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THE FC RECEPTOR SUPRAMOLECULAR COMPLEX FROM RAW MACROPHAGES

By

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M.Sc. in Molecular Science, Ryerson University, 2009

ABSTRACT

The Fc receptor is expressed on the surface of RAW macrophages that can engulf IgG opsonized particles by phagocytosis. Isolation and characterization of these receptors and the identification of proteins involved is challenging. Live-cell Affinity Receptor Chromatography (LARC) (Jankowski 2008) resulted in the identification of 336 proteins which are found to be specifically associated with the activated Fc receptor in RAW 264.7 macrophage cells. The proteins isolated were analyzed for protein-protein interactions using various analytical techniques including data mining through the use of iHOP, protein interaction databases such as Cytoscape, Osprey and STRING and literature searches, in order to create a signalling interaction pathway involving the proteins that are activated and associated with the Fcγ receptor during receptor-mediated phagocytosis. The phospholipase C family of proteins have been previously identified as important in phagocytosis, and were identified by LARC. The selected isoforms were confirmed in RAW 264.7 cells via Western Blots, antibody staining, and live-cell confocal microscopy with fluorescently linked fusion proteins to verify the localization of the phospholipases, specifically PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2 to the activated receptor complex.

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LIST OF SELECTED ABBREVIATIONS

AP2	Adaptor protein complex 2
B-PIX	PAK-interacting exchange factor
BLAST	Basic local alignment search tool
BLNK	B-cell adaptor/linker protein
BSA	Bovine serum albumin
Cy 3/5	Cyanine 3/5
DAG	Diacylglycerol
ECL	Enhanced chemiluminescence
EF hands	Helix-loop-helix structural domain (found in calcium-binding proteins)
EGFR	Epidermal growth factor receptor
ERK	Extracellular signal-regulated kinases
FASTA	Protein sequence alignment software (for protein sequence similarity searching using nucleotide or amino acid sequences)
FcγR	Receptor that binds the Fc (constant) portion of IgG
GDP	Guanosine diphosphate
GEF	Guanine nucleotide exchange factor
GFP	Green fluorescent protein
GIT1	G-protein coupled receptor kinase interactor 1
GPCR	G-protein coupled receptor
GTP	Guanosine triphosphate
IAC	Immunoaffinity chromatography
iHOP	Information hyperlinked over proteins
IgG	Immunoglobin
Ins(1,4,5)P_3/IP_3	Inositol-1,4,5-trisphosphate
ITAM	Immunoreceptor tyrosine-based activating motif
ITIM	Immunoreceptor tyrosine-based inhibitory motif
LARC	Live-cell affinity receptor chromatography
LB	Liquid broth
LC	Liquid chromatography
MHC	Major histocompatibility complex
MS/MS	Tandem mass spectroscopy
NFκB	Nuclear Factor κB
PBS	Phosphate-buffered saline
PBST	Phosphate-buffered saline + tween
PDZ	Common structural domain (post drosophila zonula protein)
PH	Pleckstin homology binding domain
PI3-K	Phosphatidylinositol 3-kinase
PI(4,5)P_2/PIP_2	Phosphatidylinositol 4,5-bisphosphate
PI(3,4,5)P_3	Phosphatidylinositol-3,4,5-triphosphate
PI(4)P	Phosphatidylinositol 4-phosphate
PI	Phosphatidylinositol
PI-PLC	Phosphoinositide-specific phospholipase C
PKA	Protein kinase A
PKC	Protein kinase C

PKG	Protein kinase G
PLC	Phospholipase C
RA	Ras-associated
SDS-PAGE	Sodium dodecyl sulphatate polyacrylamide gel electrophoresis
SEQUEST	Tandem mass spectrometry data analysis program
SH 2/3	Src homology binding domain 2/3
SHIP	Phosphoinositol polyphosphate 5-phosphatase
SLP-76	SH2 domain containing leukocyte protein of 76kDa
SQL	Structured query language (database computer language)
SRBC	Sheep's red blood cells
SRC	Sarcoma (a family of proto-oncogenic tyrosine kinases)
SYK	Spleen tyrosine kinase

INTRODUCTION

LARC has recently been used to capture an activated receptor supramolecular complex from the surface of live cells (Jankowski 2008). Receptor complexes recruit proteins to the site of phagosomal cup formation in the plasmalemma subdomain surrounding the activated receptor (Marshall J. G. 2001). A total of 336 proteins were identified by LARC, including the Phospholipase C family of proteins. Phospholipase C has been previously shown to be involved in Fcγ receptor-mediated phagocytosis (Jiang 1994; Murthy 2004; Rosales 2005; Jones 2007). Macrophages are able to promote phagocytosis via the Fcγ receptor (Crowley 1997). The determination of phospholipase C family members (specifically PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2) at the activated receptor in RAW 264.7 macrophages will be able to further our understanding of the phospholipase C family of proteins as well as the protein members involved in the regulation of phagocytosis.

Phospholipase C

Phospholipases are enzymes that are able to hydrolyze phospholipids to create products that act as membrane detergents, enzyme cofactors, and second messengers (Rosales 2005). Phosphoinositide-specific phospholipase C's (PI-PLCs) in mammalian cells play a critical role in signalling by catalyzing the hydrolysis of phosphatidylinositol 4,5-bisphosphate (PI(4,5)P_2 / PIP_2) into two secondary messengers: inositol-1,4,5-trisphosphate (Ins(1,4,5) P_3 / IP_3) and diacylglycerol (DAG) (Rhee 1989). After the formation of these two messengers, calcium is released from intracellular storages and protein kinase C (PKC) is activated by DAG (Yang 2001), making PI-PLCs important for many transduction pathways (Williams 1999) including

cell growth and transformation as well as a key mediator of calcium release (Yang 2001). To date, the mammalian isozymes of PLC have been classified into five classes: PLC-β, PLC-γ, PLC-δ, PLC-ε and PLC-ζ (Hwang 2005), where PLC-β, PLC-γ, PLC-δ and PLC-ε can be seen below as adapted from Rhee, 2001.

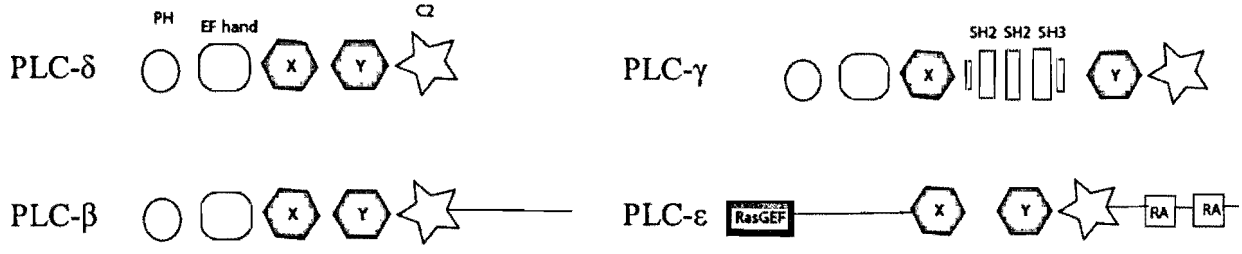

Figure 1: The domain organization of PLC-β, PLC-γ, PLC-δ and PLC-ε. The structures include the X and Y catalytic domains, Pleckstrin homology domain, EF-hands, as well as the SH2/3 domains for PLC-β, PLC-γ, PLC-δ, with PLC- γ also containing the SH2-SH2-SH3 domain. PLC-ε contains the X and Y catalytic domain and the C2 domain, plus RasGEF and RA domains. PLC structures are shown as adapted from Rhee, 1997.

One way the isozymes are distinguished is by their means of regulation (Williams 1999). Currently, PLC activity is increased during tumour growth, however the role PLC plays during drug resistance is still unknown (Yang 2001). G protein subunits are associated with the β-class of phospholipases, while the regulation of the γ-class is controlled by tyrosine kinases and the δ-class has yet to be completely characterized (Williams 1999). Of the classes of PI-PLCs, only the delta isozyme 3-dimensional structure is known, acting as a guide for the organization and functional understanding of the beta and gamma isozyme classes (Williams 1999).

All PLC's contain an X and Y domain which makes up the catalytic core of the protein (Litosch 2002) (Figure 1). The β, γ and δ isoform were initially reported as having 40-60% similarity (Rhee 1989) but today contain a 70-77% sequence homology in this region. The X and Y domains contain catalytic histidines (His32 and His82) as well as aspartate and asparagine

(Essen L.O. 1996). The PLC isozymes (β, γ and δ) are all able to hydrolyze PI, PIP and PIP_2, sharing a common catalytic mechanism(Rhee 1989). The β, γ and δ isoforms contain three protein modules – four elongation-factor-like hands (EF hands), a pleckstrin homology (PH) domain and a C2 domain (Litosch 2002; Rosales 2005).

Phagocytosis

The process of phagocytosis is essential for the immune function; it enables engulfment and elimination of foreign particles (Scott C. C. 2005). Particle internalization is initiated via interaction of receptors on the cells surface of the phagocyte with ligands on the particle's surface (Allen 1996). At the site of ingestion, actin is polymerized and the particle is internalized via an actin-based mechanism (Allen 1996; Aderem 1999). Actin is released from the phagosome after internalization and maturation of the phagosome to a phagolysosome, which occurs in a series of fusion and fission events where the vacuolar membrane with its contents fuses with late endosomes and lysosomes to form a phagolysosome (Aderem 1999) as seen in Figure 2. The understanding of phagocytosis is able to shed insight in mechanisms involving signal transduction, membrane trafficking, actin-based motility and infectious disease (Allen 1996; Aderem 1999).

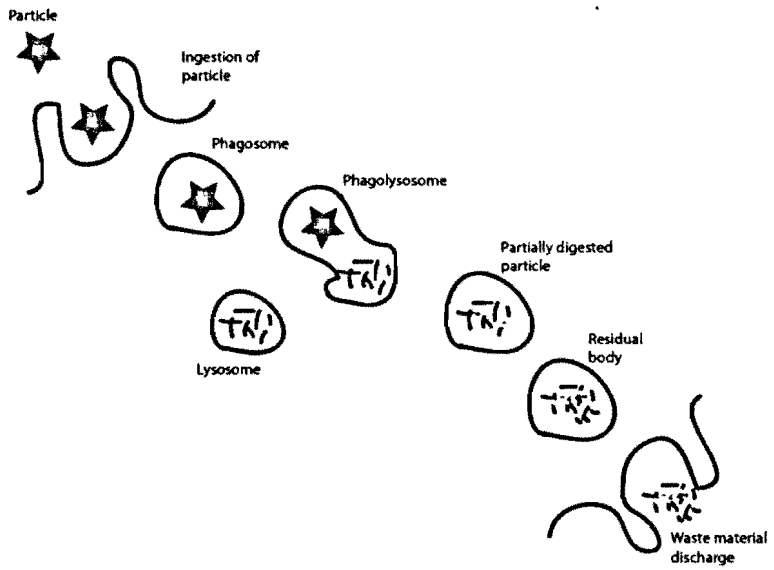

Figure 2: The phases of phagocytosis from particle invasion to cell excretion adapted from Tortora, 2004.

Engulfment of particles larger than 2 μm requires an actin-dependent mechanism, also known as phagocytosis (Allen 1996; Aderem 1999; Scott C. C. 2005). Phagocytosis is triggered via association of ligands that are located on the target particle and the corresponding receptor located on the membrane of the leukocyte (Scott C. C. 2005). Phagocytosis is essential for innate immunity (Botelho R. J. 2000). Phagocytosis is a multi-step process mechanism consisting of engulfment and destruction of particulate material (Groves 2008). It is necessary for host defence mechanisms and aids in the uptake and destruction of infectious pathogens as well as contributes to inflammation and immune response (Garcia-Garcia 2002). Phagocytes are responsible for the ingestion of invading microorganisms. These phagocytes include neutrophils, dendrite cells and macrophages (Garcia-Garcia 2002).

Numerous receptors for phagocytosis for both macrophage cells and neutrophils have been identified. The best known class of receptors is the Fc receptor, in particular the Fcγ family

of receptors that is able to recognize the Immunoglobulin (IgG) constant domain (Scott C. C. 2005). Once the ligand is cross-linked with the receptor, a complex and highly coordinated set of rearrangements occurs resulting in particle internalization or ingestion (Scott C. C. 2005) as seen in Figure 2. After internalization, the vacuole of the phagosome is converted to a microbicidal organelle through fusion with endosomes and lysosomes (Botelho R. J. 2000). The vacuole is now ready for excretion from the cell.

Phagocytosis is present in both unicellular and multicellular (or higher) organisms; in microorganisms it is used as a method of food uptake, whereas in higher organisms it is used for tissue remodelling and homeostasis (Garcia-Garcia 2002). Calcium is a key player to phagocytosis. An increase of cytosolic calcium, especially around the phagocytic cup has been linked to FcγR phagocytosis (Garcia-Garcia 2002; Rosales 2005).

Phagocytosis is mediated by the Fcγ receptor (Rosales 2005). Phagocytosis involves many processes in which calcium is involved (Figure 3). Increased levels of calcium have been observed around the phagocytic cup and near the phagosome (Garcia-Garcia 2002; Rosales 2005). This implies the endoplasmic reticulum plays a role in phagosome formation (Rosales 2005). Calcium released from the phagosome after Fcγ receptor-mediated phagocytosis into the cytoplasm has been observed. Also, waves of calcium have been reported to encircle the phagosome after Fcγ receptor-mediated phagocytosis (Rosales 2005).

Calcium near and around the phagocytic cup may also play a role in actin formation and depolymerisation. Calcium can activate gelsolin which can bind to the barbed ends of actin, preventing polymerization and enhancing depolymerisation via actin filament severing. Calcium that surrounds the phagosome may play a mediation role in vesicle fusion events during phagosome-lysosome fusion. When blocked, the receptor cannot direct calcium waves to the

phagosome, implying that the routing of calcium is important in Fcγ receptor-mediated phagocytosis (Rosales 2005).

When phagocytosis has been stimulated and a target is bound, the phagosome must enter the cytosol and be detached from the plasma membrane (Rosales 2005). Actin rearrangement is critical at this step. When the actin cytoskeleton has been remodelled by such molecules as gelsolin, the phagosome, driven by other actin binding molecules, enters the cytosol. Myosin, an actin binding molecule, is activated. It is a downstream effector of PKC and PI3-K (Rosales 2005). PKC and PI3-K activate ERK (Extracellular signal-regulated kinases). ERK activates the myosin light chain kinase that phosphorylates myosin (Cox 2001). Myosin is then able to bind actin and the phagosome can enter the cell (Rosales 2005). Closure and separation of the phagosome from the cell has been linked to PI3-K activity (Cox 2001) as well as dynamin, an actin cytoskeleton component (Rosales 2005) as seen in Figure 3. Dynamin has been suggested to wrap around the region connected to the plasma membrane, contract and pinch off the vacuole to form a phagosome, ready for excretion from the cell (Rosales 2005).

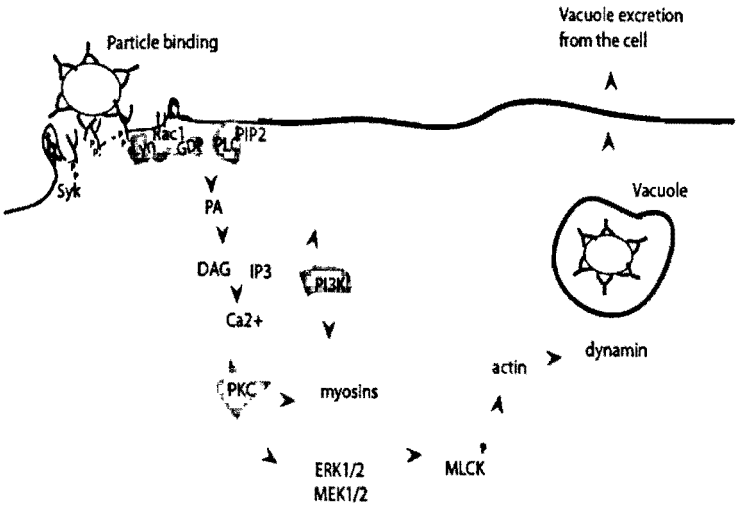

Figure 3: The phases of phagocytosis from involving actin rearrangement and separation of the vacuole from the plasma membrane.

Phagocytosis and focal exocytosis function in concert. Exocytosis is triggered by phagocytosis and occurs close to the site of and in unison with particle engulfment (Greenberg and Grinstein 2002). Since focal exocytosis is a highly localized and rapid mechanism, membrane trafficking seems to be essential for functional phagocytosis (Greenberg and Grinstein 2002).

For phagocytosis to occur, a large amount of membrane must be engulfed (Greenberg 1999). This membrane must be replenished at a steady state, accomplished by large amounts of membrane remodelling (Greenberg 1999; Rosales 2007). As macrophage cells ingest foreign particles, either individually or numerous particles at once, the membrane of the macrophage is replenished by an intracellular source, for example intracellular granules (Greenberg 1999). Cells that lack intracellular granules, for example enucleated human neutrophils must be expected to have a limited ability to ingest large numbers of particles at one time since their membrane cannot be remodelled and replenished (Greenberg 1999).

Since the process of membrane remodelling takes place during phagosome formation, the lipid composition of the plasma membrane changes (Groves 2008). The changing lipids include

phosphoinositides, which are best characterized and are derived from phosphatidylinositol (Groves 2008). Phosphatidylinositol can be phosphorylated by kinases at the 3, 4 and 5 position of the inositol ring, generating phosphatidylinositol mono-, bis- or tris-phosphate (Groves 2008). Phosphatidylinositol can interact with specific protein domains, such as the PH domain (Rosales 2005; Groves 2008).

The D3 position of the inositol ring of phosphoinositol (PI), phosphoinositol 4-phosphate [PI(4)P] and PI(4,5)P_2 can be phosphorylated, activating tyrosine kinase receptors that trigger actin polymerization (Aderem 1999; Steinberg 2008). PI(4,5)P_2 also localizes on the inner surface of the plasma membrane during the early events of phagosomal cup formation (Aderem 1999; Groves 2008).

PI(4,5)P_2 activates the small G-proteins, for example Rac1, and is recruited via Fcγ receptor ligation (Rosales 2005). PI(4,5)P_2 plays a role in actin assembly and remodelling, aiding in nucleation and uncapping filament ends including barbed, seering and cross-linking filaments. PI(4,5)P_2 is thus found around the edges of pseudopods since it helps in the polymerization of actin around the particle (Rosales 2005).

The disappearance of PI(4,5)P_2 from the phagosomal cup involved PLC (producing IP_3 and DAG) as well as phosphatidylinositol 3-kinase (PI3-K) [which aids in producing phosphatidylinositol 3,4,5-triphosphate (PI(3,4,5)P_3 / PIP_3)] (Rosales 2005; Groves 2008; Steinberg 2008). PI(3,4,5)P_3 starts to form after Fcγ receptor ligation is initiated until just after phagosomal closure. PI(3,4,5)P_3 accumulation at the phagocytic cup is dependent on PI3-K (Groves 2008; Steinberg 2008). PI3-K is recruited via a Src homology 2 (SH2) domain to the receptor complex where phosphotyrosines and tyrosine kinase Syk are located. PI3-K activity also enables membrane delivery from intracellular compartments to the phagocytosis site

allowing for formation of larger pseudopodia (Groves 2008). The timing of the disappearance of $PI(3,4,5)P_3$ occurs with the completion of particle engulfment. The SH2 domain containing inositol 5'-phosphatase (SHIP) might regulate $PI(3,4,5)P_3$ disappearance (Marshall J. G. 2001) since SHIP can associated with both the immuno tyrosine activating motif (ITAM) and immuno tyrosine inhibitory motif (ITIM) of the Fcγ receptor (Groves 2008).

Lipids are also important in the targeting of signalling proteins associated with phagosome formation and closure (Groves 2008; Steinberg 2008). Lipids during phagocytosis aid in recruiting, retaining and functionally regulating the activity of proteins (Steinberg 2008). PIP_2 is important for cytoskeletal remodelling during pseudopod extension and particle engulfment (Steinberg 2008). Membrane and lipid remodelling during phagocytosis alters the surface charge on the phagosome membrane, influencing the activation and localization of signalling molecules (Groves 2008).

Fc Receptors

An important function of white blood cells and macrophages is the ingestion of IgG-coated particles, also known as phagocytosis. The Fcγ receptors are the receptors for the constant region of IgG, allowing these cells to detect and destroy IgG-coated particles. The four classes of murine Fcγ receptors are FcγRI (CD64), FcγRII (CD32), FcγRIII (CD16) and FcγRIV (Hamaguchi Y 2006; Nimmerjahn 2006) as seen in Figure 4. These three classes, FcγRI (CD64), FcγRII (CD32), FcγRIII (CD16), have conserved extracellular Ig domains, but different cytoplasmic regions suggesting that this region may be responsible for sending of the phagocytic signal (Indik ZK 1995). Phagocytosis is one phenotype of Fcγ receptor activation (Ravetch 2001).

The Fc receptors are defined based on their specificity for IgG (Ivan 2006). The Fcγ receptors bind IgG. The Fcγ receptors are single α-chain glycoproteins, having two (FcγRII, FcγRIII and FcγRV) or three (FcγRI) N-terminal IgG ligand binding domains. They also contain a transmembrane region and a C-terminus with an intracellular tail (Ravetch 1997; Ivan 2006), as seen in Figure 4 and listed in Table 1.

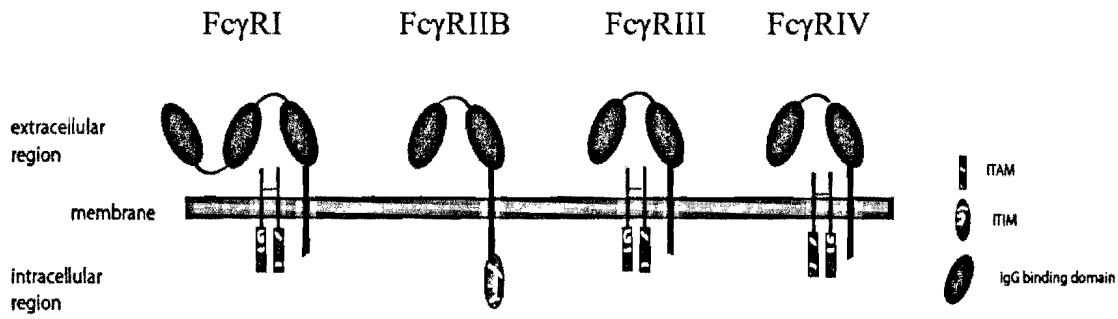

Figure 4: The murine family of receptors for the Fc portion of IgG molecules includes four classes of Fcγ receptors FcγRI, FcγRII, FcγRIII and FcγRIV adapted from Ivan, 2006.

The α-chain of the Fcγ receptor is needed for surface expression of FcγRI and FcγRIII (Ravetch 1997; Nimmerjahn 2006). The γ-chain is involved with enhancing the affinity of the α-chain ligand for IgG. FcγRI, having three extracellular IgG ligand binding domains has a high affinity for IgG (Ivan 2006). The ITAM is responsible for signalling of the receptors due to the cytoplasmic nature of the ITAM (Ravetch 1997; Ivan 2006; Nimmerjahn 2006). FcγRIIB has a low affinity for IgG since FcγRIIB contains an ITIM as its cytoplasmic tail (Ivan 2006). FcγRIII contains two genes, A and B which both bind IgG, creating an intermediate affinity for IgG (Ravetch 1997; Ivan 2006; Nimmerjahn 2006).

The genes coding for the Fcγ receptors are located on chromosome 1 in humans and mice (Ortega 2007). FcγRI is expressed on macrophages and expression can be induced in neutrophils. FcγRI has the highest affinity for IgG. Three FcγRI genes have been identified, however only the

FcγRIA form is expressed on cell membranes (Nimmerjahn 2006; Ortega 2007). FcγRII is expressed on the surface of most FcγR bearing cells. Human FcγRII have five isoforms (FcγRIIa, FcγRIIb1, FcγRIIb2, FcγRIIb3 and FcγRIIc) (Ortega 2007). All FcγRII isoforms have two IgG domains, while the cytoplasmic portions determines whether it is an activating receptor (containing an ITAM) or an inhibitory receptor (FcγRIIB, containing an ITIM) (Nimmerjahn 2006; Ortega 2007). FcγRIIa and FcγRIIc are expressed only on neutrophils and are involved in phagocytosis mediation due to the ITAM cytoplasmic portion. Mice only express the inhibitory FcγRIIB isoform (Ortega 2007).

FcγRIII contains two IgG binding domains (Ivan 2006). FcγRIIIa is expressed on macrophages, while FcγRIIIb is expressed on neutrophils. The receptor is involved in signalling via the ITAM cytoplasmic protein. Only recently identified in mice at the protein and gene level is FcγRIV. The human equivalent if FcγRIIIA (Hamaguchi Y 2006; Ivan 2006). FcγRIV and FcγRIIIA have an amino acid sequence identity of 63% (Hamaguchi Y 2006). Mouse FcγRIV binds IgG2a and IgG2b subclasses with an intermediate affinity. FcγRIV signalling, like the human FcγRIII equivalent is dependent on the cytoplasmic ITAM portion (Ivan 2006; Ortega 2007). Additionally, FcγRIV has a YEEP cytoplasmic motif, allowing for association with Crk and PI3-K in order to increase its signalling potential (Ivan 2006). A summary of Fcγ receptors and their expression can be seen below in Table 1.

Table 1: Fcγ receptors, their IgG binding domain and affinity and cell expression (Takai 2005; Hamaguchi Y 2006; Ivan 2006).

Receptor	IgG affinity	Cell expression	Cytoplasmic domain	# IgG binding domains	Effect in mice (in vivo)
FcγRIa (CD64)	IgG1, IgG2a IgG3	macrophage, neutrophil	ITAM	3	Deletion of FcγRIa results in phagocytosis deficiency
FcγRIIa (CD32a)	IgG3	macrophage, neutrophil	ITAM	2	Deletion of FcγRII results in increased predisposition to auto-immune disease
FcγRIIb (CD32b)	IgG2a, IgG2b, IgG3	macrophage, neutrophil	ITIM	2	
FcγRIIIa (CD16a)	IgG1, IgG2a, IgG2b, IgG3	macrophage	ITAM	2	Deletion of FcγRIII results in decreased predisposition to auto-immune disease
FcγRIIIb (CD16b)	IgG1, IgG2a, IgG2b, IgG3	neutrophil	ITAM	2	
FcγRIV	IgG2a, IgG2b	macrophage	ITAM	2	Unknown

The murine Fc receptors are divided into two classes, the activation receptors (FcγRI, FcγRIII and FcγRIV) and the inhibitory receptors (FcγRIIB) (Ravetch 1997; Aderem 1999; Nimmerjahn 2006). The Fc receptors share a common motif, the ITAM that is involved with the recruitment and activation of tyrosine kinases upon receptor cross-linking (Ravetch 1997; Rosales 2005; Nimmerjahn 2006), as well as an ITIM (Nimmerjahn 2006). The two receptor classes function in concert and are both present on the same cell, a point of importance in immune response balance (Nimmerjahn 2006). The magnitude of the immune response is

determined by the ratio of expression of ITAM to ITIM receptors (Ravetch 2001). The FcγRIIB is different from the other classes of Fc receptors as it lacks the ITAM motif (Ravetch 1997)

The FcγIIB receptor serves as an inhibitory receptor. The receptor is important in regulation and activation of inhibitors. The loss of this function could lead to an imbalanced immune response resulting in such conditions as auto-immune disease (Nimmerjahn 2006). The FcγRIIB receptor contains an ITIM motif in its cytoplasmic domain, a defining factor of inhibitory receptors (Nimmerjahn 2006; Rosales 2007). Recruitment of inositol phosphatase SHIP binding to the SH2 domain on the FcγRIIB allows for inhibitory function (Nimmerjahn 2006). The binding site for SHIP on the SH2 domain allows for inhibition by the ITAM activating signalling via hydrolysis of PIP_3 (Ravetch 2001). In the absence of PIP_3, PH domain proteins, including PLCγ, are released from the membrane and the sustained calcium signal is also blocked. This prevents the flow of extracellular calcium via calcium channel, inhibiting Fc receptor phagocytosis (Ravetch 2001).

The FcγRIIB receptor is expressed on all cells of the immune system, serving as a modulator of inflammatory effector cells such as macrophages during different stages of immune response. The lack of the FcγRIIB receptor causes enhanced phagocytosis (Nimmerjahn 2006)

The activation of the receptor is not completely understood, but involves the co-localization of Src kinases (Ravetch 2001; Nimmerjahn 2006) as seen in Figure 5. This leads to the recruitment of PI3-K and PLC-γ, triggering PKC activation and a sustained increase in calcium. Mediation of cell-surface expression of the Fc receptors (FcγRI, FcγRIII and FcγRIV) is required for their assembly and activation is dependent on its γ chain (Nimmerjahn 2006).

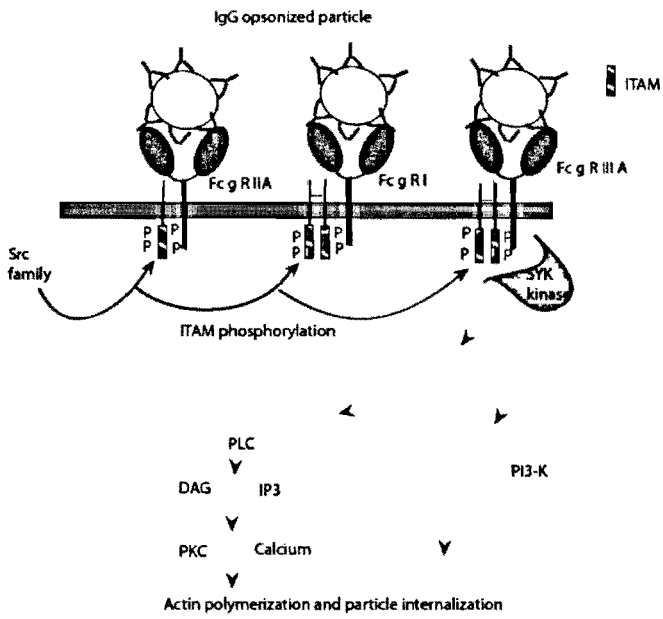

Figure 5: The interaction of the Fcγ receptors with activated Syk kinase and PI3-K, an early Fcγ receptor-mediated phagocytosis event adapted by Aderem, 1999.

Fc Receptor and Phagocytosis

The Fc receptors of IgG play a critical role in immunity via phagocytosis (Greenberg 1999). Actin assembly and pseudopod extension are triggered via IgG-mediated phagocytosis of the Fc receptors, each with distinct signalling mechanisms (Greenberg 1999). The regulatory functions of the immune system, such as the initiation of phagocytosis, has been connected to IgG-linked Fc receptors (Greenberg 1999).

When particles are opsonised with IgG, the Fcγ receptor on the phagocyte membrane interacts with the Fc portion of the IgG molecule, triggering phagocytosis (Rosales 2007). FcγR signalling is initiated, leading to changes in the plasma membrane and cytoskeleton. Pseudopods are extended around the particle, forming a cup that moves into the cell (Rosales 2007).

Phagocytosis initiates with the clustering of phagocytic receptors via ligation to numerous ligands located on the surface of the target particle (Greenberg and Grinstein 2002). For the FcγRI and FcγRII receptors, triggering is due to phosphorylation of the receptor itself or

the associated ITAM-containing subunits, carried out by members of the Src family (Greenberg and Grinstein 2002). The Src family of kinases are in close proximity to the portions of receptors that reach into the cytoplasm (Rosales 2007). These receptors cross into the cytoplasm due to their lipid anchor to the cell membrane, but are inactive until the cross-linking of the ligand binding extracellular domain occurs. The main Src family kinases found to be involved in phagocytosis include Hck, Lyn and Fgr (Rosales 2007). Once the Src family kinases are activated, they are able to phosphorylate the tyrosines located in the ITAM or even the receptor itself (Greenberg and Grinstein 2002). Activation of Src family tyrosine kinases enables mediation of the Fcγ receptor with a ligand and is essential for actin polymerization and phagocytosis (Groves 2008). The ITAM's once phosphorylated create a docking site for the SH2 domain of Syk (a Src family member), a site that is required for IgG-opsonized particle internalization (Greenberg and Grinstein 2002). Kinase activity is activated once Syk binds to the phosphorylated ITAM's of FcγR through their SH2 domains. Syk is now able to activate several signalling pathways (Rosales 2007) that can have an impact on actin dynamics (Groves 2008). The events that occur after this are not as clear, however lipid remodelling ensures that PI3-K is activated, which generates 3'-phosphoinositides located at the phagosomal cup (Greenberg and Grinstein 2002). Syk recruitment and activation has shown to be essential for FcγR-mediated phagocytosis and demonstrated by macrophages from Syk deficient mice being unable to internalize IgG-opsonized particles (Botelho R. J. 2000).

During phagocytosis, the synthesis of phosphatidylinositol bisphosphate / phosphatidylinositol-4,5-bisphosphate [PIP_2 / $PI(4,5)P_2$] is accelerated (Greenberg and Grinstein 2002). PIP_2 acts as a substrate for PI3-K (which is involved in membrane trafficking) as well as the target for PLC thereby generating DAG during phagocytosis (Greenberg and Grinstein 2002).

Fcγ receptor stimulation has allowed for the detection of numerous phosphorylated proteins as well as activated enzymes including phospholipases (in particular PLC-γ_1), Ins(1,4,5)P_3, DAG, PKC, PI3-K, Rho family GTPases and nuclear factors, in particular nuclear factor κB (NF κB) (Rosales 2007), as seen in Figure 6.

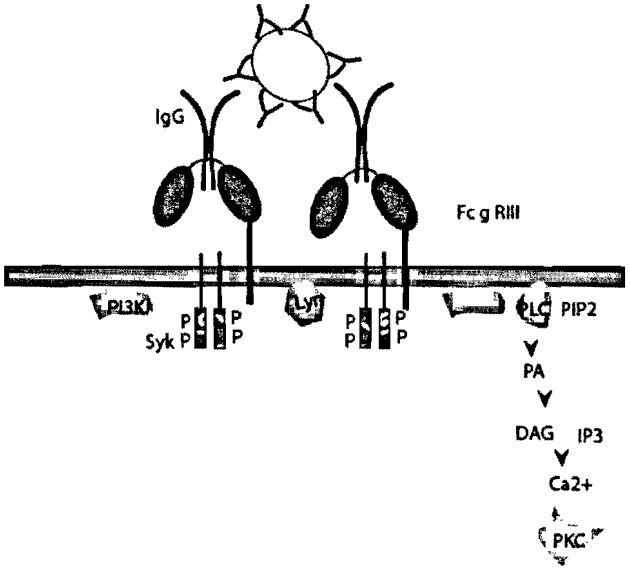

Figure 6: The interaction of the FcγRIII with the phosphorylated ITAM, activating Syk kinase and its binding to the ITAM, as well as PI3-K, which phosphorylates PIP_2 to generate IP_3 and DAG as adapted from Rosales, 2007.

Syk activity is responsible for the activation of enzymes participating in other signalling pathways, including the enzyme PLC-γ (Ortega 2007). The activation of downstream enzymes and pathways is associated with the mobilization of both extracellular and stored calcium, rearrangement of the cytoskeleton, phagocytosis and transcription factor activation (Ortega 2007).

Phospholipase C and Phagocytosis

The resolution of phospholipase activity by receptor activation is a complex series of steps and does not occur in a linear fashion, but rather is thought to involve the activation of

multiple isoforms of PLC (Kelley 2006). Before phospholipase activation and stimulation, numerous enzymes and adaptor/effector molecules must change their subcellular localization in order to participate in the intracellular signalling process (Fujii 1999). Such changes include the translocation to or from the plasma membrane, initiating signalling since signals must be moved from the plasma membrane to components located in the cytoplasm (Fujii 1999). Membrane targeting of signals is thought to involve the PH domain of the protein since this domain has been shown to bind phosphoinositides (cell membrane components) as well as inositol phosphates (the head group of phosphoinositides) (Fujii 1999), with a high affinity in PLC-γ and PLC-δ (Williams 1999).

The discovery of new adaptor molecules, SLP-76 and BLNK, are able to link Syk activation with PLCγ responses in macrophages in Fc receptor-dependent activation (Ravetch 2001; Greenberg and Grinstein 2002). PLC accumulates at the phagocytic cup and aids in production of two crucial products, IP_3 and DAG via PI(4,5)P hydrolysis (Liao 1992). DAG is able to activate PKC and IP_3 triggers the release and mobilization of calcium from the endoplasmic reticulum via the IP_3 receptor (Liao 1992; Rosales 2005). The release of calcium is important for phagosome and lysosome fusion to a phagolysosome and activation of PKC. The inhibition of PLC results in a reduction of the rate of phagocytosis (Rosales 2005).

In resting cells, PI-PLC is cytosolic; it accumulates at the membrane upon receptor cross-linking (Rosales 2005). The PH domain of $PI(4,5)P_2$ and $PI(3,4,5)P_3$ serves as a target for binding in response to cell stimulation via PI kinase activation. Metabolism of $PI(4,5)P_2$ and $PI(3,4,5)P_3$ results in membrane associated PLC release and down regulation of the signalling network (Rosales 2005).

Phospholipase C-β

Phospholipase C is also involved in phagocytosis through its interaction with the G-proteins, in particular the alpha and beta subunits (Jiang 1994). The α-subunits are GTP (guanosine triphosphate) bound and are activated while the β-subunits are free and can interact with ligand bound receptors as well as effectors such as PLC, in particular PLC-β which acts via second messengers, for example through the conversion of $PI(4,5)P_2$ to DAG and IP_3 (Jiang 1994), as depicted in Figure 7. Furthermore, the β-subunits of PLC are involved with the activation of the α-subunit of the G-protein, specifically PLC-β_3, while little is known about the function of PLC-β_4 except that it can hydrolyze phosphoinositol (Jiang 1994), so it is thought to have a similar role to PLC-β_3.

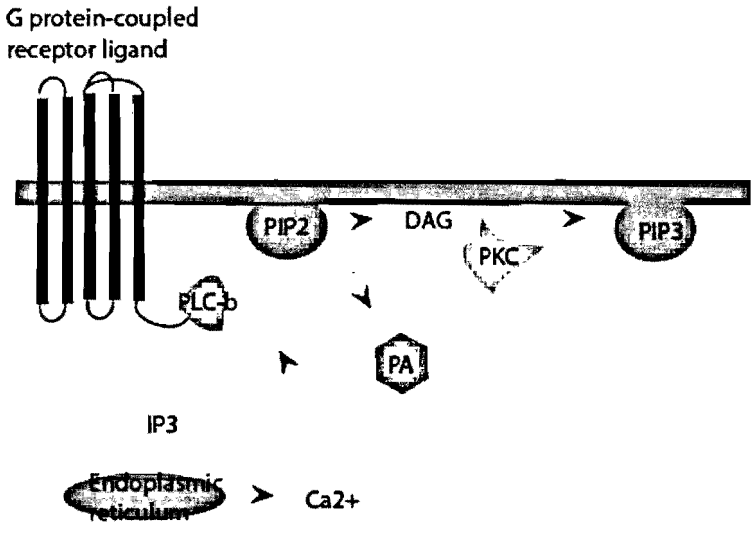

Figure 7: Receptor activation of PLC which converts PIP_2 to IP_3 and DAG adapted from Litosch, 2002.

As mentioned, the superfamilies of PLC enzymes are classified into different isoform families. The PLC-β family consists of four isozymes, PLC-β_1, PLC-β_2, PLC-β_3 and PLC-β_4 (Faenza 2004). The PLC-β family contains a long COOH-terminus located downstream from the

catalytic domain, unique due to the high concentration of arginine and lysine residues (Faenza 2004). In the PLC-β_1 isozyme, these basic residues are responsible for its location in the nucleus compared go PLC-β_3 which is mainly found in the cytoplasm (Faenza 2004).

Each phospholipase isotype is able to perform a different function depending on such factors as structure, activity and sensitivity to G-protein coupled receptor (GPCR) regulation (Litosch 2002). For example, depending on the distribution of various isozymes of PLC-β in the brain, each isozyme performs a different function. PLC-β_1 is strongly expressed in the cerebral cortex, while PLC-β_4 is observed at a high density in the cerebellum, and PLC-β_3 is expressed throughout the brain suggesting the possibility that each isozyme plays a distinctive role in the brain (Hwang 2005). PLC-β isotypes also share a consensus sequence known as the PDZ domain binding motif (Hwang 2005). These PDZ domain binding motifs are largely found in proteins that are able to mediate protein-protein interactions, in particular interactions of highly specialized sub-membrane sites including cellular junctions (Hwang 2005).

PLC-β is able to link GPCR's to intracellular signalling networks (Litosch 2002). GPCR's are able to activate PLC-β, promoting the hydrolysis of PIP_2 which generates IP_3 and DAG. Activation of PKC occurs with DAG, and IP_3 triggers calcium release from intracellular compartments, increasing the levels of intracellular calcium and activating calcium depending signalling pathways (Litosch 2002). The hydrolysis of PIP_2 also stimulates the release of proteins from the plasma membrane, for example tubby proteins which are protein transcription factors that are able to associate with the plasma membrane through their PIP_2 binding domain (Santagata S. 2001).

PLC-β has a long 450 amino acid C-terminal stretch to the catalytic Y domain (Litosch 2002). Enzyme activity activation by G-proteins requires the C-terminal region of PLC-β, the

binding of PLC-β to the membranes and the localization of PLC-β to the cell nucleus (Wu D. 1993; Kim CG 1996). For example, PLC-β_1 binding to phospholipids vesicles is improved by acidic phospholipids; the C-terminal region is essential for binding as well as residue phosphorylation of certain kinases such as PKC in order to regulate enzyme activity (Litosch 2002).

PI3-K has previously been identified in phagocytosis (Lennartz 1999). PI3-K is able to interact with the βγ-subunit of the G-proteins, much like PLC-β. The role of the G-proteins in phagocyotsis is unknown, however their mediation of signalling via βγ and other transmembrane receptors (Lennartz 1999) is important for activation of such proteins as PLC- β. Upon PLC- β activation, hydrolysis of PIP_2 to IP_3 and DAG occurs, releasing calcium and activating PKC (Litosch 2002).

G protein signalling can be regulated by receptors, promoting the exchange of GTP to GDP (guanosine diphosphate) on the G protein α subunit (Lennartz 1999). Inactive G protein occurs when GDP is bound to the α subunit; when it is active GTP is bound (Lennartz 1999). As seen in Figure 8, the activation of the receptor is promoted by the exchange of GDP with GTP (Rhee 2001; Litosch 2002). When GTP is bound, α subunit affinity for the βγ subunit is reduced, causing the dissociation of the βγ subunit. Since the α subunit is activated, it will bind to its effector, PLC-β, to stimulate activity (Rhee 2001; Litosch 2002). Signalling is deactivated by the conversion of α-GTP to α-GDP through re-association of α-GDP with βγ to form a βγ subunit (Litosch 2002). The G protein βγ subunit can also stimulate the activity of PLC-β (Rhee 2001).

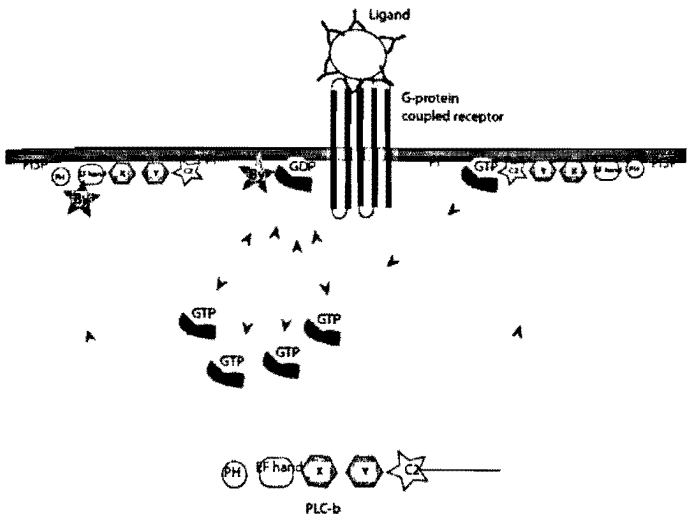

Figure 8: The exchange of GDP to GTP for activation of the GPCR's. Once the exchange of GDP to GTP, the dissociation of the α-subunit from the membrane associated βγ-subunit occurs. The membrane anchored G-βγ-subunit recruits PLC-β via PH and Y domain interactions, aided by the presence of PI3P, activating the PLC-β enzyme as adapted from Rhee, 1997.

As previously mentioned, PLC-β isoform function is dependent on such factors as their sensitivity to GPCR's (Litosch 2002). The order of enzyme activity stimulation of the PLC-β isoforms from the βγ subunit is PLC-β_3 > PLC-β_2 >> PLC-β_1 (Smrcka A.V. 1993). PLC-β_3 and PLC-β_2 binding to the βγ subunit occurs at the N-terminal PH domain of the enzyme, whereas binding of PLC-β_1 to the βγ subunit is very weak (Wang T. 1999). This suggests that the βγ subunit does not regulate PLC-β_1, but rather by another subunit such as the $G\alpha_q$ where studies show stimulation activity of the PLC-β isoforms occurs in the reverse order (Litosch 2002).

Phospholipase C-β cytosolic activity is regulated by many protein kinases, including PKC, protein kinase A (PKA) and protein kinase G (PKG) as adopted by Litosch, 2002 and illustrated in Table 2.

Table 2: PLC-β activity regulation by protein kinases (Litosch 2002).

Protein kinase	Isoform of PLC beta	Phosphorylation sites	Consequences of phosphorylation on functional activity
	Cytosolic Pool		
Protein kinase C	PLC-β1	Ser 887	βγ stimulation inhibited
	PLC-β3	Ser 1105	Gαq stimulation inhibited
		?	βγ stimulation inhibited
Protein kinase A	PLC-β3	Ser 1105	Gαq and βγ stimulation inhibited
	PLC-β2	?	βγ stimulation inhibited
Protein kinase G	PLC-β3	Ser 26, Ser 1105	Gαq and βγ stimulation inhibited
	PLC-β2	?	βγ stimulation inhibited
	Nuclear Pool		
Protein kinase C	PLC-β1	Ser 887	IGF-1 stimulation inhibited
ERK	PLC-β1	Ser 982	IGF-1 stimulation mediation

PKC acts as a negative feedback regulator for PLC-β signalling. When PLC-β is stimulated by GPCR's, DAG is generated in turn activating PKC (in its β form), which is able to phosphorylate PLC-β_3 and inhibit $G\alpha_q$ stimulation of PLC-β_3 activity but not inhibit βγ for reasons unknown but through to be related to stimulation through protein-protein interactions, preventing the binding of βγ (Litosch 2002). PKA is also able to inhibit stimulation of PLC-β_3 by $G\alpha_q$ and βγ by the serine^{1105} phosphorylation site, the same site that PKC phosphorylates (Williams 1999). Lastly, PKG can also inhibit stimulation at the serine^{1105} phosphorylation site as well as the serine^{26} site, by $G\alpha_q$ and βγ (Yue C. 1998). The signalling pathway involving PLC-β is important in regulating cell function as well as numerous feedback mechanisms, such as those that target $G\alpha_q$ and PLC-β as seen in Figure 9.

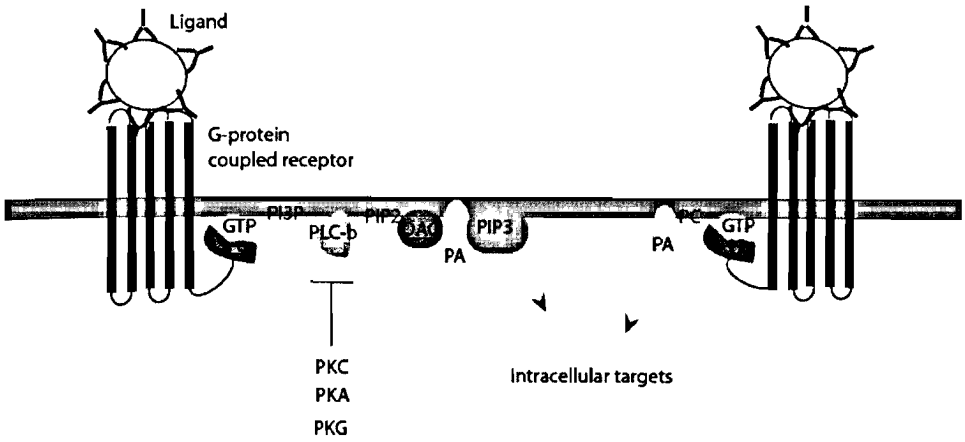

Figure 9: Gq-PLC-β signalling pathway activation is able to initiate numerous feedback mechanisms that regulate signalling as adapted from Litosch, 2002.

Phospholipase C-γ

Phospholipase C-γ (PLC-γ) is regulated by the phosphorylation of tyrosine by tyrosine kinase receptors and tyrosine kinase nonreceptors such as Src, which are activated by immunoglobulins and cytokines (Kelley 2006). Protein-protein interactions, mainly mediated by the SH2 and SH3 domains, play an important role in the localization of PLC-γ in protein complexes in different cellular components (Jones 2007).

PLC-γ contains two SH2 domains and one SH3 domain (Rhee 1997; Tvorogov 2002). Binding of various growth factors to their corresponding receptor leads to the activation of protein tyrosine kinase activity of the receptor itself as well as tyrosine phosphorylation of many intracellular proteins (Tvorogov 2002). The SH2 domain can bind to IP_3 with a high affinity (Williams 1999). This binding is thought to contribute to the tight interactions of PLC-γ with the plasma membrane (Williams 1999).

Tyrosine phosphorylation of PLC-γ_1 is mediated through the recognition of the receptor sites by the SH2 domains of PLC-γ_1 (Williams 1999; Tvorogov 2002). In order for PLC-γ to be activated, tyrosine phosphorylation must first occur followed by the movement of the enzyme to

the plasma membrane cytoplasmic face, a mechanism that is not completely understood (Tvorogov 2002). PLC-γ has two SH2 domains. The function of the SH2 domains is to associate PLC-γ with receptor tyrosine kinases for activation (Rhee 1997; Williams 1999; Wang 2001). As depicted in Figure 10, for PLC-γ_1 to be tyrosine phosphorylated, physical contact must be made between the receptors (such as the epidermal growth receptor) and PLC-γ_1. Physical contact of the receptor with PLC-γ_1 is essential for the protein's function (Wang 2001). As like other PLC isoforms, PLC-γ contains an N-terminal PH domain and a C2 domain near the C-terminus (Wang 2001). The PH domain mediates interaction with the surface of the membrane (Rhee 1997) via binding IP_3 with a strong affinity (Williams 1999). This enables its translocation (Williams 1999) and aides in membrane localization by phosphoinositide recognition while the C2 domain is involved in membrane targeting and binding as in PLC-δ (Williams 1999; Wang 2001).

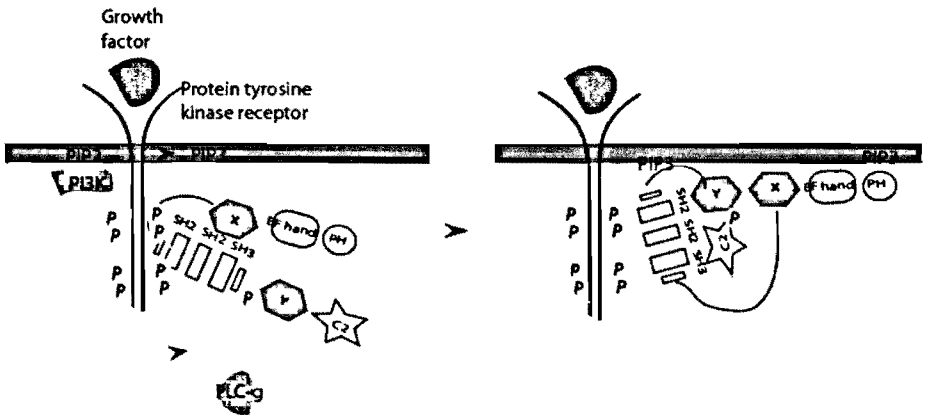

Figure 10: Tyrosine kinase-receptor activation for the tyrosine phosphorylation and activation of PLC-γ_1. The phosphorylated tyrosine protein tyrosine kinase (PTK) receptor acts as a docking site for PI3-K and PLC-γ, which aids in the conversion of PIP_2 to PIP_3. PLC-γ undergoes conformational changes, and is maintained in close proximity to the membrane via SH2 domain with PTK adapted from Rhee, 1997.

Little is known about the SH2 domain interactions, but even less is known about the interactions of the SH3 domain of PLC-γ_1, and how this domain may influence enzyme activity or function (Tvorogov 2002). In general, the SH3 domain is found in many signalling involved proteins and is used for facilitation of protein-protein association by recognition of proline-rich sequences in partner proteins (Tvorogov 2002). A similar action is thought to occur with the SH3 domain of PLC-γ_1, with the proline rich protein c-Cbl (Tvorogov 2002).

PLC-γ_1 can also be influenced by the formation of signalling complexes by the epidermal growth factor receptor (EGFR). Actin polymerization drives cell migration (Wang 2007). F-actin and the EGFR can facilitate the formation of PLC-γ_1 signalling complexes and the ability to sense extracellular stimuli (Wang 2007). PLC-γ_1 activation has been linked to numerous growth factor receptors, implying that cytoskeletal reorganization, but in particular the cytoskeleton itself, plays a critical role in mediating PLC-γ intracellular signalling since reorganization can disrupt PLC-γ activation (Wang 2007).

The actin binding protein villin is tissue-specific and expressed in many cell types such as epithelial cells (Wang 2007). It is a unique actin binding protein because it has the ability to nucleate, cap, serve and bundle filaments of actin, as well as regulate epithelial cell migration. Tyrosine phosphorylation is essential to the role villin plays in cell migration (Wang 2007). Phosphorylated villin interacts with and recruits PLC-γ_1 where it is able to regulate activity leading to modification of the phosphoinositide signal transduction pathway (Wang 2007). PLC-γ_1 is able to form complexes with surface receptors such as the platelet-derived growth factor receptor (Wang 1998). Formation of such a complex leads to phosphorylation of PLC-γ on 3 tyrosine residues and an increase in enzyme activity (Wang 1998).

The PLC-γ family is involved with several aspects of cell motility, including motility regulation and cell spreading, however the mechanisms that control these actions are not fully understood (Jones 2007). PLC-γ phosphorylation has also been linked to c-Src (Ronnstrand 1999). c-Src has the ability to phosphorylate and associate with PLC-γ (Ronnstrand 1999).

Multiple protein-protein interactions are likely to be involved with PLC-γ complex formation, including interactions with GIT1 (an adaptor protein) and β-Pix (a guanine exchange factor), and the maintenance and assembly of such complexes (Jones 2007). Also, the interaction of PLC-γ with the GIT1/β-Pix complex is needed for tyrosine phosphorylation, which is associated with the activation and function of PLC-γ (Jones 2007). The role of PLC-γ in such a model could be to increase the amount of cellular calcium released, acting as an activator for further events, such as the interaction of PLC-γ with β-Pix to activate Rac and/or Cdc42 (Jones 2007).

As mentioned, PLC-γ is a phosphoinositide specific phospholipase that is activated after Fcγ receptor stimulation (Rosales 2007). It is able to use $PI(4,5)P_2$ for the generation of IP_3 and DAG (Garcia-Garcia 2002). As seen in Figure 11, IP_3 helps to mediate the mobilization of calcium (Rosales 2007). PLC-γ allows calcium to mobilize from the endoplasmic reticulum, causing the opening of plasma membrane channels enabled to sustain calcium flow (Ortega 2007). DAG is needed to activate numerous PKC isoforms (Garcia-Garcia 2002) as well as Ras guanyl nucleotide-releasing proteins which are able to bind both calcium and DAG (Ortega 2007). PKC-δ can be activated by DAG and accumulate in the membrane of the phagosome during FcγR-mediated phagocytosis (Garcia-Garcia 2002). Through interactions with tyrosine, Fyn has been found to associate with PKC-δ (Kronfeld I 2000), and is also bound to such signalling intermediates as PLC-γ (Xing L 2004). The activation of PKC initiates other signalling

pathways such as the Ras-Erk-AP-1 and nuclear factor κB (NFκB), enabling the activation of different transcription factor families (Ortega 2007).

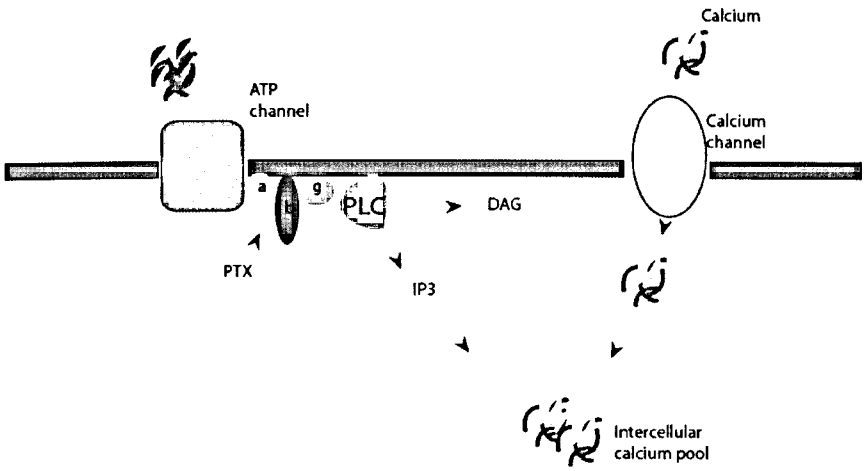

Figure 11: The production of IP_3 and DAG through the hydrolysis of $PI(4,5)P_2$ and mobilization of calcium via help of IP_3 as adapted from Parikh, 1997.

Tyrosine phosphorylation of the Fcγ receptors by membranes of the Src family kinases triggers the activation of the Fcγ receptor in macrophages (Indik ZK 1995). FcγRIIA cross-linking serves as an initiation point for phagocytosis (Indik ZK 1995). PLC-γ activation has been reported after FcγR cross-linking. The inhibition of the PLC- γ enzyme results in the impairment of phagocytosis in macrophage cells (Garcia-Garcia 2002). In addition, PLC-γ has been shown to accumulate at the phagocytic cup during Fcγ receptor-mediated phagocytosis, however the exact role that PLC-γ plays is unknown (Garcia-Garcia 2002).

Phospholipase C-δ

Most studies done on phospholipase C have been carried out on the δ isoform (Litosch 2002). The PH domain of PLC-δ is composed of 100 amino acids, and is able to bind with high

affinity to PIP_2, an essential step required to facilitate PIP_2 hydrolysis at catalytic sites (Rhee 1997; Murthy 2004). Activation of PLC-δ may occur via the PH domain, making it an essential compartment of PLC-δ, especially for membrane targeting (Rhee 1997; Fujii 1999). The PH domain binds PIP_2. The role of PIP_2 is to anchor the enzyme to the plasma membrane thereby enhancing its catalytic activity (Rhee 1997; Murthy 2004). PLC-δ is fixed in place via binding of its C2 domain to the membrane (Rhee 1997). PLC-δ alternates between two forms: one where it is membrane bound, when it interacts with PIP_2 and the other where it is cytosolic bound, where it interacts with soluble IP_3 (Sidhu 2005). The fully activated membrane form hydrolyzes PIP_2, losing the docking molecule, resulting in the dissociation of PLC from the membrane (Rosales 2005). As in PLC-β, the PH domain of PLC-δ also binds the G-protein βγ subunit, however it does this with a lower affinity making it too weak to induce enzyme activation (Murthy 2004).

PLC-δ has a C2-like domain which interacts with the EF hands (a helix loop helix structure of 2 perpendicular α-helixes linked by a short loop region) located on the catalytic region, allowing the enzyme and substrate to position correctly for binding (Litosch 2002). A PLC-δ activator, calcium, is thought to take part in activation by assisting the interaction between the PIP_2 substrate inositol head-group which is charged and the residues located in the catalytic region (Kelley 2006). EF hand domains are crucial for catalytic activity (Sidhu 2005). The EH hands have sites for calcium binding, however it is not known if they bind calcium (Williams 1999). Yet, the C2 domain contains 3 sites for calcium binding as well as the catalytic domain which contains one site for calcium binding and connects to the EF hands through a linker region suggesting that the C2 domain may be involved in membrane binding (Williams 1999).

As mentioned, most studies done on PLC's have focused on the PLC-δ isoform due to it being the most abundantly expressed isoform (Murthy 2004). PLC-δ is also thought to be the first evolutionary form of the phospholipase family since the structure of PLC-δ is the simplest as well as the most conserved since cloned isoforms of PLC-δ in different mammals (including slime mould, yeast and plants) has the most homology with one another compared to other members of the PL family (Yamaga 1999). PLC-δ has a high sensitivity to calcium, higher than that of PLC-β and PLC-γ (Rhee 1997; Murthy 2004). However, PLC-δ is not activated by the increase in calcium levels to the extent of the PLC-β and PLC-γ isoforms where calcium release activates PKC and IP_3 (Murthy 2004). The production of IP_3 generates PIP_2 which competes with PLC-δ for binding therefore inactivating the PLC-δ isoform (Murthy 2004), however PLC-δ is activated by the increase in intracellular calcium (Lad 2006).

PLC-δ_1 is able to bind $PI(4,5)P_2$, present in the lipid in the plasma membrane (Rosales 2007). In order for $PI(4,5)P_2$ to be hydrolyzed, PLC-δ_1 must be present at the membrane and physical contact must be made between PLC-δ_1 and the membrane (Fujii 1999). When pseudopods are forming phagosomes, the levels of $PI(4,5)P_2$ are increased (Rosales 2007). Once the phagosome is fully formed, these increased levels disappear due the conversion of $PI(4,5)P_2$ into $PI(3,4,5)P_3$, decreasing the levels of $PI(4,5)P_2$ at the phagosome (Rosales 2007). This allows feedback regulation of PLC-δ via dislocation from the plasma membrane (Williams 1999) and shows that the signalling mechanism of the Fcγ receptor during phagocytosis is dynamic, with certain molecules becoming activated and recruited into a process that results in the formation of a phagosome (Rosales 2007).

Phospholipase C-ε

Phospholipase C-ε (PLC-ε) is the most recently discovered group of phospholipases and is also the largest member of the phospholipase family (Kelley 2006). PLC-ε_1 is a 254kDa isozyme that contains in its structural core EF-hands, a catalytic TIM barrel and a C2 domain (which is common to all PLC isozymes) as well as additional domains at both the C and N-termini that facilitate its interactions with the Ras family GTPases (Wing 2003). PLC-ε is regulated by both the Ras and Rho family of proteins as well as G proteins including the heterotrimetic G_{12} family and the G-protein βγ subunits, GPCR's and receptor tyrosine kinases (Kelley 2006). PLC-ε contains two C-terminals which are Ras-associating domains (used for activation by Ras-p21) (Sidhu 2005) as well as a RasGEF motif at the N-terminus, which allows for activation by Ras, Rap, RhoA, G_{12} family and G-βγ (Murthy 2004).

PLC-ε_1 is activated by GPCR's (just like PLC-β) as well as various ligands (Yun 2008), including Rho and Ras. PLC-ε is also able to hydrolyze the conversion of PI(4,5)P_2 into its corresponding messengers IP_3 and DAG, the first involved in the mobilization of calcium and the latter with the activation of PKC (Yun 2008). Contained in PLC-ε_1 is a CDC25 homology domain at the N-terminus (Yun 2008). It is a guanine nucleotide exchange factor (GEF) domain for the small G protein Ras family that has GEF activity towards both Rap1 and H-Ras (Lad 2006). At the C-terminus is a pair of Ras-associated (RA) domains (Yun 2008). These RA (H-Ras/Rap1-associating) domains RA1 and RA2 are able to bind PLC-ε_1 (Lad 2006) and are involved with the signalling mechanisms of Ras suggesting that PLC-ε_1 is involved with the signalling that is supported by the superfamily of Ras (Yun 2008). H-Ras is able to bind PLC-ε in a GTP-dependent manner through the RA2 domain it contains, stimulating the hydrolysis of PI(4,5)P_2 into the secondary messengers of IP_3 and DAG (Lad 2006). Ras proteins are small

GTP-binding proteins which are able to act as switches to alternate between the active GTP-bound state and the inactive GDP-bound state enabling them to regulate numerous biological responses including cell proliferation (Song 2001).

The RA domain of PLC-ε_1 is specific for Ras superfamily member RAP 1A when activated, playing an important role in the essential step of activation and subcellular localization of PLC-ε (Yun 2008) by promoting the translocation of PLC-ε to the plasma membrane (Wing 2001). PLC-ε is characterized through the Ras domains it contains (Bai 2004). These domains as mentioned are responsible for the activation of PLC-ε_1 when the GTP-bound form of the small GTPases is bound (Bai 2004). Although the RA domain also binds other binding proteins and not just the Ras family of proteins, it is still able to bind to Ras members, activating PLC-ε (Yun 2008), as seen in Figure 12. More specifically, Ras binds the RA2 domain, along with adaptor protein complex 2 (AP2), playing a key role in the regulation of the EGFR through PLC-ε dependent regulation (Yun 2008). Even though both Ras and AP2 bind the RA2 domain for the binding region of PLC-ε, it is important to note that the binding of one factor to the domain does not affect the binding or activity of the other: both Ras and AP2 bind to the same binding domain but they do not have an influence on one another's activity, binding or function (Yun 2008). The association of Ras with PLC-ε is likely to induce the activation of PLC-ε by its recruitment to the plasma membrane, where PIP_2 is located (Song 2001).

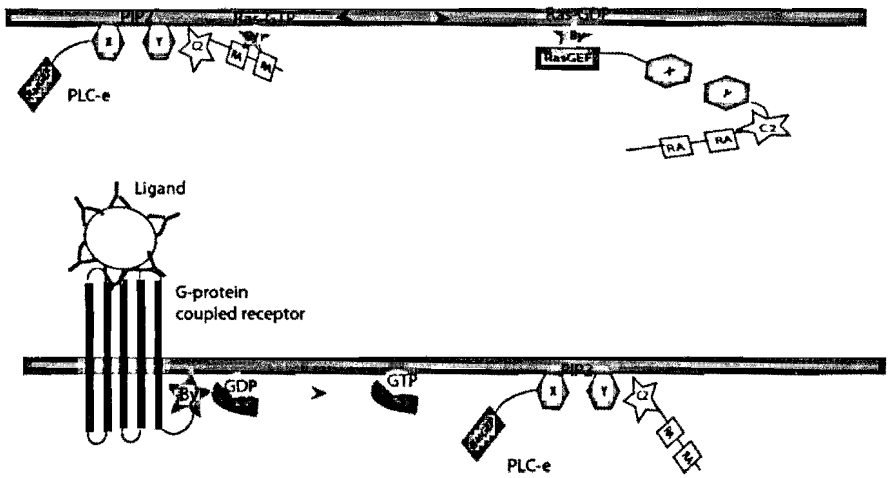

Figure 12: Receptor-mediated activation of PLC-ε. Ras-GTP promotes the translocation of PLC-ε to the membrane via RA domain binding. Ras-bound GTP hydrolysis to Ras-bound GDP turns off the activation signal. GPCR induce the exchange of GDP to GTP on the α-subunit of the G12 family of G proteins. PLC-ε is positioned closer to the membrane by the GTP-bound α-subunit, and is activated as adapted from Rhee, 2001.

PLC-ε has been implicated in additional roles such as affecting cell growth (Yun 2008). PLC-ε has been shown to reduce carcinogen-induced skin tumour formation when PLC-ε knock-out mice were studied, suggesting a mitogenic function (Yun 2008). A reduction in expression of PLC-ε has shown to reduce cell growth in numerous cancer cells (Yun 2008).

PLC-ε affects cell growth through small G-protein-dependent PLC-ε activity, an activity that is critical for both cell growth or tumour formation (Yun 2008). Cell growth occurs because PLC-ε has the ability to terminate EGFR signalling, impairing it from sending a stop signal for growth. PLC-ε is able to increase the recycling of the EGFR, enhancing receptor-mediated cell growth. This recycling of surface receptors is able to increase the activity of ligands since surface receptors are continuously being replenished and maintained to promote prolonged signalling (Yun 2008).

Phospholipase C like-2 (PLC-L_2)

Like the other classes of PLC enzymes mentioned, PLC like-2 (PLC-L_2) also has X and Y domains (Otsuki 1999). Before PLC-L_2 was discovered, another PLC-like protein was found; PLC-L which is homologous to PLC-δ in structure. It has a higher molecular weight than PLC-δ, but the X and Y domain as well as the C2 region are the same. The PH domain of PLC-L is able to bind both PI(4,5)P_2 and Ins(1,4,5)P_3 as PLC-δ. This binding is essential for protein anchoring to the plasma membrane in response to extra-cellular stimuli as well as detaching from the plasma membrane due to increasing levels of Ins(1,4,5)P_3. However, PLC-L was found to have no PLC activity, making its role to remain unclear. Another type of PLC-L, PLC-L_2, also contains the same X and Y domain, but like PLC-L does not have PLC activity. It is also able to bind both PI(4,5)P_2 and Ins(1,4,5)P_3 through the PH domain with great strength (Otsuki 1999).

The X and Y domains of PLC-L_2 are essential for its activity (Otsuki 1999). Mouse PLC-L_2 has a 63.9% similarity to human PLC-L_1 when its amino acid sequence was compared, especially in the X and Y domains as well as the PH region, with all 3 regions having approximately 69% homology or higher. The PH domain is located at the N-terminus, and has approximately 73% of its amino acids identical to PLC-L_1 and 34% of its amino acids identical to PLC-δ_1. The PH domain is considered to be a binding site for inositolphospholipids and inositolphosphates. The PH domain bound more readily and strongly to PI(4,5)P_2 and moderately to both PI(3,4,5)P_3 and PI(4)P (Otsuki 1999).

PLC-L_2 is highly expressed in skeletal muscle and is moderately expressed in both the brain and spleen, with additional expression seen in the thymus, kidney and liver (Otsuki 1999). Since PLC-L_2 is highly expressed in skeletal muscle, its intracellular localization can be examined using antibodies and/or GFP's (green fluorescent proteins). It was seen that PLC-L_2

was present throughout the cytoplasm and was also concentrated in perinuclear areas, as was the localization of the PH domain suggesting that PLC-L_2 localizes around the endoplasmic reticulum where the Ins(1,4,5)P_3 receptors are located and where it is able to interfere with Ins(1,4,5)P_3 signalling, possibly regulating it (Otsuki 1999).

A summary of the known important protein interactors that play a role in Fc receptor-mediated phagocytosis can be seen below in Table 3.

Table 3: The role of important protein interactors in Fc receptor-mediated phagocytosis (Fujii 1999; Lennartz 1999; Williams 1999; Litosch 2002; Steinberg 2008; Yun 2008).

Protein	Binding domain	Role	Regulation / Activation
PLC-β	PH	hydrolysis PIP_2 to IP_3 and DAG	G-proteins
PLC-γ	C2	hydrolysis PIP_2 to IP_3 and DAG	Tyrosine kinase receptors
PLC-δ	C2 / PH	hydrolysis PIP_2 to IP_3 and DAG	unknown
PLC-ε	RA	hydrolysis PIP_2 to IP_3 and DAG; decreases cell growth in tumours	G-proteins
PLC like-2	PH	hydrolysis PIP_2 to IP_3 and DAG	No PLC activity; unknown
IP_3	PH	calcium mobilization	PLC's
DAG	C1	PKC activation	PLC's
PIP_2	PH	PIP_3, IP_3 and DAG production	PI3-K; PLC's
PIP_3	PH	Rac activation; Actin polymerization regulation; PKC activation	PI3-K
PKC	C1 / C2	Actin assembly; Cytoskeletal reorganization; ERK pathway activation	DAG
PI3-K	PI	Actin assembly; Pseudopod extension; Phosphorylation PIP_2 --> PIP_3; Phagosome closure	G-proteins; SYK
Src	SH2	Docking site for Syk	IgG opsonized particles
Syk	SH2	Recruit secondary messengers ie. PLC	Src; phosphorylated ITAM

RATIONALE

Ligand binding can activate receptors and recruit proteins to the site of supramolecular complex formation in the plasmalemma subdomain surrounding the activated receptor (Marshall J. G. 2001). The receptor complex proteins' diffusion may be measured on the inner bilayer of the membrane using fluorescence recovery after photo bleaching (Marshall J. G. 2001). In an unstimulated membrane there was no change in mobility of the proteins (Marshall J. G. 2001). However, at sites of Fc receptor activation the mobility of some phospholipids and proteins were restricted (Marshall J. G. 2001). The inner bilayer of the membrane displayed a decrease in mobility for proteins anchored to the inner membrane, while proteins anchored to the outer layer remained unaffected (Corbett-Nelson E. F. 2006). The plasma membrane itself, local polarity of the membrane, and the cytoskeleton itself are all required to form the functional supramolecular receptor complex (Yeung, Terebiznik et al. 2006). Hence, the activated receptor supramolecular complex is comprised of the receptor, cytoskeleton and associated proteins bound together in an annulus within the associated plasma membrane subdomain.

Recently, the LARC method has been used to capture an activated receptor supramolecular complex from the surface of live cells with the receptor's ligand bound to a microbead for identification by LC-MS/MS, with superior specificity and sensitivity compared to immuno- precipitation (Jankowski 2008). A total of 336 proteins were identified by LARC, including the Phospholipase C family of proteins.

Phospholipase C has been previously shown to be involved in Fcγ receptor-mediated phagocytosis (Jiang 1994; Murthy 2004; Rosales 2005; Jones 2007). The purpose of the work described in this thesis was to identify the proteins specifically associated with Fcγ receptor-mediated phagocytosis in RAW macrophages, and investigate the role of phospholipase C as

members of the activated supramolecular receptor complex. The determination of phospholipase C family members (specifically PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2) at the activated receptor in RAW 264.7 macrophages will be able to further our understanding of the phospholipase C family of proteins as well as the protein members involved in the regulation of phagocytosis. Cell surface receptors found on the plasma membrane can act as key targets for modulating cellular responses. The phospholipase C family of proteins can interact with these cell surface receptors. Understanding their regulatory roles may shed some insight on various immune diseases.

MATERIALS AND METHODS

Reagents

Antibodies

Monoclonal rabbit anti-PLC-β_3 (C-20: sc-403), rabbit anti-PLC-β_4 (C-18: sc-404), rabbit anti-PLC-γ_1 (1249: sc-81), rabbit anti-PLC-δ_1 (H-140: sc-30062) and goat anti-PLC-ε_1 (C-18: sc-28404) was obtained from Santa Cruz Biotechnology, Inc (Santa Cruz, CA). Monoclonal mouse anti-PLC-L2 (ab57398) was obtained from Abcam (Cambridge, MA). Cy3- conjugated anti-rabbit, anti-goat and anti-mouse secondary antibodies were obtained from Jackson ImmunoResearch Laboratories (West Grove, PA). The 2 μ polystyrene beads were obtained from Bands Laboratories (Fishers, IN). Human IgG and all other reagents, unless otherwise stated, were obtained from Sigma-Aldrich.

Nculeic Acids

Plasmids encoding Phospholipase C isoforms were used in these experiments. The construct for pEGFP-C1 was generously donated by Dr. Pann-Ghill Suh (Department of Life Science, Division of Molecular and Life Science, Poland University of Science and Technology) (Hwang 2005). The GFP tagged PLC-β_3 consisted of the expression of glutathione S-transferase fusion form of the C-terminal region of PLC-β_3 in *E.coli*. PCR amplified the 337 amino acids of the C-terminal with primers. The PCR product was inserted into PGEX4T-1 as an EcoRI/XhoI fragment. Primers digested with EcoRI/SmaI and ligated into PEGFP-C1 to express GFP-tagged PLC-β_3 (Hwang 2005).

The construct for PLC-β_4-GFP was generously donated by Dr. Lucio Cocco (Cellular Signalling Laboratory, Department of Anatomical Science, Univeristy of Bologna) (Faenza 2004). The full cDNA of PLC-β_4 was produced by PCR using EcoRI sites in the 5' and 3' termini. PLC-β_3 PCR product was digested with EcoRI and subcloned into the pEGFP vector (Clonetech Labs) (Faenza 2004).

The construct for pEGFP-C1 was generously donated by Dr. Matilda Katan (Cancer Research UK Centre for Cell and Molecular Biology, Chester Beaty Laboratories, The Institute of Cancer Research) (Jones 2007). The GFP tagged PLC- γ_1 consisted of the attachment of EGFP to the carboxyl-terminus of rat PLC- γ_1 using the pEGFP-C1 vector (Clonetech labs) and standard recombination techniques (Wang 2001; Jones 2007).

The construct for $PH^{PLC-\delta}$-GFP was generously donated by Dr. Sergio Grinstein (Division of Cell Biology, The Hospital for Sick Children, Toronto, Ontario, Department of Biochemistry, University of Toronto, Toronto, Ontario) (Scott C. C. 2005). Plasmids encoding the PH domain of PLC-δ were fused to GFP (Scott C. C. 2005).

The construct for PLC- δ_1 dominant negative was generously donated by Dr. Karnam Murthy (Departments of Physiology and Medicine, Medical College of Virginia Campus, Virginia Commonwealth University, Richmond, Virginia) (Murthy 2004). Dominant negative PLC- δ_1 (E341R/D343R) was subcloned into the multiple cloning site of *Eco*RI of the pcDNA3 eukaryotic expression vector. A myc-tag was incorporated at the N-terminus. Recombinant plasmid cDNA was transfected into smooth muscle cells and cotransfected with pcDNA3 to monitor GFP expression and efficiency (Murthy 2004).

Cell Culture

The macrophage RAW 264.7 cell line was obtained from ATCC (American Type Culture Collection, VA, USA). Culturing of the macrophage cells used Dulbecco's modified Earl's alpha-MEM with 5-10% heat-inactivated fetal bovine serum in a 25 cm^2 culture flask at 37°C, with 5% CO_2 (Jankowski 2008).

Experimental Procedures

Live-cell affinity receptor chromatography (LARC) coupled to LC-MS/MS

The Fc receptor complex was captured by LARC, as previously described by Jankowski et al., 2008 (Jankowski 2008). On the surface of live cells in experimental medium, IgG-coated polystyrene beads were presented on ice for 30 minutes. The free beads were washed away in ice cold medium. In these conditions, the IgG receptor complex is not internalized, but rather remains attached to the Fc receptor on the cell's surface. The cells were warmed for various time intervals (0, 2.5, 5, 7.5 and 10 min) at 37°C to activate the receptor fully. The experiment was stopped with the addition of ice cold buffer, the cells scraped, and the beads collected before the receptor complexes were internalized by the warming cells. A French Press (FA-078A, Thermo Electron, Waltham MA, USA) was used to disrupt the cells in experimental medium. The ligand microbeads were isolated with a sucrose gradient centrifugation (Beckman, USA) (Jankowski 2008). For the control, for each LARC experiment performed, a crude lysate of RAW macrophages was run through the French Press or incubated, without the ligand but with the 2 micron polystyrene beads.

Proteins were extracted from LARC as well as crude extract control beads with salt (Foster L. J. 2006). Organics were used to digest the remaining salt insoluble proteins. Following sucrose isolation, the LARC beads were extracted in 200 μL of a step gradient of NaCl to produce 14 fractions of intact proteins as well as control beads (gradient: 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 700, 800, 900, and 1000 mM). Coomassie Brilliant Blue dye binding was used to measure protein content of all fractions (Ghosh S. 1988). Protein fractions obtained from extractions were digested with trypsin and analyzed with LC-MS/MS in a minimum of three replicates along with controls, as previously described by Jankowski et al. (Jankowski 2008).

Correlation and Conformation of Proteins Identified by SEQUEST

To eliminate false positives, manual inspection of proteins generated by search algorithms is required. A joint calculation using the manufacturer's software under recommended settings by the manufacturer and previously described conditions was used to correlate the resulting peptides from the control and LARC fractions. The full length FASTA protein sequence was correlated to the sequences from the NCBI website. The sequences for PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2 were correlated by BLAST for screening of proteins or peptides identified by SEQUEST. The peptide sequences generated from the MS/MS (tandem mass spectrometry) data were aligned with the FASTA protein sequences and only accepted as true if at least three different peptide sequences from a single protein identified by SEQUEST were present in the FASTA sequence. The peptides with a cumulative unified score of 2400 or more using BIOWORKS (Thermo Electron Corporations) identified by SEQUEST were accepted. The manufacturer's scoring settings and conditions were used to

analyze the spectra, with a cut-off score of 2400 yielding a false-positive rate of identification of about 5% (Chelius D. 2002). Only these proteins which met the criteria were determined to be proteins specifically associated with the Fc receptor complex, and proteins that failed to meet the criteria were omitted.

LARC Specific Protein Computerized Analysis

Accession numbers of proteins which attained a cumulative score of 2400 were collected in SQL (Structured query language) and complied into a non-redundant set; SQL was further used to subtract background proteins which interacted non-specifically with the control beads (Codd 1998). Proteins identified from the 3 sets of LARC experiments were combined into a non-redundant set of accession numbers through use of SQL (Zhu P. 2007). A non-redundant set of accession numbers for the crude extract, BSA, IAC and media control was complied in a similar nature with SQL. Proteins specific to the Fc receptor complex that were captured by LARC were identified after removal of proteins associated with the controls by SQL.

Fc-Ligand Specific Protein Manual Selection

Both manual and computer searches of the proteins and peptides identified by LARC, IAC and control beads from the LC-MS/MS runs were carried out ensuring all proteins collected were detected by mass spectroscopy exclusively in the captured receptor complex. Comparison of proteins captured by LARC verses traditional IAC to control beads incubated with crude extracts or growth media through manual inspection was used to search for proteins from

previous experiments identified specifically to be associated with the Fc-ligand complex (Ellis R.E. 1991; Chung S. 2000; Greenberg and Grinstein 2002).

Data mining using iHOP (Information Hyperlinked over Proteins) was used in order to search for known proteins and known protein-protein interactions. iHOP is a gene network which encompases known protein interactors. Imputing specific proteins that were found to be associated with Fc receptor-mediated phagocytosis into the iHOP search engine created a list of additional protein interactors. However, in order to keep the model specific to those only captured by the activated receptor complex, only the proteins identified by ESI-MS/MS were accepted and added to the interaction model. This added specificity to the model, ensuring it only encompassed proteins that were accepted under the previously determined criteria (score, number of peptides, ratio LARC to control).

The protein interaction databases Cytoscape, Osprey and STRING were used to visualize the interaction network created with iHOP. The protein interaction data established with iHOP was inputed into the protein interaction databases to create a visual representation of the protein-protein interactions that occur during Fc receptor-mediated phagocytosis. The protein-protein interaction models allowed for the main interactors of Fc mediated phagocytosis to be determined, displayed by the greatest number of interaction lines between proteins.

A theoretical based approach of Fc receptor-mediated phagocytosis was developed by reviewing the literature. This allowed for identification of numerous proteins that were known to be involved in the signalling of phagocytosis of the Fc receptor complex.

Confirmation by Confocal Microscopy

To confirm that the proteins identified by LARC followed by LC-MS/MS were associated with the Fc receptor complex, additional experiments had to be performed including confocal microscopy. Confocal microscopy was combined with antibody staining and/or constructs which fluoresce and are fused with the endogenous proteins. Images of both fixed RAW 264.7 and live macrophage cells were done using the Zeiss LSM 510 laser scanning confocal microscope and an oil immersion objective of 100x.

Confirmation by Western blot of RAW 264.7 cell lysates

Western blot analysis was used to confirm the presence of PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC-L2 using RAW 264.7 cell lysates. Cell lysates were prepared by growing cells to 80-90% confluency in a 75 cm^2 flask in cell culture conditions and then scraped. To the cells, approximately 5mL of 2x SDS-PAGE sample buffer [containing approximately 5mM PMSF, 5mM AEBSF, 5mM EDTA salt and eukatyotic anti-protease cocktail (Sigma-Aldrich)] was added and the cells were immediately heated at 100°C for 15 minutes. On a discontinuous polyacrylamide gel containing a 4% monomer stacking gel (Tris pH 6.8) and a 7% monomer separating gel (Tris pH 8.8), 50 μL of cell lysate was electrophoresced, alongside a molecular weight marker in tricine anode and cathode buffers (Schagger and von Jagow 1987). Proteins from the SDS-PAGE gel were transferred to Immobilon-P Transfer Membrane (pore size 0.45 μm) (Millipore, Bedford, MA) (Burnette 1981) which was first soaked in 100% methanol for activation. Once transferred, the membrane was stained with Coomassie stain containing no acetic acid, destained with 50% methanol, dried and marked with pencil to indicate the location of the molecular weight markers and protein lanes. When marked, the membrane

was fully destained with 100% methanol and blocked with 5% skim milk in PBST (PBS + 0.1% Tween) for 30 minutes. After blocking, the membranes were washed 3 times with PBST and then incubated with 1:1000 primary antibody for PLC-γ_1, PLC-δ_1 and PLC like-2 for 30 minutes, and washed again 3 times with PBST. The membrane was then incubated with 1:10,000 HRP conjugate secondary antibody in PBST for 30 minutes, followed by extensive washing with PBST. For PLC-β_3, PLC-β_4 and PLCε_1, 5% BSA in PBST was used for blocking, with the same conditions used for the primary and secondary antibodies thereafter. The membrane was developed using ECL Western blot solution (Haan 2007).

Immunofluorescence Staining

In six-well plates containing 1-2 mL of media, cells were grown on 2.5 cm glass cover slips for immunostaining for 24 to 48 hours until approximately 50% confluent. 2 μM beads were opsonized with human anti-IgG at room temperature for 30 minutes in 1x PBS. The beads that were fed to the cells stained with anti-PLC-δ_1 antibody were incubated with 5% skim milk to block the fluorescence of the bead. Beads were washed as previously described 3 times with 1x PBS (Marshall J. G. 2001). Cells grown on the glass cover slips were incubated with the IgG opsonized particles for 5, 7.5 and 10 minutes at 37°C. Cover slips were then washed with ice cold PBS and fixed with 4% paraformaldehyde in 1x PBS for 30 minutes. Upon cell fixation, they were washed 3 times with 1x PBS, left in 5% glycine in 1x PBS for 10 minutes and washed 3 times with 0.1% MgCl. The cells were blocked with 5% skim milk in 1x PBS which contained 0.1% Triton for permeablization. The cells were washed 3 times with 1x PBS. On the cover of the 6-well plate, 25 μL of PBS was spotted with 1 μL of primary antibody (PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2); the cover slips were placed cell side down into the

antibody solution and incubated for 30 minutes at room temperature. The cover slips were placed back into the wells and washed 3 times with 1x PBS. The cells were incubated for 30 minutes at room temperature with cy3-conjugated secondary antibody at 1:10,000 (Cy-3 donkey α rabbit for PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, donkey α goat for PLC-ε_1 and donkey α mouse for PLC like-2) . The cells were washed 3 times with 1x PBS and fixed onto microscope slides with DAKO (Dako, Denmark), dried and analyzed using laser confocal microscopy.

Competent Escherichia coli (E.coli) DH5α

Competence of *E.coli* DH5α strain (ATCC) was carried out as previously described by Hanahan (Hanahan 1983). *E.coli* DH5 Alpha stock was inoculated in LB broth and incubated at 37°C overnight with shaking at 200 rpm. Approximately 1 mL of overnight culture was inoculated into 5 mL of LB broth and grown at 37°C with shaking for 2 hours. Again, 1 mL of culture was inoculated into 100 mL pre-warmed LB broth and grown at 37°C with shaking for approximately 2 hours until an optical density of 0.3-0.45 was reached. The culture was chilled on ice, centrifuged at 3500 rpm / 8000 g at 4°C for 5 min. The supernantant was disgarded, the pellet was resuspended in 2/5 original volume Tfb I buffer (30 mM potassium acetate, 100 mM $RbCl_2$, 50 mM MgCl, 15% glycerol, 10 mM $CaCl_2 \bullet 2H_20$, pH 5.8) and chilled for 5 min on ice. The resuspended pellet was centrifuged at 3500 rpm / 6000 g at 4°C for 5 min, the pellet was resuspended in 1/25 original volume Tfb II buffer (10 mM MOPS, 75 mM $CaCl_2 \bullet 2H_2O$, 10 mM $RbCl_2$, 15% glycerol, pH 6.5) and chilled for 15 min on ice. Competent cells were stored at -80°C in 100 μL aliquots.

Cell Transformation

Competent *E.coli* cells were thawed on ice; 100 μL was incubated with approximately 1 mg/mL DNA on ice for 30 minutes. The cells were heat shocked at 42°C for 90 seconds and chilled for 1-2 minutes on ice. To the cell suspension 1 mL of LB was added and the cells were incubated at 37°C for 3 hours at 200 rpm. The cell suspension was plated on LB agar plates alone, LB containing 50 μg/mL kanomycin and LB containing 100μg/mL ampicillin and left overnight to grow at 37°C. Colonies grown on plates showing resistance were looped off and mixed with 3 mL LB and grown with specific antibiotics for 3 hours. After the 3 hour growth period, 1 mL of the culture was grown in 100 mL LB with the same antibiotic conditions overnight. The DNA plasmid was then extracted using the Q1Afilter Plasmid Maxi kit protocol (QIAGEN, Valencia, California). The concentration of DNA in TE buffer was determined at a wavelength of 260nm.

Cell Transfection

RAW 264.7 macrophage cells were grown in 6-well plates on 2.5 cm glass cover slips at 37°C, 5% CO_2 for 24-48 hours until 50% confluency was reached. The RAW cells were transfected using FuGENE 6 transfection reagent (Roche Diagnostics, USA) according to the manufacturer's directions. Cells were transfected with PLC-β_3-GFP, PLC-β_4-GFP, PLC-γ_1-GFP, $PH^{PLC\text{-}\delta 1}$-GFP and a pmaxGFP (provided by manufacturer) vector as a control. Cells were left for 24 hours at 37°C and analyzed using laser confocal microscopy.

Double Immunofluorescence Staining for Dominant Negative Analysis

Cells prepared for double stain were grown in 6-well plates as previously described above. Cells were transfected with PLC-δ_1-GFP-DN (E341R/D343R) as described above. Latex beads of 2 μm were opsonized with human IgG at room temperature for 30 minutes and washed as previously described 3 times with 1x PBS (Marshall J. G. 2001). Latex beads were incubated with 1 μL of Cy-3 donkey α human for 5 min and washed 3 times with 1x PBS. Cells grown on the glass cover slips were incubated with the IgG opsonized particles for 30 minutes and 2 hours at 37°C. Cover slips were then washed with ice cold PBS and fixed with 4% paraformaldehyde in 1x PBS for 30 minutes. Once the cells were fixed, they were washed 3 times with 1x PBS, left in 5% glycine in 1x PBS for 10 minutes and washed 3 times with 0.1% MgCl. The cells were blocked with 5% skim milk in 1x PBS for 30 minutes. The cells were washed 3 times with 1x PBS. The cells were incubated for 30 minutes at room temperature with Cy5-conjugated secondary antibody, with 0.2 μL per well (Cy-5 donkey α human). The cells were washed 3 times with 1x PBS and fixed onto microscope slides with DAKO (Dako, Denmark), dried and analyzed using laser confocal microscopy.

RESULTS

Proteins associated with an activated Fc receptor complex may provide insight on immune response regulation. In this experiment, latex beads coated with an Fc receptor activating ligand were exposed to RAW 264.7 macrophages and the proteins involved in the assembled Fc receptor complex were identified and analyzed using tandem mass spectrometry. Mass spectrometry data was further confirmed first by Western blots and second the visualization of macrophages undergoing phagocytosis either by immunostaining or transfections with fluorescently fused constructs using confocal microscopy.

Correlation of LC-MS/MS data to protein sequences

Data analysis obtained by live cell affinity receptor chromatography (LARC) followed by mass spectrometry identified numerous proteins associated with Fc receptor-mediated phagocytosis. Analysis identified 336 proteins to be specifically associated with Fc receptor-mediated phagocytosis. The elimination of false positive identification by SEQUEST was taken into account by only selecting proteins which had a cumulative peptide score of at least 2400 from at least three different peptide sequences (Chelius D. 2002).

Proteins identified to be associated with Fc receptor-mediated phagocytosis (Table 4) include multiple kinases such as Spleen tyrosine kinase (Syk) which is known to be involved with the activation of phagocytosis and was detected with a score of 2,709 and contained 19 peptide sequences. Phosphoinositide 3-kinase, another key player in phagocytosis, was detected in its beta, gamma and delta isoform, with scores of 3,902, 8,441 and 8,849 respectively as well as 9, 18 and 23 unique peptides respectively. Phospholipase C, known to be involved in the

activation of diacylglycerol and release of calcium in phagocytosis, was detected in numerous isoforms including the gamma isoform with a score of 6,100 and 19 peptides. The Fc receptor (IgE high affinity 1) alpha polypeptide was also detected with a score of 3,517 and 6 peptides as well as the high affinity immunoglobulin gamma Fc receptor with a score 2,284 and 7 peptides. Many GTPases were identified including the RASp21 protein activators 1-3, having scores of 13,593, 7,208 and 13,160 respectively and 23, 16 and 20 peptides. Actin and myosin motor proteins were also identified as seen fit since phagocytosis involves cell migration. Actins include actin related protein 2 and 2/3 complex having scores of 26,207 and 19,800 and 18 and 13 peptides respectively. Myosins include cofilin 1 having a score of 34,435 and 10 peptides.

Many phospholipase C molecules were detected by LARC. PLC-ζ had the highest score of 39,889 and 18 peptides, PLC-β_3 had the second highest score of 13, 940 and 26 peptides and PLC-ε_1 had the third highest score of 11,725 and 46 peptides. Other PLC molecules ranged from about 4,064 up to 13,940 (Table 4). Phospholipase C family of proteins were detected with high scores for all isoforms, suggesting that PLC may be present at the activated Fc receptor. The list of peptides correlating to the total score of each protein can be found in Appendices A to L.

Table 4: Detection of proteins in RAW 264.7 macrophages identified by LARC.

The method of LARC yielded a total of 336 proteins identified as specifically being associated with the Fcγ receptor complex and Fcγ receptor-mediated phagocytosis. Cumulative score for each protein is shown, along with the control scores (from raw extracts, French Press and BSA). Proteins all had a cumulative score of at least 2400, had at least 3x the score of the control and had 3 independent peptide sequences, indicating a 95% probability of correct identification and elimination of false-positive identification.

KINASE's			
	Accession Number	Fc Receptor Complex	Control
Serine/threonine kinase			
bone morphogenic protein receptor, type II (serine/threonine kinase) [M	6680804.0	4802.61	354.28
similar to serine/threonine kinase [Mus musculus]	38348544.0	6461.94	0.00
similar to serine/threonine kinase AIE1 [Mus musculus]	38085953.0	3895.25	998.44
similar to Serine/threonine-protein kinase PAK 6 (p21-activated kinase	28487481.0	3903.18	889.45
serine/threonine protein kinase; Murine thymoma viral (v-akt) oncogene protein kinase B kinase	4885061.0	2591.51	0.00
CHK1_MOUSE SERINE/THREONINE-PROTEIN KINASE CHK1	7531058.0	5246.87	51.80
NEK4_MOUSE Serine/threonine-protein kinase Nek4 (NimA-related protein kinase	29337019.0	5043.36	1769.81
protein kinase C-like 1; serine/threonine kinase 3 [Mus musculus]	32813439.0	3688.99	321.51
serine threonine kinase 31 [Mus musculus]	31044416.0	8382.82	1139.45
calcium/calmodulin-dependent serine protein kinase [Mus musculus]	6753276.0	4016.75	1482.17
Crk			
breast cancer anti-estrogen resistance 1; v-crk-associated tyrosine ki	40254593.0	3618.68	1035.84
CRKL_MOUSE Crk-like protein	1345822.0	2880.83	1590.97
Nck			
Nck-interacting kinase-like embryo specific kinase [Mus musculus]	6472874.0	6605.09	867.02
p21			
p21-activated kinase 2 [Mus musculus]	28493842.0	2608.54	0.00
p21-activated protein kinase 4 [Mus musculus]	29336032.0	6849.56	1729.84
p21-activated kinase 5 [Mus musculus] ix-associate	40037528.0	3189.61	0.00

Nucleoside diphosphate kinase			
similar to Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (P18	38083746.0	24545.05	3710.61
nucleoside-diphosphate kinase 1; nucleotide diphosphate kinase [Mus mu	37700232.0	100772.79	0.00
Protein kinase C			
KIMSCD protein kinase C (EC 2.7.1.-) delta - mouse	66731.0	2907.04	642.49
Tyrosine kinase			
LYN_MOUSE Tyrosine-protein kinase LYN	2507208.0	2641.95	0.00
Hematopoietic cell specific Lyn substrate 1 [Mus musculus]	13938627.0	18504.27	664.90
KSYK_MOUSE Tyrosine-protein kinase SYK (Spleen tyrosine kinase)	1711636.0	11911.30	0.00
protein tyrosine kinase TecIII [Mus musculus]	5453033.0	54184.90	21096.49
CSK_MOUSE Tyrosine-protein kinase CSK (C-SRC kinase) (Protein-tyrosine kinase M	729888.0	2709.32	328.54
FAK2_MOUSE Protein tyrosine kinase 2 beta (Focal adhesion kinase 2) (FADK 2)	20138411.0	6064.34	1648.93
megakaryocyte-associated tyrosine kinase [Mus musculus]	6754646.0	2967.88	541.86
tyrosine kinase 2; tyrosine kinase TYK2 [Mus musculus]	9055372.0	5146.30	1153.02
FMS-like tyrosine kinase 3 [Mus musculus]	6753888.0	4446.11	349.60
B39577 protein-tyrosine kinase (EC 2.7.1.112) JAK2 - mouse (fragment)	110873.0	3262.85	0.00
Mitogen activated protein kinase			
mitogen activated protein kinase kinase 1; protein kinase, mitogen acti	6678794.0	3933.63	1262.70
mitogen-activated protein kinase kinase kinase 6; apoptosis signal-reg	33186928.0	6744.04	2473.28
M4K6_MOUSE Mitogen-activated protein kinase kinase kinase kinase 6 (MAPK/ERK	29428007.0	5369.49	304.31
Mitogen activated protein kinase kinase 2 [Mus musculus]	15990388.0	2650.25	0.00
mitogen activated protein kinase binding proten 1; JNK-binding protein	6754398.0	5917.27	0.00
M4K5_MOUSE Mitogen-activated protein kinase kinase kinase kinase 5 (MAPK/ERK	30315995.0	4660.40	968.25
similar to MAP-kinase phosphatase (cpg21) [Mus musculus]	38085197.0	3195.40	724.11
MNK1_MOUSE MAP kinase-interacting serine/threonine kinase 1 (MAP kinase signa	30315972.0	5901.28	0.00
Fos			
fos-like antigen 1 [Mus musculus]	6753896.0	3160.06	0.00

unnamed protein product [Mus musculus] V-FOS TRAN	26342525.0	2811.85	0.00
Fas			
Fas-interacting serine/threonine kinase 3 [Mus musculus]	10998780.0	2957.86	343.95
Fyn			
embryonal Fyn-associated substrate [Mus musculus]	31981787.0	4347.65	987.63
Fyn protein [Mus musculus] h leukemia gene [Mus mu	21594599.0	4462.89	1398.92
FYN binding protein; FYB-120/130; SLAP130; p120/130 [Mus musculus]	33469119.0	3338.25	1353.85
similar to FYN binding protein (FYB-120/130); FYN-binding protein (FYB	38078624.0	4267.40	1189.61
Btk			
Btk protein [Mus musculus] sculus] ns and 9-cis) [	31419802.0	3079.66	153.45
Anchor kinases			
A-kinase anchor protein 3 [Mus musculus]	6753026.0	6588.68	222.06
A-kinase anchor protein 4 [Mus musculus]	6753028.0	6954.92	1145.87
similar to A-kinase anchor protein 5; RII-B-binding protein [Mus muscu	38050553.0	3200.57	0.00
A kinase anchor protein 7 isoform gamma [Mus musculus]	31580808.0	3798.07	0.00
A kinase (PRKA) anchor protein 10; protein kinase A anchoring protein	40807354.0	3440.06	252.09
type II cAMP-dependent protein kinase anchoring protein Ht31 [Mus muscul	14192799.0	2688.09	683.04
Phosphoglycerate kinase			
similar to phosphoglycerate kinase (EC 2.7.2.3) - mouse [Mus musculus]	38076512.0	72264.39	1145.87
Phosphoglycerate kinase 2 [Mus musculus]	38174603.0	162672.42	1793.86
kappaB kinase epsilon			
inhibitor of kappaB kinase epsilon; inducible IKappaB kinase; inhibito	31981053.0	3782.89	419.38
Putative kinase			
similar to putative protein kinase [Mus musculus]	38079866.0	4915.22	512.41
putative membrane-associated guanylate kinase 1 [Mus musculus]	2702351.0	2416.23	379.49
putative PKA-related protein kinase [Mus musculus]	6010221.0	6220.94	2579.39
Diacylglycerol kinase			
diacylglycerol kinase, gamma 3 [Mus musculus] mu	20893772.0	3346.56	0.00
similar to diacylglycerol kinase eta [Mus musculus]	38076892.0	8226.93	208.83
similar to diacylglycerol kinase iota-1 [Mus musculus]	38083937.0	2854.30	278.46
diacylglycerol kinase zeta [Mus musculus]	30794244.0	5423.18	619.81
Inositol kinase			
inositol 1,4,5-trisphosphate 3-kinase A; IP3-kinase A	22122643.0	2982.86	147.55

[Mus musculus]			
inositol 1,4,5-trisphosphate 3-kinase C [Mus musculus]	31712006.0	2440.16	713.66
inositol polyphosphate 5-phosphatase II splice variant [Mus musculus]	2766531.0	3337.53	0.00
inositol polyphosphate-5-phosphatase E; inositol polyphosphate-5-phosp	14916467.0	10790.96	655.57
inositol polyphosphate-5-phosphatase D; inositol polyphosphate-5-phosph	6754356.0	13813.52	1910.29
inositol polyphosphate-5-phosphatase F; cDNA sequence, clone 3-26 [Mus	31542017.0	5308.43	2230.62
inositol polyphosphate phosphatase-like 1 [Mus musculus]	33859566.0	4298.98	444.26
Phosphoinositide / Phosphatidylinositol kinase			
phosphatidylinositol 4-phosphate 5-kinase type I-beta [Mus musculus]	1622710.0	3146.63	1072.12
phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma [Mus musculus]	6679323.0	4527.08	242.76
phosphatidylinositol-4-phosphate 5-kinase, type II, beta [Mus musculus	33663294.0	4194.56	828.81
phosphatidylinositol 4-kinase, catalytic, beta polypeptide; EST AA4378	29648332.0	5801.84	792.60
phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 b	6679321.0	2769.48	1162.26
phosphatidylinositol-3-phosphatase associated protein; phosphatidylino	27370470.0	3415.38	694.59
phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A; proline-rich	27369946.0	5521.29	375.50
phosphatidylinositol 4-kinase type-II beta; likely ortholog of mouse ph	8922869.0	4592.95	799.23
1-phosphatidylinositol-4-phosphate 5-kinase; phosphatidylinositol-4-pho	6755062.0	10714.65	4057.62
phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Mus muscul	29789235.0	3902.88	1679.37
similar to Phosphatidylinositol-4-phosphate 3-kinase C2 domain-contain	38073314.0	3613.76	1581.74
phosphoinositide 3 kinase P110delta [Mus musculus]	22758919.0	8849.02	1213.99
phosphoinositide-3-kinase, catalytic, gamma polypeptide; PI3-K<gamma>; P	9937984.0	8441.50	1126.95
similar to PI 3-kinase enhancer long isoform [Mus musculus]	38090993.0	48087.97	14328.94
similar to phosphoinositide-3-kinase, class 2, beta polypeptide; PI3-K-	28482204.0	6533.84	1883.99
T42642 phosphoinositide 3-kinase (EC 2.7.1.-) - mouse	11259849.0	9807.10	4453.78
Protein kinase			
A55748 protein kinase (EC 2.7.1.37) Sak-a - mouse	1083471.0	3086.10	136.73
AMP-activated protein kinase, gamma-2 subunit; 5-AMP-activated protein	21703802.0	3316.59	182.04
protein kinase [Mus musculus]	2980671.0	4823.12	0.00
protein kinase, lysine deficient 1 [Mus musculus]	38424077.0	5435.59	1703.71
protein kinase, cGMP-dependent, type II [Mus musculus]	31982097.0	4662.78	1059.70
C32571 ribosomal protein S6 kinase II (EC 2.7.-.-) alpha	91277.0	6831.28	533.28

chain homolog (clone Mu7A) -			
DNA-dependent protein kinase catalytic subunit [Mus musculus]	3241856.0	29405.11	3919.51
homeodomain-interacting protein kinase 2b [Mus musculus]	12751417.0	4501.44	687.18
Pyruvate kinase			
M2-type pyruvate kinase [Mus musculus]	1405933.0	3369827.68	24951.66
similar to Pyruvate kinase 3 [Mus musculus] mest	38075009.0	7936.48	0.00
Hexokinase			
HXK1_MOUSE Hexokinase, type I (HK I) (Hexokinase, tumor isozyme)	30316354.0	5510.52	0.00
JNK			
protein kinase JNK2 beta 2 [Mus musculus] lus]	4558397.0	4061.58	809.69
WASP			
Wiskott-Aldrich syndrome protein interacting protein; WASP interacting	23346579.0	6762.08	2551.31
WASP family 1 [Mus musculus]	13994209.0	3697.82	485.64
Wasp-binding protein [Mus musculus]	37537556.0	3377.69	515.28
Other kinases			
cyclin-dependent kinase inhibitor 1B (P27) [Mus musculus]	31542372.0	5325.61	207.64
polynucleotide kinase 3'- phosphatase; polynucleotide kinase 3'-phosph	10946988.0	2972.92	847.98
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 [Mus	21704000.0	10742.03	6764.05
mKIAA0617 protein [Mus musculus] e 5-kinase; phos	39104526.0	2613.07	0.00
NIMA-related expressed kinase 9 [Mus musculus]	21553095.0	3488.76	672.83
unnamed protein product [Mus musculus] kinase 14	26338994.0	4030.70	0.00
polo-like kinase 2; serum-inducible kinase [Mus musculus]	22779889.0	2759.74	0.00
Falz protein [Mus musculus] t kinase 6 [Mus muscul	27370657.0	3838.83	0.00
adenylate kinase 2 [Mus musculus]	34328230.0	2709.93	0.00
vaccinia related kinase 2; vaccinia virus BIR kinase related kinase 2	21312468.0	2791.14	976.25
unnamed protein product [Mus musculus] nase PAK 6	26337801.0	24988.60	0.00
similar to protein kinase nek1 (EC 2.7.1.-) - mouse [Rattus norvegicus	34878053.0	4832.71	245.18
DnaJ (Hsp40) homolog, subfamily C, member 3; protein kinase, interfero	31542563.0	4479.39	467.85
sterile-alpha motif and leucine zipper containing kinase AZK; MLK-like	30017393.0	4723.55	1712.06
choline/ethanolamine kinase [Mus musculus]	6671748.0	3100.60	1151.63
phosphorylase kinase alpha 2 [Mus musculus]	27370156.0	4071.07	248.02
ProSAPiP2 protein [Mus musculus]	37674212.0	4760.12	1249.96

LIPASE's

	Accession Number	Fc Receptor Complex	Control
Phospholipase A			
PA2Z_MOUSE Group XIII secretory phospholipase A2 precursor (Phosphatidylcholi	20178006.0	4658.97	248.68
phospholipase A2, group IB, pancreas, receptor; PLA2-I receptor [Mus mu	6679365.0	2675.25	918.13
phospholipase A2, group VI; 85 kDa calcium-independent phospholipase A2	8393978.0	15926.07	991.79
similar to Calcium-dependent phospholipase A2 precursor (Phosphatidylc	38079191.0	2404.52	0.00
phospholipase A2, group IVB (cytosolic) [Mus musculus]	38075595.0	4523.75	1357.49
Phospholipase C			
phospholipase C, beta 3 [Mus musculus]	31982122.0	8916.15	790.84
phospholipase C beta 4 [Mus musculus]	29293803.0	9857.93	997.97
phospholipase C, epsilon [Mus musculus]	23956100.0	11725.24	4251.91
Ina protein [Mus musculus] phospholipase C zeta [M	17390900.0	39887.76	0.00
phospholipase C-like 2 [Mus musculus] musculus]	38082546.0	4064.26	419.85
Nck, Ash and phospholipase C binding protein; SH2 domain containing SO	20149738.0	2869.04	0.00
phospholipase C-L2 [Mus musculus] ive zinc finger	6705987.0	6065.06	1060.73
phospholipase C, delta; phospholipase C delta-1; PLC-delta 1 [Mus muscu	9790167.0	6458.61	532.04
dJ511B24.2.5 (phospholipase C, gamma 1 (formerly subtype 148) (1-Phosph	41393059.0	6001.40	956.88
Other lipases			
similar to Sec23-interacting protein p125; phospholipase [Mus musculus	38087445.0	2739.70	118.23
LIPS_MOUSE Hormone sensitive lipase (HSL)	1708847.0	5901.00	2632.22
lipase, member H; lipase H [Mus musculus]	23510279.0	4022.93	227.10

CDC's

	Accession Number	Fc Receptor Complex	Control
CDC-42			
similar to CDC42-binding protein kinase alpha; mytonic dystrophy kinas	38085310.0	5418.85	1498.84
Cdc42 binding protein kinase beta [Mus musculus]	33942081.0	4021.91	1049.73
Cdc42 GTPase-activating protein [Mus musculus]	9938022.0	8568.58	1110.57
sorting nexin 26; TC10/CDC42 GTPase-activating protein [Mus musculus]	30142699.0	3838.02	1838.90

CDC-2			
cell cycle p34 CDC2 kinase protein [Mus musculus]	20066967.0	2668.32	0.00
p34 cdc2 kinase [Mus musculus] musculus] mily membe	1575290.0	3022.15	0.00
CDC2-related protein kinase 7; protein kinase for splicing component [	30794424.0	4269.32	1835.76

RECEPTOR's

	Accession Number	Fc Receptor Complex	Control
CD36			
CD36_MOUSE Platelet glycoprotein IV (GPIV) (GPIIIB) (CD36 antigen) (PAS IV) (PA	729081.0	3309.04	1353.63
Insulin receptor			
insulin-like growth factor binding protein 7 [Mus musculus]	6679869.0	4620.89	1835.57
Insulin degrading enzyme [Mus musculus] n [Mus mus	27371196.0	3375.75	476.82
insulinoma-associated 1; insulinoma-associated protein (IA-1) [Mus musc	8393617.0	7882.34	0.00
IRS2_MOUSE INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS)	3024044.0	8423.91	2538.66
insulin receptor substrate 1 [Mus musculus]	29825829.0	10649.26	7257.97
insulin receptor substrate 4 [Mus musculus]	6754372.0	10812.04	4159.47
insulin receptor-related receptor [Mus musculus]	6754362.0	5279.32	1082.56
insulin-like growth factor binding protein 6 [Mus musculus]	6680387.0	2926.88	1141.87
insulinoma-associated 2; mlt 1 gene; mlt 1 [Mus musculus]	9938006.0	5150.44	801.78
insulin-like growth factor I receptor [Mus musculus]	33859572.0	4293.95	1976.75
Receptor tyrosine kinase			
BMX non-receptor tyrosine kinase [Mus musculus]	6753196.0	4673.75	639.39
endothelial-specific receptor tyrosine kinase [Mus musculus]	8567412.0	2611.93	0.00
receptor tyrosine kinase EphA1 [Mus musculus] eras	10047365.0	2572.06	406.84
Fc receptor			
Fc receptor, IgE, high affinity 1, alpha polypeptide [Mus musculus]	6753828.0	3517.37	672.99
high affinity immunoglobulin gamma Fc receptor I [Mus musculus molossinus	4973138.0	2283.71	575.15

GTP'ases

Ros	Accession Number	Fc Receptor Complex	Control
I48310 kinase-related protein ros - mouse	2117869.0	9764.98	3491.61
Rho			
Rho-associated coiled-coil forming kinase 1 [Mus musculus]	6677759.0	16083.11	3003.23
Rho GDP dissociation inhibitor (GDI) alpha; RhoGDI-1 [Mus musculus]	31982030.0	38494.87	2782.68
Rho, GDP dissociation inhibitor (GDI) beta [Mus musculus]	33663236.0	59520.62	253.83
similar to RhoGEF glutamate transport modulator GTRAP48 [Mus musculus]	38077561.0	8734.76	3262.87
similar to Rho guanine nucleotide exchange factor (GEF) 17; Rho-specif	38087046.0	12540.05	2129.10
FGD1_MOUSE Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (	1706790.0	8860.79	1551.80
Rho guanine nucleotide exchange factor (GEF) 1; lymphoid blast crisis l	6678668.0	6214.75	2438.48
Rho guanine nucleotide exchange factor (GEF) 5 [Mus musculus]	38083968.0	9087.43	375.57
Rho-GTPase-activating protein PS-GAP-b [Mus musculus]	37730280.0	7705.17	295.08
Rho GTPase-activating protein; GAB-associated CDC42; rac GTPase activa	28893539.0	8123.67	2417.66
brain stress early protein Gbi; rho GTPase activating protein 14; EST	27597098.0	7211.53	632.62
T-cell activation Rho GTPase-activating protein [Mus musculus]	22165374.0	5740.19	278.82
ARH7_MOUSE Rho guanine nucleotide exchange factor 7 (PAK-interacting exchange	18202873.0	3003.03	1182.67
Rac			
Cdc42/Rac effector kinase; PAK-3 [Mus musculus] lus	3420949.0	5646.82	604.70
Rac GTPase-activating protein 1 [Mus musculus]	6755266.0	5356.45	299.62
RAB			
GDIB_MOUSE RAB GDP dissociation inhibitor beta (RAB GDI beta) (GDI-2)	13638229.0	21477.00	698.58
rab effector MYRIP [Mus musculus] g factor l recep	21218142.0	5468.55	0.00
Rab6-interacting protein 2 [Mus musculus]	30017397.0	8788.25	3067.60
Rab11-FIP4-like [Mus musculus]	28202067.0	8256.50	895.74
hypothetical protein ((NM_017382) RAB11a, member RAS oncogene family	32414965.0	2429.55	0.00
RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind	5803135.0	3713.70	1729.25

RAB GTPase activating protein 1; rab6 GTPase activating protein (GAP a	22122645.0	4006.06	0.00
RAB guanine nucleotide exchange factor (GEF) 1; Ras negative regulator	9910316.0	3146.41	879.22
RAB2, member RAS oncogene family-like; ral guanine nucleotide dissociat	6677737.0	2900.86	682.88
regulating synaptic membrane exocytosis 2; Rab3 interacting protein 1;	16716607.0	2757.02	0.00
Ras			
ras homolog gene family, member U; Wnt1 responsive Cdc42 homolog [Mus	19923060.0	6217.52	1773.06
similar to ras-GTPase-activating protein SH3-domain binding protein [M	38077047.0	7237.55	293.53
ras-GTPase-activating protein SH3-domain binding protein [Mus musculus]	1698657.0	2573.89	1073.66
RAS p21 protein activator 3; GAPIII activator 3; Ras GTPase-activating	7110713.0	9596.83	0.00
RAS p21 protein activator 2 [Mus musculus]	16716601.0	7208.47	417.19
RAS p21 protein activator 1; p120-rasGAP; GTPase-activating protein [M	21703900.0	11271.47	0.00
RAP			
glutamate receptor, ionotropic, AMPA3 (alpha 3); cAMP-dependent Rap1 g	8393313.0	5235.53	0.00
RAP1, GTP-GDP dissociation stimulator 1; cDNA sequence BC011279 [Mus m	21704072.0	3104.99	892.70
Rap1 guanine-nucleotide-exchange factor directly activated by cAMP; ex	21450061.0	2658.92	600.14
RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s	4506413.0	63109.41	24733.93
Activating proteins			
similar to IQ motif containing GTPase activating protein 3 [Mus muscul	38077593.0	9048.40	2314.34
similar to SREBP cleavage activating protein [Mus musculus]	23593606.0	3645.31	871.78
ADP ribosylation			
ARG1_MOUSE ADP-ribosylation factor GTPase activating protein 1 (ADP-ribosylat	27923732.0	6347.77	533.27
ADP-ribosylation factor GTPase activating protein 3; ADP-ribosylation	30841021.0	10013.42	300.68
GEF (guanine exchange factor)			
4833420I20Rik protein [Mus musculus] or (GEF) 1; R	20987708.0	18301.20	0.00
Vav2 protein [Mus musculus] tumor virus] sculus]	31418561.0	6016.02	0.00
Vav2 oncogene [Mus musculus]	6678555.0	10446.42	548.21

Vav 3 oncogene [Mus musculus]	30931094.0	5071.99	995.83

G-PROTEIN's

	Accession Number	Fc Receptor Complex	Control
G protein			
G protein-coupled receptor, family C, group 2, member A [Mus musculus]	20892429.0	3892.80	852.11
G protein-coupled receptor, family C, group 2, member A, related seque	38086653.0	3984.06	1497.84
G protein pathway suppressor 2 [Mus musculus]	31980980.0	3036.86	0.00
G protein-coupled receptor 4 [Mus musculus]	28316758.0	4926.37	0.00
regulator of G-protein signaling 19 interacting protein 3; PDZ-domain	22507363.0	3260.68	0.00
G protein-coupled receptor 22 [Mus musculus]	30424810.0	3689.49	0.00
G protein-coupled receptor 37-like 1; G protein-coupled receptor 37-lk	30794242.0	3897.75	0.00
G protein-coupled receptor 39 [Mus musculus]	21492622.0	2890.26	720.13
G protein-coupled receptor 124 [Mus musculus]	16905079.0	3164.66	1156.18
G protein-coupled receptor 128 [Mus musculus]	27370236.0	5606.10	371.76
G protein-coupled receptor 135 [Mus musculus]	32306524.0	3459.07	0.00
G protein-coupled receptor 156; GABAB-related G-protein coupled recept	40254201.0	6664.17	33.35
treacle [Mus musculus] metabotropic 6; G protein-co	2145149.0	5115.74	0.00
similar to MrgA4 RF-amide G protein-coupled receptor [Mus musculus]	38086685.0	7951.84	1549.78
G protein-coupled receptor kinase 5 [Mus musculus]	3005012.0	6053.52	1597.12
G protein-coupled receptor kinase 2, groucho gene related; G protein-co	9506749.0	2869.31	0.00
G protein-coupled receptor kinase-interactor 2; ARF GTPase activating	34447227.0	5381.83	654.58
RGSE_MOUSE Regulator of G-protein signaling 14 (RGS14) (RAP1/RAP2 interacting	3914636.0	2510.75	1127.97

TYROSINE PHOSPHATASE's

	Accession Number	Fc Receptor Complex	Control
Tyrosine phosphatase			
protein tyrosine phosphatase, non-receptor type 3 [Mus musculus]	38078421.0	4736.62	1567.93
protein tyrosine phosphatase, non-receptor type 4; testis-enriched prot	9910518.0	5006.98	680.58
protein tyrosine phosphatase, non-receptor type 8; PEST domain-enriched	6679555.0	11231.00	2497.47

protein tyrosine phosphatase, non-receptor type 9; protein-tyrosine pho	9790181.0	3560.06	563.51
protein tyrosine phosphatase, non-receptor type 18 [Mus musculus]	6755236.0	9770.03	276.40
protein tyrosine phosphatase, non-receptor type 21 [Mus musculus]	6755240.0	3987.77	546.88
protein tyrosine phosphatase DPZPTP [Mus musculus]	517125.0	5616.72	1508.72
protein tyrosine phosphatase, receptor-type, F interacting protein, bin	6679435.0	8600.19	2696.09
protein tyrosine phosphatase, receptor type, F; leukocyte antigen-rela	18702313.0	9883.14	1906.53
protein tyrosine phosphatase receptor type N [Mus musculus]	14193733.0	3719.70	1275.99
protein tyrosine phosphatase, receptor type, N polypeptide 2; protein	33859598.0	4514.07	1139.64
similar to protein tyrosine phosphatase, non-receptor type 13 isoform	38075912.0	9049.74	1505.19
similar to protein tyrosine phosphatase, receptor type, Q [Mus musculu	38090755.0	8028.87	840.79
JC5981 prenylated protein tyrosine phosphatase (EC 3.1.3.-) 2 - mouse	7513774.0	5419.20	197.60
LPA2_MOUSE Liprin-alpha 2 (Protein tyrosine phosphatase receptor type f polyp	42558981.0	7460.17	2137.47
similar to receptor-type tyrosine phosphatase [Mus musculus]	38074950.0	6475.58	446.42

ADAPTOR's

14--3--3	**Accession Number**	**Fc Receptor Complex**	**Control**
14-3-3 zeta [Mus musculus] [Mus musculus]	1841387.0	28403.75	279.58
similar to 14-3-3 PROTEIN TAU (14-3-3 PROTEIN THETA) [Mus musculus]	38076709.0	4285.41	175.06
GABA			
gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1; gamma-aminobu	6679919.0	4411.17	1569.95
gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2 [Mus musculu	6679901.0	3261.65	0.00
similar to gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon	38077221.0	4482.26	201.85
similar to Mus musculus (Mouse). GABA-A receptor epsilon-like subunit [D	28850332.0	26339.31	2579.45
similar to GABA-B receptor 2 [Mus musculus] mal	38078306.0	7269.71	1646.67
GAD_MOUSE Gamma-aminobutyric-acid receptor delta subunit precursor (GABA(A) rec	120792.0	3659.92	1578.20

GRB			
Grb10 interacting GYF protein 1 [Mus musculus] us	33943105.0	7213.70	618.28
SH2			
LCP2_MOUSE Lymphocyte cytosolic protein 2 (SH2 domain-containing leucocyte pr	10720066.0	5760.77	0.00
Gprin1 protein [Mus musculus] el SH2-containing pr	34784265.0	3461.17	0.00
JC7278 adaptor protein containing PH and SH2 domains - mouse	11292017.0	13076.82	985.91
SH2 domain containing 3C; novel SH2-containing protein 3; Cas/HEF1-asso	7305329.0	5339.27	0.00
PSM/SH2-B delta [Mus musculus]	15787983.0	3716.12	1111.86
ASH2_MOUSE ASH2-like protein	32141377.0	2581.56	165.27
suppressor of cytokine signaling 1; cytokine inducible SH2-containing p	6753424.0	3251.05	451.68
Shc SH2-domain binding protein 1 [Mus musculus]	6755508.0	7474.49	0.00
SH3			
SH3-binding domain glutamic acid-rich protein like [Mus musculus]	9910548.0	53456.92	855.61
SH3 domain protein D19; SH3 domain containing protein D 19 [Mus musculu	7657564.0	7254.12	939.37
SH3 multiple domains 1; five SH3 domains [Mus musculus]	6679801.0	16536.82	3726.01
SH3/ankyrin domain gene 3; Shank3b protein [Mus musculus]	10946786.0	7273.78	1386.02
SH3 domain-containing adaptor protein METS-1 [Mus musculus]	8131948.0	3280.79	0.00
SH3 domain protein 3 [Mus musculus]	22267440.0	2588.47	379.53
SH3-domain binding protein 5 (BTK-associated) [Mus musculus]	6755498.0	2587.89	163.02
intersectin (SH3 domain protein 1A); intersection (SH3 domain protein 1	6754392.0	4571.63	1753.84
Mus musculus SrcSH3 binding protein, incomplete sequence	1928966.0	2564.47	618.36
signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 [Mus	6755668.0	5281.06	0.00
chromosome X open reading frame 9; likely ortholog of mouse SH3 gene SL	9506363.0	4538.65	0.00
SH32_MOUSE SH3-containing GRB2-like protein 2 (SH3 domain protein 2A) (Endoph	10720274.0	32216.09	1903.27
PDZ			
PDZ domain containing guanine nucleotide exchange factor (GEF) 1 [Mus	38076580.0	14181.01	4380.14
PDZ-domain protein scribble; Scribble; scribble homolog 1 (Drosophila)	20373163.0	8342.85	1797.59
PDZ and LIM domain 3; actinin alpha 2 associated LIM protein [Mus muscu	7948997.0	4331.53	0.00
PDZ domain protein GIPC2; likely ortholog of mouse	41393579.0	3374.15	0.00

semaF cytoplasmic d			
Similar to multiple PDZ domain protein [Mus musculus]	28175159.0	3730.13	1013.39
DOCK			
Dock8 protein [Mus musculus] ypeptide 9 [Mus muscu	37589935.0	2747.03	803.58
DOK1_MOUSE Docking protein 1 (p62(dok)) (Downstream of tyrosine kinase 1)	27805460.0	2854.98	0.00

PHOX PROTEIN's

	Accession Number	Fc Receptor Complex	Control
p67			
methionine aminopeptidase 2; eIF-2-associated p67; initiation factor 2-	9789873.0	3670.38	1321.51
p47			
similar to rat p47 [Mus musculus]	13386036.0	4254.55	1337.62
similar to AP47 protein - mouse [Rattus norvegicus]	34877759.0	2462.92	348.11
P4770	30704925.0	2923.61	0.00

ACTIN's

Actin	Accession Number	Fc Receptor Complex	Control
dJ562N20.1.1 (trabeculin alpha (actin binding protein ABP620) (ortholog	11137614.0	9452.05	1059.11
ADVL_MOUSE Advillin (p92) (Actin-binding protein DOC6)	14547906.0	5282.27	29.87
cytoskeletal actin-modulating protein [Mus musculus]	17222137.0	42725.17	16323.71
similar to KIAA0825 protein [Mus musculus] actin	38075392.0	11085.52	0.00
SWI/SNF related, matrix associated, actin dependent regulator of chroma	7106417.0	8344.55	1166.60
similar to actin, gamma, cytoplasmic [Mus musculus]	38089775.0	32046.32	3344.56
microtubule-actin crosslinking factor 1 [Mus musculus]	25021548.0	25710.24	6998.58
Eno1 protein [Mus musculus] ein 2 (Actin-related p	34784434.0	89548.39	0.00
nexilin; nF actin binding protein [Mus musculus]	41054994.0	8572.32	1368.75
SAC2 (supressor of actin mutations 2, homolog)-like [Mus musculus]	28499084.0	51100.65	214.30
ARP1 actin-related protein 1 homolog B [Mus musculus]	22122615.0	2781.93	374.43
actin-related protein 2; ARP2 (actin-related protein 2,	5031571.0	26207.20	0.00

yeast) homolog			
actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub	5031595.0	19800.19	474.05
ARP8 actin-related protein 8 homolog; actin-related protein 8 homolog	13937369.0	8899.80	455.30
put. beta-actin (aa 27-375) [Mus musculus]	49868.0	3074987.26	850033.95
similar to beta actin [Mus musculus] usculus] X&	38086870.0	87131.81	0.00
actin-like [Mus musculus]	8850209.0	401898.34	29730.87
B25819 actin, fetal skeletal/adult cardiac muscle - mouse (fragment)	90263.0	697183.89	61821.62
FLNB_MOUSE Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP	38257404.0	32979.13	4924.09
profilin 1; actin binding protein [Mus musculus]	6755040.0	466850.53	13772.56
CAPB_MOUSE F-actin capping protein beta subunit (CapZ beta)	1345668.0	15537.88	578.75
capping protein (actin filament), gelsolin-like [Mus musculus]	6680842.0	277641.04	250.79
Coronin, actin binding protein 1A [Mus musculus] g	31418362.0	10780.84	0.00
Shroom-related protein; F-actin-binding protein; likely ortholog of mo	18699722.0	8144.07	2434.42
actin binding protein ShroomS [Mus musculus] attus	6467992.0	13715.15	0.00
A60965 vinculin - mouse (fragment) gene [Mus musculus]	482647.0	5894.72	1211.60

MYOSIN's

	Accession Number	Fc Receptor Complex	Control
Myosin			
erythrocyte protein band 4.1-like 4b; expressed in high-metastatic cell	9506567.0	2436.21	0.00
erythrocyte protein band 4.1-like 1 [Mus musculus]	7305029.0	2792.94	0.00
erythrocyte protein band 4.1-like 3; DAL1P [Mus musculus]	7305031.0	4191.97	1750.48
erythrocyte protein band 4.1 [Mus musculus]	38570129.0	3334.41	1664.78
cofilin 1, non-muscle [Mus musculus]	6680924.0	34424.95	0.00
myosin, heavy polypeptide 3, skeletal muscle, embryonic [Mus musculus]	38091410.0	22636.88	3193.45
myosin, heavy polypeptide 6, cardiac muscle, alpha; myosin heavy chain,	6754774.0	17391.32	2809.33
tropomyosin 1, alpha; alpha tropomyosin [Mus musculus]	31560030.0	58288.56	2617.01
A44131 tropomyosin beta 2 - mouse	346655.0	120061.38	1105.25
S11390 tropomyosin 5 - mouse	111212.0	737865.99	17609.92
MYHB_MOUSE Myosin heavy chain, smooth muscle isoform (SMMHC)	13431676.0	17793.41	2987.77
nonmuscle myosin II-C heavy chain [Mus musculus] g	33638127.0	3126.81	0.00
MY1A_MOUSE Myosin Ia (Brush border myosin I) (BBM-I) (BBMI) (Myosin I heavy c	13431683.0	8468.17	1405.04

myosin 1H [Mus musculus]	29725639.0	3857.57	0.00
keratin complex 1, acidic, gene 23; type I intermediate filament cytok	15431281.0	3880.44	736.81
keratin intermediate filament 16a [Mus musculus] &	11559579.0	155966.04	25853.00
similar to Myosin light chain kinase 2, skeletal/cardiac muscle (MLCK2	38075322.0	13585.55	598.45

DYNEIN's

	Accession Number	Fc Receptor Complex	Control
Dynein			
similar to axonemal dynein heavy chain 7 [Mus musculus]	38075883.0	28113.09	3453.46
similar to axonemal dynein heavy chain 7 [Mus musculus]	38049489.0	5911.22	1532.12
similar to axonemal dynein heavy chain 7 [Mus musculus]	38049491.0	13137.79	2783.05
similar to Dynein intermediate chain 2, axonemal (Axonemal dynein inte	38091940.0	3758.10	1252.30
axonemal dynein heavy chain [Mus musculus] 959370	11991525.0	4253.69	1645.43
similar to axonemal heavy chain dynein type 3 [Mus musculus]	38348574.0	2915.94	590.13
similar to axonemal heavy chain dynein type 3 [Mus musculus]	38087391.0	10813.28	1766.08
dynein, cytoplasmic, intermediate chain 2 [Mus musculus]	6753658.0	4345.54	0.00
1-beta dynein [Mus musculus]	29243996.0	9154.41	3024.99
similar to Dynein heavy chain at 89D CG1842-PA [Mus musculus]	38080759.0	23833.99	4904.75
dynein, axonemal, heavy chain 5; dynein, axon, heavy chain 5; axonemal	20373161.0	30565.33	10864.41
dynein, axonemal, heavy chain 8; dynein, axon, heavy chain 8 [Mus musc	34328061.0	14878.18	3104.45
axonemal dynein heavy chain 8 Dnahc8 [Mus musculus]	13310482.0	26309.14	4168.28
dynein, axonemal, heavy polypeptide 9 [Mus musculus]	38091406.0	29256.48	7589.12
dynein, axonemal, heavy chain 10 [Mus musculus]	38080767.0	4217.46	1305.88
dynein, axonemal, heavy chain 11; situs inversus viscerum; dynein, axon	6753652.0	31116.64	8179.05
dynein, cytoplasmic, heavy chain 1; dynein heavy chain, retrograde tra	13384736.0	36601.91	10833.98
similar to SI:zC220F6.1 (novel protein similar to human dynein heavy c	38084535.0	35097.83	5077.14
similar to dynein, cytoplasmic, heavy chain 2; cytoplasmic dynein heav	38094407.0	2644.67	983.02

Peptides identified by LARC LC-MS/MS were manually correlated to their full length FASTA protein sequence of PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2 (Figure 13). PLC-β_3 was identified by all but one of its 24 different tryptic peptide sequences including the three highest peptides that correlated to the full length sequence where four sequences were overlapping (Figure 13, Panel A). PLC-β_4 was identified by many of the 26 different tryptic peptide sequences including the highest three peptides that correlated to the full length sequence where there were no overlapping sequences (Figure 13, Panel B). PLC-γ_1 was identified by all but two of its 19 different tryptic peptide sequences including the three highest peptides that correlated to the full length sequence where two sequences were overlapping (Figure 13, Panel C). PLC-δ_1 was identified by all but one of its 15 different tryptic peptide sequences including the highest three peptides that correlated to the full length sequence where two sequences were overlapping (Figure 13, Panel D). PLC-ε_1 was identified by all of its 42 different tryptic peptide sequences being correlated to the full length sequence including the three highest peptides with two overlapping sequences (Figure 13, Panel E). PLC like-2 was identified by all but five of its 25 different tryptic peptide sequences including the three highest peptides that correlated to the full length sequence where four sequences were overlapping (Figure 13, Panel F). Identification of these proteins by mass spectrometry assumes to be reliable since they were identified by at least 3 different peptide sequences, confirming their presence at the activated Fc receptor complex identified by LARC.

Figure 13: Correlation of peptides identified by LARC and LC-ESI-MS/MS and searched with SEQUEST to the full length FASTA protein sequence.

Panal A illustrates 23 different peptide sequences identified for PLC-β_3 correlating to the full length protein sequence. Panal B illustrates 11 different peptide sequences identified for PLC-β_4. Panal C illustrates 17 different peptide sequences identified for PLC-γ_1. Panal D illustrates 14 different peptide sequences identified for PLC-δ_1 protein sequence. Panal E illustrates 42 different peptide sequences identified for PLC-ε_1. Panal F illustrates 20 different peptide sequences identified for PLC-like 2. The accession numbers for the FASTA sequences are indicated as they appeared in NCBI. Peptides identified from LARC are highlighted in grey, with the highest scored peptide appearing in blue, second highest scored peptide in purple and the third highest scored peptide in yellow. Overlapping sequences are in red. PH protein domains are indicated in blue. C-terminal domains are indicated in green. EF hand domains are indicated in pink. X and Y catalytic domains are indicated by underlining. SH2 and SH3 domain are indicated in orange (PLC-γ_1) as well as RA and RasGEF domains (PLC-ε_1).

Panel A PLC-β_3
LARC Accession # 31982122.0 NCBI Accession # NP_032900.2

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MAGARPGVHALQLEPPTVVETLRRGSKFIKWDEEASSRNLVTLRVDPNGFFLYWTGPNME
VDTLDISSIRDTRTGRYARLPKDPKIREVLGFGGPDTRLEEKLMTVVAGPDPVNTTFLNF
MAVQDDTVKVWSEELFKLAMNILAQNASRNTFLRKAYTKLKLQVNQDGRIPVKNILKMFS
ADKKRVETALESCGLNFNRVESIRPDEFPLEIFERFLNKLCLRPDIDKILLEIGAKGKPY
LTLEQLMDFINQKQRDPRLNEVLYPPLRSSQARLLIEKYETNKQFLERDQMSMEGFSRYL
GGEENGILPLEALDLSMDMTQPLSAYFINSSHNTYLTAGQLAGPSSVEMYRQALLWGCRC
VELDVWKGRPPEEEPFITHGFTMTTEVPLRDVLEAIAEAAFKTSPYPVILSFENHVDSAK
QQAKMAEYCRSIFGDALLIDPLDKYPLSAGIPLPSPQDLMGRILVKNKKRHRPSTGVPDS
SVRKRPLEQSNSALSESSAATEPSSPQLGSPSSDSCPGLSNGEEVGLEKTSLEPQKSLGE
ESLSREPNVPMPDRDREDEEEDEEEEETTDPKKPTTDEGTASSEVNATEEMSTLVNYVEP
VKFKSFEAARKRNKCFEMSSFVETKAMEQLTKSPMEFVEYNKQQLSRIYPKGTRVDSSNY
MPQLFWNVGCQLVALNFQTLDLPMQLNAGVFEYNGRSGYLLKPEFMRRPDK[redacted]
[redacted]VKVISGQFLSDKKVGIYVEVDMFGLPVDTRRKYRTRTSQGNSFNPVWDEE
PFDFPKVVLPTLASLRIAAFEEGGKFVGHRILPVSAIRSGYHYVCLRNEANQPLCLPALL
IYTEASDYIPDDHQDYAEALINPIKHVSLMDQRAKQLAALIGESEAQASTETYQETPCQQ
PGSQLPSNPTPNPLDASPRWPPGPTTSSTSSSLSSPGQRDDLIASILSEVTPTPLEELRS
HKAMVKLRSRQDRDLRELHKKHQRKAVALTRRLLDGLAQARAEGKCRPSPSALGKATNSE
[redacted]
SGGHLSSADSESQEENTQL
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Panel B PLC-β_4
LARC Accession # 29293803.0 NCBI Accession # NP_038857.1

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MAKPYEFNWQKEVPSFLQEGAVFDRYEEESFVFEPNCLFKVDEFGFFLTWKSEGKEGQVL
ECSLINSIRQAAIPKDPKILAALEAVGKSENDLEGRILCVCSGTDLVNIGFTYMVAENPE
VTKQWVEGLRSIIHNFRANNVSPMTCLKKHWMK[redacted]SITRTFASGKTEK
VIFQALKELGLPSGKNDEIEPAAFTYEKFYELTQKICPRTDIEDLFKKINGDKTDYLTVD
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QLVSFLNEHQR AMQIIEMYEPDEELKK GLISSDGFCRYLMSDE
NAPVFLDR QEMDHPLAHYFISSSHNTYLTGRQFGGKSSVEMYRQVLLAGCRCVELD
CWDGKGEDQEPIITHGKAMCTDILFKDVIQAIKETAFVTSEYPVILSFENHCSKYQQYKM
SKYCEDLFGDLLLKQALESHPLEPGRPLPSPNDLKRKILIKNKRLKPEVEKKQLEALKSM
MEAGESAAPASILEDDNEEEIESADQEEEAHPEYKFGNELSADDYSHKEAVANSVKKTSD
DLEHENNKKGLVTVEDEQAWMASYKYVGATTNIHPYLSTMINYAQPVKFQGFHVAEERNI
HYNMSSFNESVGLGYLKTHAIEFVNYNKRQMSRIYPKGGRVDSSNYMPQIFWNAGCQMVS
LNYQTPDLAMQLNQGKFEYNGSCGYLLKPDFMRRPDRTFDPFSETPVDGVIAATCSVQVI
SGQFLSDKKIGTYVEVDMYGLPTDTIRKEFRTRMVMNNGLNPVYNEESFVFRKVILPDLA
VLRIAVYDDNNKLIGQRILPLDGLQAGYRHISLRNEGNKPLSLPTIFCNIVLKTYVPDGF
GDIVDALSDPKKFLSITEKRADQMRAMGIETSDIADVPSDTSKNDKKGKANPAKANVTPQ
SSSELRPTTTAALGSGQEAKKGIELIPQVRIEDLKQMKAYLKHLKKQQKELNSLKKKHAK
EHSTMQKLHCTQVDKIVAQYDKEKSTHEKILEKAMKKKGGSNCLEIKKETEIKIQTLTTD
HKSKVKEIVAQHTKEWSEMINT

EAEMDRRPATVV

Panel C PLC-γ_1
LARC Accession # 41393059.0 NCBI Accession # NP_067255.2

MAGVATPCANGCGPGAPSEAEVLHLCRSLEVGTVMTLFYSKKSQRPERKTFQVKLETRQI
TWSRGADKIEGSIDIREIKEIRPGKTSRDFDRYQEDPAFRPDQSHCFVILYGMEFKLKTL
SLQATSEDEVNMWIKGLTWLMEDTLQAATPLQIERWLRKQFYSVDRNREDRISAKDLKNM
LSQVNYRVPNMRFLRERLTDLEQRSGDITYGQFAQLYRSLMYSAQKTMDLPFLETNALRT
GERPEHCQVSLSEFQQFLLEYQGELWAVDRLQVQEFMLSFLRDPLREIEEPYFFLDELVT
FLFSKENSVWNSQLDAVCPDTMNNPLSHYWISSSHNTYLTGDQFSSESSLEAYARCLRMG
CRCIELDCWDGPDGMPVIYHGHTLTTKIKFSDVLHTIKEHAFVASEYPVILSIEDHCSIA
QQRNMAQHFRKVLGDTLLTKPVDIAADGLPSPNQLRRKILIKHKKLAEGSAYEEVPTSVM
YSENDISNSIKNGILYLEDPVNHEWYPHYFVLTSSKIYYSEETSSDQGNEDEEEPKEASS
STELHSSEKWFHGKLGAGRDGRHIAERLLTEYCIETGAPDGSFLVRESETFVGDYTLSFW
RNGKVQHCRIHSRQDAGTPKFFLTDNLVFDSLYDLITHYQQVPLRCNEFEMRLSEPVPQT
NAHESKEWYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAISFRAEGKIKHCRVQQE
GQTVMLGNSEFDSLVDLISYYEKHPLYRKMKLRYPINEEALEKIGTAEPDYGALYEGRNP
GFYVEANPMPTFKCAVKALFDYKAQREDELTFTKSAIIQNVEKQDGGWWRGDYGGKKQLW
FPSNYVEEMINPAVLEPEREHLDENSPLGDLLRGVLDVPACQIAIRPEGKNNRLFVFSIS
MPSVAQWSLDVAADSQEELQDWVKKIREVAQTADARLTEGKMMERRKKIALELSELVVYC
RPVPFDEEKIGTERACYRDMSSFPETKAEKYVNKAKGKKFLQYNRLQLSRIYPKGQRLDS
SNYDPLPMWICGSQLVALNFQTPDKPMQMNQALFMAGGHCGYVLQPSTMRDEAFDPFDKS
SLRGLEPCVIC

NNYSEDL
ELASLLIK PAKENGDLSPFSGISLRERASDASSQLFHVRAREGSFEARYQQPFEDF
RISQEHLADHFDSRERSTSDGPSSATNLIEDPLHDKLWKCSL

Panel D PLC-δ_1
LARC Accession # 9790167.0 NCBI Accession # NP_062650.1

MDSGRDFLTLHGLQDDPDLQALLKGSQLLKVKSSSWRRERFYKLQEDCKTIWQESRKVMR
SPESQLFSIEDIQEVRMGHRTEGLEKFARDIPEDRCFSIVFKDQRNTLDLIAPSPADVQH
WVQGLRKIIDRSGSMDQRQKLQHWIHSCLRKADKNKDNKMNFKEVKDFLKELNVQVDDSY
ARKIFRECDHSQTDSLEDEEIETFYRMLTQRAEIDRAFAEAAGSAETLSVEKLVTFLQHQ
QREEEAGPALALSLIERYEPSETAKAQRQMTKDGFLMYLLSADGNAFSLAHRRVYQDMNQ
PLSHYLVSSSHNTYLLEDQLTGPSSTEAYIRALCKGCRCLELDCWDGPNQEPIIYHGYTF
TSKILFCDVLRAIRDYAFKASPYPVILSLENHCSLEQQRVMAHHLRAILGPMLLDQPLDG

VTTSLPSPEQLKEKILLKGKKLGGLLPAGGENGPEATDVSDEDEAAEMEDEAVRSQVQHK
PKEDKLKLVPELSDMVIYCKSVHFGGFSSPSTSGQAFYEMASFSESRALRLLQESGNSFV
RHNVGHLSRIYPAGWRTDSSNYSPVEMWNGGCQIVALNFQTPGPEMDVYLGCFQDNGGCG
YVLKPAFLRDPDTTFNSRALTQGPWWAPK

NGDLHPSATLFVKISIQD

Panel E PLC-ε_1
LARC Accession # 23956100.0 NCBI Accession # NP_062534.2

MTSEEMAASVLIPVTQRKVASAQSVAEERSVKVSDAGIPRARAGRQGALIPPTISQWNKH
KEESSRSDLSKVFSIARGELVCDENSNEEGWEENAPDSPENHAMNGNSLVQSHQHQFPRS
QLCEARDSVTEDPCLQPGIPSPLERKVLPGIQLEMEDSPMDVSPAGSQPRIMESSGPHSD
RNTAVFHFHYEADRTMSDAFHTLSENLILDDCANCVTLPGGQQNKNCMAYACKLVELTRT
CGSKNGQVQCEHCTSLRDEYLCFESSCSKADEVCSGGGFCEDGFAHGPAAKTFLNPLEDF
SDNCEDVDDFFKSKKERSTLLVRRFCKNDREVKKSVYTGTRAIMRTLPSGCIGPAAWNYV
DQKKAGEIWPCGNVWCTLSAMDLQSGSQRLSEAQWCLIYSAVRRGEEIEDTVGSLLHCS
TQLPNSETAHGRIEDGPCLKQCVRDTECEFRATLQRTSIAQYITGSLLEATTSLGARSGL
LSSFGGSTGRIMLKERQLGTSMANSNPVPSSSAGISKELIDLQPLIQFPEEVASILTEQE
QNIYRRVLPMDYLCFLTRDLSSPECQRSLPRLKASISESILTSQSGEHNALEDLVMRFNE
VSSWVTWLILTAGSMEEKREVFSYLVHVAKCCWNMGNYNAVMEFLAGLRSRKVLKMWQFM
DQSDIETMRSLKDAMAQHESSVEYKKVVTRALHIPGCKVVPFCGVFLKELCEVLDGASGL
LKLCPRYSSQEEALEFVADYSGQDNFLQRVGQNGLKNSEKELTVNSIFQVIRSCSRSLEM
EEEDSASEGSGSRKNSLKDKARWQFIIGDLLDSENDIFEKSKECDPHGSEESQKAFDHGT
ELIPWYVLSIQADVHQFLLQGATVIHYDQDTHLSARCFLQLQPDNSTLTWMKPPTASPAG
ARPKLGVLSNMAEPGKFPSPGNAGVSGLAEGILDLFSVKAVYMGHPGIDIHTVCVQNKLS
SMLLSETGVTLLYGLQTTDNRLLHFVAPKHTAEMLFSGLLELTTAVRKIRRFPDQRQQWL
RKQYVSLYQEDGRYEGPTLAHAVELFGGRRWSTRNPSPGMSAKNAEKPNMQRNNTLGIST
TKKKKKMLMRGESGEVTDDEMATRKAKMYRECRSRSGSDPQDVNEQEESEANVITNPPNP
LHSRRAYSLTTAGSPNLATGMSSPISAWSSSSWHGRIRGGMQGFQSFMVSDSNMSFVEFV
ELFKSFSIRSRKDLKDIFDIYSVPCNRSASESAPLYTNLTIEENTSDLQPDLDLLTRNVS
DLGLFIKSKQQLSDNQRQISDAIAAASIVTNGIGIESTSLGIFGVGILQLNDFLVNCQGE
HCTYDEIISIIQKFEPSVSMCHQGLLSFEGFARFLMDKDNFASKNDESRENKKELQLPLS
YYYIESSHNTYLTGHQLKGESSVELYSQVLLQGCRSIELDCWDGDDGMPIIYHGHTLTTK
IPFKEVVEAIDRSAFITSDLPIIISIENHCSLPQQRKMAEIFKSVFGEKLVAKFLFETDF
SDDPMLPSPDQLRRKVLLKNKKLKAHQTPVDILKQKAHQLASMQAQAFTGGNANPPPASN
EEEEDEEDEYDYDYESLSDDNILEDRPENKSCADKLQFEYNEEVPKRIKKADNSSGNKGK
VYDMELGEEFYLPQNKKESRQIAPELSDLVIYCQAVKFPGLSTLNSSGSSRGKERKSRKS
IFGNNPGRMSPGETAPFNRTSGKGSCEGMRHTWEESSPLSPSTSLSAIIRTPKCYHISSL
NENAAKRLCRRGSQKLIQHTAYQLLRTYPAATRIDSSNPNPIMFWLHGIQLVALNYQTDD
LPLHLNAAMFEANGGCGYVLKPPVLWDKSCPMYQKFSPLERDLDNLDPAIYSL

NSRRMEENPSGSSMPAS
LMFNTEERKCSQTHKVTVHGVPGPEPFAVFTINEGTKAKQLLQQVLAVDQDTKCTATDYF
LMEEKHFISKEKNECRKQPFQRAVGPEEDIVQILNSWFPEEGYVGRIVLKPQQETLEEKS
IVFDDKEVILSSEEESFFVQVHDVSPEQPRTVIKAPRVSTAQDVIQQTLCKAKYSYSILN
NPNPCDYVLLEEVLKDAANKKSSTPKSSQRILLDQECVFQAQSKWKGAGKFILKLKEQVQ
ASREDKRRGISFASELKKLTKSTKQSRGLPSPPQLVASESVQSKEEKPVGALSSSDTVGY
QQ

PANEL F PLC like-2
LARC Accession # 38082546.0 NCBI Accession # NP_038908.2

MAECGRGAAGGALPTSPSPALGAKGALKAGAGEGGGGGGGGRLGHGR[redacted]
[redacted]TSPGRGPLGVALARTPSPAAGPVPRDSKPGGLPRRSSIIKDGTKQKRERK
KTVSFSSMPTEKKISSASDCIHSMVEGSELKKVRSNSRIYHRYFLLDADMQSLRWEPSKK
DSEKAKIDIKSIKEVRTGKNTDIFRSNGISEQISEDCAFSVIYGENYESLDLVANSADVA
NIWVTGLRYLISYGKHTLDMLESSQDNMRTSWISQMFSEIDVDGLGHITLCHAVQCIRNL
NPGLKTSKIELKFKELHK[redacted]KEEFIEVFHELRTRPEIYFLLVQFSSNK[redacted]
[redacted]QDMKQPLSHYFINSSHNTYLIEDQFRGPSDITGYIRALKMGCRSVELDVWDGPD
NEPVVYTGHTMTSQIVFRSVIDIINKYAFFASEYPLILCLENHCSIKQQKVMVQHMKKIL
GDKLYTTSPNMEESYLPSPDVLKGKILIKAKKLSSNCSGVEGDVTDEDEGAEMSQRMGKE
NVEQPNHVPVKRFQLCKELSELVSICKSVQFKEFQVSFQVQKYWEVCSFNEVLASKYANE
NPGDFVNYNKRFLARVFPSPMRIDSSNMNPQDFWKCGCQIVAMNFQTPGLMMDLNVGWFR
QNGNCGYVLRPAIMREEVSFFSANTKDSVPGVSPQL

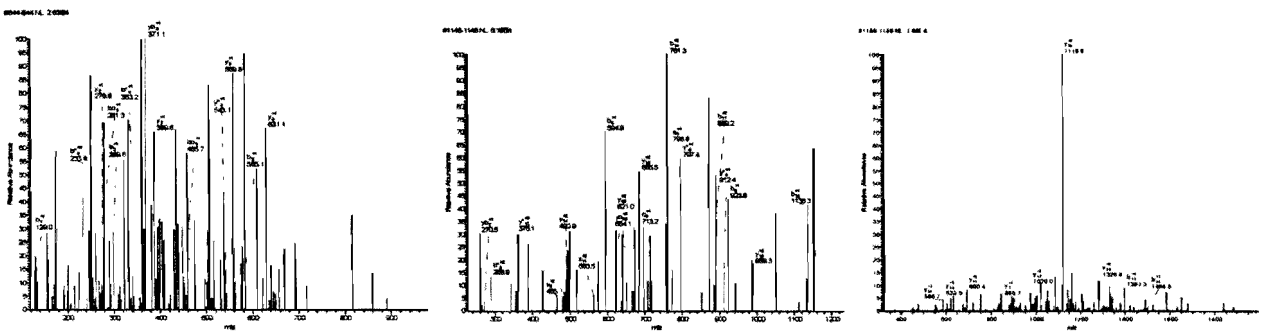
NRRGGGKPHKRGLSVRKG
KKSREYASLRTLWIKTVDEVFKNAQPPIRDATDLRENMQNAVVSFKELCGLSSVANLMQC
MLAVSPRFLGPDNNPLVVLNLSEPYPTMELQAIVPEVLKKIVTTYDMMMQSLKALIENAD
AVYEKIVHCQKAAMEFHEHLHSIGTKEGLKERKLQKAVESFTWNITILKGQADLLKYAKN
ETLENLKQIHFAAVSCGLNKPGTENSEAQKPRRSLEAIPEKASDENGD

Mass spectra of the PLC isoforms were gathered and were deemed good quality spectra. The PLC spectra of PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC-L_2 (Figure 14) show good mass accuracy (approximately within 0.2 *m/z*) and resolution. This allows for the observation of both the 2+ and 3+ charge states of the peptides, as well as the 1+ charge state. LC-MS/MS spectra from the LARC experiment for PLC-β_3 shows the 2+ peptide KAVALTR (MH+ 758.93), 3+ peptide SFDPFTEVIVDGIVANALR (MH+ 2064.33) and 3+ peptide ILLEIGAKGKPYLTLEQLMDFINQK (MH+ 2877.44) with correlating b and y series ions (Figure 14, Panel A). The fragmentation spectra of PLC-β_4 show the 3+ peptide QWVEGLRSIIHNFRANNVSPMTCLK (MH+ 2915.39), 3+ peptide LAFLTNTTGKIPVR (MH+ 1531.83) and 3+ peptide GLISSDGFCRYLMSDEANAPVFLDR (MH+ 2707.04) with correlating b and y series ions (Figure 14, Panel B). The fragmentation spectra for PLC-γ_1 show the 2+ peptide HPLYRK (MH+ 813.97), 3+ peptide PDQSHCFVILYGMEFR (MH+ 1943.24) and 2+ peptide NPGFYVEANPMPTFK (MH+ 1712.95) with correlating b and y series ions (Figure 14, Panel C). Spectra for PLC-δ_1 show the 3+ peptide MNFKEVKDFLK (MH+ 1399.68), 1+ peptide NGDLHPSATLFVKISIQD (MH+ 1956.19), and 2+ peptide HNVGHLSRIYPAGWR (MH+ 1763.99) with correlating b and y series ions (Figure 14, Panel D). Fragmentation spectra for PLC-ε_1 show the 3+ peptide KESRQIAPELSDLVIYCQAVK (MH+ 2391.77), 3+ peptide KAGLLWPCGNVMGTLSAMDIR (MH+ 2234.70) and 3+ peptide EEKPVGALSSSDTVGYQQ (MH+ 1896.00) with correlating b and y series ions (Figure 14, Panel E). Lastly, spectra for PLC-L_2 show the 2+ peptide GAAGGALPTSPSPALGAKGALK (MH+ 1893.18), 3+ peptide ARYDSGGVSNGSCSLGVSGDEAR (MH+ 2273.34) and 2+ peptide GAAGGALPTSPSPALGAK (MH+ 1523.72) with correlating b and y series ions (Figure 14, Panel F).

Figure 14: Tandem mass spectra of Phospholipase C isoforms specifically associated with the Fc receptor determined from the method of LARC.

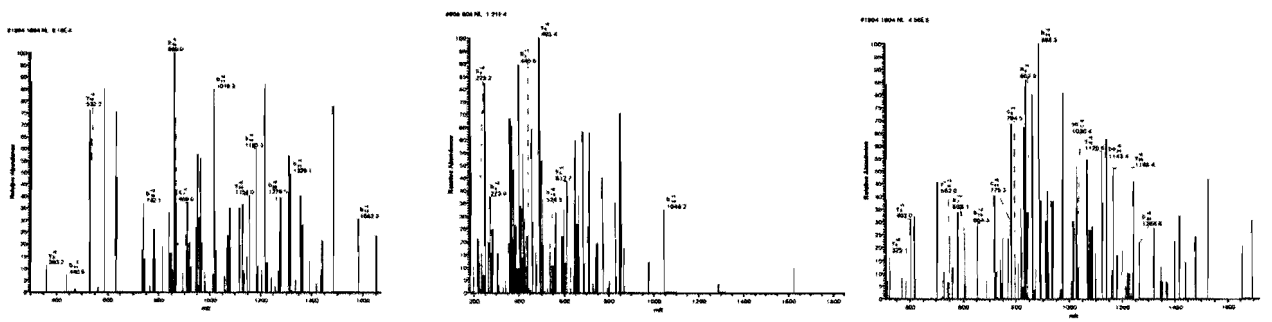
Peptide sequences for PLC-β_3 (Panel A), PLC-β_4 (Panel B), PLC-γ_1 (Panel C), PLC-δ_1 (Panel D), PLC-ε_1 (Panel E) and PLC-L_2 (Panel F) at 1+, 2+ or 3+ charge states. The fragmentation spectra were obtained from LC-MS/MS in conjunction with the SEQUEST algorithm.

Panel A PLC-β_3



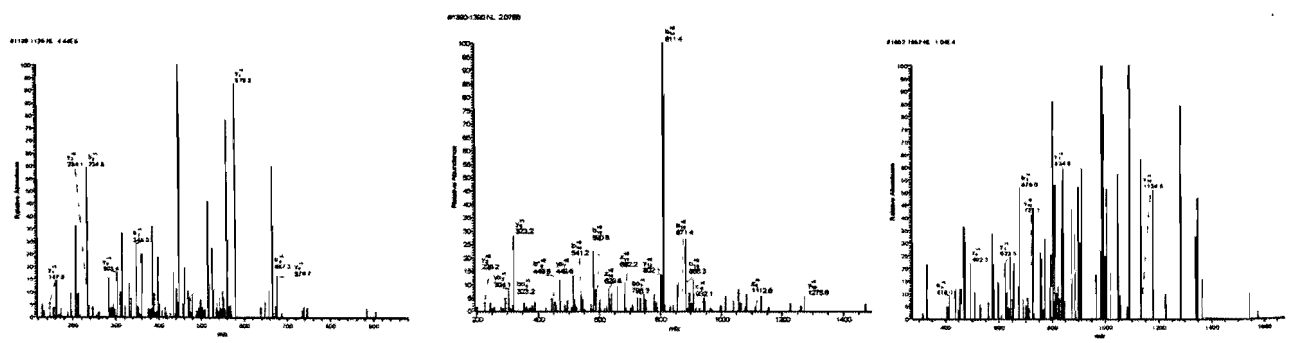
2+ -.KAVALTR.- 3+ -.SFDPFTEVIVDGIVANALR.- 3+ -.ILLEIGAKGKPYLTEQLMDFINQK.-

Panel B PLC-β_4



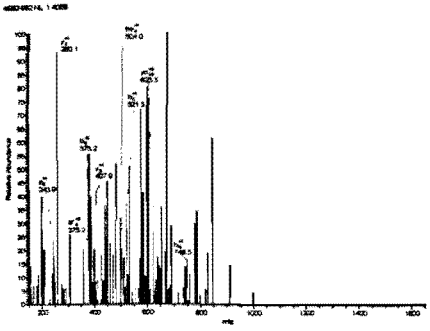
3+ -.KWVEGFRSIIHNFRANNVSPMTCLK.- 3+ -.LAFLTNTTGKIPVR.- 3+ -.FLISSDGFCRYLMSDENAPVFLDR.-

Panel C PLC-γ_1

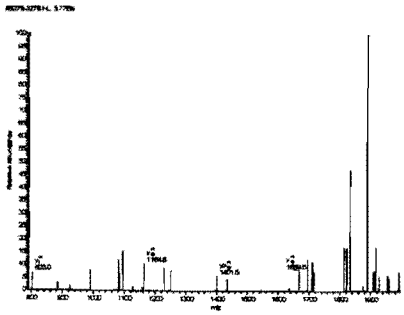


2+ -.HPLYRK.- 3+ -.PDQSHCFVILYGMEFR.- 2+ -.NPGFYVEANPMPTFK.-

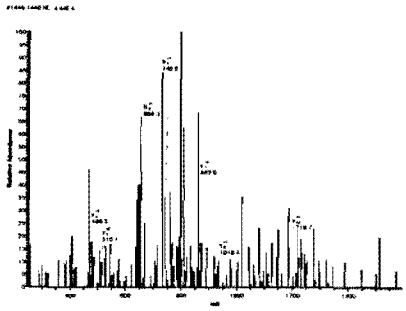
Panel D **PLC-δ_1**



3+ -.MNFKEVKDFLK.-

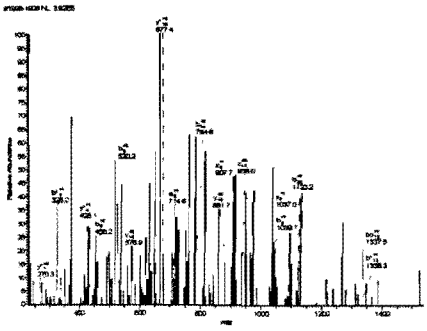


1+ -.NGDLHPSATLFVKISIQD.-

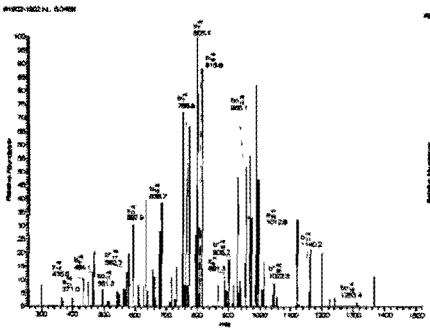


2+ -.HNVGHLSRIYPAGWR.-

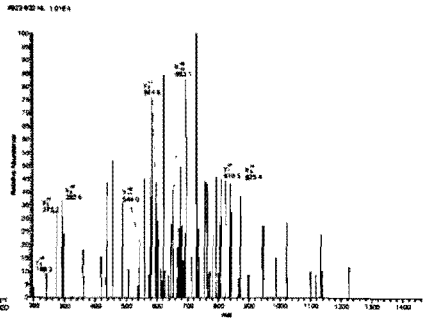
Panel E **PLC-ε_1**



3+ -.KESRQIAPELSDLVIYCQAVK.-

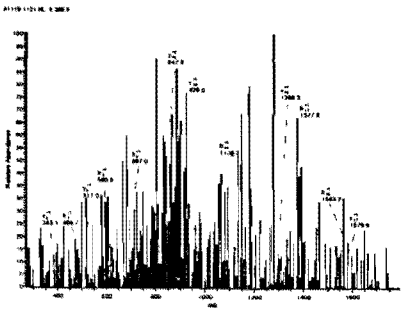


3+ -.KAGLLWPCGNVMGTLSAMDIR.-

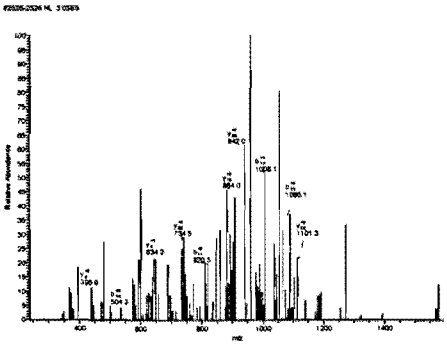


3+ -.EEKPVGALSSSDTVGYQQ.-

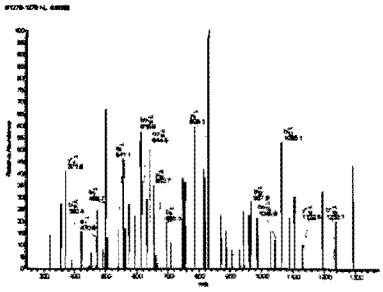
Panel F **PLC-L_2**



2+ -.GAAGGALPTSPSPALGAKGALK.-



3+ -.ARYDSGGVSNGDCSLGVSGDEAR.-



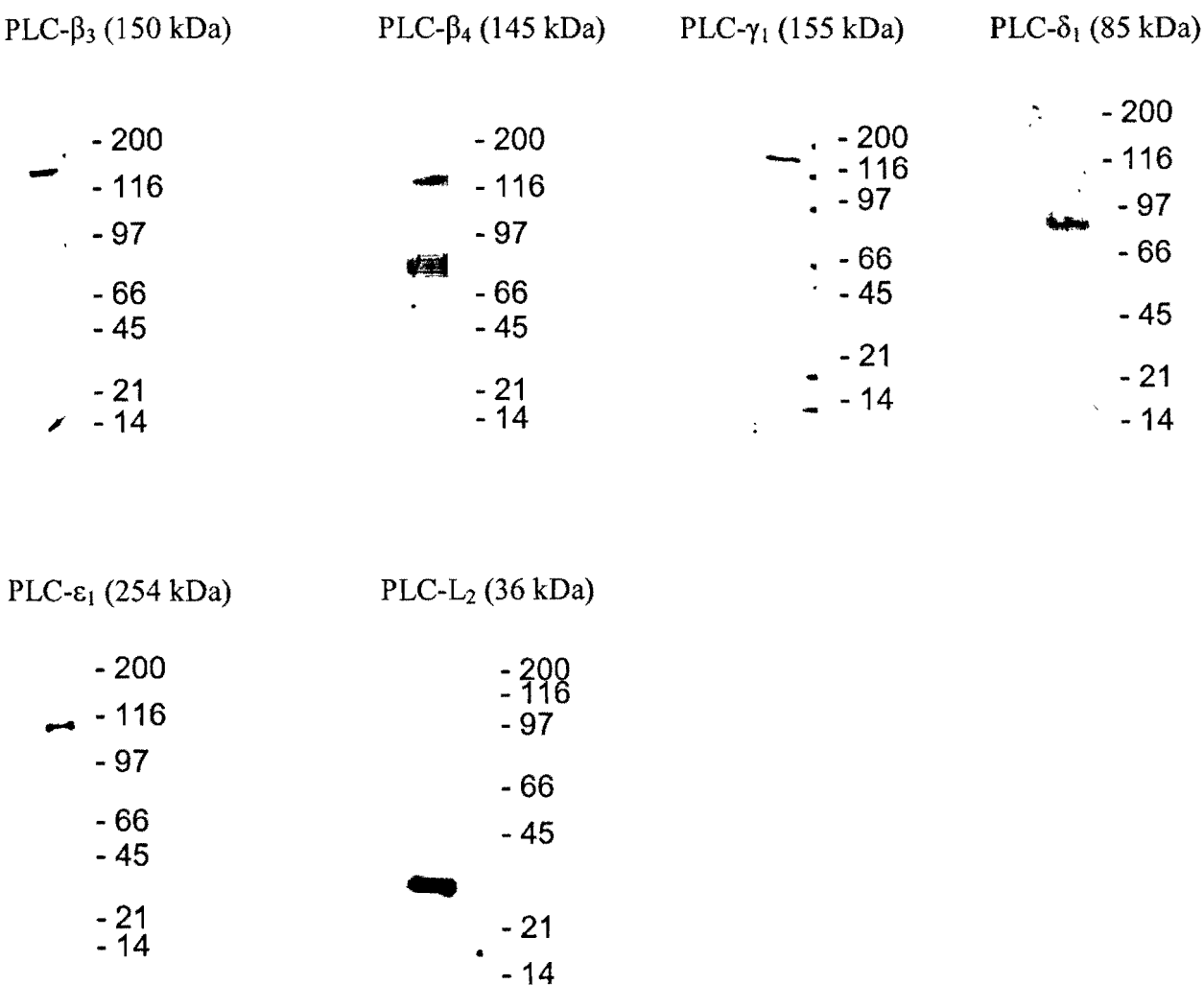
2+ -.GAAGGALPTSPSPALGAK.-

Western Blot confirmation of proteins

Phospholipase proteins PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC-L_2 were confirmed to be present in RAW 264.7 cell lines by Western Blot (Figure 15). A lone band was seen at approximately 150kDa for the blot incubated with PLC-β_3 rabbit polyclonal antibody, signifying the presence of PLC-β_3 in the macrophage cell lysate. The blot incubated with rabbit polyclonal antibody PLC-β_4 had a band at approximately 145 kDa, as well as a band at approximately 85 kDa. The second band can be attributed to the secondary antibody, as a band at this weight was sometimes observed. The detection of a lone band at approximately 155 kDa shows the presence of the PLC-γ_1 protein in the macrophage cell lysate, at the expected size. The band for the PLC-δ_1 protein appeared at 85 kDa at the appropriate position, signifying that the protein is present in the cell lysate. The detection of PLC-ε_1, a protein of 254 kDa, was a faint band at approximately 254 kDa. A stronger band is seen at approximately 116 kDa, however this band can be attributed to the secondary antibody since a band of that weight was sometimes observed (Figure 15). The band for PLC-L_2 mouse monoclonal antibody is strong band located at approximately 36 kDa, implying that the protein is present within the RAW macrophage cell lysates.

Figure 15: Western blots of Phospholipase C isoforms in RAW 264.7 cell lysates specifically associated with the Fc receptor determined from the method of LARC.

Cells were boiled in SDS-PAGE in the presence of eukaryotic anti-protease cocktail before being presented with 1 μL of each PLC isoform. Blotting was completed using goat anti rabbit HRP conjugated secondary (PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1), donkey anti goat HRP (PLC-ε_1) or goat anti mouse HRP (PLC-L_2) followed by detection with ECL.



Immunostaining with confocal microscopy confirmation

The localization of PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC-L_2 to the IgG bound particle of cell was observed by fixing the cells at various time intervals (5 min, 7.5 min and 10 min) followed by immunostaining with rabbit polyclonal anti-PLC-β_3, anti-PLC-β_4, anti-PLC-γ_1 and anti-PLC-δ_1 as well as goat polyclonal anti-PLC-ε_1 and mouse monoclonal anti-PLC-L_2 followed by detection using Cy-3 secondary antibody and visualization with laser confocal microscopy.

The accumulation of rabbit anti-PLC-β_3 was clearly seen at all time intervals monitored. At 5, 7.5 and 10 minutes, PLC-β_3 protein accumulation was noted at the site of IgG-opsonized particle binding, demonstrated by the increase in fluorescence around the bead (Figure 16, Panel A).

The accumulation of rabbit anti-PLC-β_4 displayed similar results to rabbit anti-PLC-β_3 at all time intervals monitored. At 5, 7.5 and 10 minutes, accumulation of PLC-β_4 protein was seen as an increase in fluorescence around the bead that was attached to the Fc receptor (Figure 16, Panel B).

The accumulation of rabbit anti-PLC-γ_1 displayed similar results to those described above all time intervals. At 5, 7.5 and 10 minutes, PLC-γ_1 protein accumulation was noted around the bead at the site of IgG-opsonized particle binding, represented by an increase in fluorescence (Figure 16, Panel C).

PLC-δ_1 protein for the rabbit anti- PLC-δ_1 showed similar results to both the beta and gamma isoforms. At 5, 7.5 and 10 minutes, PLC-δ_1 protein accumulation was marked around the bead, represented as a slight increase in fluorescence (Figure 16, Panel D).

To confirm that the cell staining and fluorescence of the secondary antibody was specific for the primary antibody, control cells were incubated with cells that were opsonised with IgG, fixed and stained with only the donkey anti-rabbit Cy-3 fluorescent secondary antibody. Images were taken at the same settings as those stained with the primary antibody and secondary antibodies. The control slide for the donkey anti-rabbit Cy-3 displays no non-specific binding; therefore there was no fluorescence at the bead for both PLC-β_3 and PLC-β_4, signifying that the signal obtained for these reactions is the true signal of the protein. The images taken for the control cells at the PLC-γ_1 and PLC-δ_1 settings displayed minimal fluorescence at the bead, as well as throughout the entire cell. The fluorescence around the bead in the PLC-γ_1 cells was slightly more intense than that of the rest of the cell. The fluorescence throughout the cell for PLC-δ_1 was present, however at a lower intensity compared to the cells with the primary antibody present.

The accumulation of fluorescence was clearly seen for goat anti-PLC-ε_1 at all time intervals. At 5, 7.5 and 10 minutes, PLC-ε_1 protein accumulation at the site of IgG-opsonized particle binding was visualized by an increase in fluorescence around the bead that is attached to the Fc receptor at the site of phagocytosis (Figure 16, Panel E).

To again confirm that the fluorescence of cell staining of the secondary antibody was specific for the primary antibody, control cells were incubated as previously mentioned stained with only the donkey anti-goat Cy-3 fluorescent secondary antibody. Images were taken as stated above. The control slide for the donkey anti-goat Cy-3 displays no non-specific binding, no fluorescence at the bead signifying the signal obtained for PLC-ε_1 is the true signal of the protein.

Accumulation of fluorescence was observed for mouse anti-PLC like-2 at all time intervals. At 5, 7.5 and 10 minutes, PLC like-2 protein was noted by the increase in fluorescence around the bead at the site of IgG-opsonized particle binding (Figure 16, Panel F).

To confirm that the cell staining and fluorescence of the secondary antibody was specific for the primary antibody control cells were incubated, as previously mentioned, stained with only the donkey anti-mouse Cy-3 fluorescent secondary antibody and images were taken as stated above. The donkey anti-mouse Cy-3 control displayed no non-specific binding, no fluorescence at the bead signifying the signal obtained for PLC like-2 is the true signal of the protein.

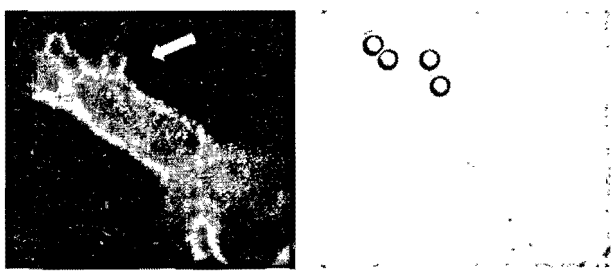
Figure 16: Immunostaining of PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC-L_2 of RAW 264.7 macrophages

Cells were grown in 6-well plates on glass coverslips for 24 to 48 hours in DMEM and then exposed to IgG-opsonized beads for 5, 7.5 and 10 minute intervals. Cells were washed, fixed and stained with 1 μL of primary PLC antibody followed by Cy-3 conjugated fluorescent secondary antibody. Control images exhibit cells only stained with Cy-3 secondary antibody and illustrate non-specific binding. Images below illustrate the localization and accumulation of rabbit anti-PLC-β_3 (Panel A), anti-PLC-β_4 (Panel B), anti-PLC-γ_1 (Panel C) and anti-PLC-δ_1 (Panel D) as well as goat anti-PLC-ε_1 (Panel E) and mouse anti-PLC-L_2 (Panel F). Protein accumulation at the site of cup formation is indicated by arrows. Images are displayed with the rhodamine (red) light channel and the while light channel.

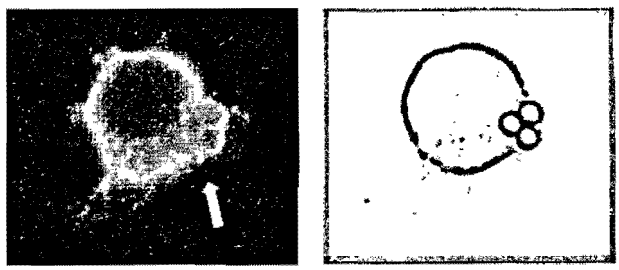
Panel A PLC-β_3

Localization and accumulation of rabbit anti-PLC-β_3 in RAW 264.7 macrophage cells.

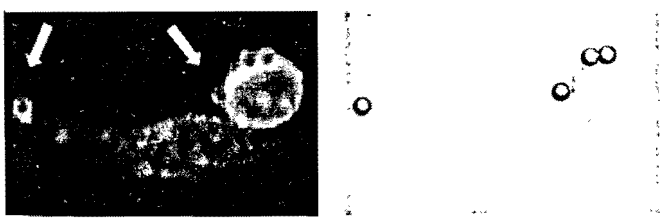
5 minutes



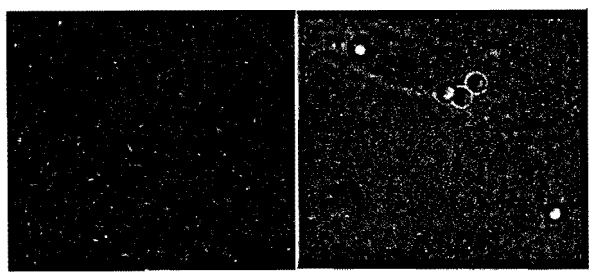
7.5 minutes



10 minutes



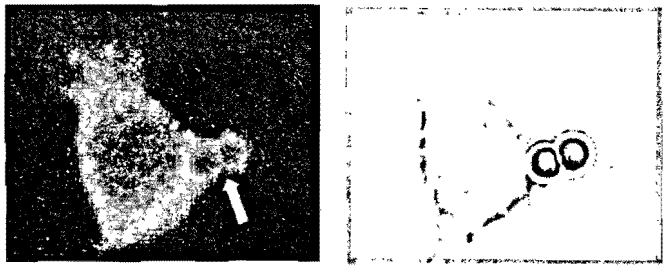
Cy-3 secondary donkey anti rabbit



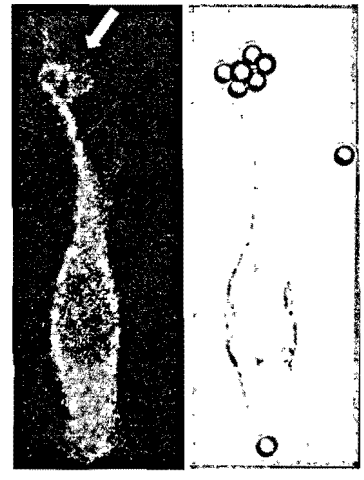
Panel B **PLC-β_4**

Localization and accumulation of rabbit anti-PLC-β_4 in RAW 264.7 macrophage cells.

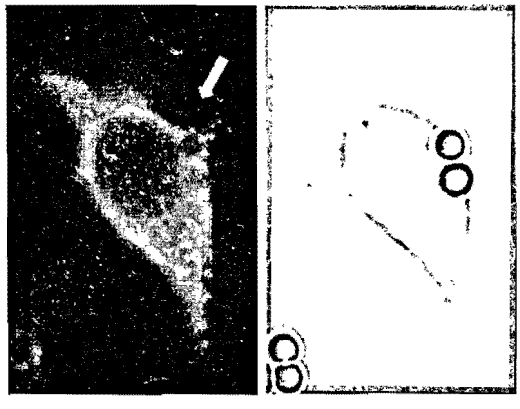
5 minutes



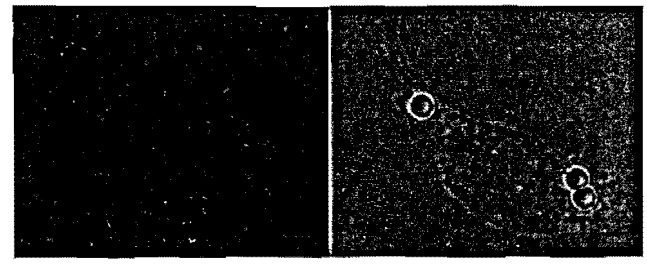
7.5 minutes



10 minutes



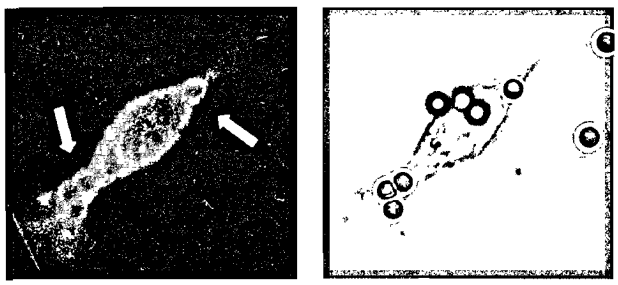
Cy-3 secondary donkey anti rabbit



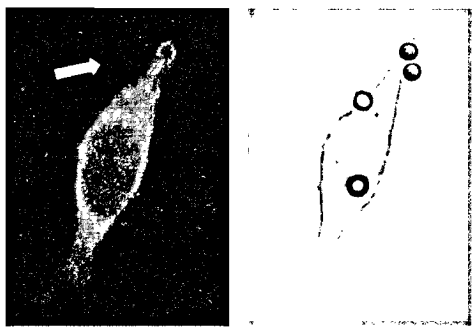
Panel C **PLC-γ_1**

Localization and accumulation of rabbit anti-PLC-γ_1 in RAW 264.7 macrophage cells.

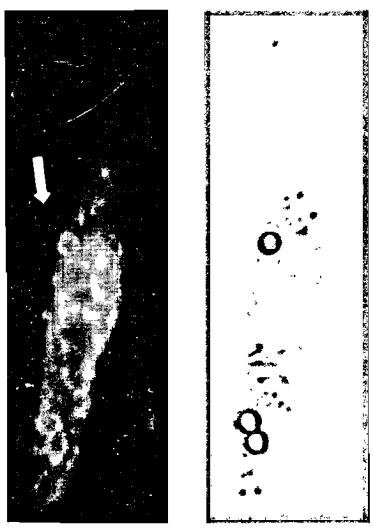
5 minutes



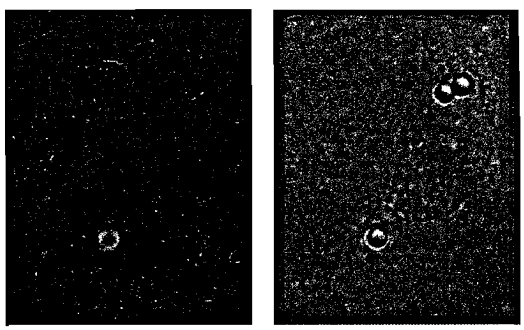
7.5 minutes



10 minutes



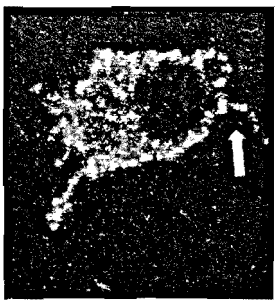
Cy-3 secondary donkey anti rabbit



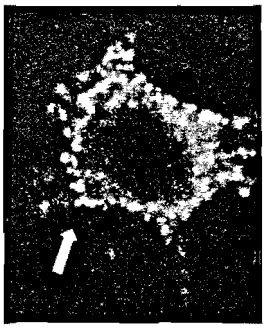
Panel D **PLC-δ_1**

Localization and accumulation of rabbit anti-PLC-δ_1 in RAW 264.7 macrophage cells.

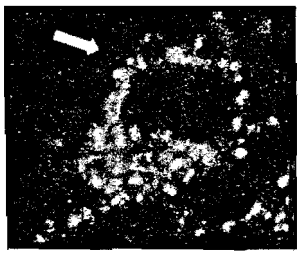
5 minutes

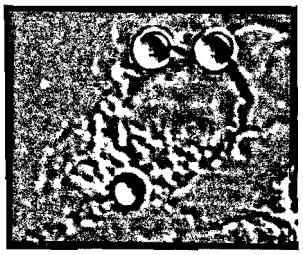


7.5 minutes

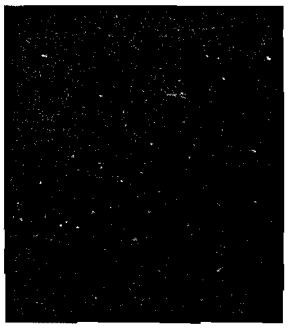


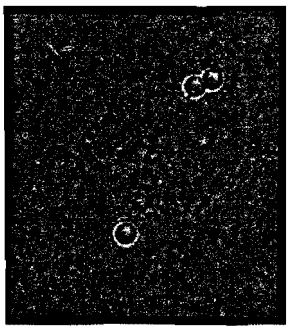
10 minutes





Cy-3 secondary donkey anti rabbit

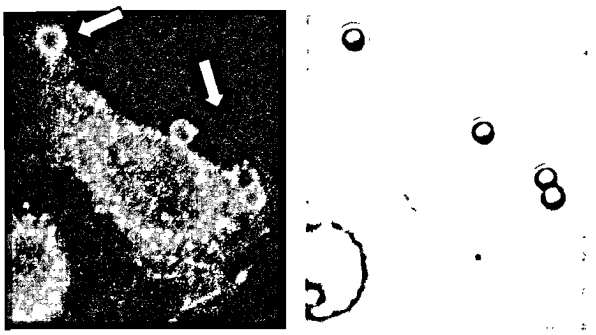




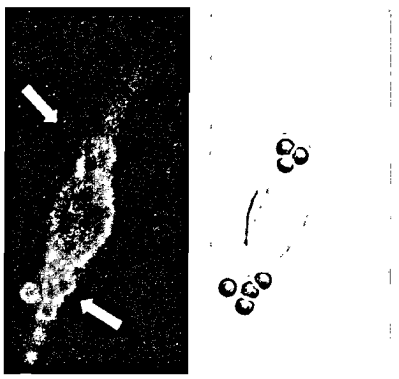
Panel E **PLC-ε_1**

Localization and accumulation of goat anti-PLC-ε_1 in RAW 2647 macrophage cells.

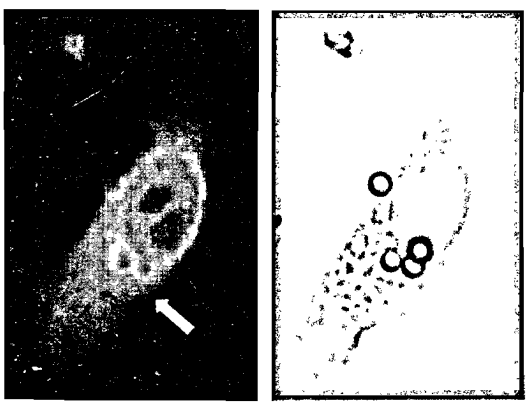
5 minutes



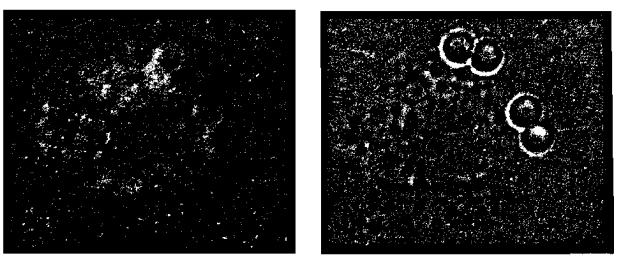
7.5 minutes



10 minutes



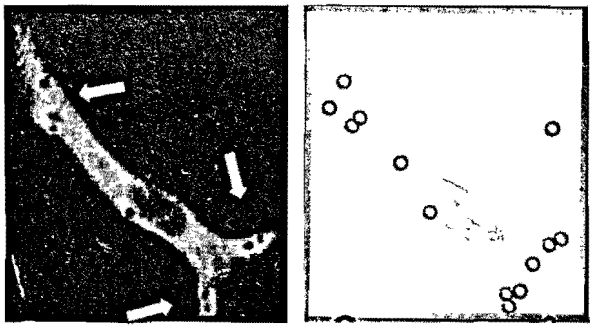
Cy-3 secondary donkey anti goat



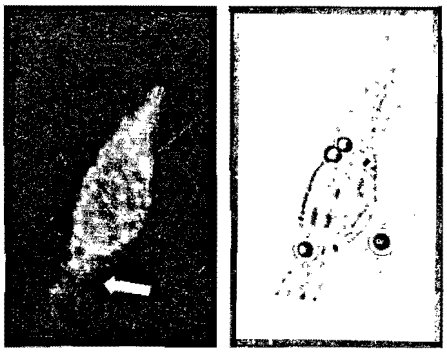
Panel F **PLC-L_2**

Localization and accumulation of mouse anti-PLC-L_2 in RAW 2647 macrophage cells.

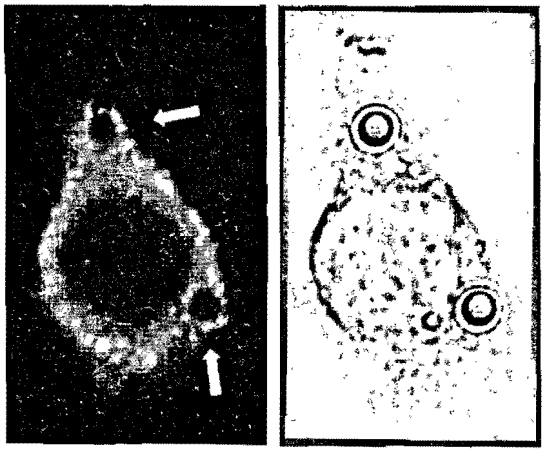
5 minutes



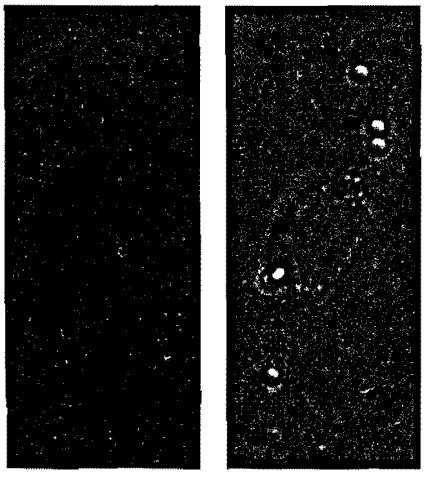
7.5 minutes



10 minutes



Cy-3 secondary donkey anti mouse



Transfected fusion protein with confocal microscopy confirmation

The accumulation of PLC-β_3, PLC-β_4, PLC-γ_1 and PLC-$\delta_1$was also studied in stimulated RAW macrophages using transfections of fusion proteins linked to GFP. Live-cell confocal microscopy was used to visualize the cells that were transfected with GFP-tagged PLC-β_3, GFP-tagged PLC-β_4, GFP-tagged PLC-γ_1 and GFP-tagged PLC-δ_1. The localization of the protein at the plasma membrane where the Fc receptor is activated was monitored by inducing phagocytosis with sheep's red blood cells (SRBC).

Cells transfected with PLC-β_3 linked to GFP displayed fluorescence throughout the cytoplasm of the cell and the plasma membrane with a slight increase in intensity, but not in the nucleus (Figure 17, Panel A). A slight increase in intensity of fluorescence near the SRBC at the formation of the phagocytic cup can also be seen. The line scan of the cell displays consistent fluorescence intensity within the cell with where no SRCB is present, a decrease of intensity in the nucleus of the cell, and an increase at the plasma membrane near the SRBC. Additional images of PLC-β_3 linked to GFP can be seen in Appendix M, Panel A.

Cells transfected with GFP that was linked with PLC-β_4 linked illustrated fluorescence in the nucleus of the cell as well as fluorescence throughout the cytoplasm and equally at the plasma membrane (Figure 17, Panel B). Even through there is fluorescence throughout the entire cell, there is an increase in fluorescence intensity at the phagocytis cup around the SRBC. The line scan of the cell where no SRBC was present shows consistant fluorescence intensity within the cell, with an increase in intensity body of the cell near the nucleus, a decrease of intensity in the nucleus and an increase at the plasma membrane near the SRBC. Additional images of PLC-β_4 linked to GFP can be seen in Appendix M, Panel B.

PLC-γ_1 transfected cells linked to GFP displayed a similar fluorescence pattern to PLC-β_4 with consistent fluorescence throughout the cytoplasm and plasma membrane, but not in the nucleus (Figure 17, Panel C). There was also an increase in intensity of fluorescence at the formation of the phagocytic cup around the SRBC. The consistent fluorescence within the cell (although minimal) is confirmed by a consistent intensity of the line scan where no SRCB is present, followed by an intensity decrease in the nucleus of the cell, and an increase near the SRBC. Additional images of PLC-γ_1 linked to GFP can be seen in Appendix M, Panel C.

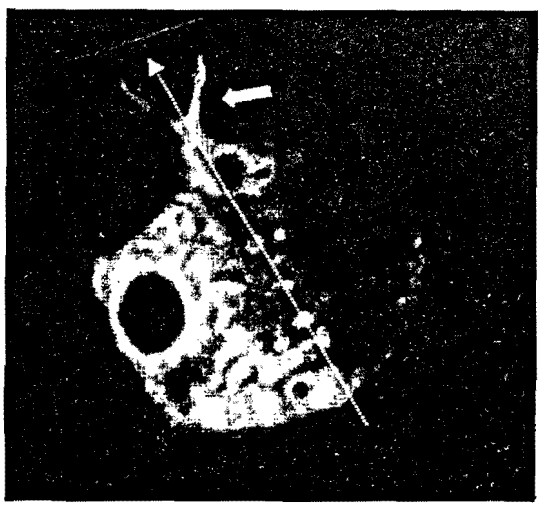
PLC-δ_1 linked GFP transfected cells showed fluorescence at the plasma membrane, with slight fluorescence throughout the cell and no fluorescence in the nucleus of the cell (Figure 17, Panel D). An increase in fluorescence can be seen around the SRBC with the formation of the phagocytic cup. Where no SRBC was present, the fluorescence intensity of the cell with the line scan is consistent. The line scan shows a decrease in intensity across the nucleus representing the lack of fluorescence in the nucleus as well as an increase in intensity of the line scan near the SRBC. Additional images of PLC-δ_1 linked to GFP can be seen in Appendix M, Panel D.

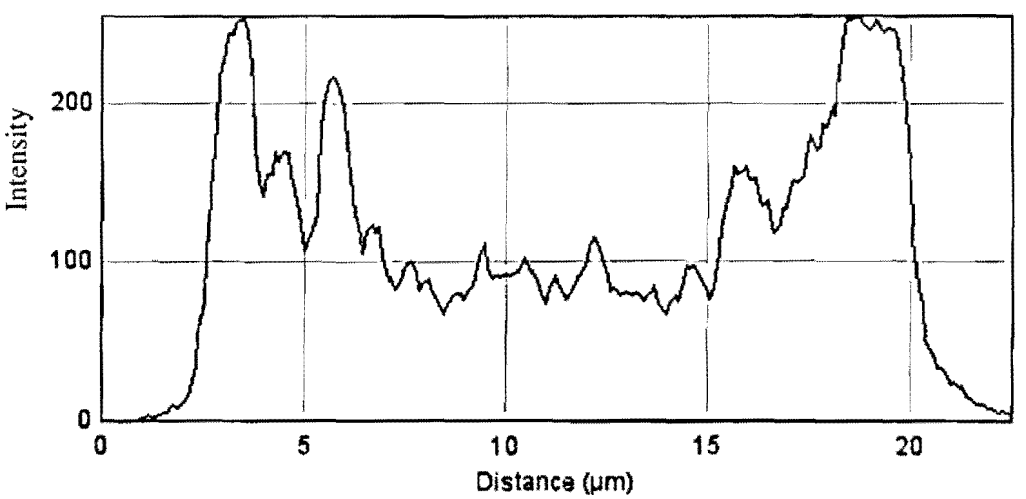
Figure 17: GFP transfection of pEGFP-PLC-β_3, pEGFP-PLC-β_4, pEGFP-PLC-γ_1 and $PH^{PLC-\delta 1}$-GFP in RAW macrophages displaying localization and quantitation of phospholipase proteins.

RAW 264.7 macrophages were transfected with pEGFP-PLC-β_3, pEGFP-PLC-β_4, pEGFP-PLC-γ_1 and $PH^{PLC-\delta 1}$-GFP and phagocytosis was induced with SRBC's. Images were taken every 30 seconds using confocal microscopy. Images below represent cells transfected with GFP-PLC-β_3 (Panel A), GFP-PLC-β_4 (Panel B), GFP-PLC-γ_1 (Panel C) or $PH^{PLC-\delta 1}$-GFP (Panel D), arrows indicating site of phagocytosis, and corresponding line intensity graph for that cell. To quantify the accumulation of the isoform of phospholipase transfected in the cell, a line was drawn through the cell and the site of phagocytosis for comparison.

Panel A pEGFP-PLC-β_3

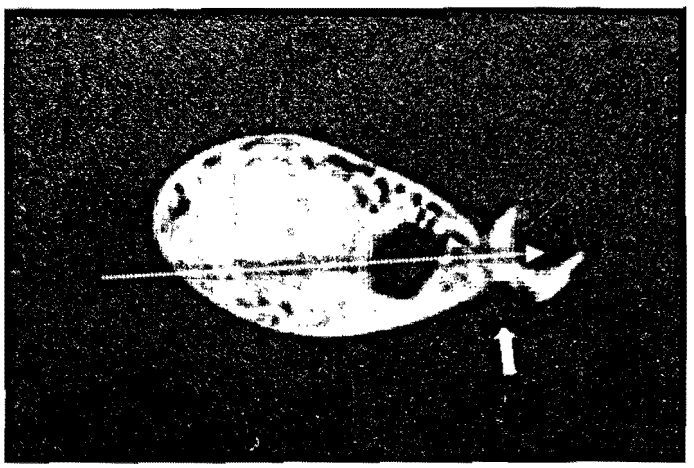
RAW 264.7 macrophage cell transfected with GFP-PLC-β_3.

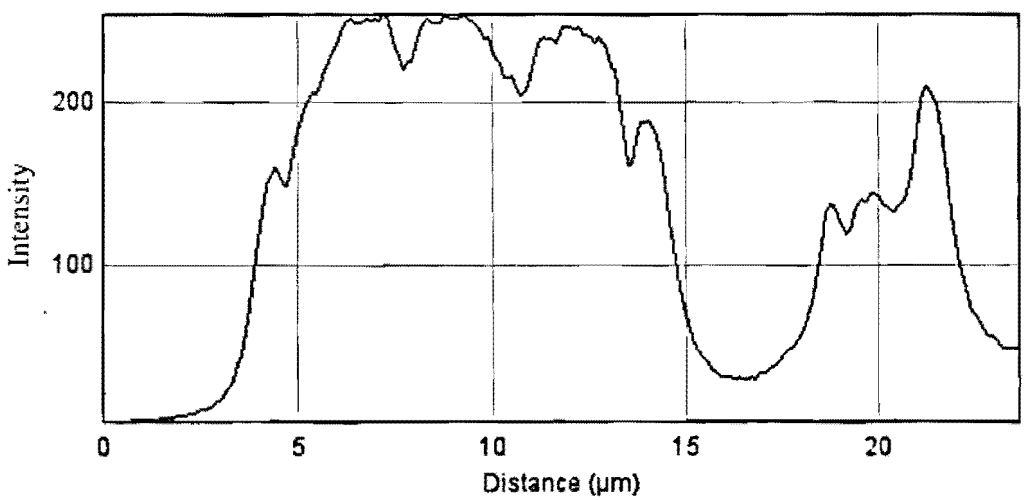




Panel B **pEGFP-PLC-β_4**

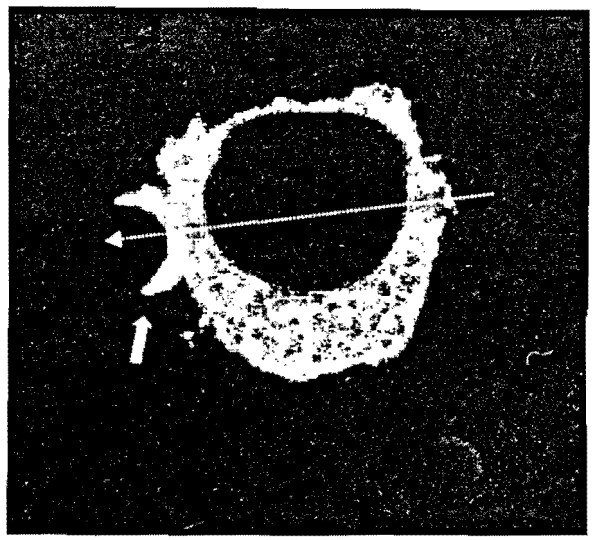
RAW 264.7 macrophage cell transfected with GFP-PLC-β_4.

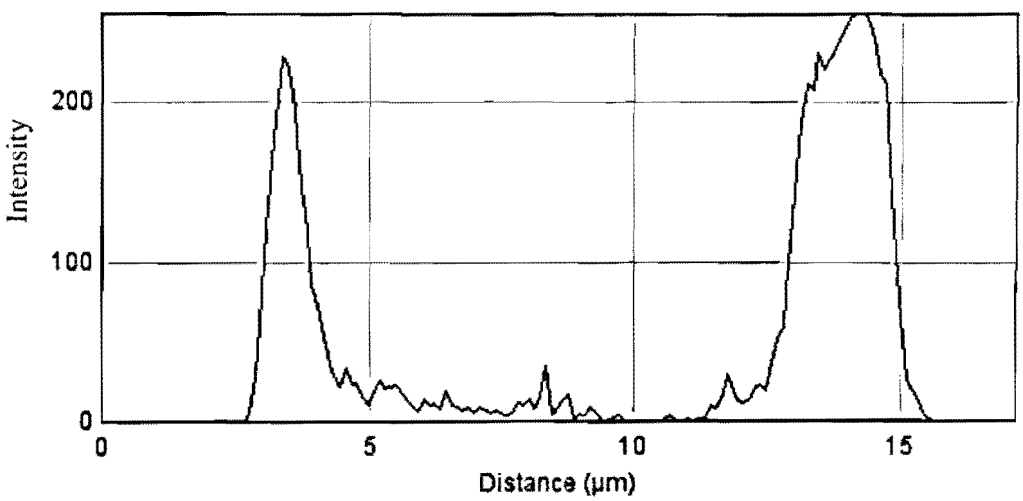




Panel C **pEGFP-PLC-γ_1**

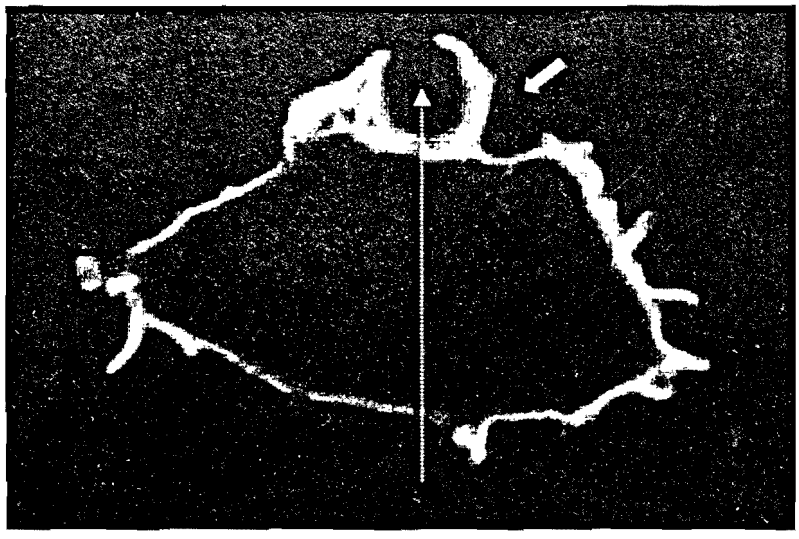
RAW 264.7 macrophage cell transfected with GFP-PLC-γ_1.

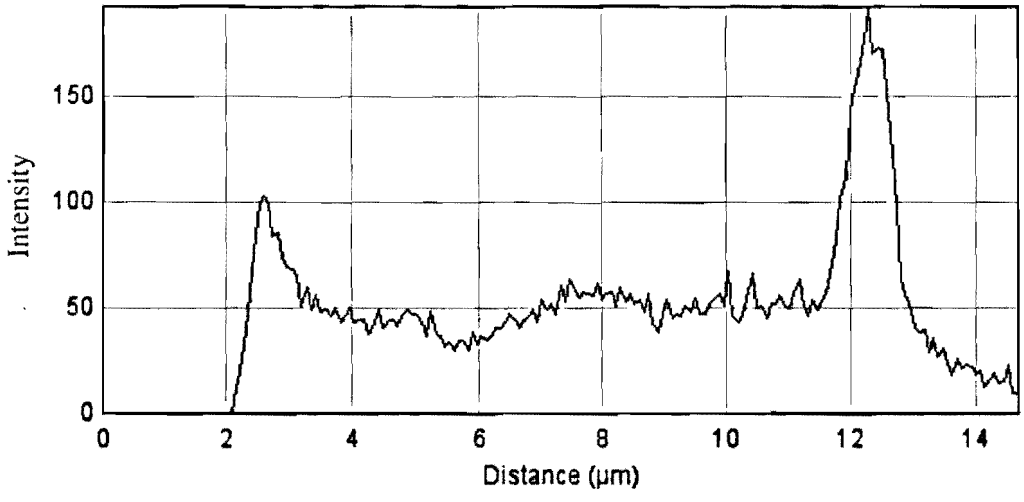




Panel D **$PH^{PLC-\delta 1}$-GFP**

RAW 264.7 macrophage cell transfected with $PH^{PLC-\delta 1}$-GFP.





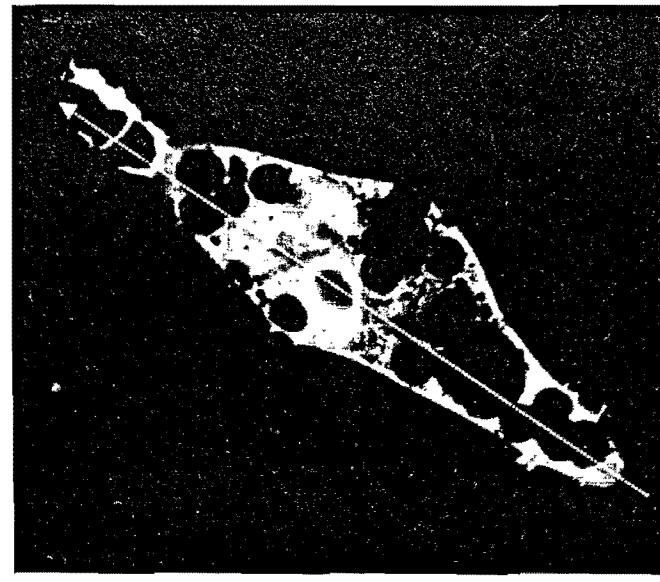
Dominant negatives can affect the number of particles that are consumed by the cell compared to that of the control. The accumulation of PLC-δ_1 was studied in stimulated RAW macrophages using transfections of fusion protein of PLC-δ_1 linked to GFP. Live-cell confocal microscopy was sued to visualize the cells that were transfected with the dominant negative PLC-δ_1 (E41R/D343R). The localization of the protein at the plasma membrane where the Fc receptor is activated was monitored by inducing phagocytosis with SRBC.

Cells transfected with the dominant negative PLC-δ_1 linked to GFP illustrated fluorescence in the nucleus as well as throughout the cytoplasm of the cell and at the plasma membrane (Figure 18). The line scan of the cell where no SRBC was present shows consistent fluorescence within the cell, in the nucleus and a slight increase in fluorescence at the plasma membrane around the SRBC with phagocytic formation. Additional images of the dominant negative PLC-δ_1 linked to GFP can be seen in Appendix M, Panel E.

The dominant negative for PLC-δ_1 that binds to the PLC binding region may have an effect on the number of SRBC consumed. The cells that have been transfected with the dominant negative PLC-δ_1 consume less of the beads coated with IgG than the cells that are transfected with the wild-type $PH^{PLC-\delta 1}$-GFP as well as its neighbouring non-transfected cells, however the decrease in consumption was found not to be significant at the $p = 0.05$ level at both the 7.5, 10 and 30 minute interval as well as the 2 hour time interval (7.5 minutes: $t = 1.43$, $T = 2.36$; 10 minutes: $t = 0$, $T = 2.36$; 30 minutes: $t = 1.30$, $T = 2.23$; 2 hours: $t = 1.64$, $T = 2.05$) (Figure 19). Additional images and the average number of consumed beads for each type of cell (wild-type $PH^{PLC-\delta 1}$-GFP, dominant negative PLC-δ_1 and empty GFP) for each time interval can be seen in Appendix M, Panel F.

Figure 18: Transfection of PLC-δ_1 dominant negative (E341R/D343R) in RAW macrophages displaying localization and quantitation.

RAW 264.7 macrophages were transfected with PLC-δ_1 dominant negative (E341R/D343R) and phagocytosis was induced with SRBC's. Images were taken every 30 seconds using confocal microscopy. Arrows indicating site of phagocytosis, and corresponding line intensity graph for that cell. To quantify the accumulation of the isoform of phospholipase transfected in the cell, a line was drawn through the cell and the site of phagocytosis for comparison.



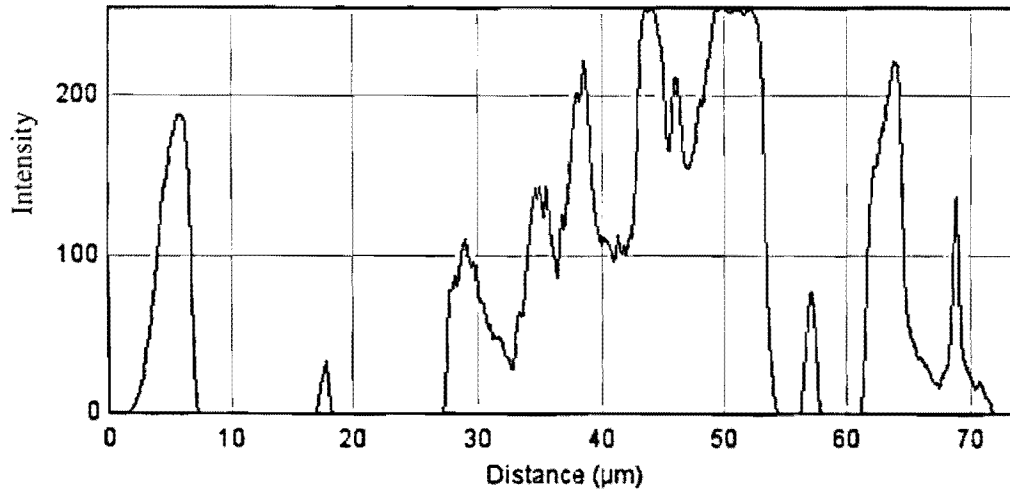
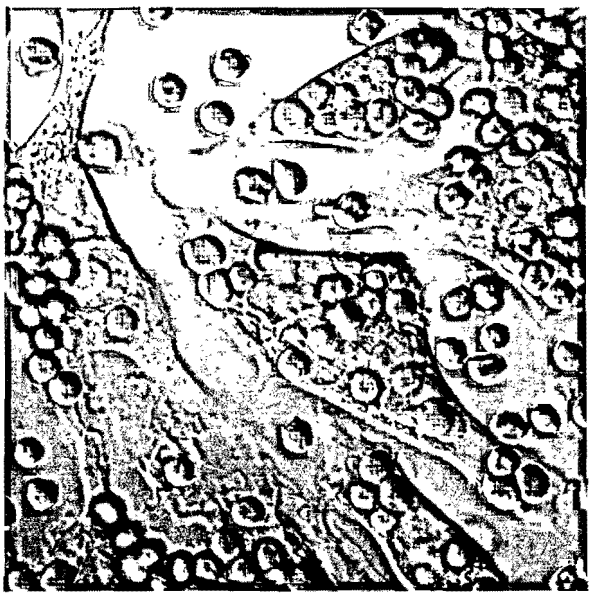


Figure 19: Transfection of PLC-δ_1 dominant negative (E341R/D343R) in RAW macrophages displaying localization and expression.

RAW 264.7 macrophages were transfected with PLC-δ_1 dominant negative (E341R/D343R) and phagocytosis was induced with SRBC's. Images were taken every 30 seconds using confocal microscopy. Image below illustrates a transfected PLC-δ1 dominant negative (E341R/D343R) cell engulfing less SRBC's than its neighbouring non-transfected cells.



t-Test: Paired Two Sample for Means
Cells transfected with WT-GFP-PLCd1 compared to DN-GFP-PLCd1 at 7.5 minutes

	Variable 1	*Variable 2*
Mean	2.38	0.88
Variance	6.55	0.70
Observations	8	8
Pearson Correlation	-0.38	
Hypothesized Mean Difference	0	
df	7	
t Stat	[illegible]	
P(T<=t) one-tail	0.10	
t Critical one-tail	1.89	
P(T<=t) two-tail	0.20	
t Critical two-tail	[illegible]	

t-Test: Paired Two Sample for Means
Cells transfected with WT-GFP-PLCd1 compared to DN-GFP-PLCd1 at 10 minutes

	Variable 1	*Variable 2*
Mean	5.88	5.88
Variance	22.98	10.13
Observations	8	8
Pearson Correlation	0.16	
Hypothesized Mean Difference	0	
df	7	
t Stat	[illegible]	
P(T<=t) one-tail	0.50	
t Critical one-tail	1.89	
P(T<=t) two-tail	1.00	
t Critical two-tail	2.36	

t-Test: Paired Two Sample for Means
Cells transfected with WT-GFP-PLCd1 compared to DN-GFP-PLCd1 at 30 minutes

	Variable 1	*Variable 2*
Mean	20.55	12.55
Variance	348.27	61.47
Observations	11	11
Pearson Correlation	-0.03	
Hypothesized Mean Difference	0	
df	10	
t Stat	[illegible]	
P(T<=t) one-tail	0.11	
t Critical one-tail	1.81	
P(T<=t) two-tail	0.22	
t Critical two-tail	[illegible]	

t-Test: Paired Two Sample for Means
Cells transfected with WT-GFP-PLCd1 compared to DN-GFP-PLCd1 at 2 hours

	Variable 1	*Variable 2*
Mean	36.45	28.52
Variance	527.04	336.90
Observations	29	29
Pearson Correlation	0.22	
Hypothesized Mean Difference	0	
df	28	
t Stat	[illegible]	
P(T<=t) one-tail	0.06	
t Critical one-tail	1.70	
P(T<=t) two-tail	0.11	
t Critical two-tail	2.05	

Protein Network Analysis of LARC

Analyzing RAW mass spectroscopy data that has been collected via stimulation of macrophage phagocytosis by LARC (Olsen J. V. 2004; Jankowski 2008), the proteins associated with the FcγR receptor signalling pathway were determined, as well as any isoforms associated. Manual and computer searches of proteins and peptides LARC identified were carried out. Peptides with a cumulative score of 2400 or greater were accepted since a cut-off score of 2400 has a false-positive identification rate of about 5% (Chelius D. 2002; Moore 2002). Cumulative scores of 2400 must have also come from at least 3 different peptide sequences.

The use of proteins and peptides obtained from the LARC method yielded a total of 336 proteins identified as specifically being associated with the Fcγ receptor complex and Fcγ receptor-mediated phagocytosis. Signalling between proteins was examined by literature review, data mining and protein interaction databases. The resulting signalling pathway of proteins associated with the Fcγ receptor is shown in the Figures below. Figure 20 displays Fc receptor-mediated phagocytosis pathway derived from data mining and protein interaction database Cytoscape. In Figure 21, Fc receptor-mediated phagocytosis involves the same criteria but uses the Osprey database. Figure 22 illustrates Fc receptor-mediated phagocytosis also involves the same criteria but uses the STRING database. All protein interaction databases include similar proteins to be major players in phagocytosis, including tyrosine kinases (Syk, Ptk2), lipases ($PLC\gamma_1$, $PLC\beta_3$), GTPases (RAP1A), phosphatidylinositol kinases (PI3-Kβ, PI3-Kγ) and MAPKs (MAP2K1) as seen in Table 5. In Figure 23, is illustrated with Adobe Illustrator and is derived from literature review. Protein interaction network models for the PLC's ($PLC\beta_3$, $PLC\beta_4$, $PLC\gamma_1$, $PLC\delta_1$, $PLC\varepsilon_1$ and PLC-like 2) can be found in Appendix N. Mass spectra as well as protein

interaction network models for the main interactors in Fcγ receptor-mediated phagocytosis can be found in Appendix O and Appendix P respectively.

Figure 20: Model pathway of Fc receptor-mediated phagocytosis in macrophage cells illustrated with Cytoscape.

Fc receptor-mediated phagocytosis involves many proteins identified by LARC. The major key interactors of phagocytosis in RAW macrophage cells are seen in areas of multiple line intensity, with the secondary interactors having less connecting lines present.

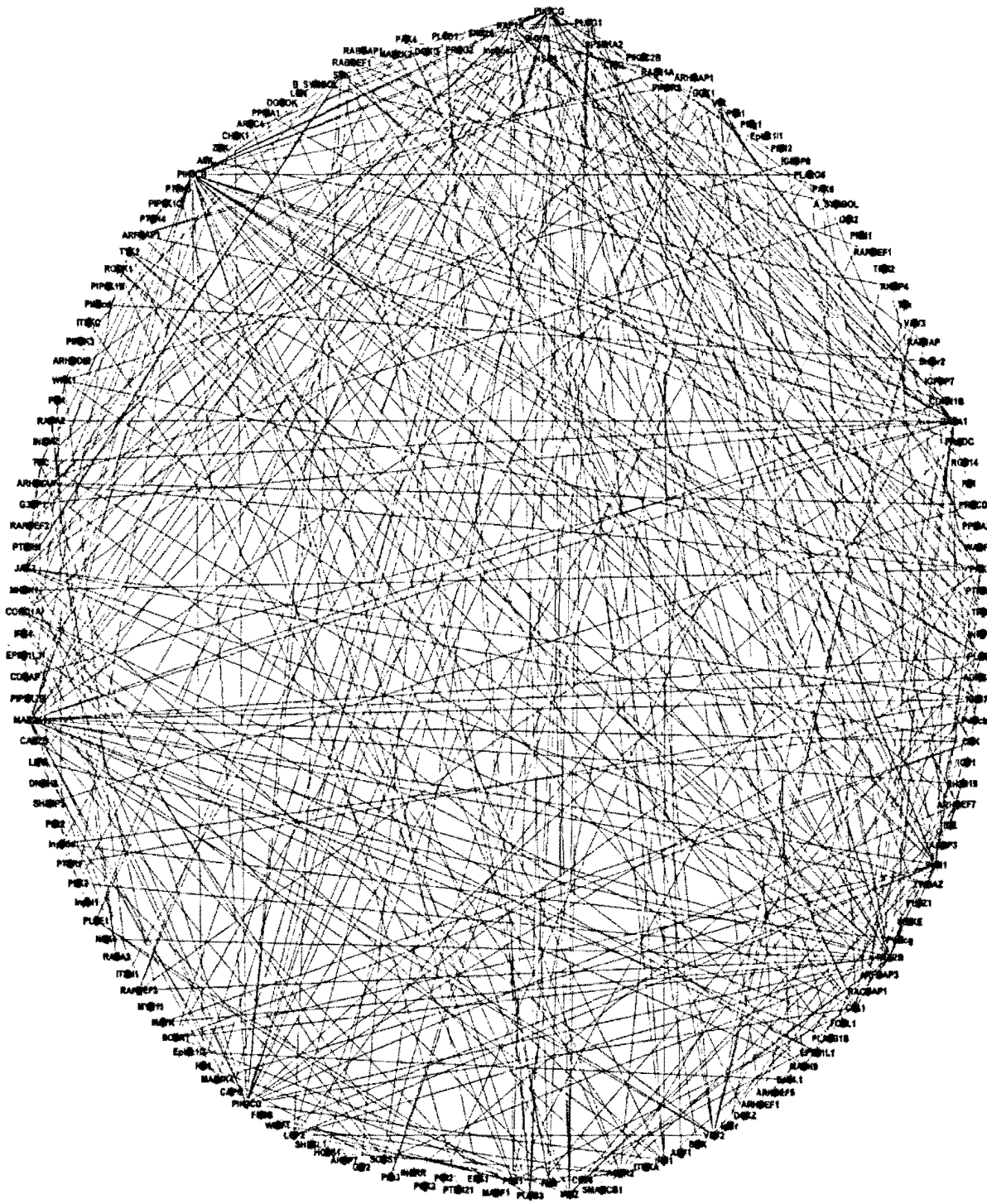


Figure 21: Model pathway of Fc receptor-mediated phagocytosis in macrophage cells illustrated with Osprey.

Fc receptor-mediated phagocytosis involves many proteins identified by LARC. The major key interactors of phagocytosis in RAW macrophage cells are seen in the inner circle, with the secondary interactors protruding outside the circle. All proteins have at least 3 known protein-protein interactions.

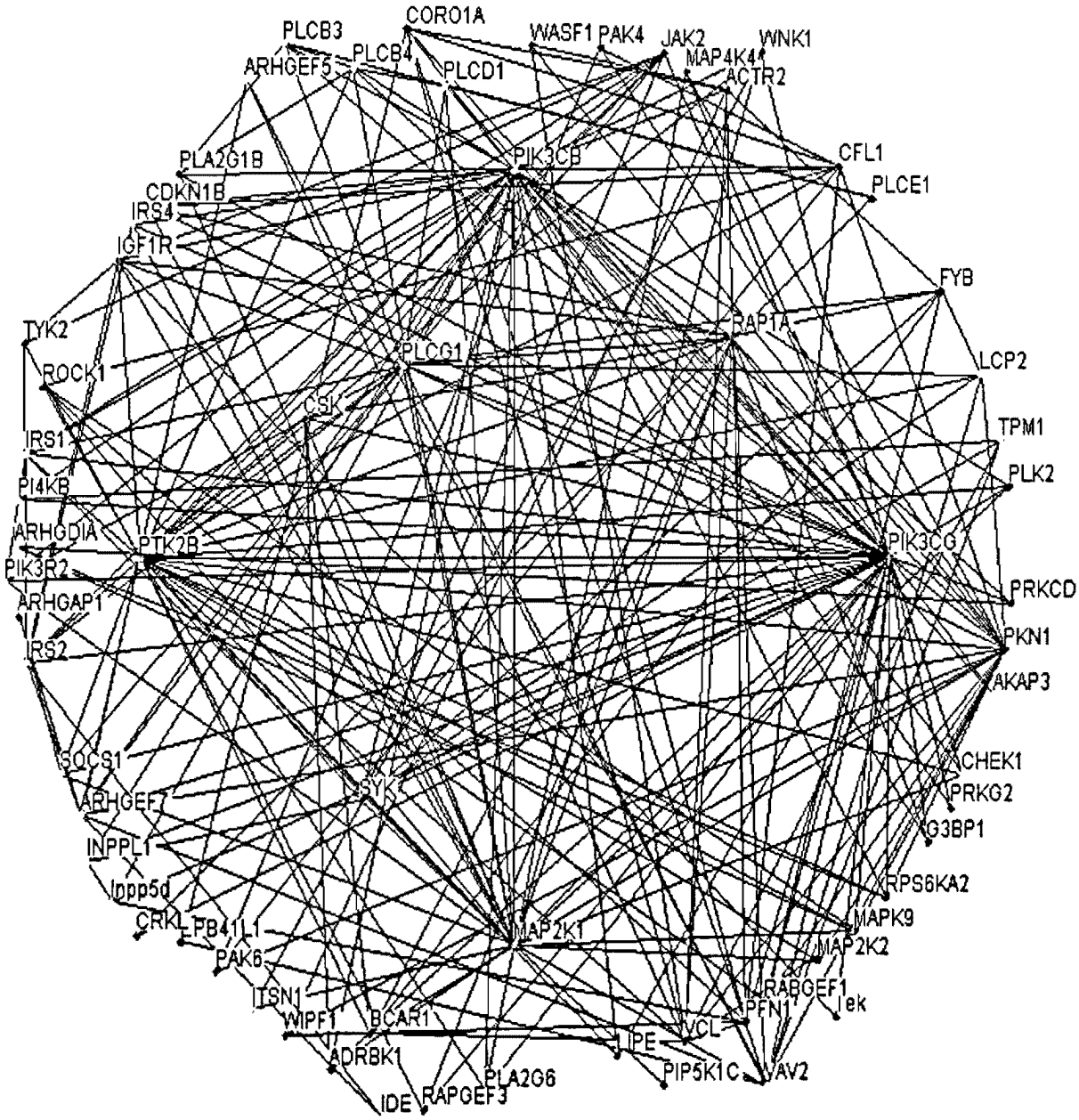


Figure 22: Model pathway of Fc receptor-mediated phagocytosis in macrophage cells illustrated with STRING.

Fc receptor-mediated phagocytosis involves many proteins identified by LARC. The major key interactors of phagocytosis in RAW macrophage cells are represented by white circles and have at least 3 known protein-protein interactions.

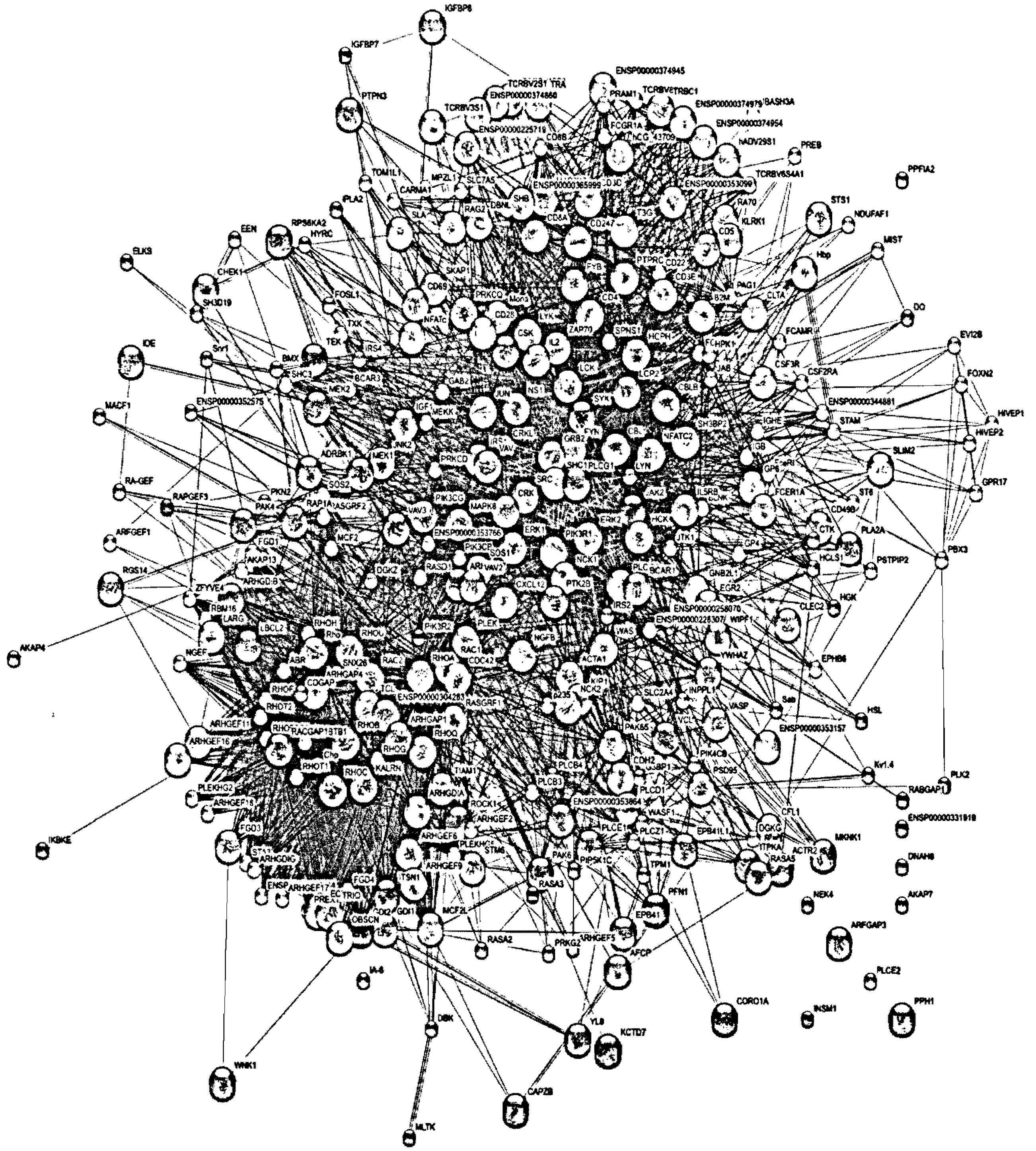


Table 5: Major key interactors of Fcγ receptor-mediated phagocytosis in RAW 264.7 macrophage cells.

Major interactors include tyrosine kinases (Syk, Ptk2), lipases ($PLC\gamma_1$, $PLC\beta_3$), GTPases (RAP1A), phosphatidylinositol kinases (PI3-Kcβ, PI3-Kcγ) and MAPKs (MAP2K1). Main interactors predicted by each model: Cytoscape (Table 3a), Osprey (Table 3b) and STRING (Table 3c) are shown below.

Table 5a: Main protein interactors in Fc receptor-mediated phagocytosis predicted by Cytoscape.

Cytoscape: Main Protein Interactors

Protein	Accession Number	Fc Receptor Complex	Control
KSYK_MOUSE Tyrosine-protein kinase SYK (Spleen tyrosine kinase)	1711636.0	14346.20	0.00
FAK2_MOUSE Protein tyrosine kinase 2 beta (Focal adhesion kinase 2) (FADK 2)	20138411.0	6064.34	1648.93
phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Mus muscul	29789235.0	3902.88	1679.37
phosphoinositide-3-kinase, catalytic, gamma polypeptide; PI3K<gamma>; P	9937984.0	8441.50	1213.99
phospholipase C, beta 3 [Mus musculus]	31982122.0	8916.15	790.84
Coronin, actin binding protein 1A [Mus musculus] g	31418362.0	10780.84	0.00
mitogen activated protein kinase kinase 1; protein kinase, mitogen acti	6678794.0	3933.63	1262.70
dJ511B24.2.5 (phospholipase C, gamma 1 (formerly subtype 148) (1-Phosph	13560998.0	6405.30	956.88
RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s	4506413.0	63109.41	24733.93
A60965 vinculin - mouse (fragment) gene [Mus musculus]	482647.0	5894.72	1211.60
protein kinase C-like 1; serine/threonine kinase 3 [Mus musculus]	32813439.0	3688.99	321.51
RAS p21 protein activator 1; p120-rasGAP; GTPase-activating protein [M	21703900.0	11271.47	0.00
phosphoinositide 3 kinase P110delta [Mus musculus]	22758919.0	8849.02	1213.99
cofilin 1, non-muscle [Mus musculus]	6680924.0	34424.95	0.00

Table 5b: Main protein interactors in Fc receptor-mediated phagocytosis predicted by Osprey.

Osprey: Main Protein Interactors

Protein	Accession Number	Fc Receptor Complex	Control
KSYK_MOUSE Tyrosine-protein kinase SYK (Spleen tyrosine kinase)	1711636.0	14346.20	0.00
CSK_MOUSE Tyrosine-protein kinase CSK (C-SRC kinase) (Protein-tyrosine kinase M	729888.0	2709.32	328.54
FAK2_MOUSE Protein tyrosine kinase 2 beta (Focal adhesion kinase 2) (FADK 2)	20138411.0	6064.34	1648.93
phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Mus muscul	29789235.0	3902.88	1679.37
phosphoinositide-3-kinase, catalytic, gamma polypeptide; PI3K<gamma>; P	9937984.0	8441.50	1213.99
phospholipase C, beta 3 [Mus musculus]	31982122.0	8916.15	790.84
Vav2 oncogene [Mus musculus]	6678555.0	10446.42	548.21
mitogen activated protein kinase kinase 1; protein kinase, mitogen acti	6678794.0	3933.63	1262.70
dJ511B24.2.5 (phospholipase C, gamma 1 (formerly subtype 148) (1-Phosph	13560998.0	6405.30	956.88
RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s	4506413.0	63109.41	24733.93
B39577 protein-tyrosine kinase (EC 2.7.1.112) JAK2 - mouse (fragment)	110873.0	3262.85	0.00
protein kinase C-like 1; serine/threonine kinase 3 [Mus musculus]	32813439.0	3688.99	321.51
A60965 vinculin - mouse (fragment) gene [Mus musculus]	482647.0	5894.72	1211.60
Coronin, actin binding protein 1A [Mus musculus] g	31418362.0	10780.84	0.00

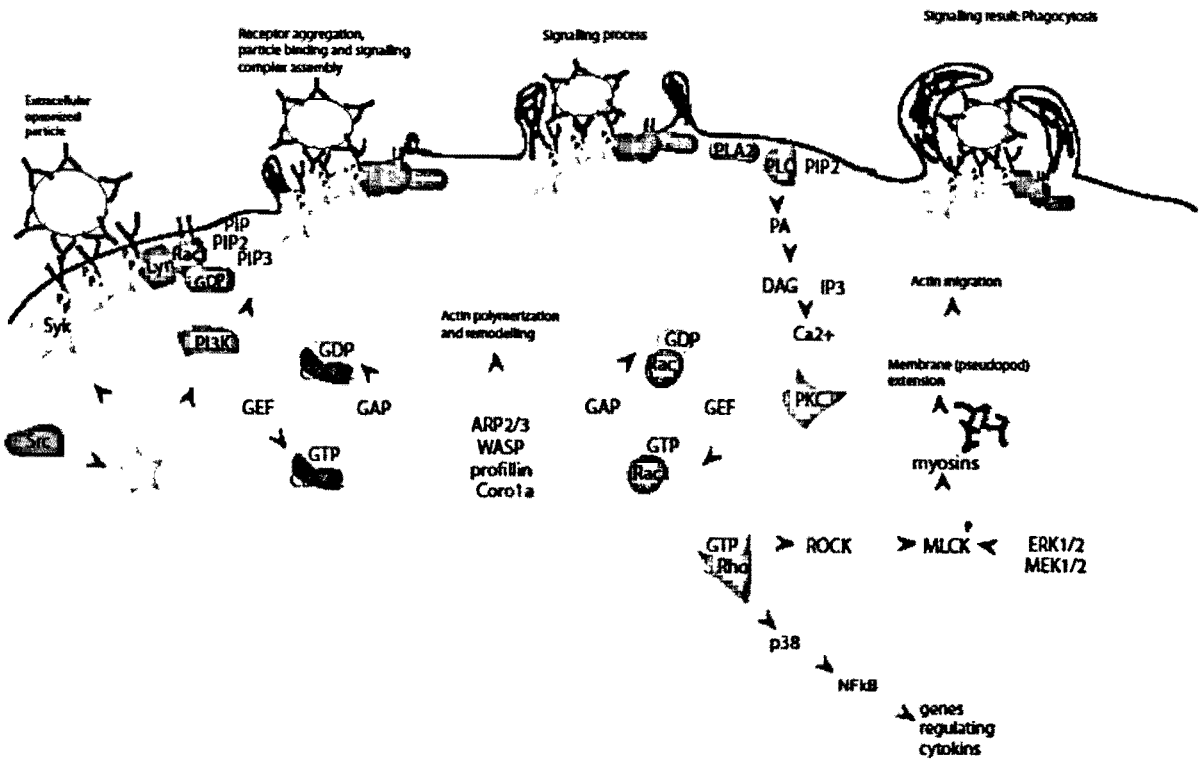
Table 5c: Main protein interactors in Fc receptor-mediated phagocytosis predicted by STRING.

STRING: Main Protein Interactors

Protein	Accession Number	Fc Receptor Complex	Control
KSYK_MOUSE Tyrosine-protein kinase SYK (Spleen tyrosine kinase)	1711636.0	14346.20	0.00
CSK_MOUSE Tyrosine-protein kinase CSK (C-SRC kinase) (Protein-tyrosine kinase M	729888.0	2709.32	328.54
FAK2_MOUSE Protein tyrosine kinase 2 beta (Focal adhesion kinase 2) (FADK 2)	20138411.0	6064.34	1648.93
phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Mus muscul	29789235.0	3902.88	1679.37
phosphoinositide-3-kinase, catalytic, gamma polypeptide; PI3K<gamma>; P	9937984.0	8441.50	1213.99
phospholipase C, beta 3 [Mus musculus]	31982122.0	8916.15	790.84
phospholipase C beta 4 [Mus musculus]	29293803.0	9857.93	997.97
mitogen activated protein kinase kinase 1; protein kinase, mitogen acti	6678794.0	3933.63	1262.70
dJ511B24.2.5 (phospholipase C, gamma 1 (formerly subtype 148) (1-Phosph	13560998.0	6405.30	956.88
B39577 protein-tyrosine kinase (EC 2.7.1.112) JAK2 - mouse (fragment)	110873.0	3262.85	0.00
Vav2 oncogene [Mus musculus]	6678555.0	10446.42	548.21
A60965 vinculin - mouse (fragment) gene [Mus musculus]	482647.0	5894.72	1211.60
Rho-associated coiled-coil forming kinase 1 [Mus musculus]	6677759.0	16083.11	3003.23
phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 b	6679321.0	2769.48	1162.26

Figure 23: Model pathway of Fc receptor-mediated phagocytosis in macrophage cells illustrated with Adobe Illustrator.

Fc receptor-mediated phagocytosis involves many proteins identified by LARC. The major key interactors of phagocytosis in RAW macrophage cells are shown below.



DISCUSSION

LARC

Many proteins were observed with the Fc receptor complex with IgG on the LARC beads, but not control beads. Many of these proteins have been previously shown to be associated with the Fc receptor. From this we conclude that at least some of the Fc receptor supramolelcular complex remained bound to the ligand coated microbeads. Presuming the ligand coated beads bind and activate the receptor, and that the receptor complex forms, which can be confirmed by the direct visual observation that the beads are eventually engulfed, then there is no reason to suppose the complex would necessarily fall apart or dissociate itself from the beads during isolation on ice in the presence of physiological buffers and added biochemical preservatives.

LC-ESI-MS/MS

The proteins associated with the Fc receptor complex were detected by LC-ESI-MS/MS along side controls for non specific biding. Proteins previously found to be associated with the Fc receptor, including members of the Fc receptor family itself, its binding partners and effectors were found to show multiple peptides and significant scores compared to control beads. From this we conclude that the process of LC-ESI-MS/MS analysis and SEQUEST correlation is sensitive and accurate enough to identify proteins from the Fc receptor supramolecular complex captures from live cells in at least some or many cases.

Among the proteins identified by the protein interaction network to be crucial to the formation of the Fc receptor complex identified were lipases, including phospholipase C and its various isoforms. Phospholipases, in particular PLC's have been previously reported in Fcγ

receptor-mediated phagocytosis (Lennartz 1999; Greenberg and Grinstein 2002; Steinberg 2008). Of the main interacting proteins, we have chosen to focus on the PLC's. Upon Syk activation in macrophages, SH2 containing signalling molecules bind the ITAM which has been phosphorylated by Src (Ravetch 2001). Subsequent PI3-K activation leads to PIP_3 production and recruitment of PLC-γ to the phosphorylated ITAM of the IgG receptors, generating IP_3 and DAG as well as sustained calcium mobilization (Rhee 1989). DAG is responsible for PKC activation and IP_3 triggers calcium release from the endoplasmic reticulum. Calcium is important for phagolysosome fusion as well as PKC activation (Greenberg and Grinstein 2002). PLC inhibition has shown to result in a decrease in phagocytosis (Rosales 2005).

The full length FASTA sequence of PLC-β_3 correlated to 23 of 24 peptides identified with mass spectrometry indicating the alignment of the native sequence with the sequences generated by tandem mass spectrometry. The full length FASTA sequence of PLC-β_4 was able to correlate 12 of 26 peptides to the native sequence listed by NCBI. PLC-γ_1 aligned 17 of 19 peptides from the sequences generated by tandem mass spectrometry to the sequence listed by NCBI. PLC-δ_1 aligned 14 of 15 peptides to the native sequence. The full length FASTA sequence aligned all peptides identified using tandem mass spectrometry of PLC-ε_1 as listed on NCBI. Lastly, 20 of 25 peptides were identified with tandem mass spectrometry for PLC like-2 using the full length FASTA sequence and that listed on NCBI. The mass spectra for all PLC isoforms displayed good fragmentation patterns with relatively high abundance and low noise for the 3 spectra corresponding to the 3 highest scored peptides. It can be concluded that relevant isoforms of PLC can be identified with LARC with high accuracy, suggesting that these PLC isoforms may localize to the Fc receptor complex upon activation.

Western Blot

Based on detection and mass we conclude that the proteins detected by LC-ESI-MS/MS may be confirmed in terms of immunological character and protein size to be typically in agreement with the PLC molecules predicted by mass spectrometry and peptide sequence correlation. PLC-β_3 has a molecular weight of 150 kDa, represented by the single band identifying the protein in RAW 264.7 macrophages. PLC-β_4 has a molecular weight of 145 kDa, represented by the single band. The second band, about 60 kDa lower, can be attributed to secondary binding of the antibody. PLC-γ_1 has a molecular weight of 155 kDa, corresponding to the single band at the correct weight. PLC-δ_1 has a molecular weight of 85 kDa, identified by the single band on the blot in RAW 264.7 cell lysate. PLC-ε_1 has a molecular weight of 254 kDa, and is denoted by a faint band located above the 116 kDa marker. PLC-ε_1 has a relatively low abundance in macrophage cells, making its detection difficult and weak. The second band located at approximately 116 kDa can be linked to secondary antibody binding. PLC like-2 has a molecular weight of 36 kDa, indicated by the strong single band at this weight. Identification of all 6 isoforms of phospholipase C using Western blots confirms their presence in RAW 264.7 macrophages.

Laser Confocal Microscopy

Although there are theoretical reason to believe that the protein complex has been captured and direct tandem mass spectrometric data showing that known Fc associated proteins are detected, these observations can also be directly and independently tested using both antibodies and fluorescent proteins using the laser confocal microscope. We observed that in many cases the proteins indicated by LC-ESI-MS/MS were shown to co-localize with the Fc

receptor complex activated by IgG coated microbeads. Immunofluorescent staining of cells with PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2 illustrated an increase in fluorescence occurring near the site of phagocytic cup formation around the IgG-coated bead at the site of phagocytosis. PLC isoforms can be detected at the site of the activated receptor complex in RAW 264.7 macrophages near the bound particle. Hence it remains possible that the PLC proteins observed to the proximal to the activated Fc receptor do play a role in the function of the Fc receptor.

Functional Assays

Using fluorescent fusion proteins to further detect PLC-β_3-GFP, PLC-β_4-GFP, PLC-γ_1-GFP and $PH^{PLC\text{-}\delta 1}$-GFP the accumulation of the PLC isoforms is illustrated near the site of initial phagocytic cup formation. Whether the PLC isoform fluorescence is throughout the cytoplasm of the cell (PLC-β_3-GFP, PLC-β_4-GFP, PLC-γ_1-GFP) or located just at the plasma membrane ($PH^{PLC\text{-}\delta 1}$-GFP), upon phagocytosis stimulation with SRBC, the fluorescence intensity of the cell changes, with an increase in intensity seen near and around the SRBC at the site of cup formation. Live-cell imaging of RAW 264.7 macrophages denotes an increase in fluorescence around the SRBC to be engulfed, near the site of the activated receptor.

A further method to test the validity of the LC-ESI-MS/MS data is to use the expression of mutant proteins or silencing RNA to inhibit the specific molecular function of the detected proteins. We have attempted this approach with the regard to the PLC delta, the most prominently studied PLC where molecular reagents such as wild type GFP fusion proteins and dominant negative mutant constructs are available. In this regard we have observed that in general the exogenous expression of GFP fusion proteins show a general reduction in the

phagocytosis of RAW macrophages. However compared to the GFP control, the expression of functional PLC-δ showed an increase in the phagocytic activity of the Fc receptor complex. PLC-δ has many protein domains including the a, b, & c domains. Expression of a mutant construct with a mutation (described) in the x domain was found to show lower, but not significantly lower or decreased phagocytosis. However, since it is difficult to know with certainty which domain and isoform of PLC is required for the initial phagocytic engulfment step, this experiment could be further supported by the use of silencing RNA.

CONCLUSION

LARC was able to capture the activated receptor complex and associated proteins that were identified by mass spectrometry and confirmed with confocal microscopy (Jankowski 2008). Proteins associated with the Fc receptor complex were detected and identified with ESI-MS/MS. Therefore, we conclude that the proteins exist in RAW 264.7 macrophage cells at the site of the activated receptor complex. LARC identified numerous proteins, a total of 336 that were specifically associated with Fcγ receptor-mediated phagocytosis in RAW 264.7 macrophages. Of the 336 proteins identified was the PLC family, specifically the isozymes studied: PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2. Alignment of FASTA peptides identified by mass spectrometry to full length NCBI sequence further confirmed protein identification. Western blots confirmed the presence of the PLC isoforms in RAW 264.7 macrophages. Antibody staining of PLC isoforms has shown recruitment of the PLC's to the cell membrane at the site of the activated receptor near phagocytic cup formation. Fusion proteins of the PLC isoforms linked to GFP illustrated expression of the PLC's at the site of cup formation in RAW macrophages. Initial dominant negative data illustrates a slight decrease in phagocytosis compared to non-transfected cells; however t test confirmation shows a non-significant decrease. The PLC's studied, PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2 may play a role in Fcγ receptor-mediated phagocytosis in RAW 264.7 macrophages, however further evidence is necessary to establish and verify the mechanisms involved.

FUTURE OBJECTIVES

Future objectives that could help shed additional insight and support for the topics discussed in this study could help establish the mechanisms that involve the phospholipase C isozymes in phagocytosis. Using mass spectrometry coupled with confocal microscopy allows for a foundation of the fundamentals involved to be discussed, however further evidence is needed to further develop these fundamentals. Additional support could come from the use of silencing RNA (siRNA) in order to enhance the knowledge behind the activated Fc receptor and Fc receptor-mediated phagocytosis in macrophage cells. siRNA has the ability to silence or greatly reduce a specific protein's expression within a cellular network. This would allow the study of the protein's function in phagocytosis since activity at the site of the activated receptor could be monitored. When combined with the visualization of confocal microscopy, the protein would be determined to whether it is essential in the uptake of opsonised particles. Mass spectrometry, immunostaining and GFP transfections have determined that the phospholipase C's (PLC-β_3, PLC-β_4, PLC-γ_1, PLC-δ_1, PLC-ε_1 and PLC like-2) are present upon Fc receptor activation in RAW 264.7 macrophages, however further experimentation is required for identification of the molecules and isoforms of both phospholipases and other proteins identified by LARC that are associated with the activated Fc receptor complex.

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APPENDIX A – KINASE SUMMATION OF IONS

The summation of peptides from Kinases found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
bone morphogenic protein receptor, type II (serine/threonine kinase) [M					4802.61	6680804.0	12		
jmIgG300rawphag3007,1008-1010	-.MEYLLVMEYYPNGSLCK.-	2054.44	3	1227.73	1.78	0.2	163	15/64	
jmIgG400rawphag3007, 1044	-.MEYLLVMEYYPNGSLCK.-	2054.44	3	593.24	1.61	0.1	335	19/64	
jmraw5minigg250mmnaclsyringdnase, 1146	-.MEYLLVMEYYPNGSLCK.-	2054.44	3	968.25	1.50	0.2	319	17/64	
jm5miniggrawlowonic, 1574	-.ISHENGTILCSKGSTCYGLWEKSK.-	2642.99	3	393.20	1.34	0.0	280	17/92	
jmrawf5minbsareebeads,1050-1052	-.MEYLLVMEYYPNGSLCK.-	2054.44	3	273.25	1.45	0.1	133	13/64	
jmldl250naclrawphag3007, 1042	-.MEYLLVMEYYPNGSLCK.-	2054.44	3	173.64	1.22	0.0	128	13/64	
jmldl300naclrawphag3007, 1206	-.MEYLLVMEYYPNGSLCK.-	2054.44	3	496.89	1.19	0.0	417	21/64	
rawsucrfp_60MeOHphagigg_MAr04,664-666	-.MEYLLVMEYYPNGSLCK.-	2054.44	3	581.23	1.67	0.1	315	5/16	
rawsucrfp_actinphagigg_Mar04, 1912	-.VPWLLWAVLLVSTTAASQNQERLCAFK.-	3046.58	2	95.18	0.78	0.1	60	2/13	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
bone morphogenic protein receptor, type II (serine/threonine kinase) [M					354.28	6680804.0	7		
rawextr_900beadigg_Mar04, 734	-.MEYLLVMEYYPNGSLCK.-	2054.44	3	354.28	1.58	0.1	198	1/4	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to serine/threonine kinase [Mus musculus]					6461.94	38348544.0	15		
JMFAGNACL10_2B21E3, 118	-.TTKKPDPR.-	943.08	2	368.49	1.37	0.0	269	1/2	2
jmlagfrench20minigg1mnackdtt, 424	-.QQSAWENKTTK.-	1321.42	3	702.04	1.52	0.1	341	7/20	2
jmraw5minigg500mmnaclsd, 1354	-.SHGGSHGIRAFRGTVLPEK.-	2007.25	3	368.13	1.52	0.0	242	19/72	
jmrawigg5minbeadsfreezethaw, 1396	-.NCFNEETTPLHSICPQLVQKAHYR.-	2830.20	3	176.73	1.72	0.0	103	4/23	1
jmraw5minigg1000mmsd, 1522	-.GEGPALQQRESR.-	1328.42	2	166.92	0.83	0.1	160	4/11	
JMFAGNACL10_2B21E3, 1796	-.FDQVMATYLMLKQQSAWENKTTK.-	2763.19	2	195.39	1.19	0.1	122	9/44	2
jmrawigg5min150mmnacl, 1838	-.ESRPSSPNTLQGHLHGR.-	1874.01	2	858.70	1.57	0.2	261	11/32	1
jmldl150naclrawphag3007, 1464	-.DLKPENILLDHR.-	1463.66	2	200.30	1.22	0.0	160	4/11	2
rawsucrfp_900phagigg_Mar04,1203-1205	-.TDMVSKAMSCDPVQYGHGQLLSSSLQK.-	2912.31	3	1937.18	2.62	0.2	178	21/104	
phagrawF350_dec20,1324-1326	-.YGHGQLLSSSLQKTDMVSKAVSCGPVQYDHR.-	3393.80	3	147.92	1.19	0.0	105	1/8	
rawsucrfp_350phagigg_Mar04, 1824	-.YGHGQLLSSSLQK.-	1418.58	2	546.19	1.01	0.1	351	1/2	
rawsucrfp_actinphagigg_Mar04,1020-1022	-.IHTLQTSMGVSKAGSTYSK.-	1997.26	3	144.57	1.29	0.0	109	7/36	1
rawsucrfp_600phagigg_Mar04, 2446	-.ESRPSSPNTLQGHLHGRHQTAPQAPFQR.-	3136.39	2	70.44	0.89	0.1	49	1/9	
ajrawphagjun20dpi1MNaCl, 1942	-.SHGGSHGIRAFRGTVLPEK.-	2007.25	3	578.93	1.10	0.2	182	7/36	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to serine/threonine kinase AIE1 [Mus musculus]					3895.25	38085953.0	4		
jmfag5minigg1000mmnacl, 118	-.SSNTGHNSCGTSR.-	1308.32	3	1400.60	1.98	0.1	638	5/12	
jmfag5minigg500mmnacl, 1350	-.LLGRAKFGCVYLAWLK.-	1839.28	3	408.45	1.24	0.0	329	1/4	
jmigg600rawphage3007, 1524	-.LAGLQLALTLLEFR.-	1558.89	3	333.03	1.34	0.0	245	1/4	
phagrawF1000_Dec23, 1806	-.PYKSGRTHTSAFSMDR.-	1842.03	2	402.89	1.00	0.2	134	4/15	
ajrawmediapbsnocells, 1592	-.QSAPKSVLLSPTGSKR.-	1656.91	2	675.14	1.25	0.2	234	1/3	
ajrawmediapbsnocells, 1592	-.QSAPKSVLLSPTGSKR.-	1656.91	2	675.14	1.25	0.2	234	1/3	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to serine/threonine kinase AIE1 [Mus musculus]					998.44	38085953.0	5		
rawextr_350beadigg2_Mar04,218-220	-.SSNTGHNSCGTSR.-	1308.32	3	727.90	1.70	0.0	422	3/8	
FPbeads500_dec19, 1724	-.FCGLISSSLSTIDFWHLLVDGRPKK.-	2821.29	3	270.54	1.27	0.0	196	3/16	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Serine/threonine-protein kinase PAK 6 (p21-activated kinase					3903.18	28487481.0	11		
jmfag5minigg300mmnacl, 1728	-.PNSAFRPPQKDSSSNLVAK.-	2044.26	3	1874.18	2.14	0.2	550	19/72	
jmIgG250rawphag3007, 1816	-.SMFLSTPATGAASSSKPVPLPQNK.-	2417.77	3	232.05	1.59	0.0	131	19/92	
JMMAGNEGB16D3, 300	-.LSVISSNTLR.-	1090.28	2	234.05	0.96	0.0	243	4/9	
phagrawF450_dec20, 908	-.HSSEEARPQSCLVGSAIGRPGGEGSPSPK.-	2879.12	3	296.04	1.59	0.0	175	17/112	
phagrawFsuc250_dec22, 1231	-.SMFLSTPATGAASSSKPVPLPQNK.-	2417.77	3	448.69	1.69	0.1	170	5/23	
phagrawFsuc800_dec23, 1526	-.KRPEISAPQNFQHR.-	1708.91	2	112.91	0.84	0.0	131	4/13	
jmbeads250rawphag3007, 526	-.WASERAGQR.-	1061.14	2	172.24	1.11	0.1	92	5/16	
jmbeads500rawphag3007, 1384	-.SMFLSTPATGAASSSKPVPLPQNK.-	2417.77	3	733.01	2.26	0.1	264	1/4	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Serine/threonine-protein kinase PAK 6 (p21-activated kinase					889.45	28487481.0	8		
rawextr_60MeOHbeadigg_Mar04, 1130	-.TAPAAGPLPGRSSPAGSPRTR.-	2005.23	3	426.27	1.05	0.2	150	3/20	
jmbsa600naclrawphag3007, 1690	-.SMFLSTPATGAASSSKPVPLPQNK.-	2417.77	3	463.18	1.45	0.1	277	1/4	

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Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
serine/threonine protein kinase; Murine thymoma viral (v-akt) oncogene protein kinase B kinase					2591.51	4885061.0	5		
a1MNaClphagigGDPIPJun18, 968	- DEVAHTLTENRVLQNSR.-	1983.13	2	74.46	1.09	0.0	67	7/32	1
phagrawFsuc500_dec20 2568	- ..FELILMEEIAFPRTLGPEAK -	2418.88	3	536.99	1.37	0.0	392	19/80	
phagrawFsucchlfbead_dec23, 1962	- PEDFKFQKILGEGSFSTVVLAR -	2398.74	3	1047.47	1.60	0.2	274	3/14	2
jmfag1mnacl2,5minigg,308-310	- KIQEVR -	772.92	2	932.60	1.64	0.0	561	4/5	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
CHK1_MOUSE SERINE/THREONINE-PROTEIN KINASE CHK1					5246.87	7531058.0	19		
jmfagfrench5minigg1mnackdlt, 263	-.KIDSAPLALLHK.-	1306.58	3	2436.83	1.60	0.2	906	21/44	3
jmIgG300rawphag3007, 820	-.FSSSQPEPR.-	1035.09	2	462.35	1.51	0.0	306	5/8	3
jmfag5minigg600mmnacl, 1014	-.INLVEMDEKILVDFR.-	1835.16	3	325.43	1.28	0.1	222	13/56	3
jmrawigg5minbeadsyringdnase,1049-1051	-.ITIPDIK.-	799.98	1	330.83	1.14	0.0	266	7/12	3
jmrawigg5min150mmnacl, 1126	-.SYQCLKETFEKLGYQWK.-	2152.46	3	289.78	1.31	0.1	148	17/64	3
jmfag5minigg500mmnacl, 1580	-.ATSGGMSESSSGFSK.-	1420.49	2	288.49	1.23	0.0	214	5/14	3
jmfag5minigg400mmnacl, 2130	-.PRATSGGMSESSSGFSK.-	1673.79	2	1113.16	1.56	0.2	336	11/32	3

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
CHK1_MOUSE SERINE/THREONINE-PROTEIN KINASE CHK1					51.80	7531058.0	2		
FPbeads250_Dec19, 2032	-.GKLSDVVSSQKVWFPVT.-	1878.16	2	51.80	1.04	0.0	50	7/32	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
NEK4_MOUSE Serine/threonine-protein kinase Nek4 (NimA-related protein kinase					5043.38	29337019.0	23		
jmfag5minigg350mmnacl,827-829	- KLNLRNASSR -	1159.33	2	536.81	1.48	0.1	178	1/2	2
ajrawphagjun20dpi1MNaCl,912-914	-.INIDILPAERR.-	1310.53	3	234.43	1.23	0.0	189	13/40	2
jmfag1mnacl7,5minigg,926-928	-.KLNLRNASSR.-	1159.33	2	572.89	1.56	0.1	238	2/3	2
jmfag1mnacl5minigg, 1078	-.KLNLRNASSR.-	1159.33	2	408.44	1.43	0.0	284	11/18	2
jmraw5minigg250mmnaclsyringdnase, 1178	- VVGRGSYGEVTLVKHR.-	1758.02	3	641.90	1.36	0.2	182	1/4	2
jmIgG350naclrawphag3007, 1315	- KLNLRNASSR -	1159.33	2	192.15	1.30	0.0	141	1/2	2
jm5miniggrawlowionic, 1544	- KLNLRNASSR.-	1159.33	2	245.87	1.45	0.0	158	1/2	2
jmkdlactinrawphag3007, 1248	- TNIIKVGDLGIAR.-	1370.62	2	733.04	1.11	0.2	330	11/24	2
jmkdl600naclrawphag3007, 2494	-.PDQDQVTGIIENQDSIHPR.-	2163.29	2	84.21	1.13	0.0	74	2/9	1
rawsucrfp_300phagigg_Mar04, 1671	- PDQDQVTGIIENQDSIHPR.-	2163.29	2	288.19	1.43	0.1	118	1/4	1
jmkdlactinrawphag3007, 1248	-.TNIIKVGDLGIAR.-	1370.62	2	733.04	1.11	0.2	330	11/24	2
jmkdl600naclrawphag3007, 2494	-.PDQDQVTGIIENQDSIHPR -	2163.29	2	84.21	1.13	0.0	74	2/9	1
rawsucrfp_300phagigg_Mar04, 1671	-.PDQDQVTGIIENQDSIHPR -	2163.29	2	288.19	1.43	0.1	118	1/4	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
NEK4_MOUSE Serine/threonine-protein kinase Nek4 (NimA-related protein kinase					1769.81	29337019.0	9		
rawextr_500beadigg_Mar04, 954	-.KLNLRNASSR.-	1159.33	2	576.01	1.49	0.2	168	5/9	2
jmraw5minbsafreezthaw,1414-1416	- KLNLRNASSR -	1159.33	2	298.63	1.39	0.1	144	5/9	2
jmraw5minbsafreezthaw,1414-1416	- KLNLRNASSR.-	1159.33	2	298.63	1.39	0.1	144	5/9	2
jmraw5minbsafreezthaw, 2684	- PVAAVVSRKEESNTDVIHYQPR.-	2496.76	3	496.53	1.76	0.1	183	4/21	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein kinase C-like 1; serine/threonine kinase 3 [Mus musculus]					3688.99	32813439.0	14		
jmfag1mnacl7,5minigg, 736	-.AVFYSACVVLGLQFLHEHK.-	2162.54	3	152.04	1.17	0.0	123	13/72	
jmfag1mnacl5minigg, 1004	-.QLAIELK.-	814.99	2	595.78	1.59	0.0	356	3/4	
JMFAGNACL5B2153, 1808	-.GEAENATEVSTVLKLDNTVVGQTAWK.-	2762.02	3	600.51	1.55	0.1	169	9/50	
jmag5mincon500mmnacl, 2268	-.SLGWDVLLARRLPPPFVPTLSGR.-	2549.01	3	304.91	1.40	0.0	211	17/88	
jmag5mincon500mmnacl, 2428	-.LLRRLIPSAVATGTFSPNASPGAEIR.-	2696.10	3	661.16	1.47	0.1	254	19/100	
jmraw5minigg1000mmsd, 794	-.LLSGAKAPDRK.-	1156.36	3	353.84	1.46	0.0	234	3/8	1
jmkdl450naclrawphag3007, 1260	-.DARPLTAAEQAAFRDFDFVAGGY.-	2489.68	3	87.76	1.01	0.0	85	5/44	2
jmkdl500naclrawphag3007, 1965	-.SGSLSGRSSLRGEAENATEVSTVLK.-	2536.74	2	250.07	0.88	0.1	132	5/24	1
phagrawFsuc150_dec22, 684	-.PAPLTGTLEVR.-	1154.34	2	143.82	1.14	0.0	121	7/20	1
phagrawF150_dec22, 2436	-.FLSAEAIGIMRRLLR.-	1747.15	2	539.08	1.21	0.2	104	2/7	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein kinase C-like 1; serine/threonine kinase 3 [Mus musculus]					321.51	32813439.0	14		
jmbsa300naclrawphag3007, 1995	-.QLAIELKVKQGAENMIQTYSNGSSK.-	2739.10	3	321.51	1.26	0.1	150	1/6	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
serine threonine kinase 31 [Mus musculus]					8382.82	31044416.0	28		
jmfag1mnacl5minigg, 442	-.LIEENEKLK.-	1116.29	3	904.02	1.96	0.0	441	7/16	
jmfagfrench5minigg1mnacldtt, 1027	-.ASVNAMVGGLSLLSPELK.-	1787.12	2	578.51	1.38	0.1	294	6/17	
ajrawphag1MNaCl20,1116-1118	-.LIEENEKLK.-	1116.29	3	587.37	2.17	0.1	237	13/32	
jmfag5minfrench1mnacldttdpi, 1378	-.HINISIR.-	853.01	2	298.39	0.91	0.1	225	1/2	
jmfag_20_minfrench1mnacldttdpi, 1378	-.HINISIR.-	853.01	2	298.39	0.91	0.1	225	1/2	
JMFAGNACL5B21E3, 1656	-.SESQRASVNAMVGGLSLLSPELK.-	2374.70	3	1256.23	2.22	0.2	323	21/88	
jmfagfrench20minigg1mnacldtt, 2032	-.IKATYQDGTVIAQAEYGTVDIGEEVAK.-	2871.15	3	583.46	1.37	0.1	290	5/26	
jmfag1mnacl7,5minigg, 2428	-.IKQDQKLIEENEK.-	1615.81	2	106.23	1.08	0.0	92	7/24	
jmraw5minigg250mmnaclsyringdnase, 2694	-.FGNDLSDAMQVLDEGSFTTLASLNELEK.-	3046.31	2	122.76	1.01	0.0	112	5/27	
JMFAGNACL15B21E3, 2942	-.NSVFQEIYHEREEYEKLNSLTQK.-	2886.12	3	295.00	1.27	0.1	202	2/11	
JMFAGNACL10_1B21E3, 3330	-.FGNDLSDAMQVLDEGSFTTLASLNELEK.-	3046.31	2	58.36	0.76	0.0	53	7/54	
jmldl250naclrawphag3007,1496-1498	-.SLKNPIPLWGR.-	1281.53	2	1003.68	1.64	0.2	374	3/5	
jmldl1000naclrawphag3007, 1690	-.SLKNPIPLWGR.-	1281.53	2	1252.78	1.86	0.1	448	13/20	
phagrawFsuc500_dec20, 84	-.IWAEYNVAQEKIQTCLNENEGNILIAER.-	3263.63	2	278.81	1.00	0.1	82	4/27	
phagrawFsuc500_dec20, 94	-.TCVGTRLK.-	878.08	1	189.75	0.70	0.1	64	2/7	
phagrawFsuc800_dec23, 1502	-.IKQDQKLIEENEK.-	1615.81	3	456.77	1.53	0.0	298	5/16	
phagrawFsuc450_dec20, 1932	-.ATYQDGTVIAQAEYGTVDIGEEVAK.-	2629.81	2	112.31	0.95	0.1	84	1/6	

control

serine threonine kinase 31 [Mus musculus]					1139.45	31044416.0	15		
rawextr_150beadigg2_Mar04, 1358	-.ESLAAGDFNLGSNVSLAKIKQDQK.-	2534.81	3	555.60	1.94	0.0	286	5/23	
rawextr_300beadigg_Mar4, 1808	-.DIMKIGCSLSEVCPLANSVFGNLDPKK.-	2880.40	2	72.11	1.03	0.0	58	2/13	
FPbeads150_Dec19, 2039	-.ATYQDGTVIAQAEYGTVDIGEEVAKK.-	2757.99	3	270.05	1.50	0.0	173	4/25	
jmraw5minbsafreezthaw, 152	-.LIEENEKLK.-	1116.29	3	241.68	1.37	0.0	166	1/4	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
calcium/calmodulin-dependent serine protein kinase [Mus musculus]					4016.75	6753276.0	18		
jmrawigg5minbeadsfreezethaw, 320	- KTSVLLGAHGVGR.-	1295.52	3	1669.09	1.63	0.2	705	11/24	
jmraw5minigg500mmnaclsd, 960	-.FACPIPHTTRPPKK -	1593.92	2	217.62	0.97	0.1	99	7/28	
jmrawigg5miniggfreebead, 1574	- VGTPHFMAPEVVKREPYGK.-	2143.50	3	701.36	1.39	0.0	490	1/4	1
ajrawphagjun20actinDPI, 1952	- HNAVLIIDLVTYEEVVKLPAFK.-	2512.97	3	363.04	1.38	0.0	264	17/84	
jmigG250rawphag3007, 2078	- EINGISVANQTVEQLQK.-	1872.07	2	847.47	1.86	0.1	338	13/32	1
jmfag5minigg1000mmnacl, 3024	-.LVQFQKNTDEPMGITLKMNELNHCIVAR.-	3244.80	2	43.62	0.75	0.0	58	5/27	1
ajrawphag1MNaCl20, 3128	-.DLDFLHSVFQDQHLHTLLDLYDKINTK.-	3270.64	2	42.72	0.69	0.0	46	7/52	1
phagrawF300_dec20, 1573	- KDEENGKNYYFVSHDQMMR.-	2392.61	2	85.76	1.00	0.0	84	7/36	
phagrawF500_dec20, 2026	- QGTLHVGDEIREINGISVANQTVEQLQK -	3078.38	2	46.07	0.82	0.1	31	7/54	1

control

calcium/calmodulin-dependent serine protein kinase [Mus musculus]					1482.17	6753276.0	13		
rawextr_250bead_Mar04, 1646	- ENSAPVKLGGFGVAIQLGESGLVAGGR.-	2584.91	3	717.74	1.52	0.0	464	11/52	
rawextr_200beadigg_Mar04, 1775	- TAEFPPFVVFIAAPTITPGLNEDESLQRLQK.-	3430.90	3	244.24	1.29	0.1	150	7/40	
rawextr_150bead_Mar04, 2175	-.VGTPHFMAPEVVKREPYGK.-	2143.50	3	359.48	1.10	0.1	202	7/36	
FPbeads800_Dec19, 2378	-.NPPSQAVQRAKEVLEEISCYPENNDAK -	3018.26	2	160.72	0.91	0.1	81	7/52	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
breast cancer anti-estrogen resistance 1; v-crk-associated tyrosine ki					3618.88	40254593.0	18		
ajrawphag1MNaCl20, 556	- QTSTFSK.-	798.87	2	133.90	1.07	0.0	109	1/2	1
jmfag5minigg150mmnacl, 668	- VGQGYVYEAAQTEQDEYDTPR.-	2420.49	3	787.02	1.62	0.2	227	17/80	1
JMFAGNACL5B21E3, 894	-.VGQGYVYEAAQTEQDEYDTPR.-	2420.49	3	190.20	1.35	0.0	140	7/40	1
jmigg600rawphag3007, 1032	- QTSTFSK.-	798.87	2	212.69	1.15	0.0	161	1/2	1
jmrawigg5minbeadsfreezethaw, 1356	-.AAVAAVHGAVHELLEFAR -	1862.13	3	603.20	1.37	0.0	423	9/34	1
JMFAGNACL10_1B21E3, 1672	-.VLPPEVADGSVVDDGVYAVPPPAEREAPTDGKR.-	3404.73	2	100.61	0.99	0.1	32	1/8	1
jmfag1mnacl5mncon, 1698	-.ALYDNVAESPDELSFR.-	1826.94	2	639.66	1.50	0.2	188	3/10	1
jm5miniggrawlowonic, 2722	-.QAKAADVRSQVTHYSNLLCDLLR.-	2602.96	3	611.58	1.57	0.0	369	19/88	1
phagrawF500_dec20, 1388	-.VLPPEVADGSVVDDGVYAVPPPAER.-	2549.82	3	208.43	1.50	0.0	123	17/98	1
phagrawF800_Dec23, 2814	- LEQEVSRPIDHDLANWTPAQPLVPGR.-	2940.26	2	131.39	1.22	0.0	98	9/50	1

control

breast cancer anti-estrogen resistance 1; v-crk-associated tyrosine ki					1035.84	40254593.0	14		
rawextr_350beadigg2_Mar04, 216	- RVLGQLAAA.-	899.07	3	336.88	1.00	0.1	125	9/32	1
rawextr_350beadigg2_Mar04,480-482	-.PPAKVVVPTR.-	1064.31	3	210.09	1.12	0.1	125	13/36	1
rawextr_900beadigg_Mar04, 1430	-.VLPPEVADGSVVDDGVYAVPPPAER.-	2549.82	2	158.77	1.19	0.1	89	5/24	1
FPbeads400_Dec19, 2036	-.LEQEVSRPIDHDLANWTPAQPLVPGR.-	2940.26	2	88.53	0.95	0.0	67	4/25	1
jmbsaactinrawphag3007,1431-1433	-.FVILSAHK.-	915.12	1	281.56	1.15	0.0	227	4/7	8

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
CRKL_MOUSE Crk-like protein					**2880.83**	1345822.0	2		
RawPhg2007MeEthmeth3digest, 1624	-.GLFPFTHVKIFDPQNPDDNE.-	2331.52	3	404.75	1.68	0.0	237	5/19	1
jmldl400firstnaclrawphag3007,2194-2196	-.GELLVIIEKPEEQWWSARTK.-	2413.76	3	649.63	1.67	0.2	108	13/76	
jmraw5minigg500mmnaclsd, 1482	-.GELLVIIEK.-	1014.24	2	379.48	1.31	0.1	180	9/16	1
jmrawrminigg200mmnaclsyringdnas,1486-1488	-.GELLVIIEK.-	1014.24	2	798.65	1.78	0.1	256	5/8	1
rawsucrfp_actinphagigg_Mar04, 838	-.IHYLDTTTLIEPAPR.-	1740.98	2	135.26	1.12	0.1	84	2/7	1
ajrawmediapbsnocells, 996	-.GELLVIIEK.-	1014.24	2	331.50	1.21	0.1	125	7/16	1
phagrawFsuc450_dec20, 2000	-.TALALEVGDIVKVTRMNINGQWEGEVNGR.-	3171.58	3	181.57	1.10	0.0	153	9/56	1

control

CRKL_MOUSE Crk-like protein					**1590.97**	1345822.0	2		
FPbeads500_dec19, 2152	-.TLYDFPGNDAEDLPFKKGELLVIIEK.-	2966.37	2	74.05	0.94	0.0	78	7/50	1
FPbeads300_Dec19, 2618	-.TLYDFPGNDAEDLPFKKGELLVIIEK.-	2966.37	2	89.65	1.03	0.0	74	4/25	1
jmraw5minbsabeads, 2650	-.TKDGRVGMIPVPYVEK.-	1790.12	2	1427.28	1.44	0.3	246	1/3	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Nck-interacting kinase-like embryo specific kinase [Mus musculus]					**6605.09**	6472874.0	28		
jmrawgg5min150mmnacl, 418	- ILNNDPKSKK -	1157.35	3	450.57	1.61	0.1	198	7/18	1
jmrawgg5min450mmnaclsd, 932	- HRRWEDIFNQHEEQLR.-	2194.36	3	786.87	1.71	0.1	433	3/10	1
jmrawgg5minbeadsyringdnase, 979	- AAGVFMPLHSQDNTSKLFPK -	2189.52	3	242.77	1.12	0.1	120	13/76	1
jmrawgg5min450mmnaclsd,1072-1074	- SLQSTILENELK.-	1375.55	2	662.11	2.02	0.0	324	1/2	1
jmfagfrench20minigg1mnacldtt, 1308	-.PVSSTTMGFPIGRSSPR.-	1778.03	3	274.77	1.31	0.0	206	1/4	1
jmIgG150rawphag3007, 1442	- SLQSTILENELK -	1375.55	2	302.91	1.27	0.0	225	1/2	1
jm5miniggrawlowonic,1582-1584	- AIEVRSLQSTILENELK.-	1944.22	3	465.83	1.82	0.0	256	1/4	1
jmfag5minigg500mmnacl, 1768	- AQAWDLEASRAVGAVQALIEGLSR -	2512.81	3	679.69	1.65	0.1	330	19/92	1
jmfag1mnacl2,5minigg, 1848	- AQAWDLEASRAVGAVQALIEGLSRDLLR.-	3010.40	2	146.98	0.94	0.1	110	5/27	1
JMFAGNACL10_1B21E3, 3154	-.QIQVVEQLNLLITISGK.-	1897.25	1	57.78	0.79	0.0	49	5/32	1
phagrawFsuc250_dec22, 875	- AGILKNGHNDGRALNR.-	1706.89	2	143.70	0.86	0.0	166	3/10	1
rawsucrfp_350phagigg_Mar04, 946	- EKKGIPVAFEGEEAAK.-	1703.92	3	383.02	1.56	0.0	244	19/60	1
phagrawFsuc200_dec22, 1091	- SLQSTILENELK.-	1375.55	2	341.03	1.66	0.0	196	9/22	1
phagrawFsuc60MeOH_dec23, 1154	-.VYLMSLGKLEELHR.-	1689.02	2	293.69	1.27	0.1	174	11/26	2
rawsucrfp_500phagigg_Mar04, 1440	- SQSSPPYSTIDQKLLIDIHVPDGFK.-	2787.12	3	1173.90	1.66	0.2	268	7/32	1
phagrawFsuc600_dec20, 2364	-.NCLNPQNFQAQSDSSSEEDSPVTR.-	2654.72	2	115.77	0.79	0.1	79	7/46	1
phagrawF1000_Dec23, 3068	-.NCLNPQNFQAQSDSSSEEDSPVTR.-	2654.72	2	83.73	0.89	0.0	91	4/23	1

control

Nck-interacting kinase-like embryo specific kinase [Mus musculus]					**867.02**	6472874.0	28		
jmraw5minbsabeads, 1548	-.AIEVRSLQSTILENELK.-	1944.22	2	867.02	2.21	0.0	386	3/8	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
p21-activated kinase 2 [Mus musculus]					**2608.54**	28493842.0	9		
jmfag5minigg200mmnacl, 716	-.QKYLSFTPPEK.-	1338.53	3	737.67	1.61	0.0	457	9/20	
jmrawigg5minbeadsfreezethaw, 1566	-.MSDNGELEDKPPAPPVR.-	1853.05	2	117.52	1.24	0.0	94	9/32	
jmrawrminigg200mmnaclsyringdnas, 1592	-.SVIDPIPAPVGDSNVDSGAK.-	1939.11	2	1518.14	1.73	0.3	190	6/19	
jmfag5minigg300mmnacl, 1788	-.AKMTDEEIMEK.-	1325.54	2	235.21	1.05	0.1	180	9/20	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
p21-activated protein kinase 4 [Mus musculus]					**6849.56**	29336032.0	4		
jmldl150naclrawphag3007, 1248	-.AGPPASIVPLMR.-	1209.49	2	965.92	1.29	0.0	737	13/22	4
rawsucrfp_chlfphagigg_Mar04, 696	-.AALQLVVDPGDPR.-	1351.53	3	251.73	1.28	0.0	186	5/16	3
rawsucrfp_60MeOHphagigg_MAr04, 1076	-.AGPPASIVPLMRQHRTR.-	1888.23	3	354.36	1.32	0.0	269	1/4	4
phagrawF150_dec22, 1404	-.LLVRDPAQRATAAELLK.-	1866.20	2	83.14	0.95	0.0	84	7/32	3
jmIgG350naclrawphag3007,1357-1359	-.VHTGFDQHEQK.-	1326.40	2	430.13	1.33	0.0	303	1/2	2
jmIgG250rawphag3007, 1564	-.GAPSPGVLGPHASEPQLAPPAR.-	2107.36	3	707.21	1.66	0.2	156	3/14	3
jmfag5minigg150mmnacl, 1832	-.SDSILLTHDGRVK.-	1441.62	2	115.78	0.84	0.0	134	7/24	4
jmIgG400rawphag3007, 1848	-.ATGHSEAGSGSGDR.-	1289.25	2	1075.23	1.38	0.2	306	6/13	2
jmfag1mnacl5minigg, 2030	-.DGALTLLLDEFENMSVTRSNSLR.-	2582.87	3	755.24	1.68	0.1	388	19/88	2
jmfag5minigg1000mmnacl,2370-2372	-.DGPGGPQEASRDK.-	1314.34	2	569.54	1.59	0.1	307	5/12	2
jmbeads250rawphag3007, 1040	-.GAPSPGVLGPHASEPQLAPPAR.-	2107.36	3	235.11	1.65	0.0	126	4/21	3
jmbeads350rawphag30072nd, 1416	-.VHTGFDQHEQK.-	1326.40	2	786.26	1.55	0.1	384	11/20	2
jmfagcon5min1000mmnacl_030601180404, 1422	-.DIKSDSILLTHDGRVK.-	1798.04	2	247.39	1.18	0.0	210	1/3	4
jmbeads350rawphag30072nd, 1634	-.GAPSPGVLGPHASEPQLAPPAR.-	2107.36	3	272.51	1.46	0.0	185	19/84	3

control

p21-activated protein kinase 4 [Mus musculus]					**1729.84**	29336032.0	11		
rawextr_250beadigg_Mar04, 1548	-.ATGHSEAGSGSGDRR.-	1445.44	2	696.48	1.33	0.1	437	11/28	2
rawextr_actinbeadigg_Mar04, 1559	-.PKPLIDPACITSIQPGAPKTIVR.-	2416.91	3	798.66	1.59	0.1	446	5/22	2
jmbsa150naclrawphag3007, 1145	-.ATAAELLKHPFLTK.-	1540.83	2	234.70	1.34	0.0	173	9/26	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
p21-activated kinase 5 [Mus musculus] ix-associate					**3189.61**	40037528.0	10		
jmfag1mnacl5minigg,628-630	-.YRDRSLYGDDLDLYYK.-	2056.22	3	263.35	1.39	0.0	190	4/15	2
jmIgG400rawphag3007, 792	-.SDSILLTSDGR.-	1164.25	3	1215.54	1.36	0.2	451	7/20	2
jmfag1mnacl0minigg, 898	-.ALSYLHNQGVIHR.-	1508.71	2	1610.03	1.30	0.3	316	5/12	2
jmrawigg5min1mnacl, 2193	-.IGEGSTGIVCIATEKHTGK.-	1902.16	2	100.69	0.94	0.1	50	2/9	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (P18					**24545.06**	38083746.0	3		
jmfag5minigg350mmnacl, 915	-.DRPFFPGLVK.-	1176.39	2	506.66	1.40	0.0	361	4/9	2
jmfag5minigg350mmnacl, 919	-.DRPFFPGLVK.-	1176.39	2	2603.33	1.96	0.3	618	13/18	2
jmfag5minigg600mmnacl,936-938	-.DRPFFPGLVK.-	1176.39	2	4275.45	2.85	0.2	917	7/9	2
jmfag1mnacl2,5minigg,1020-1022	-.DRPFFPGLVK.-	1176.39	2	1310.28	1.92	0.1	588	13/18	2
jmfag1mnacl7.5minigg,1032-1034	-.DRPFFPGLVK.-	1176.39	2	1801.46	2.18	0.2	535	13/18	2
jmfag5minigg400mmnacl,1076-1078	-.DRPFFPGLVK.-	1176.39	2	1928.83	2.19	0.2	387	11/18	2
jmfag5minigg200mmnacl, 1138	-.DRPFFPGLVK.-	1176.39	2	1741.61	1.72	0.0	1011	7/9	2
jmfag1mnacl5minigg, 1186	-.DRPFFPGLVK.-	1176.39	2	677.60	1.33	0.1	480	11/18	2
jmIgG400rawphag3007, 1332	-.TGXVMLGETNPADSKPGTIR.-	2058.35	3	825.09	1.39	0.0	575	11/38	
jmfag5minigg450mmnacl_030527025134,1628-1630	-.DRPFFPGLVK.-	1176.39	2	841.34	1.46	0.1	400	5/9	2
jmfag5minigg200mmnacl, 1698	-.EIHLWFKPEELIDYK.-	1961.25	2	3706.25	1.85	0.3	798	15/28	1
jmIgG500rawphag3007,1145-1147	-.HQTTYWFSNQGK.-	1497.60	3	360.35	1.38	0.1	139	3/11	
jmrawigg5min1mnacl, 1295	-.TNKDSGT.-	722.73	2	210.53	0.87	0.1	201	1/2	
jmrawigg5min150mmnacl, 1348	-.TNKDSGT.-	722.73	2	239.72	0.86	0.1	192	1/2	
jm5miniggrawlowionic, 2054	-.TNKDSGT.-	722.73	2	1062.46	1.02	0.3	166	1/2	
jm5miniggrawlowionic, 2062	-.TNKDSGT.-	722.73	2	305.82	0.81	0.1	241	7/12	
ajrawphag1MNaCl20, 2260	-.TNKDSGT.-	722.73	2	255.48	0.95	0.1	124	5/12	
jmldl150naclrawphag3007, 1888	-.GQIIKCFEQK.-	1194.43	2	582.66	1.46	0.1	291	11/18	
jmraw5minigg500mmnaclsd, 328	-.PDGGQRSLR.-	986.07	3	893.16	1.54	0.1	492	3/8	
jmrawigg5min400mmnaclsd, 1311	-.GFCLVAMKFLHTSEK.-	1712.07	2	212.02	1.06	0.0	177	9/28	
rawsucrfp_actinphagigg_Mar04,1196-1198	-.TNKDSGT.-	722.73	1	204.99	0.80	0.1	88	1/2	

control

similar to Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (P18					**3710.61**	38077292.0	3		
rawextr_800beadigg_Mar04, 1068	-.AHDWGYEQTWINRNPFWHY.-	2521.69	3	1218.83	2.06	0.2	234	19/72	
jmraw5minbsareebeads, 896	-.QHYTVLK.-	889.03	2	245.46	0.98	0.1	154	1/2	
jmraw5minbsareebeads, 908	-.QHYTVLK.-	889.03	2	505.29	1.53	0.1	290	2/3	
jmraw5minbsareebeads, 1842	-.PQVHFHCHQARWCTAGLLWAR.-	2518.91	3	856.95	1.66	0.2	266	19/80	
jmrawbsa5minlowionic, 1838	-.TNKDSGT.-	722.73	2	560.60	0.90	0.2	104	5/12	
jmraw5minbsafreezthaw, 1926	-.TNKDSGT.-	722.73	2	178.15	0.98	0.0	169	1/2	
jmrawbas5min1mnacl,2054-2056	-.TNKDSGT.-	722.73	2	145.35	1.01	0.0	144	5/12	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
nucleoside-diphosphate kinase 1; nucleotide diphosphate kinase [Mus mu					100772.79	37700232.0	4		
jmfag5minggbead,543-545	- VMLGETNPADSKPGTIR.-	1787.03	3	3938.95	2.62	0.3	447	21/64	5
jmfag1mnacl0mingg,604-606	-.VMLGETNPADSKPGTIR.-	1787.03	3	6479.78	2.43	0.4	693	29/64	5
JMMAGNEGB16D3, 646	-.VMLGETNPADSKPGTIR.-	1787.03	3	3609.89	2.34	0.3	430	11/32	5
jmfag1mnacl2.5mingg, 686	- VMLGETNPADSKPGTIR.-	1787.03	3	4972.65	2.41	0.4	354	11/32	5
jmfag1mnacl7.5mingg, 702	- VMLGETNPADSKPGTIR.-	1787.03	3	10689.45	3.26	0.5	507	27/64	5
jmfag5mingg1000mmnacl, 772	-.VMLGETNPADSKPGTIR.-	1787.03	3	6952.82	2.96	0.4	666	7/16	5
jmfag5mingg200mmnacl,780-782	-.VMLGETNPADSKPGTIR.-	1787.03	3	5610.78	2.39	0.4	501	25/64	5
jmfag1mnacl5mingg, 816	-.VMLGETNPADSKPGTIR -	1787.03	3	3690.92	2.16	0.4	309	21/64	5
jmfag1mnacl5mingg, 824	-.VMLGETNPADSKPGTIR.-	1787.03	3	2647.29	2.31	0.3	290	11/32	5
jmfag5mingg350mmnacl, 935	- FLQASEDLLK.-	1164.33	2	3429.93	2.39	0.3	758	13/18	1
jmfag5mingg250mmnacl, 1056	- VMLGETNPADSKPGTIR -	1787.03	3	5622.91	2.53	0.4	611	27/64	5
jmfag5mingg450mmnacl_030527025134, 1216	- VMLGETNPADSKPGTIR.-	1787.03	3	4722.39	2.69	0.4	264	5/16	5
jmfag5mingg300mmnacl, 1234	- VMLGETNPADSKPGTIR -	1787.03	3	3782.12	2.07	0.4	432	3/8	5
ajrawmediapbsnocells, 602	- VMLGETNPADSKPGTIR -	1787.03	3	2807.29	2.07	0.3	258	19/64	5
jmfag5mingg350mmnacl, 613	-.VMLGETNPADSKPGTIR.-	1787.03	3	1766.67	1.70	0.3	318	23/64	5
jmfag5mingg600mmnacl, 618	- VMLGETNPADSKPGTIR.-	1787.03	3	944.55	1.64	0.2	196	9/32	5
jmfag5mingg600mmnacl, 622	- VMLGETNPADSKPGTIR.-	1787.03	3	5324.67	2.57	0.4	296	11/32	5
jmfag5mingg150mmnacl, 642	-.VMLGETNPADSKPGTIR.-	1787.03	3	970.87	1.81	0.1	388	23/64	5
jmfag1mnacl2.5mingg, 686	- VMLGETNPADSKPGTIR.-	1787.03	3	4972.65	2.41	0.4	354	11/32	5
jmfag5mingg400mmnacl,736-738	- VMLGETNPADSKPGTIR.-	1787.03	3	1453.95	1.66	0.2	393	3/8	5
jmfag1mnacl7.5mingg, 762	- TFIAIKPDGVQR.-	1345.57	3	1489.30	2.01	0.2	313	15/44	4
jmfag5mingg1000mmnacl, 772	- VMLGETNPADSKPGTIR.-	1787.03	3	6952.82	2.96	0.4	666	7/16	5
jmfag5mingg250mmnacl, 1052	-.VMLGETNPADSKPGTIR -	1787.03	3	2069.95	1.68	0.3	276	9/32	5
jmfag5mingg450mmnacl_030527025134, 1220	-.VMLGETNPADSKPGTIR.-	1787.03	3	1651.53	1.72	0.3	238	19/64	5
jmidlactinrawphag3007, 1528	- TGRVMLGETNPADSK.-	1576.76	3	494.79	1.39	0.1	322	3/8	5
ajrawmediapbsnocells, 598	-.VMLGETNPADSKPGTIR.-	1787.03	3	1758.80	1.81	0.2	460	11/32	5
ajrawmediapbsnocells, 678	- TFIAIKPDGVQR.-	1345.57	3	1965.10	1.64	0.3	356	9/22	4

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
KIMSCD protein kinase C (EC 2.7.1.-) delta - mouse					2907.04	66731.0	12		
phagrawFsucchlf_dec23, 1482	-.LDTTESVGIYQGFEK.-	1687.83	2	743.11	1.12	0.2	227	5/14	3
phagrawFsuc600_dec20, 3152	- MAPFLRISFNSYELGSLQVEDEASQPFCAVK.-	3478.94	2	52.27	0.77	0.0	48	7/60	3
ajrawphagactin20, 642	-.FNIDMPHRFK.-	1305.53	3	627.68	1.36	0.0	458	7/18	2
jmrawigg5min150mmnacl, 1200	-.IIGRCTGTATNSR.-	1350.53	2	386.08	1.38	0.0	256	5/12	2
jmIgG300rawphag3007, 1862	-.EALSTERGKTLVQK -	1560.78	2	219.87	1.33	0.1	52	3/13	3
jm5miniggrawlowionic, 3126	-.VIQIVLMRAAEDPVSEVTVGVSVLAER.-	2882.37	2	257.80	0.91	0.1	118	11/52	3
jmfagtimecon2.5min.2142.2142.3	-.SPSDYSNFDPEFLNEKPQLSFSDK.-	2792.95	0	289.57	1.29	0.0	220	21/92	2
RawPhg2007MeEthmeth3digest, 2166	-.DTIFQKERFNIDMPHR.-	2048.31	3	278.39	1.39	0.0	177	13/60	2
phagrawFsuc600_dec20, 3152	-.MAPFLRISFNSYELGSLQVEDEASQPFCAVK -	3478.94	2	52.27	0.77	0.0	48	7/60	3

control

KIMSCD protein kinase C (EC 2.7.1.-) delta - mouse					642.49	66731.0			
rawextr_200beadigg_Mar04, 1963	- EFVWGLNKQGYKCR.-	1729.00	2	642.49	1.32	0.2			

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
LYN_MOUSE Tyrosine-protein kinase LYN					2641.95	2507208.0	6		
jmfag5mingg500mmnacl, 2826	-.AEERPTFDYLQSVLDDFYTATEGQYQQQP.-	3441.62	2	715.20	1.14	0.2	47	1/8	1
jmraw5mingg500mmnaclsd, 1664	-.DAERQLLAPGNSAGAFLIR.-	2000.25	3	1299.87	1.58	0.2	470	7/24	1
jmfagfrench20mingg1mnacldtt, 2694	-.SDEGGKVLLPKLIDFSAQIAEGMAYIER.-	3052.49	2	124.85	0.89	0.1	90	5/27	2
rawphag2007chlfsol2, 1440	-.NTDRTIYVRDPTSNK.-	1780.92	2	184.30	1.08	0.0	171	9/28	1
rawphag2007chlfsol2, 2828	-.KDNLNDDEVDSKTQPVR.-	1974.08	1	181.19	0.83	0.1	124	1/4	1
jmrawbas5min1mnacl, 2118	-.KNYIHR.-	830.96	2	136.55	0.80	0.1	65	2/5	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Hematopoietic cell specific Lyn substrate 1 [Mus musculus]					**18504.27**	13938627.0		4	
jmrawigg5minigg freebead, 880	-.SAVGFNEMEAPTTAYK.-	1716.89	2	2714.07	2.22	0.3	545	1/2	1
jmfag1mnacl5minigg, 354	- SAVGHEYVADVEK.-	1404.51	3	720.99	1.94	0.1	335	3/8	2
jmfag1mnacl0minigg, 696	-.KTTPIEAASSGARGLK.-	1587.80	2	1478.87	1.89	0.0	780	17/30	1
jmIgG300rawphag3007, 1214	-.DRVDKSAVGFNEMEAPTTAYK.-	2330.56	3	231.35	1.20	0.0	191	17/80	1
jmraw5minigg1000mmsd, 1356	-.ELESGPKASHGYGGR.-	1545.64	2	311.51	1.18	0.1	208	5/14	1
jmIgG250rawphag3007,2318-2320	-.HSSQTDAARGFGGKYGVER.-	2024.14	3	593.03	1.56	0.0	379	5/18	2
jmfag1mnacl5minigg, 2740	-.EEEEKAQQMARQQQER.-	2019.14	3	1205.68	2.08	0.0	578	7/20	1
jmfag1mnacl5mincon, 378	-.SAVGHEYVADVEK.-	1404.51	3	4792.17	2.53	0.4	631	1/2	2
AJRAWSoluteContr_jun13, 736	-.TTPIEAASSGARGLK.-	1459.63	2	482.59	1.70	0.0	265	5/14	1
jmfag5mincon250mmnacl, 1324	-.QSPLQNHLEDNEEPPALPPR.-	2282.46	3	660.97	1.58	0.0	416	9/38	1
jmfreebeadsrawphag3007,1212-1214	- KTTPIEAASSGARGLK.-	1587.80	2	1821.17	2.19	0.1	629	7/15	1
rawsucrfp_350phagigg_Mar04, 1428	- KTTPIEAASSGARGLK.-	1587.80	2	617.64	1.44	0.1	309	2/5	1
rawsucrfp_600phagigg_Mar04,1450-1452	-.KTTPIEAASSGARGLK.-	1587.80	2	500.69	1.48	0.0	335	1/3	1
phagrawF200_dec22, 1617	- ISSEVWPPAESHLPPESQPVRSRR.-	2743.03	3	371.74	1.45	0.0	240	9/46	1
phagrawFsuc450_dec20, 2178	- KTTPIEAASSGARGLK.-	1587.80	2	2001.81	1.67	0.2	643	13/30	1

control

hematopoietic cell specific Lyn substrate 1 [Mus musculus]					**664.90**	6680187.0		2	
rawextr_450beadigg_Mar04, 864	- ELESGPKASHGYGGQFGVER.-	2106.24	3	664.90	1.59	0.1	325	9/38	
FPbeads300_Dec19, 1510	-.KTTPIEAASSGARGLK.-	1587.80	2	576.32	1.43	0.0	398	2/5	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
KSYK_MOUSE Tyrosine-protein kinase SYK (Spleen tyrosine kinase)					11911.30	1711636.0		14	
JMMAGTube1B16E3, 160	- GMKGSEVTAMLEKGER.-	1724.00	3	760.75	1.91	0.0	398	19/60	
jmfag5minigg150mmnacl,562-564	- NVLLVTQHYAK.-	1286.51	2	1829.32	1.55	0.3	361	11/20	
jmfag1mnacl7.5minigg,602-604	- NVLLVTQHYAK.-	1286.51	2	605.58	1.38	0.1	293	1/2	
jmfag1mnacl5mincon,734-736	-.NVLLVTQHYAK.-	1286.51	2	447.03	1.32	0.0	339	11/20	
rawsucrfp_900phagigg_Mar04,1239-1241	-.EMYDLMNLCWTYDVENRPGFTAVELRLR.-	3436.93	3	861.38	2.00	0.2	125	4/27	2
phagrawFsuc500_dec20, 2356	- KPFNRPPGVQPK.-	1365.61	2	421.71	1.36	0.1	274	5/11	2
jmfagfrench20minigg1mnacldtt,1842-1844	-.PQLEKLIATTAHEK.-	1579.82	2	2210.47	2.67	0.0	805	15/28	2
jmfagtimecon2.5min,680,682.2	-.NVLLVTQHYAK.-	1286.51	0	1793.67	1.62	0.3	300	9/20	2
jmfagtimecon7.5min,850,850.2	-.NVLLVTQHYAK.-	1286.51	0	852.54	1.54	0.2	253	9/20	2
jmfagtimecon10min, 70	- EALPMDTEVYESPYADPEEIRPKEVYLDR.-	3458.78	2	230.06	0.88	0.1	167	5/28	2
jmfag1mnacl5mincon,734-736	- NVLLVTQHYAK.-	1286.51	2	447.03	1.32	0.0	339	11/20	2
AJRAWpellet1_contr_jun13, 1352	- AHASPADLCHYHSQEPDGLICLLK.-	2619.96	3	451.24	1.28	0.0	333	5/23	2
jmbeads400rawphag3007, 1602	-.LSIPEGKKFDTLWQLVEHYSYK.-	2683.05	3	176.65	1.16	0.0	136	17/84	2
jmfag5mincon250mmnacl, 2040	- KAHHYTIER.-	1155.29	2	274.29	0.98	0.1	122	3/8	2
jmfagcon5minn600mmnacl, 2065	- VVKTVAVK.-	844.08	1	96.71	0.69	0.0	122	5/14	2
phagrawFsuc500_dec20, 2356	-.KPFNRPPGVQPK.-	1365.61	2	421.71	1.36	0.1	274	5/11	2
jmfagtimecon10min, 3700	-.SLLTLEDNELGSGNFGTVK.-	1995.18	1	31.18	0.65	0.0	45	1/6	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine kinase TecIII [Mus musculus]					**54184.90**	5453033.0		7	
rawsucrfp_350phagigg_Mar04, 1006	-.NNNNIMIK.-	961.12	2	1753.53	2.24	0.1	757	6/7	6
rawsucrfp_300phagigg_Mar04, 1095	-.NNNNIMIK	961.12	1	524.88	1.54	0.0	336	9/14	6
phagrawFsuc450_dec20, 1882	-.NNNNIMIK.-	961.12	1	548.65	1.51	0.0	356	9/14	6
JMMAGNEGB16D3, 764	-.NNNNIMIK.-	961.12	2	1149.77	1.81	0.0	634	11/14	6
JMMAGNEGB16D3, 1056	-.MNFNTILEEILIKRSQQK.-	2206.60	3	361.77	1.85	0.0	191	5/17	6
JMFAGNACL10_1B21E3, 1250	-.NNNNIMIK.-	961.12	1	564.82	1.63	0.0	330	9/14	6
jmidl600naclrawphag3007,1210-1212	-.NNNNIMIK.-	961.12	2	2749.51	2.80	0.0	976	6/7	6
jmidl400firstnaclrawphag3007,1210-1212	-.NNNNIMIK.-	961.12	2	1987.46	2.43	0.0	817	6/7	6
jmidl250naclrawphag3007,1228-1230	-.NNNNIMIK.-	961.12	2	2301.69	2.73	0.1	799	6/7	6
jmidl60MeOHrawphag3007, 1236	-.NNNNIMIK.-	961.12	2	1003.08	1.98	0.0	505	5/7	6
jmidl500naclrawphag3007,1305-1307	-.NNNNIMIK.-	961.12	2	1757.93	2.37	0.0	738	6/7	6
jmidl300naclrawphag3007,1410-1412	-.NNNNIMIK.-	961.12	2	2007.32	2.33	0.0	848	6/7	6
jmidl150naclrawphag3007,1460-1462	-.NNNNIMIK.-	961.12	2	1888.05	2.22	0.1	824	6/7	6
rawphag2007chfbead2, 650	-.NNNNIMIK.-	961.12	2	1696.81	2.05	0.1	798	6/7	6
rawphag2007chfbead2, 654	-.NNNNIMIK.-	961.12	2	2164.88	2.41	0.1	858	6/7	6
rawphag2007chfsol3, 879	-.NNNNIMIK.-	961.12	2	368.46	0.86	0.0	417	4/7	6
rawphag2007chfbead1, 1290	-.NNNNIMIK.-	961.12	1	312.62	1.38	0.0	220	1/2	6
RawPhag2007EtBeadsdigest_030718152503, 2166	-.EGGFMVRDSSQPGLYTVSLYTKFGGEGSSGFR.-	3418.74	2	18.78	0.70	0.0	27	3/31	7
jmbeads300rawphag3007,700-702	-.NNNNIMIK.-	961.12	2	2250.61	2.48	0.0	903	6/7	6
jmbeads450naclrawphag3007,762-764	-.NNNNIMIK.-	961.12	2	1102.08	1.99	0.0	553	11/14	6
jmbeads450naclrawphag3007, 903	-.NDDGVIPCQNK.-	1203.31	2	1909.51	2.13	0.1	816	13/20	6
jmbeads600naclrawphage3007,928-932	-.NNNNIMIK.-	961.12	2	1739.31	2.29	0.1	729	6/7	6
jmbeads350rawphag30072nd,1312-1314	-.NNNNIMIK.-	961.12	2	1382.80	2.27	0.1	579	11/14	6
jmbeads500rawphag3007, 1475	-.LERGQEYIILEKNDLHWWR.-	2499.81	2	249.12	1.43	0.1	139	2/9	7
jmfagtimecont10min_030601202502, 2314	-.MNFNTILEEILIKR.-	1735.09	2	170.78	1.36	0.1	93	7/26	6
jmfagtimecon10min, 2344	-.DMLLSMCQDVCEGMEYLER.-	2266.65	3	692.14	1.55	0.2	312	19/72	7
jmbeads150rawphag3007, 2556	-.NAPTTAGFSYDKWEINPSELTFMR.-	2777.06	2	94.55	0.91	0.0	83	7/46	7
jmfagtimecon10min, 2718	-.FWADGSYQCCRQTEK.-	1823.00	2	300.71	1.23	0.1	115	1/4	6
jmrawigg5min300mmnaclsyringednase, 619	-.NNNNIMIK.-	961.12	1	449.36	1.25	0.0	349	9/14	6
jmrawigg5min300mmnaclsyringednase, 623	-.NNNNIMIK.-	961.12	1	838.72	1.69	0.1	433	9/14	6
jmrawigg5min150mmnacl,806-808	-.NNNNIMIK.-	961.12	2	1506.23	2.13	0.0	694	6/7	6
jmrawigg5min450mmnaclsd,818-820	-.NNNNIMIK.-	961.12	1	963.48	2.00	0.1	320	9/14	6
jmraw5minigg1000mmsd, 994	-.NNNNIMIK.-	961.12	1	1232.72	1.89	0.1	512	9/14	6
jmraw5minigg500mmnaclsd, 1202	-.NNNNIMIK.-	961.12	1	719.47	1.99	0.0	361	9/14	6
jmIgG250rawphag3007,1202-1204	-.NNNNIMIK.-	961.12	2	2262.98	2.77	0.0	812	6/7	6
jmIgG300rawphag3007, 1212	-.NNNNIMIK.-	961.12	2	1923.07	2.11	0.1	836	6/7	6
jmIgG400rawphag3007,1220-1222	-.NNNNIMIK.-	961.12	2	1940.40	2.80	0.0	692	6/7	6
jmIgG350naclrawphag3007, 1235	-.NNNNIMIK.-	961.12	2	1466.82	2.06	0.0	689	11/14	6
jmigg450rawphag3007,1242-1244	-.NNNNIMIK.-	961.12	2	2047.67	2.40	0.0	846	6/7	6
JMFAGNACL10_1B21E3, 1250	-.NNNNIMIK.-	961.12	1	564.82	1.63	0.0	330	9/14	6
jmigg450rawphag3007, 1252	-.NNNNIMIK.-	961.12	1	579.03	1.58	0.0	353	9/14	6
jmigg450rawphag3007, 1262	-.NNNNIMIK.-	961.12	1	1088.77	1.61	0.2	390	9/14	6
jmigg600rawphage3007, 1416	-.NNNNIMIK.-	961.12	2	1619.06	2.30	0.0	698	6/7	6
jmIgG1000naclrawphag3007,1638-1640	-.NNNNIMIK.-	961.12	2	1352.30	2.01	0.0	670	6/7	6
jmIggactinrawphag3007, 2788	-.SDVWSFGVLMWEIFTEGRMPFEK.-	2793.21	3	378.40	1.40	0.0	268	19/88	7

control

protein tyrosine kinase TecIII [Mus musculus]					**21096.49**	5453033.0		16	
FPbeads350_Dec19, 1055	-.NNNNIMIK.-	961.12	1	607.61	1.85	0.0	329	9/14	6
rawextr_chfbead_Mar04, 2028	-.DMLLSMCQDVCEGMEYLERNSFIHR.-	3021.49	2	189.74	1.26	0.0	151	5/24	7
rawextr_300beadigg_Mar4, 2126	-.FPVKWCPPEVFNYSR.-	1870.17	2	526.22	1.56	0.1	225	9/28	7
jmbsa250naclrawphag3007, 138	-.VMMKLTHPK.-	1085.41	3	154.66	0.73	0.0	203	5/16	7
jmbsa350naclrawphag3007,674-676	-.NNNNIMIK.-	961.12	2	2676.57	2.45	0.1	1051	6/7	6
jmbsa250naclrawphag3007,676-678	-.NNNNIMIK.-	961.12	1	607.76	1.93	0.0	314	4/7	6
jmbsa400naclrawphag3007_030802135631,691-693	-.NNNNIMIK.-	961.12	2	1825.79	2.47	0.0	732	6/7	6
jmbsa350naclrawphag3007, 712	-.NNNNIMIK.-	961.12	1	877.78	1.92	0.1	387	9/14	6
jmbsa500naclrawphag3007,764-766	-.NNNNIMIK.-	961.12	2	2780.36	2.72	0.1	969	6/7	6
jmbsa150naclrawphag3007,853-855	-.NNNNIMIK.-	961.12	2	2003.86	2.61	0.0	765	6/7	6
jmbsa150naclrawphag3007,865-867	-.NNNNIMIK.-	961.12	1	758.64	1.91	0.0	388	9/14	6
jmbsa300naclrawphag3007,895-897	-.NNNNIMIK.-	961.12	2	1681.94	2.01	0.0	827	6/7	6
jmbsa450naclcrawphag3007,897-899	-.NNNNIMIK.-	961.12	2	2240.50	2.58	0.1	822	6/7	6
jmbsa300naclrawphag3007, 913	-.NNNNIMIK.-	961.12	1	554.33	1.53	0.1	285	4/7	6
jmbsa1000naclrawphag3007, 1385	-.NNNNIMIK.-	961.12	2	2022.51	2.27	0.0	882	6/7	6
jmraw5minbsabeads,1428-1430	-.NNNNIMIK.-	961.12	2	1588.22	2.36	0.1	646	6/7	6

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions
CSK_MOUSE Tyrosine-protein kinase CSK (C-SRC kinase) (Protein-tyrosine kinase M					**2709.32**	729888.0		14
jmfag5minigg350mmnacl, 615	-.DVVPRVEKGYK.-	1290.49	2	105.35	0.86	0.0	119	3/10
jmraw5miniggiowionic, 651	-.DVVPRVEK.-	942.10	2	239.41	1.25	0.1	159	4/7
jmfag5miniggbead, 775	-.IPLKDVVPR.-	1037.28	2	368.92	1.45	0.0	243	5/8
jmfag1mnacl7,5minigg, 792	-.NCSHLDAATR.-	1088.18	3	273.31	1.38	0.1	143	11/36
jmfag1mnacl2,5minigg, 1284	-.VSDFGLTK.-	866.98	2	917.89	1.15	0.2	501	9/14
jmfag1mnacl5mincon, 1492	-.VSDFGLTK.-	866.98	2	232.45	1.13	0.0	205	3/7
jmfag5minigg450mmnacl_030527025134, 1972	-.VSDFGLTK.-	866.98	2	422.61	1.36	0.1	257	1/2
jmIgG350naclrawphag3007, 2669	-.NKVGREGIIPANYVQK.-	1787.06	2	149.38	1.13	0.0	114	4/15

control

CSK_MOUSE Tyrosine-protein kinase CSK (C-SRC kinase) (Protein-tyrosine kinase M					**328.54**	729888.0		5
rawextr_150beadigg2_Mar04, 84	-.MDAPDGCPPAVYDVMK.-	1709.99	3	328.54	1.47	0.0	223	3/10

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
FAK2_MOUSE Protein tyrosine kinase 2 beta (Focal adhesion kinase 2) (FADK 2)					**6064.34**	20138411.0	31		
jmfag5minigg250mmnacl, 444	- VKVGTLR -	772.96	2	482.77	0.97	0.2	201	1/2	3
jmfawigg5mn150mmnacl, 668	- INVAVKTCK.-	976.22	2	2007.49	1.51	0.3	392	5/8	1
JMFAGNACL10_2B21E3, 930	- SNFELLEKEVGLDLFFPKQMQENLK -	2998.44	3	443.45	1.40	0.1	252	3/16	3
jmfag5minigg600mmnacl, 958	- YRPPKILEPTTFQEPPPK -	2139.48	3	214.62	1.30	0.0	158	4/17	1
JMFAGNACL15B21E3, 1596	- QMLTASHTLAVDAK -	1488.72	2	300.68	1.20	0.1	160	9/26	1
jmfag5mintrench1mnackitdpi, 1734	-.YDLQIRYLPEDFMESLK.-	2161.46	2	130.25	0.97	0.0	134	1/4	3
jmfag_20_mintrench1mnackitdpi, 1734	- YDLQIRYLPEDFMESLK.-	2161.46	2	130.25	0.97	0.0	134	1/4	3
jmIgG500rawphag3007,2231-2233	- YDLQIRYLPEDFMESLK.-	2161.46	2	240.11	1.14	0.1	155	9/32	3
JMFAGNACL15B21E3, 3012	-.ILKVCFYSNSFNPGKNFK -	2107.46	3	64.95	0.83	0.0	78	5/34	3
jmkdl600nacirawphag3007, 1798	- LVKCTVQTEIQEITSILLSGR.-	2445.91	2	125.74	0.87	0.1	31	1/7	3
jmkdl500nacirawphag3007, 1911	-.LPIKWMSPESINFRR.-	1875.23	3	364.99	1.30	0.1	128	15/56	1
phagrawFsuc800_dec23, 1304	- YDLQIRYLPEDFMESLK -	2161.46	2	159.55	1.13	0.1	106	1/4	3
rawsucrfp_150phagigg_Mar04, 1556	-.YDLQIRYLPEDFMESLK.-	2161.46	2	552.36	1.62	0.2	90	1/4	3
phagrawFsuc400_dec20, 1658	- IGPNIQLAECYGLRLK.-	1789.14	2	94.37	1.11	0.1	47	7/30	3
phagrawF800_Dec23, 2148	- RSHLSESCSIESDIYAEIPDETLR.-	2751.97	3	580.31	1.52	0.1	183	17/92	3
phagrawFsuc400_dec20, 3070	- YDLQIRYLPEDFMESLK.-	2161.46	2	172.45	1.09	0.0	153	9/32	3

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
FAK2_MOUSE Protein tyrosine kinase 2 beta (Focal adhesion kinase 2) (FADK 2)					**1848.93**	20138411.0	7		
rawextr_900beadigg_Mar04, 1172	-.RNSLPQIPTLNLEARR.-	1879.16	2	543.02	1.30	0.1	315	11/30	3
rawextr_700beadigg_Mar04, 1554	- YDLQIRYLPEDFMESLK.-	2161.46	2	180.67	1.23	0.0	143	9/32	3
FPbeads800_Dec19, 2006	- DLAELINKMKLAQQNAVTSLSEDCK.-	2764.17	2	74.69	0.85	0.1	63	7/46	1
jmrawbsa5minlowionic, 1324	- NKLGQLPPEDYVVVVKNVGLNLR -	2566.00	3	850.54	1.62	0.0	504	21/88	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
megakaryocyte-associated tyrosine kinase [Mus musculus]					**2967.88**	6754646.0	13		
jmfag5minigg150mmnacl, 258	-.EALSTDPK.-	860.93	2	733.87	1.28	0.1	521	5/7	3
phagrawFsuc600_dec20, 1240	-.RSSRVSWLAFEGWESR.-	1954.14	3	185.40	1.22	0.0	143	11/60	1
rawsucrfp_60MeOHphagigg_MAr04, 1388	- KGDMVTILEACEDK.-	1552.80	2	394.40	1.05	0.1	299	9/26	5
JMFAGNACL5B21E3, 1880	-.SVGVSAPAGGQEAEGSAPTR.-	1828.92	2	338.46	1.55	0.1	153	6/19	4
JMFAGNACL5B21E3, 2150	-.ELRSVGVSAPAGGQEAEGSAPTRSQDP.-	2654.79	2	955.46	1.20	0.3	150	5/26	4
jmfag1mnacl5minigg, 2456	-.AKHHGSGQEGLLAAAALR.-	1788.01	2	360.30	1.43	0.1	171	5/17	5

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
megakaryocyte-associated tyrosine kinase [Mus musculus]					**541.86**	6754646.0	7		
rawextr_400beadigg_Mar04, 1264	-.GAICTKLVKPR.-	1186.50	2	541.86	1.14	0.2	93	1/4	5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
tyrosine kinase 2; tyrosine kinase TYK2 [Mus musculus]					**5146.30**	9055372.0	21		
jmkdl1000nacirawphag3007, 1006	-.GSRAHTRPLNLSQLSFHR.-	2078.33	3	427.49	1.80	0.1	203	7/34	1
phagrawF600_dec20, 1294	-.LALQGCSLRAGDDCFPLHXCCLPR.-	2603.11	2	64.50	0.84	0.0	63	7/46	1
rawsucrfp_actinphagigg_Mar04, 1930	-.LQPQNLVGTSAVNSDSPASDPTVFHKRYLK.-	3271.63	2	459.82	1.10	0.2	70	9/58	2
phagrawFsuc150_dec22, 2326	-.LQPQNLVGTSAVNSDSPASDPTVFHK.-	2710.94	2	44.71	0.75	0.0	59	7/50	2
phagrawFchll_dec23, 3300	-.NCWETEASFRPTFQNLVPILQTAQEK.-	3052.41	2	163.11	1.21	0.0	131	9/50	2
jmfag1mnacl5minigg, 694	-.TNVYEGLLR.-	1065.21	2	122.58	1.03	0.0	113	3/8	1
jmfag5minigg450mmnacl_030527025134, 1274	-.RAILEDSK.-	932.06	2	192.50	0.80	0.1	191	1/2	1
jmfag5minigg500mmnacl, 1312	-.YKGCCEDQGEKSVQLVMEYVPLGSLR.-	2933.37	3	223.19	1.47	0.0	147	9/50	2
jmIggactinrawphag3007,1408-1410	-.MPLCGRR.-	833.06	2	254.14	1.24	0.1	118	1/2	1
jmfag5minigg350mmnacl, 1443	-.NCIPHSFRQHIR.-	1508.74	2	159.13	0.94	0.0	161	4/11	2
jmfag5minigg450mmnacl_030527025134, 2282	-.VSLYCYDPTNDGTGEMVAVKALK.-	2475.82	3	541.07	1.11	0.1	313	9/44	2
jmfag5minigg300mmnacl,2476-2478	-.FYFRNWHGMNPQEPAVYR.-	2313.59	3	2382.28	2.19	0.2	480	5/17	2
jmrawigg5min1mnacl, 2911	-.DLSSEEEIHHFKNESLGMAFLHLCHLALSR.-	3465.91	2	111.76	0.87	0.1	63	9/58	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
tyrosine kinase 2; tyrosine kinase TYK2 [Mus musculus]					**1153.02**	9055372.0	5		
rawextr_chlfbeadIgG_Mar04, 1898	-.CLLLCLCSQAEALSFVALVDGYFR.-	2636.15	3	1153.02	1.43	0.2	513	6/23	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
FMS-like tyrosine kinase 3 [Mus musculus]					**4446.11**	6753888.0	20		
jmrawigg5minbeadsyringdnase,413-415	-.VFGQWVSSSTLNMSEAGK.-	1929.14	3	1466.38	2.28	0.0	643	21/68	1
jmfag5minigg350mmnacl, 675	-.VMNATAYGISKTGVSIQVAVK.-	2138.52	3	497.23	1.50	0.0	324	17/80	1
JMFAGNACL10_2B21E3, 2030	-.CTWIFSQASFPCEQRGLEDGYSISK.-	2854.17	3	343.47	1.64	0.0	193	5/32	1
jmfag5minigg200mmnacl, 2822	-.NDTGYYTCSSSKHPSQSALVTILEK.-	2730.99	2	163.07	1.04	0.1	129	5/24	2
jmkdl500nacirawphag3007, 1425	-.TSIHLPKQAAPQQR.-	1575.80	2	368.67	1.01	0.1	160	9/26	
phagrawF200_dec22, 2119	-.PSFPNLTSFLGCQLAEAEEACIR.-	2497.83	2	294.27	1.23	0.1	150	5/22	
rawsucrfp_300phagigg_Mar04, 2359	-.TWTEIFKEHNFSSYPTFQAHSNSSMPGSR.-	3375.63	2	157.05	1.06	0.1	84	9/56	
ajrawmediapbsnocells, 476	-.MLKEKADSCEK.-	1282.51	3	1155.99	1.93	0.0	594	17/40	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
FMS-like tyrosine kinase 3 [Mus musculus]					**349.60**	6753888.0	5		
rawextr_chlfbeadIgG_Mar04, 598	-.TGVSIQVAVKMLK.-	1374.72	3	349.60	1.69	0.0	200	17/48	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
B39577 protein-tyrosine kinase (EC 2.7.1.112) JAK2 - mouse (fragment)					3262.85	110873.0	14		
jmrawigg5minbeadsynngdnase, 435	-.DLSFGWIKSGTV -	1310.48	3	154.96	0.94	0.0	164	7/22	
JMFAGNACL10_2B21E3, 564	-.NKNSINILWK -	1230.44	2	289.65	0.87	0.0	316	1/2	2
jmrawigg5min350mmnaclsynngednase, 709	- FLQQLGKGNFGSVEMCR.-	1915.23	2	379.78	1.84	0.1	172	9/32	2
ajrawphag1MNaCl20, 2862	-.QGQMIVFHLIELLKSNGRLPR.-	2450.94	3	132.61	1.16	0.0	114	17/80	2
phagrawFsuc200_dec22, 917	- LSDPGISITVLPK -	1340.59	2	396.74	1.02	0.1	178	3/8	2
rawsucrfp_700phagigg_Mar04, 1455	-.EPGESPIFWYAPESLTESK -	2168.35	3	144.61	1.24	0.0	104	11/72	1
phagrawFsuc200_dec22, 1517	-.WSFGTTLWEICSGGDKPLSALDSQR.-	2756.04	3	1027.75	1.77	0.1	389	7/32	2
phagrawF350_dec20, 1570	-.RNLRLIMEYLPYGSLR -	1995.38	1	141.42	0.93	0.0	146	4/15	2
phagrawFsuc150_dec22, 2452	-.YDPLQDNTGEVVAVKK -	1776.97	2	167.78	1.00	0.0	165	3/10	2
rawsucrfp_450phagigg_Mar04, 2472	-.NSINILWKLGVAKQLAWAMHFLEEK.-	2941.49	2	114.94	0.75	0.0	147	11/48	2
phagrawFsuc400_dec20, 2834	- MIGNDKQGQMIVFHLIELLKSNGR.-	2743.25	2	312.61	1.05	0.2	36	3/23	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
mitogen activated protein kinase kinase 1; protein kinase, mitogen acti					3933.63	6678794.0	13		
jmfag1mnacl5minigg, 180	-.ISELGAGNGGVVFKVSHK.-	1800.05	3	616.49	1.77	0.0	347	5/17	2
rawsucrfp_400phagigg_Mar04, 1003	-.VSIAVIKGLTYLR -	1433.77	3	979.97	1.73	0.0	543	19/48	1
rawsucrfp_400phagigg_Mar04, 2565	-.KPTPIQLNPAPDGSAVNGTSSAETNLEALQK.-	3150.44	2	82.17	0.95	0.0	87	2/15	2
JMFAGNACL10_1B21E3, 1618	-.ISELGAGNGGVVFK.-	1348.53	2	1249.75	1.21	0.3	216	6/13	3
jmfag1mnacl5minigg,1672-1674	-.ISELGAGNGGVVFK.-	1348.53	2	143.51	1.10	0.0	111	9/26	3
jmfag1mnacl5minigg, 2066	-.DDDFEKISELGAGNGGVVFKVSHK.-	2549.78	3	469.03	1.76	0.1	241	19/92	2
jmfag5minigg300mmnacl, 2212	-.ISELGAGNGGVVFK.-	1348.53	2	392.71	1.06	0.2	144	9/26	3

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
mitogen activated protein kinase kinase 1; protein kinase, mitogen acti					1262.70	6678794.0	8		
FPbeads450_Dec19, 2154	-.DDDFEKISELGAGNGGVVFKVSHK.-	2549.78	3	543.60	1.65	0.0	318	19/92	2
FPbeads300_Dec19, 4012	-.RSDAEEVDFAGWLCSTIGLNQPSTPTHAASI.-	3275.55	2	584.05	1.06	0.2	48	7/60	1
jmraw5minbsafreezthaw,2106-2108	-.ISELGAGNGGVVFK.-	1348.53	2	135.05	0.84	0.1	121	4/13	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
mitogen-activated protein kinase kinase kinase 6; apoptosis signal-reg					6744.04	33186928.0	2		
jmrawigg5min400mmnaclsd, 599	- RQLAQELRTLQAQLR.-	1825.11	3	290.50	1.15	0.0	227	1/4	
jmrawigg5min1mnacl, 725	- AGSCWQDPLAEALSRGR.-	1818.01	2	676.25	1.17	0.2	202	9/32	
jmrawigg5min300mmnaclsyringednase, 1431	-.HTRVRIAIK.-	1094.34	2	386.07	0.83	0.0	448	9/16	
jmIgG150rawphag3007, 1668	- GTYGVVYAGRDR.-	1314.43	1	308.58	0.96	0.1	136	4/11	
JMFAGNACL5B21E3, 1768	-.CLREACAQLQGTRPPPQLR.-	2138.51	3	599.86	1.53	0.2	46	7/36	
jmfag5minigg400mmnacl, 2520	-.SPGSPRHTPRPSGAPSGPSSPSADSATQSQTFPR.-	3381.57	2	33.83	0.98	0.0	27	4/33	
phagrawFsuc150_dec22, 288	-.IWRAILAQRAGATSVTPVPR.-	2164.54	3	1648.77	1.63	0.2	676	21/76	
phagrawF150_dec22, 1016	- VHPPVPGSLSAEAQAFLLR.-	1990.30	3	180.95	1.35	0.1	85	13/72	
phagrawF600_dec20, 1834	- VPEEPAAEEPASPEESSGLSLLHQESKRR.-	3161.38	2	107.23	0.92	0.1	53	1/8	
rawsucrfp_actinphagigg_Mar04, 1858	-.IWRAILAQRAGATSVTPVPR -	2164.54	2	259.85	1.43	0.0	174	5/19	
rawsucrfp_600phagigg_Mar04, 2114	-.RLAGITPCTETFTGTLQYMAPEIIDQGPRG.-	3181.63	2	1311.01	1.11	0.3	75	1/8	
phagrawF450_dec20, 2172	-.RMLAAVLEQEVPTLAENLLEQEQDSRLSK.-	3312.74	2	231.08	0.90	0.1	78	1/7	
phagrawFsuc300_dec20, 3344	-.IWRAILAQRAGATSVTPVPR -	2164.54	3	710.07	1.38	0.0	514	11/38	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
mitogen-activated protein kinase kinase kinase 6; apoptosis signal-reg					2473.28	33186928.0	12		
FPbeads600_Dec19, 876	- MAGPCPRAGVLER.-	1357.63	2	857.68	1.13	0.2	222	5/12	
rawextr_actinbeadigg_Mar04,1811-1813	-.LAGITPCTETFTGTLQYMAPEIIDQGPRGYGK.-	3430.90	3	242.92	1.70	0.1	72	7/62	
rawextr_250beadigg_Mar04, 2378	-.IWRAILAQRAGATSVTPVPR -	2164.54	2	160.14	1.10	0.1	96	4/19	
FPbeads500_dec19, 3376	-.CQRFCGLIQVLVMNPDSSAPTEEAEGAR.-	3023.42	2	112.54	0.86	0.1	45	1/6	
jmraw5minbsareebeads, 516	-.RNRPGDR.-	870.94	2	587.46	1.48	0.0	377	3/4	
jmraw5minbsareebeads, 1000	-.PLSVVYVLTR.-	1147.39	3	213.99	0.98	0.0	214	1/3	
jmrawbsa5mniowonic, 1672	-.MAPPQEDQCLVLVLEINK.-	2041.42	3	298.55	1.03	0.1	82	13/68	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
M4K6_MOUSE Mitogen-activated protein kinase kinase kinase kinase 6 (MAPK/ERK					5369.49	29428007.0	24		
ajrawphag1MNaCl20, 366	-.ASNPDLR.-	772.83	2	437.51	0.93	0.1	436	2/3	3
jmrawigg5minbeadsfreezethaw,482-484	-.GLAHLHAHK.-	984.14	2	93.57	0.82	0.0	112	1/2	4
jmfag1mnacl7,5minigg, 1446	-.SLDDIDLSALR.-	1218.34	2	314.51	1.11	0.0	281	9/20	3
AJRAWActinIgG_june13, 1542	-.IKFLVIALKNSVEVYAWAPK.-	2290.77	2	284.29	1.32	0.1	123	5/19	3
jmraw5minigg600mmnaclsd, 1598	-.IKFLVIALKNSVEVYAWAPK.-	2290.77	2	113.61	1.06	0.0	100	9/38	3
ajrawphagjun20dpi1MNaCl, 1614	-.RLEDMQALRR.-	1288.51	2	176.06	0.84	0.0	199	7/18	4
jmfag1mnacl5minigg, 1620	- EDCIAYICREILR.-	1597.89	2	428.37	1.38	0.1	274	5/12	4
jmrawigg5minbeadsfreezethaw, 3166	-.FMAFKSFADLPHR.-	1567.84	3	152.78	1.04	0.1	100	13/48	4
phagrawF350_dec20,1206-1208	-.TSSIATALNTSGAGGSRPAQAVRASNPDLR.-	2928.17	3	821.66	1.79	0.0	458	11/58	2
jmfag5mincon450mmnacl, 1510	-.PDNEAPPKVPQRTSSIATALNTSGAGGSR.-	2881.11	3	2547.14	2.15	0.3	388	23/112	4

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
M4K6_MOUSE Mitogen-activated protein kinase kinase kinase kinase 6 (MAPK/ERK					304.31	29428007.0	9		
rawextr_350beadigg2_Mar04, 1498	-.GNALKEDCIAYICR.-	1569.83	2	304.31	1.17	0.1	208	9/26	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Mitogen activated protein kinase kinase 2 [Mus musculus]					**2650.25**	15990388 0	15		
jmfag5minigg500mmnacl, 1102	- PSGLIMARK.-	973.22	2	679 67	1 26	0 1	512	5/8	1
ajrawphagjun20dpi1MNaCl,1734-1736	- SEGEEVDFAGWLCR.-	1598 72	3	337.58	1 46	0 1	94	1/4	3
ajrawphagjun20actinDPI, 1806	- IPEDILGKVSIAVLR.-	1623 96	2	305.87	0.91	0.1	180	9/28	2
jmIgG300rawphag3007, 2114	- ADLKLLMNHAFIK.-	1514.86	2	215.18	0.90	0 1	202	3/8	3
jmfag1mnacl0minigg, 2646	- PVLPALTINPTIAEGPSPTSEGASEANLVDLQKK -	3459.89	2	334 63	0.95	0.2	83	2/11	2
rawsucrfp_400phagigg_Mar04, 1049	- PISGHGMDSR.-	1057.17	2	204 97	0.95	0 1	183	1/2	
phagrawFsuc350_dec20, 1228	- ISELGAGNGGVVTK.-	1302.46	2	201 26	1.09	0.1	135	4/13	2
rawsucrfp_150phagigg_Mar04, 1582	- PVVDGADGEPHSVSPRPRPPGR -	2280.49	3	371 30	1 63	0.0	212	19/84	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
mitogen activated protein kinase binding proten 1; JNK-binding protein					5917.27	6754398.0	14		
jmfag5minigg350mmnacl, 609	-.PHALGTDIASITEASR -	1639 79	3	447 32	1 49	0 0	300	17/60	
jmfag1mnacl0minigg, 920	-.VLGVTVSGGRGLACEPR.-	1671.95	3	1247 86	1.98	0.1	487	11/32	
jmfag5minigg1000mmnacl, 1490	- QLFETLANGTAPGGPARVLERTESR.-	2671.95	3	245.09	1.57	0.0	156	1/6	
jmfag5minigg500mmnacl,1800-1802	-.QLFETLANGTAPGGPARVLERTESR.-	2671.95	3	483.84	1 98	0.0	244	3/16	
jmIggactinrawphag3007, 2174	- HKQHHILNSSR.-	1357.51	1	84.60	0.97	0.0	86	7/20	
jmfagfrench20minigg1mnacldtt, 2306	- LFNPSNLHFLSTLPRPHALGTDIASITEASR.-	3377 80	2	146.96	0.90	0.1	63	2/15	
jmfagtimecon7.5min.2134.2134.3	- SGLLGELRNNLFTDVACGRGEK.-	2350.64	0	352.19	1.24	0.1	242	3/14	
jmfag5mincon450mmnacl,808-810	- KAHTTVEK.-	914.04	2	640.22	1.29	0 1	347	9/14	
jmbeads450nacirawphag3007 1541-1543	- KTITALAFSPDGKYLVTGESGHMPAVR.-	2848.27	3	414 90	1 66	0.0	233	19/104	
jmfagtimecont10min_030601202502, 1964	- QLFETLANGTAPGGPAR.-	1700.88	2	330.78	1 39	0.1	191	9/32	
jmfagcont5minbead, 2638	-.ADSTFCITSSGLLCEFSDRRLLDK.-	2679.02	2	164.33	1.01	0.0	152	11/46	
rawphag2007chitsolt, 577	-.TSKVNATVPLLGR.-	1356 60	2	230.58	1.26	0 1	139	5/12	
phagrawFchlf_dec23, 2358	-.SGLVAYPAGCVVVLFNPRKHK.-	2256 70	2	314.59	1.16	0.1	209	1/4	
jmldl450nactrawphag3007, 2572	-.YIVSVGYQHDMIVNVWAWKKNIVVASNK.-	3263.80	2	499.42	1.29	0.2	125	1/8	
phagrawFchlf_dec23, 2358	-.SGLVAYPAGCVVVLFNPRKHK.-	2256.70	2	314.59	1.16	0.1	209	1/4	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
M4K5_MOUSE Mitogen-activated protein kinase kinase kinase kinase 5 (MAPK/ERK					4660.40	30315995.0	18		
jmfag1mnacl7,5minigg, 170	-.RCPDLEAR -	960.09	2	610.06	1.30	0.0	469	5/7	3
jmrawigg5min400mmnaclad, 306	-.TASEINFDK.-	1025.10	2	556.45	1.27	0.0	434	1/2	3
jmfag5minigg250mmnacl, 772	-.KPGLAAHIQTHR.-	1329.54	3	436 59	1.16	0 1	335	17/44	5
jmraw5minigg250mmnaclsyringdnase, 1046	-.IVNLQGKLK.-	1013.26	2	212 41	0 92	0.1	169	9/16	5
jmIggactinrawphag3007, 1678	- ITATIAK -	717.88	1	64 20	0.71	0.0	79	5/12	4
rawsucrfp_250phagigg_Mar04, 710	-.ETLQGLAYLHTKGKMHR.-	1984.31	3	353.72	1.48	0.0	238	15/64	4
phagrawFsucchlfbead_dec23, 992	- RAIPPPLPPKPR -	1339 66	2	175.50	0 90	0.0	195	9/22	3
rawsucrfp_500phagigg_Mar04, 1140	- IESVVCLQDSVLAFWKHGMQGK.-	2478.90	3	996.78	2.20	0.1	423	1/4	5
phagrawF200_dec22, 2315	- RDFPKPTINGLPPTPK.-	1779.08	2	114.65	0.86	0.0	127	4/15	4
jmldl500nactrawphag3007, 1613	-.IESVVCLQDSVLAFWKHGMQGK.-	2478.90	3	1023.32	1 89	0.1	380	19/84	5
jmldl250nactrawphag3007, 2528	-.ECKHCNIVAYFGSYLSREK.-	2248.57	3	116.72	1 04	0.0	98	5/36	3

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
M4K5_MOUSE Mitogen-activated protein kinase kinase kinase kinase 5 (MAPK/ERK					**968.25**	30315995.0	6		
rawextr_900beadigg_Mar04, 1036	-.RQSSPSCVPVAETSSSIGNGDGISK.-	2464.65	3	968.25	1.80	0.1	336	7/32	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to MAP-kinase phosphatase (cpg21) [Mus musculus]					3195.40	38085197.0	13		
JMFAGNACL10_1B21E3, 150	- LAGAGAGYSSNFYYGK -	1626.75	3	1318.49	1.72	0.1	697	23/60	
ajrawphagjun20dpi1MNaCl, 1128	-.SPVATATSC.-	836.94	1	357 71	0.83	0.2	126	7/16	
jmIgG400rawphag3007,1200-1202	- MLRKEAEAR.-	1104.31	2	364.81	1.24	0.1	158	5/8	
jmfag5minigg250mmnacl,2048-2050	-.IEGERSLLSQCGKPVLSVAYR -	2306 67	3	439.93	1.44	0.0	305	1/4	
ajrawphagjun20actinDPI, 2566	-.PTSQEKIEGER.-	1274.36	2	6.90	0.47	0.0	15	1/10	
jmfag5minigg300mmnacl, 2860	-.CVVLDCRPYLAFAASSVRGSLNVNLNSVVLR.-	3337 91	2	280 14	0 93	0.1	102	11/60	
rawsucrfp_400phagigg_Mar04, 2567	-.SGGNVLERSPQYQDDQATPHLGSSQR.-	2828 95	3	427 42	1.22	0.1	251	1/5	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to MAP-kinase phosphatase (cpg21) [Mus musculus]					**724.11**	38085197.0	5		
jmrawigg5miniggfreebead,530-532	-.EAFDYVK.-	871.96	2	571.77	1.44	0 1	309	2/3	
FPbeads600_Dec19, 1160	-.LLQEGGGGVAAVVVLDQGSR.-	1926.16	3	152.35	1.19	0.0	120	7/38	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
MNK1_MOUSE MAP kinase-interacting serine/threonine kinase 1 (MAP kinase signa					5901.28	30315972.0	13		
ajrawphagjun20actinDPI,662-664	- DLKPENILCESPEK.-	1615.83	2	433.88	1.42	0.1	188	9/26	
jmIgG150rawphag3007,816-818	-.IIEKQAGHSRSR -	1382.56	3	234.90	1.69	0.1	114	7/22	
jmfagfrench20minigg1mnacldtt,1526-1528	- NSSTMDLTLFAAEAIALNR.-	2039.30	3	489.78	1.69	0.1	256	17/72	
jmraw5minigg600mmnaclsd, 1772	-.QRLSAAQVLQHPWVQGQAPER.-	2400.69	3	2687 56	1.85	0.3	463	1/4	
jmfag5mintrench1mnacldttdpi, 1858	-.NSSTMDLTLFAAEAIALNR.-	2039.30	3	376.38	1.51	0.0	238	17/72	
jmfag_20_minfrench1mnacldttdpi, 1858	-.NSSTMDLTLFAAEAIALNR.-	2039.30	3	376.38	1.51	0.0	238	17/72	
JMFAGNACL10_1B21E3, 1500	-.NSSTMDLTLFAAEAIALNR.-	2039.30	3	825.12	1.67	0.1	445	11/36	1
phagrawFsuc150_dec22, 480	-.PENILCESPEKVSPVK.-	1770.04	2	277 29	1.03	0.0	269	3/10	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
fos-like antigen 1 [Mus musculus]					**3160.06**	6753896.0	3		
jmraw5minigg1000mmsd, 1336	-.ELTDFLQAETDK.-	1410.51	2	154.98	1.03	0.0	140	4/11	1
jmfagcon5minn600mmnacl, 581	-.PLAYPQYSPPQPR.-	1514.71	3	634.81	1.50	0.1	368	3/8	1
rawsucrfp_chlfphagigg_Mar04,1114-1116	-.KELTDFLQAETDKLEDEK.-	2153.33	3	1323.67	2.19	0.0	596	21/68	1
ajrawmediapbsnocells,894-896	-.KSSSSSGDPSSDPLGSPTLLAL.-	2104.26	3	1046.60	1.93	0.1	515	23/84	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
unnamed protein product [Mus musculus] V-FOS TRAN					**2811.85**	26342525.0	5		
phagrawFsuc150_dec22, 892	-.VVEDIEYLK.-	1108.27	2	175.36	0.99	0.1	89	3/8	2
phagrawF450_dec20, 1248	-.VTSAYLQDIENAYK.-	1615.77	3	471.35	1.30	0.0	361	1/4	2
phagrawF60MeOH_dec23, 2554	-.FYDDPKSNDGNSYR.-	1678.70	2	2165.14	1.65	0.3	653	7/13	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Fas-interacting serine/threonine kinase 3 [Mus musculus]					**2957.86**	10998780.0	12		
ajrawphagjun20dpi1MNaCl, 518	-.KNKLCQNR.-	1004.19	2	1041.17	1.71	0.2	337	4/7	2
jmfag5minigg500mmnacl, 3942	-.HLLDFPHSNHVK.-	1444.62	2	439.12	0.93	0.1	430	5/11	2
jmrawigg5miniggfreebead, 1212	-.EASVRQDSSVSDKQR.-	1692.77	3	730.68	1.51	0.1	457	9/28	3
jmkdl150naclrawphag3007, 1576	-.VLAAQAQQAGVEAPRAVVWR.-	2121.43	3	385.23	1.47	0.0	260	9/38	2
phagrawF200_dec22, 2677	-.SCFHIMDICKSPSSCETNNHSK.-	2469.78	3	361.67	1.33	0.0	259	4/21	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Fas-interacting serine/threonine kinase 3 [Mus musculus]					**343.05**	10998780.0	13		
rawextr_chlfbeadigG_Mar04, 1522	-.IPFTKPRGHSFSLQAGAIVVK.-	2254.66	2	343.05	1.71	0.1	135	9/40	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
embryonal Fyn-associated substrate [Mus musculus]					**4347.65**	31981787.0	7		
jmfag5minigg600mmnacl, 1418	-.RVVVAAHRLVFVGDTLGR.-	1966.32	2	88.92	1.02	0.0	83	4/17	2
jmrawigg5min150mmnacl, 268	-.FTTLLDGLLP.-	1090.30	3	418.86	1.30	0.1	279	1/3	
jmfagcont5minbead, 412	-.PRLPSTESLSR.-	1243.40	3	1286.10	1.44	0.2	513	2/5	2
jmfagcont5minbead, 1754	-.VKLLPAGPAPK.-	1091.37	2	215.31	1.00	0.1	154	9/20	2
jmbeads1000naclrawphag3007, 1773	-.EGAGGLDGWCLCSLHGQQGIVPANR.-	2539.84	3	159.34	1.44	0.0	88	17/96	2
RawPhag200760MeBeadsdigest, 1684	-.PLPPPPPCLPGYGGLK.-	1603.95	3	177.76	1.02	0.0	175	13/60	2
jmkdl600naclrawphag3007, 1950	-.SCSPSSDSIYKVPRGNGMQLTASR.-	2542.84	3	691.20	1.96	0.1	219	11/46	
phagrawFsuc700_dec23, 1165	-.EPGPPLYAAPSNLKR.-	1610.84	3	573.70	1.53	0.1	251	13/56	2
phagrawF250_dec22, 1795	-.ALYDNTAESPQELSFR.-	1841.96	2	616.08	1.35	0.1	237	1/3	2
phagrawF350_dec20, 2856	-.PLPALPVSEAPAPSPAPSPAPGRKGSIQDR.-	2962.35	2	120.39	0.92	0.1	68	4/29	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
embryonal Fyn-associated substrate [Mus musculus]					**987.63**	31981787.0	8		
rawextr_150beadigg2_Mar04, 538	-.RVVVAAHRLVFVGDTLGR.-	1966.32	3	361.17	1.18	0.0	306	9/34	2
rawextr_500bead_Mar04, 1780	-.GVDTAQGSRPLDKAFPVDPELLER.-	2611.89	3	626.46	1.71	0.1	255	9/46	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Fyn protein [Mus musculus] h leukemia gene [Mus mu					**4462.89**	21594599.0	9		
jmrawigg5minbeadsfreezethaw, 556	-.EVLEQVERGYR.-	1378.52	3	506.86	1.57	0.1	198	13/40	5
JMFAGNACL15B21E3, 1142	-.LPNLVDMAAQVAAGMAYIER.-	2134.51	3	1167.61	1.54	0.1	681	21/76	1
ajrawphagactin20, 1508	-.KLGQGCFAEVWLGTWNGNTK.-	2210.50	3	411.38	1.42	0.0	279	5/19	1
jmiggactinrawphag3007, 1644	-.VPYPGMNNREVLEQVERGYR.-	2407.70	3	772.63	1.43	0.1	357	9/38	1
jmraw5minigg250mmnaclsynngdnase, 2288	-.ADGLCFNLTVVSSSCTPQTSGLAK.-	2400.72	3	205.49	1.32	0.0	152	15/92	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Fyn protein [Mus musculus] e inhibitor EIC [Mus mu					**1398.92**	21594599.0	6		
FPbeads150_Dec19, 655	-.EVLEQVERGYR.-	1378.52	3	518.83	1.43	0.0	343	2/5	5
FPbeads250_Dec19, 2702	-.GYRMPCPQDCPISLHELMIHCWK.-	2759.31	2	125.03	0.91	0.0	137	9/44	1
rawextr_400beadigg_Mar04, 2968	-.LTEERDGSLNQSSGYR.-	1812.88	2	203.88	0.98	0.1	149	4/15	1
jmraw5minbsafreezthaw,1370-1372	-.DAERQLLSFGNPR.-	1503.65	3	551.18	1.54	0.1	255	17/48	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
FYN binding protein; FYB-120/130; SLAP130; p120/130 [Mus musculus]					**3338.25**	**33469119.0**	7		
ajrawphagjun20actinDPI, 284	-.ADSANSATK.-	864.88	2	317.84	1.16	0.0	259	1/2	2
ajrawphagjun20actinDPI, 1794	-.QGEDIEIIRITDNPEGK.-	1928.09	3	329.59	1.23	0.0	263	1/4	1
jmrawgg5min450mmnaclsd, 2234	-.QKALPPLSVLGPPPPK.-	1640.01	2	83.49	0.82	0.1	77	1/5	2
jmfag5mincont400_030531151834,690-692	-.MAKFNTGSNPTEEAATSSR.-	2000.14	3	752.31	1.91	0.0	394	7/24	2
jmfagtimecont0min_030601230741, 856	-.ALPPLSVLGPPPPK.-	1383.70	3	500.37	1.54	0.1	291	17/52	2
jmbeads250rawphag3007, 894	-.DPEVKVGFLKPVSPK.-	1640.95	2	209.29	1.29	0.0	157	9/28	2
jmfagcon5minn600mmnacl, 1211	-.PFKVAGQSSPSGIQSR.-	1646.83	3	492.01	1.71	0.0	276	4/15	2
jmfag5mincont200mmnacl, 1590	-.YDGEIRVLYSTK.-	1444.62	2	173.89	0.87	0.1	140	7/22	1
rawsucrfp_900phagigg_Mar04,1568-1571	-.QKALPPLSVLGPPPPK.-	1640.01	3	264.07	1.42	0.1	148	13/60	2
rawsucrfp_350phagigg_Mar04, 1900	-.NVPVQKGSPVQLGAKSK.-	1738.03	2	215.38	1.29	0.0	163	5/16	2

control

FYN binding protein; FYB-120/130; SLAP130; p120/130 [Mus musculus]					**1353.85**	**33469119.0**	6		
rawextr_350bead_Mar04, 974	-.KWGARDLQIK.-	1215.43	1	389.86	1.48	0.1	211	1/2	1
rawextr_200bead_Mar04, 1892	-.GSPVQLGAKSKGAPFK.-	1572.83	2	239.60	1.10	0.1	171	3/10	2
jmbsa250naclrawphag3007, 1378	-.KKNSLNAVPPR.-	1224.44	1	295.60	0.92	0.1	173	2/5	1
jmbsa150naclrawphag3007, 1607	-.KKNSLNAVPPR.-	1224.44	1	428.80	1.12	0.2	113	7/20	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to FYN binding protein (FYB-120/130); FYN-binding protein (FYB					**4267.40**	**38078524.0**	7		
JMMAGTube1B16E3, 3270	-.DFQKAAVPLDVTK.-	1432.65	3	165.74	0.99	0.1	138	11/48	
jmigG150rawphag3007, 1812-1814	-.TSSSSGTPEKSTVCPER.-	1753.87	2	583.39	1.65	0.1	223	11/32	
jmfag1mnacl5mincon, 812	-.STVCPERDFQK.-	1310.46	3	365.03	1.44	0.0	241	7/20	
jmbeeds150rawphag3007, 1008	-.TSSSSGTPEKSTVCPER.-	1753.87	2	220.54	1.51	0.1	120	1/4	
jmfag5mincon450mmnacl, 1080	-.YGYVLVEHLDFK.-	1483.69	3	529.65	1.49	0.0	355	4/11	
jmfag5mincon250mmnacl,1514-1516	-.EIVSNGFSVSLPDLGPR.-	1788.00	2	240.39	1.44	0.1	43	7/32	
phagrawFchlfbead_dec23,2473-2475	-.HSQDKSGYVEALEVTK.-	1791.94	2	73.87	0.85	0.0	76	1/5	
jmidichtfsclblerawphag3007, 1612	-.ETPSPSTIRSSSSSEKTYDAVECSR.-	2705.85	3	482.35	1.78	0.1	201	1/6	
jmidl300naclrawphag3007, 1964	-.EILVINRAVACASNSR.-	1716.99	2	627.54	1.26	0.2	188	4/15	
jmidt150naclrawphag3007, 2088	-.TSSSSGTPEKSTVCPER.-	1753.87	2	310.92	1.20	0.1	201	9/32	
jmidlactinrawphag3007, 2140	-.HDRGSTQPAQDLANR.-	1666.74	2	353.14	1.13	0.0	309	5/14	
rawsucrfp_400phagigg_Mar04,1452-1454	-.TSNEEKGMTLSSFRYK.-	1879.09	2	240.98	1.33	0.1	73	4/15	
phagrawFchlfbead_dec23,2473-2475	-.HSQDKSGYVEALEVTK.-	1791.94	2	73.87	0.85	0.0	76	1/5	

control

similar to FYN binding protein (FYB-120/130); FYN-binding protein (FYB					**1189.61**	**38078524.0**	14		
rawextr_actinbead_Mar04, 968	-.LEKNRMEK.-	1048.24	2	505.58	1.41	0.1	238	9/14	
rawextr_400bead_Mar04, 1703	-.NQTLKSAQGDELQKTSSSSGTPEK.-	2522.67	3	616.17	1.82	0.0	379	19/92	
rawextr_400beadigg_Mar04, 2884	-.LFPEDVTLTRHSQDKSGYVEALEVTK.-	2964.28	2	67.88	0.93	0.0	67	7/50	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Btk protein [Mus musculus] ; novel lectin [Mus mus					**3079.66**	**31419802.0**	25		
jmfag1mnacl2,5minigg, 558	-.WIHQLKNVIR.-	1307.57	3	363.41	1.39	0.0	261	13/36	1
jmigG250rawphag3007, 990	-.GQYDVAIKMIR.-	1294.55	3	452.12	1.40	0.1	278	2/5	2
jmigG400rawphag3007, 1136	-.LSYYEYDFERGR.-	1598.70	3	252.97	1.23	0.0	204	3/11	2
jmfagtrench20minigg1mnacldtt, 1196	-.KRWIHQLK.-	1109.35	2	975.44	1.27	0.2	499	9/14	1
jmraw5minigg1000mmsd,1212-1214	-.QEGKEGGFIVGDSSK.-	1538.64	2	413.40	1.25	0.1	213	11/28	
jmigG1000naclrawphag3007, 1618	-.EGGFIVGDSSKAGK.-	1352.48	3	396.64	1.32	0.1	218	15/52	
jmfag5minigg500mmnacl, 1780	-.VSDFGLSRYVLDDEYTSSVGSK.-	2425.59	3	134.13	1.32	0.0	100	5/28	2
jmidl350naclrawphag3007, 2348	-.ELGTGQFGVVKYGKWR.-	1826.09	2	91.54	1.04	0.0	88	4/15	2

control

Btk protein [Mus musculus] ; novel lectin [Mus mus					**153.45**	**31419802.0**	7		
FPbeads800_Dec19, 2000	-.YTVSVFAKSTGEPQGVIR.-	1940.19	2	153.45	1.17	0.0	130	9/34	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
A-kinase anchor protein 3 [Mus musculus]					**6588.68**				
jmfag1mnacl0minigg, 200	-.ENLFSTCK.-	942.07	2	535.00	1.34	0.1	222	4/7	
jmfag5minigg350mmnacl, 343	-.ENLFSTCK.-	942.07	2	940.00	1.33	0.2	284	9/14	
ajrawphag1MNaCl20, 596	-.QLDEAVGNVTR.-	1202.30	3	933.21	1.31	0.1	496	2/5	
jmIgG350naclrawphag3007, 931	-.ENLFSTCK.-	942.07	2	302.14	1.12	0.0	252	4/7	
jmfag5minigg150mmnacl, 956	-.EINEKIHGAENK.-	1382.51	2	742.64	1.78	0.0	416	6/11	
jmfag5minigg500mmnacl, 1130	-.PPPPSPVVQDECKLK.-	1634.92	2	168.62	0.98	0.0	161	9/28	
jmIgG300rawphag3007, 1192	-.VDWLQSQSGVCK.-	1350.53	2	263.93	1.29	0.0	204	4/11	
JMFAGNACL10_1B21E3, 2066	-.IHGAENKCVHQSLYMGDEPTPHK.-	2592.90	3	905.65	1.62	0.2	123	2/11	
jmldichlfsolblerawphag3007,1652-1654	-.IQVKDTTIATILLKK.-	1686.07	2	423.40	1.38	0.0	308	5/14	
phagrawFsuc60MeOH_dec23, 1082	-.DLMSVIFNFIR.-	1355.63	2	244.28	0.89	0.0	271	2/5	
rawsucrfp_400phagigg_Mar04, 1172	-.CVHQSLYMGDEPTPHK.-	1843.08	3	402.25	1.63	0.0	246	1/4	
phagrawF200_dec22, 1657	-.SLPGDQKLFRTSPDNR.-	1832.01	2	191.84	1.23	0.0	144	11/30	
phagrawFsucchlf_dec23,1856-1858	-.SLPGDQKLFRTSPDNR.-	1832.01	3	437.82	1.21	0.0	343	4/15	
phagrawF600_dec20, 2312	-.EINEKIHGAENKCVHQSLYMGDEPTPHK.-	3206.56	2	97.89	0.84	0.1	75	1/6	

control

A-kinase anchor protein 3 [Mus musculus]					**222.06**	6753026.0	24		
jmbsa1000naclrawphag3007, 1125	-.LCLIIAKSCDSPLSELGEEK.-	2149.52	2	93.48	0.91	0.0	88	4/19	
jmraw5minbsabeads, 2476	-.AGDPKLSNLNFAMKSESK.-	1938.20	2	128.58	1.05	0.0	122	7/34	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
A-kinase anchor protein 4 [Mus musculus]					**6954.92**	6753028.0	2		
jmfag5minigg1000mmnacl, 158	-.SLTSAERVSEHILK.-	1570.77	3	376.32	1.37	0.0	273	17/52	3
jmfag1mnacl7,5minigg, 448	-.QQMCPKDSKEFADSISK.-	1943.19	3	411.15	1.73	0.1	146	15/64	4
jmfag5minigg500mmnacl, 960	-.GAAGPRSEGELNLENLEEK.-	2014.14	3	289.66	1.11	0.0	254	1/4	
JMFAGNACL15B21E3, 1132	-.RVLLKHTK.-	995.25	2	373.25	1.15	0.1	219	9/14	4
ajrawphagjun20actinDPI, 1368	-.LEMAASKNTNNNQSPSNPATK.-	2218.39	3	265.34	1.35	0.1	150	1/5	4
jmraw5minigglowionic, 1443	-.GPQNLRLEMAASK.-	1415.65	3	210.62	1.29	0.0	161	11/48	4
jmfag5minigg1000mmnacl, 1638	-.SLTSAERVSEHILK.-	1570.77	2	121.36	0.86	0.0	135	7/26	3
jmIgG500rawphag3007, 2357	-.SEGELNLENLEEKEIIVIKDTEK.-	2673.95	3	710.04	1.37	0.1	348	5/22	
jmldlactinrawphag3007, 2040	-.VSEHILKESLTMWNNQK.-	2058.35	3	748.35	1.52	0.2	219	9/32	2
jmldl150naclrawphag3007, 2254	-.VSEHILKESLTMWNNQK.-	2058.35	3	289.83	1.29	0.1	146	7/32	2
rawsucrfp_350phagigg_Mar04, 1508	-.GLMVYANQVASDMMVSVMKTLKVHSCGK.-	3029.68	2	165.51	1.26	0.1	98	1/6	4
phagrawFchlf_dec23,1862-1864	-.KTFLYSELSNK.-	1330.51	2	1489.71	1.45	0.2	491	3/5	
phagrawFsuc500_dec20, 3486	-.GKDPCEEECPGSSMGYMSQSAQYEK.-	2742.98	2	560.42	1.11	0.2	139	5/24	2
jmrawigg5miniggfreebead, 410	-.ESLTMWNNQKQGTQGR.-	1879.05	3	551.06	1.48	0.0	348	3/10	
jmrawigg5miniggfreebead,1482-1484	-.GPQNLRLEMAASK.-	1415.65	3	352.16	1.35	0.0	237	13/48	4
jmrawigg5miniggfreebead, 1690	-.GYSVGDLLQEVMKFAKETQLDEAVGNMAR.-	3201.62	2	40.16	0.86	0.0	38	3/28	

control

A-kinase anchor protein 4 [Mus musculus]					**1145.87**	6753028.0	12		
FPbeads450_Dec19, 2014	-.AGTHDPKCKNQSLEFSAMK.-	2093.37	2	127.99	0.92	0.1	113	2/9	
jmrawf5minbsareebeads, 1900	-.NLFNHGKQNAADIMEAMLK.-	2146.48	3	365.25	1.44	0.0	244	19/72	4
jmbsa600naclrawphag3007, 1072	-.RGVCKVDLYSPK.-	1365.63	3	489.28	1.54	0.0	316	4/11	4
jmrawbsa5minlowionic, 2056	-.GPQNLRLEMAASK.-	1415.65	3	163.36	0.98	0.0	164	11/48	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to A-kinase anchor protein 5; RII-B-binding protein [Mus muscu					**3200.57**	38050553.0	10		
jmigg600rawphage3007, 1178	-.ETVLSQAKEGELSQAK.-	1718.89	3	686.75	1.36	0.0	505	1/3	
jmraw5minigg500mmnaclsd,1346-1348	- SRHSKLTEDSGYVR.-	1635.76	2	207.04	1.12	0.1	69	4/13	
jmIgG350naclrawphag3007, 2363	- METSVSEIQVETKDEKGPVAASPQK.-	2689.98	3	203.14	1.22	0.0	186	1/6	
phagrawFsucchlfbead_dec23, 1260	-.QPAGAWASIKGLVTHRK.-	1821 12	2	46.36	0 86	0.0	46	3/16	
rawsucrfp_150phagigg_Mar04, 1323	-.PPEAEVQPEDGALPK.-	1577.72	2	223 11	1.61	0.0	139	9/28	
phagrawFsuc500_dec20, 1718	- LTEDSGYVRVQGEADDLEIK.-	2238.40	3	885.88	1.65	0.1	391	1/4	
phagrawFsuc150_dec22, 1946	-.SQESHISNSVTSGENVIAIELELENK.-	2829.02	3	423.93	1.42	0.0	298	21/100	
rawsucrfp_900phagigg_Mar04, 2817	-.AQTQPDDQAIQAGSTQGLQEGVLVRDGK.-	2912.12	2	524.36	1.53	0.2	86	1/6	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
A kinase anchor protein 7 isoform gamma [Mus musculus]					**3798.07**	31580808.0	7		
jmfag5minigg1000mmnacl, 218	-.GDKNDHVKK.-	1041.14	2	323.61	1.13	0.0	265	9/16	
jmfag5minigg600mmnacl, 516	-.GDKNDHVK.-	912.97	2	225.04	0.90	0.0	243	4/7	
jmraw5minigg1000mmsd, 1182	-.LVENAVLKAAQQYLEETQNK.-	2290.56	3	848.27	2.16	0.1	276	9/38	
phagrawFsuc150_dec22, 336	-.EKGILAGESRTFK.-	1436.64	2	321.00	1.16	0.1	242	1/3	
phagrawFsuc150_dec22, 576	-.SLQNSILQQDKRLTK.-	1773.03	2	284.28	1.16	0.1	119	2/7	
rawsucrfp_60MeOHphagigg_MAr04, 902	-.DYQPNYFLSIPITNKKITTGIK.-	2555.95	3	1795.86	2.29	0.2	325	3/14	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
A kinase (PRKA) anchor protein 10; protein kinase A anchoring protein					**3440.06**	40807354.0	17		
jmIgG1000naclrawphag3007, 90	- MRGAGPSPR -	929.08	2	1004.01	1.59	0.1	505	11/16	
jmfag5minigg1000mmnacl, 604	- ASIKILK.-	773.00	2	372.34	1.27	0.0	292	2/3	3
jmrawgg5min1mnacl,1587-1589	-.ASVAVHSPQK.-	1024.16	2	288.16	1.08	0.1	144	1/2	
jmfag5minigg1000mmnacl, 1882	-.IAKMIVSDVMQQAHHDQPLEKSTK -	2736.17	3	734.99	2.38	0.1	271	5/23	2
jmfag5minigg350mmnacl, 2041	- NHALLEAAGPSHVAINAISANMDSFSSSR -	2969.24	2	36.49	1.06	0.0	32	1/8	
rawsucrfp_800phagigg_Mar04, 1342	-.QSSLAEPVSPSKR.-	1386.54	2	578.71	0.96	0.0	604	11/24	1
phagrawF150_dec22, 1498	-.ASVAVHSPQKSTK.-	1340.51	2	167.94	0.94	0.1	155	1/3	
phagrawF350_dec20, 1560	-.KGQYDGQEAQNDAMILYDK -	2188.36	3	257.42	1.48	0.0	173	2/9	3

control

A kinase (PRKA) anchor protein 10; protein kinase A anchoring protein					**252.09**	40807354.0	1		
rawextr_350beadigg2_Mar04, 2634	- QPSHMEAAHFGDLGRSCLDYQTQETK.-	2951.20	2	154.68	0.84	0.1	156	1/5	
jmrawbsa5miniowionic, 1204	-.TLDVKSTK.-	892.03	2	97.41	1.07	0.0	76	3/7	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
type II cAMP-dependent protein kinase anchoring protein Ht31 [Mus muscul					**2688.09**	14192799.0	15		
jmfag5minigg400mmnacl, 308	-.SLPSDPPPSSAVELR.-	1552.71	3	383.02	1.07	0.1	164	17/56	
jmrawigg5min1mnacl,967-969	-.ESWCAIEPCPEAASLLASK.-	2006.29	3	860.78	1.90	0.0	451	7/24	1
jmfag5minigg500mmnacl, 1422	-.SFIDVGLGTECASK.-	1427.61	2	362.54	1.07	0.0	333	11/26	1
jmldl1000naclrawphag3007, 1174	-.SLPSDPPPSSAVELR.-	1552.71	3	246.62	1.24	0.0	189	3/14	
rawsucrfp_450phagigg_Mar04, 804	-.AQQHTPSACLKTETK.-	1643.85	3	454.18	1.60	0.0	278	15/56	1
rawsucrfp_chltphagigg_Mar04, 1624	-.AQQHTPSACLKTETK.-	1643.85	2	266.44	1.26	0.1	142	2/7	1
jmrawbsa5miniowionic, 1160	-.IVEAVIRQVR.-	1183.43	2	114.50	0.92	0.0	111	1/2	1

control

type II cAMP-dependent protein kinase anchoring protein Ht31 [Mus muscul					**683.04**	14192799.0	5		
rawextr_200beadigg_Mar04, 1329	-.SLPSDPPPSSAVELR.-	1552.71	2	130.25	0.96	0.1	98	2/7	
rawextr_chltbeadIgG_Mar04,1536-1538	-.PSSSLEMSSANSSELR.-	1682.79	2	552.79	1.80	0.0	307	2/5	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Phosphoglycerate kinase 2 [Mus musculus]					**162672.42**	38174603.0	1		
ajrawmediapbsnocells,890-892	-.LGDVYVNDAFGTAHR.-	1635.76	3	9695.13	4.34	0.3	1198	15/28	6
jmfag1mnacl0minigg,848-850	-.VDFNVPMK.-	950.14	2	905.04	2.10	0.1	396	5/7	6
jmfag5minigg350mmnacl, 861	-.LGDVYVNDAFGTAHR.-	1635.76	3	2545.15	2.49	0.2	572	11/28	6
JMFAGNACL5B21E3, 890	-.VSHVSTGGGASLELLEGK.-	1741.93	2	2030.29	2.00	0.3	204	11/34	4
JMFAGNACL5B21E3,958-960	-.LGDVYVNDAFGTAHR.-	1635.76	3	14891.60	3.91	0.5	1588	31/56	6
JMFAGNACL5B21E3, 964	-.LGDVYVNDAFGTAHR.-	1635.76	2	19271.78	3.90	0.6	1718	3/4	6
jmfag5minigg600mmnacl, 972	-.IQLIKNMLDK.-	1216.52	2	149.36	0.94	0.1	123	1/3	3
JMMAGTube1B16E3, 976	-.LGDVYVNDAFGTAHR.-	1635.76	3	6012.66	3.39	0.3	1040	13/28	6
JMFAGNACL10_1B21E3, 980	-.VDFNVPMKNNQITNNQR.-	2033.26	3	1126.07	2.14	0.1	452	23/64	6
jmfag5minigg200mmnacl, 998	-.VSHVSTGGGASLELLEGK.-	1741.93	3	3116.40	2.32	0.3	657	5/17	4
jmfag5minigg400mmnacl, 1014	-.LGDVYVNDAFGTAHR.-	1635.76	3	3554.68	2.63	0.3	553	5/14	6
jmfag1mnacl5minigg, 1062	-.VDFNVPMK.-	950.14	2	2534.89	2.03	0.3	415	5/7	6
JMFAGNACL10_1B21E3, 1072	-.LGDVYVNDAFGTAHR.-	1635.76	3	9377.94	2.79	0.5	1269	27/56	6
jmfag5minigg500mmnacl,1268-1270	-.LGDVYVNDAFGTAHR.-	1635.76	3	15489.85	3.62	0.5	1291	15/28	6
jm5miniggrawlowionic, 1548	-.VDFNVPMK.-	950.14	2	308.99	1.72	0.0	171	4/7	6
jmraw5minigg1000mmsd, 1700	-.ATSNGCVTIIGGGDTATCCAKWGTEDK.-	2660.94	3	483.45	1.72	0.0	272	21/104	2
jmfag5minigg150mmnacl, 2050	-.ALMDEVVKATSNGCVTIIGGGDTATCCAK.-	2830.27	2	149.66	0.96	0.1	81	9/56	2
jm5miniggrawlowionic, 2406	-.VSHVSTGGGASLELLEGK.-	1741.93	2	181.45	1.12	0.0	157	9/34	4
rawsucrfp_250phagigg_Mar04, 1636	-.VEAFQASLSKLGDVYVNDAFGTAHR.-	2696.96	3	1292.79	1.77	0.2	345	5/24	1
rawsucrfp_250phagigg_Mar04, 2028	-.GTKALMDEVVKATSNGCVTIIGGGDTATCCAK.-	3116.60	2	348.35	1.08	0.2	84	9/62	2
rawsucrfp_900phagigg_Mar04, 2362	-.INAQIVAQAKLIVWNGPIGVFEWDAFAKGTK.-	3386.93	2	62.93	0.75	0.0	82	2/15	2
jmraw5minbsafreezthaw, 1442	-.VDFNVPMK.-	950.14	2	2634.16	1.92	0.3	567	11/14	6
jmraw5minbsafreezthaw, 2610	-.VSHVSTGGGASLELLEGK.-	1741.93	2	265.71	1.24	0.0	213	5/17	4
jmfagtimecon2.5min.1056.1058.3	-.LGDVYVNDAFGTAHR.-	1635.76	0	11618.82	3.62	0.5	1067	27/56	6
jmfagtimecon2.5min.968.968.3	-.VDFNVPMKNNQITNNQR.-	2033.26	0	2768.43	2.70	0.3	343	19/64	6
jmfag5mincont150mmnacl, 901	-.LGDVYVNDAFGTAHR.-	1635.76	3	6747.72	3.10	0.4	795	25/56	6
jmfag5mincont200mmnacl, 1008	-.VSHVSTGGGASLELLEGK.-	1741.93	3	7481.16	2.98	0.3	1387	7/17	4
jmfag5mincont200mmnacl, 1018	-.VSHVSTGGGASLELLEGK.-	1741.93	3	3048.35	2.42	0.2	660	11/34	4
jmfagtimecont0min_030601230741, 1392	-.LGDVYVNDAFGTAHR.-	1635.76	3	5920.66	2.33	0.4	556	3/8	6
jmfagtimecont0min_030601230741, 1398	-.LGDVYVNDAFGTAHR.-	1635.76	3	5531.67	2.45	0.4	740	11/28	6
jmfagtimecont10min_030601202502, 1490	-.VDFNVPMKNNQITNNQR.-	2033.26	3	2822.02	2.52	0.2	509	23/64	6
jmfagtimecon10min,1588-1590	-.LGDVYVNDAFGTAHR.-	1635.76	3	9680.49	3.33	0.4	1274	27/56	6
jmfagtimecont10min_030601202502,1608-1610	-.LGDVYVNDAFGTAHR.-	1635.76	3	10624.77	3.17	0.4	1730	15/28	6

control

Phosphoglycerate kinase 2 [Mus musculus] us]					**1793.86**	38174603.0	7		
FPbeads600_Dec19, 620	-.VSHVSTGGGASLELLEGK.-	1741.93	3	265.49	1.31	0.0	195	9/34	4
FPbeads200_Dec19, 965	-.LGDVYVNDAFGTAHR.-	1635.76	3	1528.37	1.75	0.1	672	5/14	6

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to phosphoglycerate kinase (EC 2.7.2.3) - mouse [Mus musculus]					722642.39	38076512.0	16		
jmigG150rawphag3007, 892	- AHSSMVGVNLPQK -	1368.59	3	6186.71	3.38	0.3	1298	11/24	4
jmigG250rawphag3007, 920	- AHSSMVGVNLPQK -	1368.59	3	2782.60	2.52	0.2	804	7/16	4
jmigG250rawphag3007, 924	- AHSSMVGVNLPQK -	1368.59	2	8617.62	3.11	0.4	1341	3/4	4
jmigG350naclrawphag3007 995	- AHSSMVGVNLPQK -	1368.59	3	5212.63	3.00	0.3	1083	11/24	4
jmigG250rawphag3007, 1886	- VLPGVDALSNV -	1084.25	2	3650.40	1.73	0.3	927	13/20	2
jmraw5miniigg250mmnaclsyringdnase, 2052	- VLPGVDALSNV -	1084.25	2	9184.34	2.67	0.5	1395	4/5	2
ajrawmediapbsnocells, 390	-.AHSSMVGVNLPQK -	1368.59	3	10090.92	3.75	0.4	1183	9/16	4
ajrawmediapbsnocells, 394	- AHSSMVGVNLPQK -	1368.59	3	2651.78	2.88	0.2	665	7/16	4
ajrawmediapbsnocells,1336-1338	- VLPGVDALSNV -	1084.25	2	7473.60	2.89	0.4	1213	3/4	2
ajrawmediapbsnocells, 2378	-.VADKIQLINNMLDKVNEMIIGGGMAFTFLK.-	3326.00	2	4077.54	1.93	0.4	287	7/29	2
ajrawmediapbsnocells, 1438	- ITLPVDFVTADKFDENAK.-	2024.26	3	1813.47	1.89	0.2	508	8/17	3
jmraw5minbsabeads, 1640	- AEPAKIDAFRASLSK	1604.83	3	221.49	1.24	0.0	175	2/7	2
jmraw5minbsafreezthaw, 2796	-.DCVGPEVENACANPAAGTVILLENLR -	2670.02	3	1508.22	2.19	0.1	560	11/50	2
jmraw5minbsafreezthaw,2106-2108	- ITLPVDFVTADKFDENAK -	2024.26	3	1729.51	1.74	0.2	432	23/68	3
jmfag1mnacl0minigg, 208	- AGGFLMK -	723.91	2	2207.13	2.12	0.1	825	11/12	2
JMFAGNACL5B21E3, 412	- AHSSMVGVNLPQK -	1368.59	2	4368.89	2.61	0.2	1240	3/4	4
jmfag5minigg600mmnacl, 420	- AHSSMVGVNLPQK -	1368.59	2	13016.96	3.67	0.4	1785	5/6	4
JMFAGNACL10_1B21E3, 422	-.AHSSMVGVNLPQK -	1368.59	2	5331.41	2.61	0.3	1040	17/24	4
jmfag5minigg400mmnacl, 428	-.AHSSMVGVNLPQK -	1368.59	3	2743.67	2.79	0.2	725	5/12	4
jmfag1mnacl5minigg, 432	- AHSSMVGVNLPQK -	1368.59	3	3891.32	2.27	0.3	1066	11/24	4
jmfag1mnacl2,5minigg, 432	- AHSSMVGVNLPQK -	1368.59	2	9051.07	3.28	0.4	960	2/3	4
jmfag5minigg400mmnacl, 432	- AHSSMVGVNLPQK -	1368.59	3	8642.71	3.36	0.3	1390	1/2	4
jmfag5minigg200mmnacl, 432	- AHSSMVGVNLPQK -	1368.59	3	1940.42	2.11	0.1	835	5/12	4
jmfag5minigg1000mmnacl, 432	- AHSSMVGVNLPQK -	1368.59	3	2889.81	2.41	0.2	809	5/12	4
jmfag5minigg1000mmnacl, 438	-.AHSSMVGVNLPQK -	1368.59	3	5101.15	3.43	0.2	1230	25/48	4
jmfag1mnacl2,5minigg, 440	- AHSSMVGVNLPQK -	1368.59	2	10364.16	3.27	0.4	1186	3/4	4
jmfag1mnacl5minigg, 440	- AHSSMVGVNLPQK.-	1368.59	3	4705.39	2.68	0.2	1262	25/48	4
jmfag1mnacl5minigg, 458	- AHSSMVGVNLPQK.-	1368.59	2	9565.09	3.32	0.4	1402	3/4	4
jmfag1mnacl5minigg, 462	- AHSSMVGVNLPQK.-	1368.59	2	13828.63	3.51	0.5	1497	3/4	4
jmfag5minigg350mmnacl, 879	- SVVLMSHLGRPDGVPMPDK.-	2036.41	3	5378.16	2.67	0.3	996	1/3	1
jmfag5minigg500mmnacl, 918	- AHSSMVGVNLPQK.-	1368.59	3	3198.21	2.05	0.2	1128	7/16	4
jmigG250rawphag3007, 926	- AHSSMVGVNLPQK.-	1368.59	3	1079.60	1.80	0.1	433	1/3	4
jmfag5minigg150mmnacl, 946	- SVVLMSHLGRPDGVPMPDK -	2036.41	3	8369.62	2.96	0.4	916	25/72	1
jmfag5minigg250mmnacl, 960	-.AHSSMVGVNLPQK.-	1368.59	3	4587.98	2.66	0.3	895	23/48	4
jmfag1mnacl2,5minigg, 1076	- IQLINNMLDK.-	1202.45	2	1431.89	1.89	0.1	658	7/9	2
jmraw5minigg250mmnaclsyringdnase, 1132	-.DLMSKAEK.-	922.08	2	205.99	1.33	0.0	144	9/14	2
jmfag1mnacl5minigg, 1152	-.SVVLMSHLGRPDGVPMPDK.-	2036.41	3	9137.67	3.19	0.4	1185	13/38	1
jmfag5minigg400mmnacl, 1162	-.VLPGVDALSNV.-	1084.25	2	210.64	1.15	0.1	134	9/20	2
jmrawigg5min300mmnaclsyringednase, 1179	- VLPGVDALSNV -	1084.25	2	1807.10	1.51	0.3	561	11/20	2
ajrawphagactin20, 1252	-.SVVLMSHLGRPDGVPMPDK.-	2036.41	3	763.89	1.65	0.1	313	5/18	1
jmfag5miniggbead, 1261	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3721.32	2.20	0.3	473	23/68	3
jmfag5minigg500mmnacl, 1304	-.SVVLMSHLGRPDGVPMPDK.-	2036.41	3	4224.55	2.11	0.3	1216	3/8	1
jmfag5minigg350mmnacl, 1311	- ALESPERPFLAILGGAK.-	1770.07	3	1125.58	1.62	0.2	406	5/16	2
jmfag5minigg600mmnacl, 1342	-.ALESPERPFLAILGGAK.-	1770.07	3	7748.10	3.17	0.4	608	13/32	2
jmfag5minigg250mmnacl, 1372	-.SVVLMSHLGRPDGVPMPDK.-	2036.41	3	4584.12	2.39	0.3	704	23/72	1
jmfag1mnacl0minigg, 1386	-.ALESPERPFLAILGGAK.-	1770.07	3	3662.00	2.65	0.2	768	25/64	2
jmfag1mnacl2,5minigg, 1388	-.VLPGVDALSNV -	1084.25	2	12486.67	3.36	0.5	1193	3/4	2
jmrawigg5minbeadsfreezethaw, 1402	-.ALESPERPFLAILGGAK.-	1770.07	3	783.97	1.41	0.1	390	19/64	2
jmfag1mnacl7,5minigg, 1408	-.VLPGVDALSNV -	1084.25	2	5241.35	2.27	0.4	1002	7/10	2
JMFAGNACL5B21E3, 1410	-.VLPGVDALSNV.-	1084.25	2	5949.66	2.16	0.4	1145	7/10	2
jmrawigg5min150mmnacl, 1414	- VLPGVDALSNV.-	1084.25	2	694.16	1.52	0.1	387	1/2	2
jmfag1mnacl2.5minigg, 1430	-.ALESPERPFLAILGGAK.-	1770.07	3	3198.81	2.07	0.3	590	25/64	2
JMFAGNACL5B21E3,1442-1444	-.ALESPERPFLAILGGAK.-	1770.07	3	10900.14	4.41	0.4	1177	15/32	2
jmfag5minigg400mmnacl,1474-1476	- ALESPERPFLAILGGAK -	1770.07	3	2735.61	2.08	0.2	798	25/64	2
JMMAGNEGB16D3,1484-1486	-.ITLPVDFVTADKFDENAK.-	2024.26	3	5496.09	2.68	0.4	485	23/68	3
jmfag5minigg1000mmnacl, 1488	-.VLPGVDALSNV.-	1084.25	2	6500.28	2.73	0.4	1078	3/4	2
JMMAGTube1B16E3,1518-1520	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3344.91	2.15	0.3	460	23/68	3
jmfag1mnacl5minigg,1570-1572	-.VLPGVDALSNV.-	1084.25	2	4183.55	2.74	0.3	843	13/20	2
jmfag1mnacl5minigg,1610-1612	- ALESPERPFLAILGGAK.-	1770.07	3	7743.49	3.35	0.4	878	7/16	2
jmfag5minigg300mmnacl, 1766	-.VLPGVDALSNV.-	1084.25	2	437.20	1.12	0.2	163	9/20	2
jmigG250rawphag3007, 1886	- VLPGVDALSNV.-	1084.25	2	3650.40	1.73	0.3	927	13/20	2
jmfag5minigg600mmnacl, 1928	- DCVGPEVENACANPAAGTVILLENLR.-	2670.02	2	3744.49	3.45	0.2	473	17/50	2
jmfag5minigg250mmnacl,1938-1938	- VLPGVDALSNV.-	1084.25	2	9666.86	2.62	0.5	1352	3/4	2
jmfag5minigg150mmnacl, 2020	- DCVGPEVENACANPAAGTVILLENLR.-	2670.02	2	436.35	1.96	0.0	220	6/25	2
jmrawigg5minbeadsfreezethaw, 2026	- DCVGPEVENACANPAAGTVILLENLR.-	2670.02	2	2176.18	2.30	0.3	251	13/50	2
jmraw5minigg250mmnaclsyringdnase, 2052	-.VLPGVDALSNV.-	1084.25	2	9184.34	2.67	0.5	1395	4/5	2
jmfag5minigg450mmnacl_030527025134, 2130	- VLPGVDALSNV.-	1084.25	2	2581.30	1.69	0.2	1022	3/4	2
jmfag5minigg1000mmnacl, 2146	- DCVGPEVENACANPAAGTVILLENLR.-	2670.02	2	988.43	2.62	0.0	375	3/10	2
jmfag5minigg200mmnacl, 2162	-.DCVGPEVENACANPAAGTVILLENLR.-	2670.02	2	1029.54	2.23	0.1	294	13/50	2
jmag5mincon500mmnacl,2218-2220	-.ITLPVDFVTADKFDENAK.-	2024.26	3	2539.56	2.03	0.3	474	8/17	3
ajrawphagjun20dpi1MNaCl, 2334	-.FCLDNGAKSVVLMSHLGRPDGVPMPDK.-	2885.38	3	415.89	1.55	0.0	260	19/104	1
JMFAGNACL5B21E3, 2466	- IQLINNMLDKVNEMIIGGGMAFTFLK.-	2912.53	3	1315.80	2.00	0.2	380	1/5	2
jmfag5minigg250mmnacl, 2716	-.DCVGPEVENACANPAAGTVILLENLR.-	2670.02	3	1544.18	2.01	0.1	670	23/100	2
JMFAGNACL10_1B21E3, 574	-.YAEAVGRAK.-	965.09	2	574.42	1.20	0.0	465	11/16	3
jmfag5minigg600mmnacl, 1394	- ITLPVDFVTADKFDENAK.-	2024.26	3	571.55	1.20	0.1	398	5/17	3
jmfag1mnacl0minigg, 1446	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3410.39	1.92	0.4	404	23/68	3
jmfag5minigg150mmnacl,1460-1462	-.ITLPVDFVTADKFDENAK.-	2024.26	3	2788.02	2.35	0.3	483	25/68	3
jmrawigg5minbeadsfreezethaw,1462-1464	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3250.01	2.89	0.2	755	7/17	3
jmrawigg5minbeadsfreezethaw, 1468	-.ITLPVDFVTADKFDENAK.-	2024.26	2	1139.21	1.77	0.1	465	7/17	3
jmfag1mnacl2,5minigg,1480-1482	-.ITLPVDFVTADKFDENAK.-	2024.26	3	6947.88	2.54	0.4	767	7/17	3
JMFAGNACL5B21E3,1504-1506	-.ITLPVDFVTADKFDENAK.-	2024.26	3	7449.49	2.93	0.4	706	13/34	3
JMFAGNACL5B21E3,1510-1512	-.ITLPVDFVTADKFDENAK.-	2024.26	2	2184.38	2.05	0.2	498	8/17	3
jmfag1mnacl7,5minigg,1510-1512	-.ITLPVDFVTADKFDENAK.-	2024.26	3	7209.56	3.22	0.4	646	7/17	3
jmfag1mnacl2,5minigg,1564-1566	-.IVWNGPVGVFEWEAFARGTK.-	2264.57	3	644.15	1.72	0.1	252	4/19	

jmfag5minigg200mmnacl, 1610	-.ITLPVDFVTADKFDENAK.-	2024.26	3	709.84	1.25	0.1	388	23/68	3
jmfag1mnacl5minigg, 1618	-.ITLPVDFVTADK.-	1319.53	2	3898.53	2.13	0.4	237	13/22	3
jmfag1mnacl5minigg,1672-1674	-.ITLPVDFVTADKFDENAK.-	2024.26	3	988.87	1.44	0.2	392	21/68	3
jmfgG350nacfrawphag3007, 1905	-.ITLPVDFVTADKFDENAK.-	2024.26	2	232.66	0.98	0.0	224	5/17	3
jmfag5minigg500mmnacl, 1912	-.ITLPVDFVTADKFDENAK.-	2024.26	3	2764.36	1.75	0.3	365	21/68	3
jmfgG300rawphag3007, 1922	-.ITLPVDFVTADKFDENAK.-	2024.26	3	1987.86	1.80	0.2	502	6/17	3
jmfgG300rawphag3007, 1930	-.ITLPVDFVTADKFDENAK.-	2024.26	3	319.70	1.26	0.0	238	9/34	3
jmrawmminigg200mmnaclsyringdnas, 1958	-.ITLPVDFVTADKFDENAK.-	2024.26	3	5213.51	2.49	0.4	542	25/68	3
jmfag5minigg250mmnacl, 2010	-.ITLPVDFVTADKFDENAK.-	2024.26	3	729.86	1.58	0.2	149	15/68	3
jmfag5minigg450mmnacl_03052702513A, 2188	-.ITLPVDFVTADKFDENAK.-	2024.26	3	731.04	1.52	0.1	286	9/34	3
jmfag5minigg450mmnacl_03052702513A, 2196	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3981.00	2.29	0.4	469	6/17	3
jmfag5minigg300mmnacl, 2212	-.ITLPVDFVTADKFDENAK.-	2024.26	3	880.26	1.66	0.1	369	5/17	3
jmfgG150rawphag3007, 3070	-.ATSRGCITIIGASLELLEGKVLPGVDALSNF.-	3146.65	2	29.77	0.72	0.0	33	7/60	
jmfag5minigg350mmnacl, 917	-.YSLQPVAAELK.-	1219.41	2	6784.84	2.40	0.5	759	17/20	
jmfag1mnacl0minigg, 962	-.YSLQPVAAELK.-	1219.41	2	4301.35	1.90	0.4	621	4/5	
jmfag1mnacl2.5minigg, 1012	-.YSLQPVAAELK.-	1219.41	2	5163.00	2.53	0.4	563	3/4	
jmfag5minigg450mmnacl_03052702513A, 1114	-.AHSSMVGINLPQK.-	1382.82	2	1571.28	1.68	0.1	823	7/12	
jmfag1mnacl5minigg, 1178	-.YSLQPVAAELK.-	1219.41	2	5165.70	2.12	0.4	592	4/5	
jmfag1mnacl5minigg, 1184	-.YSLQPVAAELK.-	1219.41	2	1596.88	1.53	0.3	381	3/5	
jmfag5minigg250mmnacl, 1470	-.YSLQPVAAELK.-	1219.41	2	5498.17	2.28	0.4	652	4/5	
jmfag5minigg300mmnacl, 1650	-.YSLQPVAAELK.-	1219.41	2	2523.85	1.78	0.3	317	3/5	
jmfagtmecon2.5min,1544,1546.3	-.ALESPERPFLAILGGAK.-	1770.07	0	8040.72	3.30	0.3	1341	33/64	2
jmfagtmecon7.5min,1996,1996.3	-.ALESPERPFLAILGGAK.-	1770.07	0	5062.53	3.42	0.3	747	7/16	2
jmfagtmecon2.5min,456,456.2	-.AHSSMVGVNLPQK.-	1368.59	0	14034.25	3.81	0.5	1504	3/4	4
jmfagtmecon2.5min,452,452.3	-.AHSSMVGVNLPQK.-	1368.59	0	5621.05	3.18	0.2	1316	9/16	4
jmfagtmecon2.5min,243,243.2	-.AGGFLMK.-	723.91	0	3291.82	2.12	0.3	772	11/12	2
jmfagtmecon2.5min,459,459.3	-.AHSSMVGVNLPQK.-	1368.59	0	5707.63	2.86	0.3	1229	1/2	4
jmfagtmecon2.5min,1504,1504.2	-.VLPGVDALSNV.-	1084.25	0	4213.50	2.06	0.3	981	7/10	2
jmfagtmecon2.5min,1488,1488.3	-.SVVLMSHLGRPDGVPMPDKYSLEPVAAELK.-	3237.78	0	37753.18	6.19	0.7	1713	10/29	1
jmfagtmecon7.5min,2000,2000.3	-.ALESPERPFLAILGGAK.-	1770.07	0	7290.25	2.73	0.4	877	13/32	2
jmbeads250rawphag3007, 370	-.AHSSMVGVNLPQK.-	1368.59	2	13354.01	3.73	0.5	1206	17/24	4
jmfag5mincont150mmnacl,417-419	-.AHSSMVGVNLPQK.-	1368.59	3	3271.47	3.07	0.2	768	11/24	4
jmfag1mnacl5mincon,432-434	-.AHSSMVGVNLPQK.-	1368.59	3	3170.35	2.67	0.1	1059	25/48	4
jmfag5mncont200mmnacl, 464	-.AHSSMVGVNLPQK.-	1368.59	3	6519.75	2.98	0.3	1177	13/24	4
jmfag1mnacl5mincon, 464	-.AHSSMVGVNLPQK.-	1368.59	2	10832.67	3.81	0.4	929	17/24	4
jmfag5mincont200mmnacl, 466	-.AHSSMVGVNLPQK.-	1368.59	3	4898.65	3.23	0.2	975	25/48	4
jmfag1mnacl5mincon, 468	-.AHSSMVGVNLPQK.-	1368.59	2	5369.09	2.51	0.3	1183	3/4	4
jmfag5mincon250mmnacl,948-950	-.AHSSMVGVNLPQK.-	1368.59	3	3312.32	3.08	0.1	919	23/48	4
jmfagtmecont0min_030601230741, 1012	-.AHSSMVGVNLPQK.-	1368.59	3	4153.03	2.71	0.2	1229	13/24	4
jmfagtmecont0min_030601230741, 1016	-.AHSSMVGVNLPQK.-	1368.59	3	4011.11	2.52	0.3	803	9/12	4
jmfagtmecon10min, 1142	-.AHSSMVGVNLPQK.-	1368.59	2	13845.04	3.31	0.5	1499	3/4	4
jmfagtmecont10min_030601202502,1158-1160	-.AHSSMVGVNLPQK.-	1368.59	3	5870.13	3.82	0.2	1032	1/2	4
jmfagtmecont10min_030601202502, 1162	-.AHSSMVGVNLPQK.-	1368.59	2	6106.44	2.71	0.3	1579	17/24	4
jmbeads300rawphag3007, 1260	-.VLPGVDALSNV.-	1084.25	2	8044.29	2.49	0.4	1347	3/4	2
jmbeads250rawphag3007, 1266	-.VLPGVDALSNV.-	1084.25	2	9533.49	2.92	0.5	1208	4/5	2
jmfag5mincont150mmnacl, 1327	-.VLPGVDALSNV.-	1084.25	2	6634.78	2.30	0.4	1360	3/4	2
jmfag5mincont150mmnacl, 1373	-.ALESPERPFLAILGGAK.-	1770.07	3	4719.03	2.33	0.4	388	11/32	2
jmfag5mincont150mmnacl, 1377	-.ALESPERPFLAILGGAK.-	1770.07	3	2810.76	2.30	0.2	634	27/64	2
jmfag5mincon250mmnacl, 1902	-.VLPGVDALSNV.-	1084.25	2	3310.84	2.21	0.2	1006	7/10	2
jmfagtmecont0min_030601230741,1960-1962	-.VLPGVDALSNV.-	1084.25	2	8483.96	2.51	0.4	1357	4/5	2
jmfag5mincon300mmnacl, 2090	-.VLPGVDALSNV.-	1084.25	2	4933.89	2.20	0.3	1068	7/10	2
jmfagtmecon10min,2192-2194	-.VLPGVDALSNV.-	1084.25	2	6300.22	2.64	0.3	1395	3/4	2
jmfagtmecont10min_030601202502, 2210	-.VLPGVDALSNV.-	1084.25	2	7789.39	2.90	0.4	870	13/20	2
jmfagtmecont10min_030601202502, 2214	-.VLPGVDALSNV.-	1084.25	2	3118.92	1.82	0.3	831	7/10	2
jmfagtmecont10min_030601202502, 2226	-.ALESPERPFLAILGGAK.-	1770.07	3	7007.25	2.51	0.4	1139	15/32	2
jmfagtmecon2.5min,1596,1600.3	-.ITLPVDFVTADKFDENAK.-	2024.26	0	5744.42	2.62	0.4	601	27/68	3
jmfagtmecon2.5min,1606,1608.2	-.ITLPVDFVTADKFDENAK.-	2024.26	0	8971.55	2.58	0.5	539	8/17	3
jmbeads250rawphag3007, 1348	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3438.92	2.21	0.3	338	23/68	3
jmbeads250rawphag3007, 1352	-.ITLPVDFVTADKFDENAK.-	2024.26	3	6387.97	2.57	0.4	694	7/17	3
jmfag5mincont400_030531151834,1404-1406	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3357.00	2.42	0.3	729	13/34	3
jmfag5mincont350,1434-1436	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3652.60	2.76	0.3	457	6/17	3
jmfag5mincon250mmnacl, 1970	-.ITLPVDFVTADKFDENAK.-	2024.26	3	4580.45	2.44	0.4	529	13/34	3
jmfagtmecont0min_030601230741,2030-2032	-.ITLPVDFVTADKFDENAK.-	2024.26	3	2697.68	2.19	0.3	394	6/17	3
jmag5mincon500mmnacl,2218-2220	-.ITLPVDFVTADKFDENAK.-	2024.26	3	2539.56	2.03	0.3	474	6/17	3
jmfagtmecon10min,2262-2264	-.ITLPVDFVTADKFDENAK.-	2024.26	3	3684.39	2.53	0.3	573	27/68	3
jmfagtmecont10min_030601202502, 2294	-.ITLPVDFVTADKFDENAK.-	2024.26	2	4748.64	2.31	0.4	426	7/17	3

control

similar to phosphoglycerate kinase (EC 2.7.2.3) - mouse [Mus musculus]					**1145.87**	**38076512.0**		**5**	
rawextr_900beadigg_Mar04, 1480	-.PDGVPMPDKYSLEPVAAELKSLLGK.-	2656.09	3	499.41	1.70	0.1	248	3/16	2
rawextr_900beadigg_Mar04, 1952	-.TGQATVASGISAGCLGLDCGTESSK.-	2314.54	2	179.61	0.92	0.1	143	5/24	
rawextr_actinbeadigg_Mar04, 1083	-.ATSRGCITIIGGGASLELLEGK.-	2147.48	3	466.85	1.74	0.0	263	1/4	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inhibitor of kappaB kinase epsilon; inducible IKappaB kinase; inhibito					**3782.89**	**31981053.0**	**16**		
jmfag1mnacl5minigg, 874	-.AQNHLHLIGHSVATCNSEAR.-	2159.39	3	234.22	1.32	0.0	172	15/76	2
jmrawigg5min150mmnacl,1584-1586	-.PGLSYNEEQIHK.-	1415.53	3	359.67	1.26	0.0	260	7/22	2
jmIgG500rawphag3007, 1903	-.DQIHEDNKSIQKIQCCLDK.-	2259.55	3	809.57	1.45	0.2	334	1/4	2
jmrawmminigg200mmnaclsyringdnas, 2056	-.PGLSYNEEQIHK.-	1415.53	3	245.69	0.95	0.0	238	7/22	2
ajrawphagactin20, 2324	-.PGLSYNEEQIHK.-	1415.53	3	343.99	0.99	0.0	329	15/44	2
ajrawphag1MNaCl20, 2538	-.PGLSYNEEQIHK.-	1415.53	3	559.58	1.23	0.1	294	7/22	2
rawsucrfp_800phagigg_Mar04, 928	-.LIERLHRVPSAPDV.-	1602.86	3	387.31	1.25	0.0	311	17/52	2
phagrawFsuc1000_dec23, 2387	-.DPALDVPKFVPKVDLQADYSTAK.-	2518.85	3	259.68	1.11	0.1	112	3/22	2
phagrawF150_dec22, 2704	-.RLLQVFQEECVQTYQVSLVTHGKR.-	2863.29	3	583.19	1.52	0.1	327	21/92	2

control

inhibitor of kappaB kinase epsilon; inducible IKappaB kinase; inhibito					**419.38**	**31981053.0**		**6**	
FPbeadsz250_Dec19, 3486	-.LLQVFQEECVQTYQVSLVTHGKRMR.-	2994.49	2	83.57	0.88	0.0	90	1/8	2
jmrawbsa5minlowionic, 2050	-.PGLSYNEEQIHK.-	1415.53	3	335.81	1.15	0.0	277	15/44	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to putative protein kinase [Mus musculus]					**4915.22**	38079866.0	12		
jmigG250rawphag3007,1410-1412	-.LAHHRLTGTAVAIKVLLK.-	1942.39	3	2275.01	2.68	0.2	524	23/68	
jmfag5minigg250mmnacl, 2012	-.PVQPGITPFPTLTDPTNFR.-	2099.38	3	221.07	1.28	0.0	172	19/72	
jmfag5minigg200mmnacl, 1466	-.KSDLWALGVILYYMVVGK.-	2056.50	3	607.55	1.81	0.0	311	19/68	1
JMFAGNACL5B21E3, 1920	-.VGNAIRTLCCCIPSRK.-	1735.14	1	213.49	1.13	0.0	189	4/15	2
jmfag5minigg250mmnacl, 2612	-.APFPSMDAGAASCLKIKR.-	1864.23	2	184.55	1.23	0.1	93	4/17	2
jmraw5minigg600mmnaclsd, 3100	-.SIHEEPFPVRPDPDIVDAMQYIGFQAKDIR.-	3485.91	2	92.34	0.72	0.1	14	2/29	
phagrawF200_dec22, 1339	-.PCFQPAMKEANIMK.-	1608.98	2	166.13	0.83	0.0	193	4/13	
jmkdt250naclrawphag3007, 1978	-.MFAKTRGYLIMELVEGQELYEYIK.-	2926.44	3	175.38	1.25	0.0	138	15/92	
jmkdt500naclrawphag3007, 1579	-.VLLAKHWLTGTPVAVK.-	1734.12	2	169.04	0.92	0.0	168	3/10	
rawsucrfp_600phagigg_Mar04, 2286	-.LYNEPMATYGLLQCQARQQDDYTSLPK.-	3148.52	2	48.06	0.82	0.0	54	2/13	
phagrawF200_dec22, 2627	-.MDPSYPDPAIMAAMAAMGFDPLDVQK.-	2784.25	3	417.33	1.29	0.0	317	19/100	
rawsucrfp_700phagigg_Mar04, 2181	-.IDVWTLGVVLYFMVTGKIPFDACSIK.-	2917.52	2	130.47	1.12	0.0	114	9/50	1
jmraw5minbsafreezthaw, 176	-.SLYQHR.-	917.05	3	214.78	1.19	0.1	94	7/24	5

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to putative protein kinase [Mus musculus]					**512.41**	38093504.0	1		
FPbeads600_Dec19, 636	-.LTGTPVAVKVLVKNK.-	1567.94	3	512.41	1.45	0.1	221	2/7	
rawextr_150beadigg2_Mar04, 1182	-.NKPCFQPAMKEANIMK.-	1851.25	2	196.74	1.66	0.0	94	1/5	
FPbeads250_Dec19, 94	-.PGDLLDEPCGAYAFGAPELFLWERYDGRK.-	3287.65	2	84.22	0.89	0.0	72	1/7	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
putative membrane-associated guanylate kinase 1 [Mus musculus]					**2416.23**	2702351.0	9		
jmrawigg5min150mmnacl, 20	-.PHPALESSYPPELHK.-	1702.89	2	187.80	0.87	0.1	188	9/28	
jmfag1mnacl5minigg, 128	-.RAHAKDPK.-	923.06	2	357.19	1.08	0.0	321	9/14	
jmfag5minigg200mmnacl, 438	-.EAQPERTATNGSK.-	1389.45	3	1152.04	1.62	0.2	234	5/16	
jmfag5minigg200mmnacl, 578	-.AHAKDPKGNR.-	1094.21	3	256.99	0.97	0.1	208	13/36	
jmrawbas5min1mnacl, 842	-.RSLERLLDQR.-	1286.47	3	462.21	1.34	0.0	324	5/12	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
putative membrane-associated guanylate kinase 1 [Mus musculus]					**93.52**	2702351.0	2		
rawextr_actinbeadigg_Mar04,1379-1381	-.SPRNPPEQR.-	1081.17	2	93.52	1.15	0.0	63	3/8	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
putative PKA-related protein kinase [Mus musculus]					**6220.94**	6010221.0	20		
jmrawigg5min300mmnaclsyringednase, 344	-.LKPPIVPK.-	892.16	2	141.33	1.34	0.0	95	1/2	1
jmrawigg5minbeadsyringdnase, 563	-.TKVSAPAADPK.-	1085.24	2	1151.39	1.38	0.2	368	1/2	2
jmfagfrench20minigg1mnacldit, 626	-.TPSVSDKDLETFK.-	1467.60	3	1313.82	1.42	0.1	819	5/12	1
jmfag5minigg350mmnacl, 671	-.GVEWESVPQRKLK.-	1556.79	2	323.76	1.36	0.1	167	3/8	1
ajrawphag1MNaCl20, 1352	-.LTDFGFAKK.-	1027.20	2	150.44	1.08	0.1	104	7/16	2
jmfag5minigg500mmnacl, 1542	-.IDFPRQLDFTSKDLIK.-	1937.23	3	555.79	1.36	0.1	362	17/60	1
jmigg600rawphage3007, 1802	-.MEPPAGAAATVKDPDHDPVKTK.-	2276.56	3	383.09	1.36	0.0	266	3/14	2
jmrawminigg200mmnaclsyringdnas,2084-2086	-.KLVDRTWTLCGTPEYLAPEVIQSK.-	2749.18	3	617.07	1.79	0.1	200	11/46	2
jmrawbas5min1mnacl,1550-1552	-.VNLVKEKTGR.-	1144.35	2	494.59	1.50	0.1	251	1/2	2
phagrawF450_dec20, 775	-.LKQGQHVQNEK.-	1309.46	2	251.49	1.26	0.0	182	9/20	
rawsucrfp_450phagigg_Mar04, 1184	-.PPIVPKLSGDGDISNFETYPESELDR.-	2877.11	3	395.97	1.63	0.1	214	1/5	
rawsucrfp_300phagigg_Mar04,1635-1637	-.RLGNMKNGAEDIK.-	1446.66	2	417.47	1.45	0.0	269	5/12	1
phagrawFsuc1000_dec23, 2355	-.AGHSLQDWDTIATVGTGTFGRVNLVK.-	2745.04	2	24.74	0.70	0.0	34	3/25	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
putative PKA-related protein kinase [Mus musculus]					**2579.39**	6010221.0	8		
FPbeads150_Dec19, 905	-.LGNMKNGAEDIK.-	1290.47	3	536.74	1.66	0.0	323	17/44	
rawextr_700beadigg_Mar04, 1264	-.MEPPAGAAATVKDPDHDPVKTK.-	2276.56	3	1461.55	2.41	0.0	592	1/4	
FPbeads1000_Dec19, 2074	-.MEPPAGAAATVKDPDHDPVKTK.-	2276.56	3	581.10	1.73	0.0	336	5/21	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol 1,4,5-trisphosphate 3-kinase A; IP3-kinase A [Mus musculus]					**2982.88**	22122643.0	9		
JMFAGNACL15B21E3, 504	-.CAAVAAAAAAGEPRAR.-	1456.66	3	514.65	1.75	0.0	281	17/60	
JMFAGNACL10_1B21E3, 562	-.TMVNLPVMSPFR.-	1392.72	3	448.73	1.43	0.0	313	7/22	
jmrawigg5minbeadsyringdnase, 823	-.IEGIKKADGSCSTDFK.-	1699.91	2	468.95	1.46	0.1	253	11/30	
jmrawigg5minbeadsfreezethaw, 1202	-.TTRSREQVTR.-	1234.35	2	432.85	0.97	0.0	442	11/18	
jmrawigg5min150mmnacl, 1618	-.CAAVAAAAAAGEPRAR.-	1456.66	2	478.66	1.21	0.1	367	2/5	
jm5miniggrawlowionic, 3132	-.LSTSSLSSTGSSSLLEDSEDDLLSDSESRSR.-	3249.31	2	72.43	0.80	0.1	57	2/15	
jmkdi400firstnaclrawphag3007, 1392	-.KADGSCSTDFK.-	1159.25	2	136.70	0.82	0.0	157	7/20	
rawsucrfp_500phagigg_Mar04, 1622	-.RHEVIGSSLLFVHDHCHR.-	2143.42	3	249.06	1.62	0.0	150	1/4	
phagrawF250_dec22, 2039	-.LSTSSLSSTGSSSLLEDSEDDLLSDSESRSR.-	3249.31	2	180.83	1.01	0.1	61	3/20	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol 1,4,5-trisphosphate 3-kinase A; IP3-kinase A [Mus musculus]					**147.55**	22122643.0	3		
rawextr_500beadigg_Mar04, 1006	-.EGISSSTTLGFRIEGIKK.-	1924.19	2	147.55	1.26	0.0	111	9/34	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol 1,4,5-trisphosphate 3-kinase C [Mus musculus]					**2440.16**	31712006.0	15		
jmrawigg5min1mnacl, 721	- VLEDFVNGDLGILR.-	1560.78	2	367.97	1.21	0.0	304	5/13	
jmrawigg5min450mmnaclsd, 1270	- SLELLMGDPLRPFVPAYYGMVQR.-	2654.15	3	304.07	1.70	0.1	148	15/88	
jmfag5minigg500mmnacl, 1572	- ADGTCNTNFKK.-	1199.32	2	1188.25	1.23	0.3	214	7/20	
jmIgG350naclrawphag3007, 1941	-.QPGSDGFSSKDTESALTQPGTDGLR.-	2552.65	3	233.25	1.31	0.1	146	1/6	
phagrawFsuc800_dec23, 1232	-.CPCRGSLSEAEAGALPAEAR.-	1989.22	3	289.03	1.08	0.1	171	15/76	
phagrawFsuc450_dec20, 3660	-.TPHDTDGFWIESQTDDSLKGPSTQTACR.-	3095.26	2	57.59	0.76	0.0	76	4/27	

control

inositol 1,4,5-trisphosphate 3-kinase C [Mus musculus]					**713.66**	31712006.0	12		
rawextr_300beadigg_Mar4, 392	-.KLKTVLK.-	830.09	2	168.77	0.95	0.0	176	1/2	
rawextr_900beadigg_Mar04, 912	-.TDLHRSDLQSR.-	1328.42	2	544.90	1.32	0.1	385	9/20	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol polyphosphate 5-phosphatase II splice variant [Mus musculus]					**3337.53**	2766531.0	11		
jmfag5minigg200mmnacl, 774	-.LEEADWEMSAGGGSR.-	1595.67	3	586.58	1.55	0.1	301	1/4	1
phagrawF500_dec20, 922	-.MSFQQGNKGGVAIR.-	1493.72	3	439.93	1.27	0.0	341	19/52	1
ajrawphagjun20dpi1MNaCl, 952	-.NGCVFIIR.-	922.13	1	139.43	1.10	0.0	126	9/14	
JMFAGNACL10_1B21E3, 1236	-.CNKGTQTLDNLIQKK.-	1704.97	3	855.80	1.74	0.1	424	5/14	
jmIgG400rawphag3007, 1258	-.MSFQQGNKGGVAIR.-	1493.72	2	307.47	1.16	0.0	255	5/13	1
JMFAGNACL10_1B21E3, 2006	-.LEEADWEMSAGGGSRER.-	1880.98	2	740.51	1.67	0.2	168	9/32	1
ajrawphag1MNaCl20, 2476	-.LEEADWEMSAGGGSRER.-	1880.98	2	267.80	1.16	0.0	230	11/32	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol polyphosphate-5-phosphatase E; inositol polyphosphate-5-phosp					**10790.96**	14916467.0	8		
rawsucrfp_350phagigg_Mar04,1412-1414	-.SYLEGSLLASGALLGAEELARYFPDR.-	2800.12	3	818.81	2.54	0.1	172	1/5	
phagrawFsuc450_dec20, 1672	-.GDICPMKYSSCPGIKTSDHR.-	2196.52	3	285.29	1.24	0.0	228	4/19	
phagrawF350_dec20, 2300	-.HTEAPGQLEGRMLQGQPPNTEKK.-	2547.83	3	1631.40	1.65	0.3	324	5/22	
JMFAGNACL10_2B21E3, 720	-.PRSPLAGDDHSIHSAR.-	1716.84	3	826.13	2.05	0.0	402	19/60	
jmfag5minigbead, 821	- LSGGRVAVEAFLKQK.-	1603.89	3	392.65	1.23	0.0	303	1/4	
JMFAGNACL10_1B21E3,878-880	-.PRSPLAGDDHSIHSAR.-	1716.84	3	2788.05	2.94	0.1	760	11/30	
JMFAGNACL15B21E3,902-904	-.PRSPLAGDDHSIHSAR -	1716.84	3	1545.64	2.62	0.0	570	7/20	
jmfag5minigg150mmnacl,1342-1344	-.AHSNLGPSRPR.-	1192.31	2	150.57	1.03	0.0	131	7/20	
JMMAGNEGB16D3, 1430	-.ELYLIGIK.-	949.17	1	384.46	1.06	0.1	319	4/7	
jmfag5minigg1000mmnacl,1598-1600	- ANLITPQPPIRPK.-	1445.74	2	1056.51	1.24	0.3	85	7/24	
jmidl350naclrawphag3007, 1358	-.DTYDSTSKQRTPSYTDR.-	2022.08	3	306.32	1.25	0.0	245	15/64	
jmrawrminigg200mmnaclsyringdnas, 1630	-.DIRSRSYLEGSLLASGALLGAEELAR.-	2749.07	3	805.13	1.70	0.0	354	11/50	

control

inositol polyphosphate-5-phosphatase E; inositol polyphosphate-5-phosp					**655.57**	14916467.0	9		
rawextr_chifbeadIgG_Mar04,1314-1316	-.LSGGRVAVEAFLK.-	1347.59	2	655.57	1.58	0.0	400	1/2	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol polyphosphate-5-phosphatase D; inositol polyphosphate-5-phosph					13813.52	6754356.0	25		
jmfagtimecon7 5min.826 826 2	- LSLSETLFQR -	1194.36	0	230.80	1.42	0.0	154	4/9	5
jmfag5mincont350, 196	- AQEVESVK.-	889.97	2	500.90	1.21	0.1	263	4/7	6
jmfag5mincont400_030531151834,810-812	-.NQNYMNILRFLALGDK -	1911.22	3	1360.10	1.93	0.2	226	4/15	7
jmfag5mincont350, 2446	-.FTVQASEGVPMRFFTKLDQLIDFYK.-	2982.45	2	102.24	0.88	0.1	85	1/6	6
ajrawphagactin20,1230-1232	-.LTRDKYAYTK -	1259.44	3	212.08	1.08	0.1	145	7/18	7
rawsucrfp_500phagigg_Mar04, 1252	-.ITSWFLSKGQGKTR -	1609.85	2	343.65	1.27	0.1	114	5/13	7
rawsucrfp_700phagigg_Mar04, 1299	- QAPVPVLGPTPRIRSFTCSSSAEGR.-	2614.97	3	290.55	2.00	0.0	145	5/32	6
rawsucrfp_actinphagigg_Mar04, 1392	-.LVILVETEKEKILR -	1684.06	2	186.92	1.10	0.0	186	4/13	7
phagrawFsuc600_dec20, 1464	- LSQLTSLLSSIEDK -	1534.74	2	194.40	1.02	0.1	150	4/13	7
phagrawFsucchlf_dec23, 1468	-.PKASASSQAPVPVK.-	1367.58	2	216.97	1.20	0.0	167	5/13	6
phagrawFsuc200_dec22, 1537	- LMSLLCKELHGEVIR.-	1742.14	2	403.61	1.09	0.1	211	9/28	5
JMFAGNACL5B21E3, 358	- NQNYMNILR -	1166.34	3	748.34	1.49	0.1	431	15/32	7
jmfag5minigg500mmnacl, 1172	- NQNYMNILRFLALGDK -	1911.22	3	527.12	1.45	0.1	312	1/4	7
jmfag5minigg250mmnacl, 1256	- NQNYMNILRFLALGDK.-	1911.22	3	799.36	1.57	0.1	403	17/60	7
jmfag5minigbead_030528200105, 1325	- TVAIHTLWNIRIVVLAKPEHENR -	2711.16	3	311.58	1.59	0.1	102	13/88	7
JMFAGNACL10_2B21E3, 1578	- PSRSEMSQQTTPIPAPRPPLPVK -	2515.92	3	555.59	1.52	0.1	338	17/88	6
JMFAGNACL10_1B21E3, 2408	-.LSQLTSLLSSIEDKVK.-	1762.04	2	366.15	1.18	0.1	201	3/10	7
JMFAGNACL5B21E3, 2658	-.KEPPPCPDPGISSPSIVLPKAQEVESVK.-	2930.37	2	117.71	0.81	0.0	135	11/54	6
jmfag1mnacl0minigg, 2670	- NIPMSAGPSEAKDLPLATENPRAPEVTR -	2963.32	2	300.84	1.23	0.1	76	4/27	5
JMFAGNACL5B21E3, 358	- NQNYMNILR.-	1166.34	3	748.34	1.49	0.1	431	15/32	7
jmrawigg5min1mnacl,1157-1159	- QQQYSDLLAHDQLLLER.-	2071.28	3	197.15	1.15	0.0	171	15/64	7
ajrawphagactin20,1230-1232	- LTRDKYAYTK -	1259.44	3	212.08	1.08	0.1	145	7/18	7
jmrawigg5min450mmnaclsd,1458-1460	- PSRSEMSQQTTPIPAPRPPLPVK -	2515.92	3	165.86	1.45	0.1	69	1/8	6
jmraw5minigg250mmnaclsyringdnase, 1622	- SEMSQQTTPIPAPR -	1543.73	2	150.98	1.27	0.1	75	4/13	6
ajrawphagjun20dpi1MNaCl,1778-1780	- LFDQQLSPGLRPR.-	1527.75	2	149.58	1.06	0.0	139	3/8	5
jmrawigg5minbeadsfreezethaw, 2052	- AYALCVLFRNCVYTYR.-	1956.32	1	133.64	0.72	0.1	83	7/30	4
jmraw5minigg500mmnaclsd, 2082	- PSRSEMSQQTTPIPAPRPPLPVK.-	2515.92	3	209.58	1.09	0.1	166	17/88	6
ajrawphagjun20actinDPI, 2084	- VQEARPGDLGK -	1170.30	2	151.23	0.76	0.0	189	7/20	6
AJRAWActinIgG_june13, 2150	-.GAAGVSFMFIGTSLGFVNSHLTSGSEK.-	2703.02	3	490.52	1.79	0.1	171	2/13	
JMFAGNACL10_1B21E3, 2408	-.LSQLTSLLSSIEDKVK.-	1762.04	2	366.15	1.18	0.1	201	3/10	7
JMFAGNACL5B21E3, 2658	- KEPPPCPDPGISSPSIVLPKAQEVESVK -	2930.37	2	117.71	0.81	0.0	135	11/54	6
jmfag1mnacl0minigg, 2670	-.NIPMSAGPSEAKDLPLATENPRAPEVTR.-	2963.32	2	300.84	1.23	0.1	76	4/27	5
jmrawigg5miniggfreebead, 868	-.SEMSQQTTPIPAPRPPLPVK.-	2175.54	3	2650.99	2.17	0.2	652	13/38	6

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol polyphosphate-5-phosphatase D; inositol polyphosphate-5-phosph					1910.29	6754356.0	15		
rawextr_150bead_Mar04, 669	-.KEQESPKMLR.-	1246.46	3	291.04	1.21	0.0	219	7/18	6
rawextr_200bead_Mar04, 1586	- PQVPGEASPITMVAKLSQLTSLLSSIEDKVK.-	3268.81	3	351.86	1.25	0.1	141	17/120	5
FPbeads600_Dec19, 1248	-.LFDQQLSPGLRPR -	1527.75	2	124.96	0.96	0.0	129	7/24	5
rawextr_300beadigg_Mar4, 2146	-.IRSFTCSSSAEGRMTSGDK -	2021.22	3	480.41	1.11	0.1	377	19/72	6
FPbeads800_Dec19, 2850	-.VFLHFEEEEITFAPTYRFERLTR.-	2932.28	2	299.96	0.90	0.1	111	9/44	7
FPbeads1000_Dec19, 2998	-.ELHGEVIRTLPSLESLQRLFDQQLSPGLR.-	3333.79	2	64.50	1.15	0.0	35	1/7	5
jmraw5minbsafreezthaw, 434	-.DSSLGPGR.-	788.83	2	297.57	0.95	0.1	259	4/7	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol polyphosphate-5-phosphatase F; cDNA sequence, clone 3-26 [Mus					5308.43	31542017.0	4		
jmbsa250naclrawphag3007,436-438	-.MNDLSEIRSVAQK.-	1491.70	3	683.97	2.18	0.0	310	17/48	3
jmldl1000naclrawphag3007,1848-1850	-.QAMGLDVPIIEK.-	1314.58	1	131.84	1.03	0.0	128	9/22	3
phagrawFsuc150_dec22, 82	-.VVMEQQLKKLGVMPPEQPLPVK.-	2490.07	3	625.51	1.57	0.1	286	17/84	1
jmrawigg5min450mmnaclsd,182-185	-.MNDLSEIR.-	978.11	3	420.33	1.57	0.1	184	13/28	3
jmfag5minigg200mmnacl, 404	-.FSSLNQKVK.-	1051.22	2	535.19	1.30	0.1	387	5/8	3
JMFAGNACL10_2B21E3, 702	-.PMDVYCQR.-	1012.19	2	400.52	1.20	0.0	322	1/2	3
jmfag5miniggbead, 1127	-.QAVIDLMQGVPVTEDLYSIFTK.-	2468.85	3	1446.36	2.19	0.1	542	1/4	1
jmIgG250rawphag3007,1424-1426	-.VSNEETQSEPMGQTPPR.-	1868.01	3	854.51	1.79	0.1	412	9/32	3
jmfag5minigg600mmnacl, 2264	-.QLANSLESVGPIDYILPSCGIIVSAPR.-	2814.25	2	77.84	0.83	0.0	79	2/13	3
jmrawigg5min450mmnaclsd, 2944	-.PSQLNVSCSVAGPPFLSVEPVHSVLSQK.-	2908.32	2	132.37	0.88	0.1	46	4/27	3

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol polyphosphate-5-phosphatase F; cDNA sequence, clone 3-26 [Mus					2230.62	31542017.0	8		
rawextr_200beadigg_Mar04, 457	-.KLAGVMKDGVNSANR.-	1560.81	3	296.54	1.41	0.1	92	11/56	1
rawextr_400beadigg_Mar04, 832	-.PEMKVNFLK.-	1106.36	2	684.76	1.62	0.0	417	9/16	3
FPbeads400_Dec19, 1290	-.DTLQCIAEMLQITKQAMGLDVPIIEK.-	2903.47	3	384.95	1.43	0.0	268	19/100	2
FPbeads250_Dec19, 1376	-.VSNEETQSEPMGQTPPR.-	1888.01	3	773.80	1.44	0.2	223	15/64	3
FPbeads1000_Dec19, 2028	-.IRSSMVQVANITQAGLTHGINLAVAKVQK.-	3049.59	2	90.58	0.90	0.0	99	5/28	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol polyphosphate phosphatase-like 1 [Mus musculus]					4298.98	33859566.0	10		
phagrawFsucchlf_dec23, 2400	-.PEHENRISHVSTSSVKTGIANTLGNK.-	2778.03	3	304.07	1.59	0.0	189	9/50	1
phagrawFsuc300_dec20, 2958	- ALDEVTVTIPHDIYVFGTQENSVGDR.-	2877.11	3	1088.02	1.94	0.2	264	19/100	1
phagrawFsuc300_dec20, 3154	- GAVGVSFMFNGTSFGFVNCHLTSGNEKTTRR.-	3323.71	2	396.97	0.95	0.2	65	2/15	1
jmldl30naclrawphag3007, 1286	-.FSEEEISFPPTYR.-	1602.73	2	316.81	1.25	0.1	123	1/3	1
jmldl150naclrawphag3007, 1536	-.ILPDGEDFLAVQTSQGVPVRR.-	2298.59	3	404.05	1.50	0.1	216	17/80	1
phagrawFsucchlf_dec23, 2400	-.PEHENRISHVSTSSVKTGIANTLGNK.-	2778.03	3	304.07	1.59	0.0	189	9/50	1
phagrawFsuc300_dec20, 2958	-.ALDEVTVTIPHDIYVFGTQENSVGDR.-	2877.11	3	1088.02	1.94	0.2	264	19/100	1
phagrawFsuc300_dec20, 3154	-.GAVGVSFMFNGTSFGFVNCHLTSGNEKTTRR.-	3323.71	2	396.97	0.95	0.2	65	2/15	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
inositol polyphosphate phosphatase-like 1 [Mus musculus]					444.26	33859566.0	10		
jmbsa350naclrawphag3007, 922	-.YERGSRDTYAWHK.-	1669.78	2	90.72	0.81	0.0	111	1/3	1
jmbsa150naclrawphag3007, 2229	-.FTLSVDVEGGRLVLLRR.-	1931.27	2	353.54	0.96	0.1	152	1/4	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol 4-phosphate 5-kinase type I-beta [Mus musculus]				3146.63	1622710.0	14		
jmIgG250rawphag3007, 846 - KIPLKPSPTK.-	1109.39	2	256.29	1.23	0.0	200	4/9	2
jmldlactinrawphag3007,1004-1006 - ATVSEGPSASVMPVKK.-	1588.85	3	608.92	1.68	0.1	450	19/60	2
ajrawphagactin20, 1332 - FYGLYCVQAGGK.-	1306.52	3	1846.37	1.58	0.3	539	19/44	2
jmfag5minigg500mmnacl, 1872 -.EPTSNDTQYSADTR.-	1585.57	3	233.05	1.44	0.0	153	7/26	1

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol 4-phosphate 5-kinase type I-beta [Mus musculus]				1072.12	1622710.0	6		
FPbeads800_Dec19, 164 - DLDFLQDIPDGLFLDADMYSALCKTLQR -	3218.65	2	24.44	0.78	0.0	30	5/54	1
rawextr_350beadigg_Mar04, 596 - AEVEPDVHLGR.-	1222.33	3	389.02	1.53	0.1	146	3/10	2
rawextr_450beadigg_Mar04, 1226 - SGPSFSRRSGPSGNSCTSQLMASGEHR -	2781.99	3	658.66	2.09	0.1	267	11/52	2

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma [Mus musculus]				4527.08	6679323.0	10		
jmfagfrench20minigg1mnacldtt, 318 -.FDLKGSTYKR.-	1215.38	3	1103.68	1.94	0.0	555	4/9	2
jmrawigg5min1mnacl, 1381 -.GEAIETDDTMGGIPAVNGRGER.-	2246.40	3	1462.06	1.91	0.2	450	5/21	2
jmIgG350naclrawphag3007,1899-1901 -.ITVQVEPVCGVGVVPK.-	1624.97	2	355.23	1.42	0.0	231	11/30	2
jm5miniggrawlowionic, 2124 -.ALVHDGDTVSVHR.-	1406.53	2	612.79	1.09	0.2	305	1/2	4
phagrawF400_dec20, 884 -.GAIQLGIGYTVGNLSSK.-	1678.91	3	171.82	1.04	0.0	159	11/64	2
phagrawF200_dec22, 1113 -.KLGHRGVDASGETTYK.-	1719.88	2	454.56	1.28	0.2	89	1/5	2
phagrawF200_dec22, 2037 -.RTQSSGQDGRPQEEPHAEDLQK.-	2494.58	2	366.95	0.95	0.2	127	4/21	2

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma [Mus musculus]				242.76	6679323.0	9		
rawextr_actinbeadigg_Mar04, 763 -.PASDGESDT.-	878.82	2	242.76	0.99	0.1	209	1/2	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol-4-phosphate 5-kinase, type II, beta [Mus musculus				4194.56	33563294.0	12		
JMFAGNACL5B21E3,978-980 -.LKRDVEFLAQLK.-	1460.75	3	1035.29	2.31	0.0	448	9/22	2
phagrawF300_dec20, 1189 -.FLTTYDR.-	916.01	2	253.13	1.10	0.1	202	1/2	1
phagrawFsuc450_dec20, 2750 -.IMDYSLLVGIHDVDR.-	1747.01	2	581.43	1.25	0.1	367	3/7	2
jmldl150naclrawphag3007, 1172 -.MSSNCTSTTAVAVAPLSASK.-	1927.19	3	308.71	1.20	0.1	157	15/76	
jmldl1000naclrawphag3007, 1692 - KYHQFIVECHGNTLLPQFLGMYR.-	2796.27	3	1076.87	1.40	0.2	249	2/11	1
jmldl150naclrawphag3007, 2058 -.FVIKTVSSEDVAEMHNILK.-	2161.51	3	939.14	1.58	0.2	290	5/24	1

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol-4-phosphate 5-kinase, type II, beta [Mus musculus				828.81	33563294.0	7		
FPbeads300_Dec19, 1426 -.FVIKTVSSEDVAEMHNILK.-	2161.51	3	828.81	1.71	0.1	407	19/72	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol 4-kinase, catalytic, beta polypeptide; EST AA4378				5801.84	29648332.0	21		
ajrawphagjun20dpi1MNaCl, 678 -.VENEDEPVRLAPER.-	1653.78	3	386.46	1.51	0.0	246	9/26	1
jmfagfrench20minigg1mnacldtt, 726 -.VWLPTAGFDHHVVR.-	1634.87	2	186.35	1.01	0.0	184	9/26	1
jmigg450rawphag3007, 986 -.VPHTQAVVLNSKDK.-	1536.76	3	1359.50	1.91	0.1	569	5/13	1
jm5miniggrawlowionic, 1116 -.STRSVENLPECGITHEQR -	2057.24	3	236.97	1.17	0.0	186	13/68	1
jmfag5minigg1000mmnacl, 1280 -.SKSDATASISLSSNLKR -	1765.95	2	787.43	1.58	0.1	290	13/32	1
jmfag5minigg200mmnacl, 1296 -.SKSDATASISLSSNLKR.-	1765.95	2	387.79	1.52	0.0	254	3/8	1
JMFAGNACL5B21E3, 1496 -.NFVQSCAGYCLVCYLLQVK.-	2152.59	3	381.86	1.32	0.1	263	1/4	1
jmrawmminigg200mmnaclsyringdnas, 3078 -.VWLPTAGFDHHVVRVPHTQAVVLNSKDK.-	3152.60	2	310.74	1.03	0.2	51	7/54	1
jmfag5minigg300mmnacl, 4066 -.FHMSMTEEQLQLLVEQMVDGSMRSITTK.-	3271.80	2	82.55	0.82	0.1	43	1/9	2
jmldl300naclrawphag3007, 1134 -.EEEDEMGAGVASGTAKGARR.-	2022.15	3	528.60	1.22	0.1	357	17/76	1
phagrawF150_dec22, 1908 -.LISELSLLNHKLPAR.-	1705.04	2	1153.60	1.34	0.3	148	2/7	1

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol 4-kinase, catalytic, beta polypeptide; EST AA4378				792.60	29648332.0	21		
jmrawfminbsalreezthaw,1130-1132 -.EPVFIAAGDIR.-	1188.36	2	568.46	1.37	0.0	413	11/20	1
jmbsa150naclrawphag3007, 1345 -.LAPEREFIK.-	1103.30	1	224.14	0.83	0.1	233	1/2	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 b				2789.48	6679321.0	5		
JMMAGNEGB16D3, 178 -.FLLQHLGR.-	984.18	2	224.88	1.22	0.0	167	3/7	
JMFAGNACL10_2B21E3, 636 - TWYVGKINRTQAEEMLSGK.-	2212.51	3	317.72	1.54	0.0	204	5/24	
jmfag1mnacl5mncon, 2092 -.LVEAIEQAELDSECYSK.-	1928.11	2	537.25	1.57	0.1	239	11/32	
jmldlactinrawphag3007, 2384 -.EDSVEAVGAQLK.-	1248.35	2	302.47	1.16	0.1	154	9/22	
jmfag5minfrench1mnacldtdpi, 1012 -.TQAEEMLSGKRDGTFLIR.-	2053.33	3	693.58	1.78	0.0	387	1/4	
jmfag_20_minfrench1mnacldtdpi, 1012 -.TQAEEMLSGKRDGTFLIR.-	2053.33	3	693.58	1.78	0.0	387	1/4	

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 b				1162.26	6679321.0	8		
FPbeads150_Dec19, 1275 -.GDFPGTYVEFLGPVALAR.-	1910.16	2	602.09	1.11	0.2	151	11/34	
rawextr_700beadigg_Mar04, 2136 -.EVAGPVGLVLEPPTLPLHQALTLRFLLQHLGR.-	3487.14	2	23.01	0.75	0.0	20	5/62	
rawextr_350beadigg2_Mar04, 2792 -.VARRAPSPDTAVHALASAFGPLLLR.-	2588.01	3	537.17	1.63	0.0	312	7/32	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol-3-phosphatase associated protein; phosphatidylino					**3415.38**	27370470 0	16		
jmfag5minigg500mmnacl, 1004	- LSSLFPFALLQR -	1392.67	3	485 70	1 28	0 1	328	15/44	
jmfag5minigbead_030528200105, 1711	- GFFREETGHLIKNLLGK -	2018.31	3	421.63	1.34	0 1	241	15/64	
jmfag5minigg200mmnacl, 2560	- ISKLINSSDDLQDSSREFYDSWHSK -	2959 13	2	112.42	0.88	0.0	107	5/24	
rawsucrfp_chlfphagigg_Mar04, 1398	- ISKLINSSDDLQDSSR -	1778.90	2	831 94	1 52	0 2	183	3/10	2
phagrawFsuc400_dec20, 1612	- QLSLPLTQSKSSPK -	1514 75	2	290.37	1.06	0 0	260	9/26	2
rawsucrfp_chlfphagigg_Mar04, 1632	- EWVMGGHSFLDRCNHLHQSDK -	2497 76	3	1273.32	1 84	0 2	151	7/40	3

control

phosphatidylinositol-3-phosphatase associated protein; phosphatidylino					**594.59**	27370470 0	9		
rawextr_1000_beadigg_Mar04, 933	- NKIIGVNDVPLHCVDQIYGVFDEKK.-	2845.27	3	490.24	1.55	0 0	316	11/48	2
rawextr_500beadigg_Mar04, 1040	- QLSLPLTQSKSSPK -	1514.75	2	204.35	1 27	0 0	152	4/13	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A; proline-rich					**5521.29**	27369946.0	11		
jmfag1mnacl2,5minigg, 292	- APSGGPSPSGRESHR.-	1479 54	3	707 97	1.56	0.0	440	19/56	
JMMAGTube1B16E3, 1400	- VKAPSGGPSPSGR.-	1197 33	1	247.85	0.92	0.1	188	1/3	
rawsucrfp_800phagigg_Mar04, 872	- SPGLARFPSLALHPSSR.-	1794.05	3	1080.83	1 60	0 1	465	17/64	
phagrawFchlfbead_dec23, 1093	- MQGVILLLFAK.-	1233 59	2	236 86	1 29	0 1	145	2/5	
phagrawFsuc400_dec20, 2336	- SPSRSPSRSPNR -	1328.42	2	326 91	1.28	0.0	255	9/22	
phagrawF200_dec22,2365-2367	-.FPSLALHPSSRERR.-	1653 87	2	356.97	1.21	0 1	216	9/26	
phagrawF150_dec22, 2592	- ILWKVKAPSGGPSPSGR -	1738 03	2	80.67	0.84	0 0	95	1/4	
jmfggactinrawphag3007,64-66	- NSGPASSEPRLTLAPVGPR -	1907 12	2	438 63	1.83	0.0	226	7/18	
ajrawphag1MNaCl20, 944	-.VGFRHCK.-	847 02	2	602.93	1.29	0.1	400	2/3	
jmfagtrench5minigg1mnacldtt, 1101	- SGSARPGTRTGLGPLPGTHGVLQAEIPSK.-	2843.19	3	375.44	1.51	0.1	170	17/112	
ajrawphag1MNaCl20, 1276	-.LSPSFRAR.-	934.08	2	489.99	1.24	0.2	120	4/7	
jmraw5minigg600mmnaclsd, 1664	- LAAFGHMLCFLNCHLPAHMDK.-	2370 87	3	325 47	1.44	0 1	185	17/80	
jmraw5minigg600mmnaclsd, 3562	-.PGIPSSQTVPPPLRKPPR.-	1925.27	2	250.76	0.94	0.1	155	5/17	

control

phosphatidylinositol (4,5) biasphosphate 5-phosphatase, A; proline-rich					**375.50**	27369946.0	9		
rawextr_chlfbeadigG_Mar04, 376	-.LEVADEWARPEQAVVR.-	1869.07	2	136 90	1 10	0.1	79	3/10	
jmbsa300nacirawphag3007, 2046	- SPNRSPCLPPAPEVALPK.-	1874.20	2	238.60	1.26	0 1	93	7/34	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol 4-kinase type-II beta; likely ortholog of mouse ph					**4592.95**	8922869.0	15		
jmfag1mnacl5minigg, 1270	-.TKVVWLVSETFNYNAIDRAK.-	2355.68	3	419.31	1.44	0.0	291	4/19	
ajrawphagactin20, 1802	-.IIGVFKPKSEEPYGQLNPK.-	2145.49	3	339.76	1 71	0.0	194	7/36	
jmfag5minigg600mmnacl, 2118	-.QFQSQFERLVILDYIIR.-	2169.51	3	399.70	1.06	0.0	352	9/32	
jmbsa350nacirawphag3007, 1045	-.KIIGVFK.-	805.04	1	485.20	0.96	0.1	320	7/12	
jmbsa150nacirawphag3007, 1247	-.KIIGVFK.-	805.04	1	384.34	1.15	0.1	238	1/2	
phagrawF250_dec22, 1411	-.IGLPPKIGSFQLFVEGYK.-	1994 37	2	208.09	1.86	0.1	73	4/17	
phagrawF350_dec20,1554-1556	-.IGLPPKIGSFQLFVEGYK.-	1994.37	2	75.69	1.29	0.0	45	7/34	
rawsucrfp_450phagigg_Mar04, 1708	-.IGLPPKIGSFQLFVEGYK.-	1994 37	2	469.70	1 42	0.2	85	9/34	
phagrawFsuc150_dec22, 1956	- IGLPPKIGSFQLFVEGYKEAEYWLR.-	2942.40	2	406.86	1.02	0.2	105	3/16	
phagrawF800_Dec23, 2398	-.IGLPPKIGSFQLFVEGYK.-	1994.37	2	606.50	1.49	0.2	66	7/34	
phagrawF800_Dec23, 2404	- IGLPPKIGSFQLFVEGYK.-	1994.37	2	40.19	0.98	0.0	35	3/17	
rawsucrfp_700phagigg_Mar04, 2853	-.IVHLSNSFTQTVNCRK.-	1848.12	2	757.61	0.98	0.3	103	7/30	

control

phosphatidylinositol 4-kinase type-II beta; likely ortholog of mouse ph					**799.23**	8922869.0	4		
rawextr_1000_beadigg_Mar04, 1831	-.ATFESQMSVMRGQILNLTQALR.-	2495.91	3	500.94	1.50	0.1	303	17/84	
FPbeads450_Dec19, 2204	-.IGLPPKIGSFQLFVEGYK.-	1994.37	2	298.29	1 48	0.1	80	4/17	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
1-phosphatidylinositol-4-phosphate 5-kinase; phosphatidylinositol-4-pho					**10714.65**	6755062.0	52		
jmag5minconf500mmnacl, 624	- RQAPLK.-	712 86	2	377.36	0 80	0.2	150	1/2	
jmrawrminigg200mmnaclsyringdnas, 816	- TDTFSKTR -	956.04	2	172.41	1 29	0.0	133	3/7	
JMFAGNACL5B21E3, 860	- KLEMVVKSTGILGGQGK -	1746.11	3	1362.34	1 83	0.1	609	21/64	
jmfag1mnacl5minigg, 882	- ILLLKCSIEYLYR -	1628 02	3	549.86	1.34	0.0	390	17/48	
jm5miniggrawlowionic, 1042	- TDTFSKTR.-	956 04	2	668.02	1 42	0.2	171	3/7	
ajrawphag1MNaCl20, 1170	- TDTFSKTR.-	956.04	2	401 06	1 11	0.1	328	4/7	
jmrawigg5minbeadsfreezethaw, 1256	- QLNEELHRR -	1195.31	2	658.68	1.30	0 1	296	1/2	
jmigg450rawphag3007, 1332	- SSPTLDSANDLPRSPASPSHLTHFK -	2663 88	3	218 03	1 64	0 0	125	17/96	
jmrawrminigg200mmnaclsyringdnas, 1398	- KASGMLSFFRGTAGK.-	1558 83	2	89 67	0.90	0.1	39	2/7	
jmiggactinrawphag3007, 2466	- LLEVCVPLPKIFIKR.-	1769.27	2	529 41	1.36	0.2	164	9/28	
jmfagfrench20minigg1mnacldtt, 3036	- LCGQIFCSRCCNQEIPGKFMGYTGDLR.-	3041 57	2	37.59	0 76	0.0	33	5/52	
jmrawigg5min150mmnacl, 3044	- ELVNWLIRNGHIATR.-	1793.07	2	326.82	0.87	0.2	54	3/14	
jmldactinrawphag3007, 2234	-.THPNCIVGKELVNWLIRNGHIATR.-	2743 19	3	71.51	0.98	0.0	73	4/23	
phagrawF600_dec20, 694	-.LRQGEESK.-	947 03	2	86.23	0.89	0.0	94	5/14	
rawsucrfp_700phagigg_Mar04,1185-1187	- DNPLYIRSHSK.-	1330 48	2	1003 97	1 66	0.2	369	9/20	
phagrawF450_dec20, 1466	- KQLLRDLSGLQGMNGSVQAK.-	2144.49	3	742 17	1 44	0.2	171	15/76	
rawsucrfp_300phagigg_Mar04, 1895	- MEDIFAQKEMEEGEFKNWTEK.-	2620.90	3	475.27	1.73	0.1	220	1/5	
rawsucrfp_350phagigg_Mar04, 2796	-.ICHHTSGMEFQDHR.-	1698 87	2	156 47	1.05	0.1	120	9/26	
ajrawmediapbsnocells, 880	- FYMQIFQLPNEQTK.-	1788 06	3	873.94	1 43	0.1	508	9/26	
jmrawbas5min1mnacl,1048-1050	- TDTFSKTR.-	956.04	2	511 15	1 62	0.1	150	3/7	
jmrawbas5min1mnacl, 1682	- DNPLYIRSHSK.-	1330 48	2	1362.70	1 58	0.2	274	9/20	

control

1-phosphatidylinositol-4-phosphate 5-kinase; phosphatidylinositol-4-pho					**4057.82**	6755062.0	40		
rawextr_actinbeadigg_Mar04, 409	- KIPGGKK.-	727 92	2	417 25	1 31	0.1	145	5/6	
FPbeads600_Dec19, 506	- DDTSNELVVGIIDYIR.-	1823.00	2	69.92	0 73	0.0	87	1/5	
rawextr_350beadigg2_Mar04, 554	-.INAMDTSPR -	1005.13	2	141 98	0 86	0.0	150	7/16	
rawextr_60MeOHbeadigg_Mar04, 888	-.RKAEPACGGHDPR.-	1394.55	2	729 19	1.58	0.1	415	13/24	
rawextr_60MeOHbeadigg_Mar04,1398-1400	-.EPFLLTEK.-	977 14	2	98.35	0.90	0.1	55	1/2	
rawextr_1000bead_Mar04, 1648	-.DNPLYIRSHSK -	1330.48	2	175.69	0.86	0.1	178	2/5	
FPbeads450_Dec19, 1956	-.KQSLCEVLQAWNSR.-	1662.90	2	115.92	1.14	0.1	57	4/13	
rawextr_250bead_Mar04, 2054	-.LVSVQEDAGKSPARNR -	1727.91	2	532 45	1.12	0.0	475	7/15	
rawextr_800beadigg_Mar04, 2130	-.MLADYRARGGEFSQNIWNPFVHSK.-	2825.16	3	189.07	1.11	0.0	162	17/92	
rawextr_200beadigg_Mar04, 2573	- KFDSVVVNGFVCTK.-	1543.81	2	249.48	0.91	0.1	178	9/26	
FPbeads300_Dec19, 2834	-.KLEMVVKSTGILGGQGK.-	1746.11	1	321.20	1.31	0.0	244	13/32	
jmraw5minbsabeads, 204	-.EMEEGEFK.-	999 08	3	290.49	1.25	0.1	179	5/14	
jmraw5minbsafreezthaw, 962	-.TDTFSKTR.-	956.04	2	299.27	1 20	0.1	221	1/2	
jmraw5minbsabeads, 976	-.TDTFSKTR.-	956.04	2	427.35	1.14	0.1	295	4/7	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Mus muscul					**3902.88**	29789235.0	7		
ajrawphagjun20actinDPI, 1048	-.FLLERALDNR.-	1247.43	2	424.97	0.94	0.1	370	1/2	
jmfag5minfrench1mnackdttdpi, 1120	-.RIGQFLFWHLR.-	1473.75	2	558.11	1.09	0.2	273	9/20	
jmfag_20_minfrench1mnackdttdpi, 1120	-.RIGQFLFWHLR.-	1473.75	2	558.11	1 09	0.2	273	9/20	
jmrawigg5minbeadsyringdnase, 1233	-.LCFAVYAVLDKVKTK.-	1699.09	3	351.12	1.12	0.0	301	15/56	
phagrawF450_dec20, 753	-.QDCRENFPQSLPK.-	1562.73	3	228.75	1.11	0.1	131	3/16	
phagrawF350_dec20, 1428	-.TLNSLIKLNAVK.-	1314.60	1	102.47	0.82	0.1	78	4/11	

control

phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Mus muscul					**1679.37**	29789235 0	4		
FPbeads500_dec19, 3930	-.LPPREALELLDFNYPDQYVR.-	2449.75	3	737.31	1.21	0.2	208	15/76	
jmraw5minbsafreezthaw, 1122	-.LNAVKLSR.-	901.09	2	576.82	1.19	0.2	225	1/2	
jmraw5minbsafreezthaw, 1180	-.QPCYYPPFDK.-	1258.43	3	365.24	1.26	0.0	285	7/18	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Phosphatidylinositol-4-phosphate 3-kinase C2 domain-contain					**3613.76**	38073314.0	27		
jmigG400rawphag3007, 874	-.RDRAPFVFTSDMAYVINGGDK.-	2360.64	3	523.87	2.12	0.0	242	19/80	
jmigG400rawphag3007, 878	- RDRAPFVFTSDMAYVINGGDK.-	2360.64	3	366.85	1.72	0.0	206	17/80	
jmigG400rawphag3007, 990	-.CFSTGRGK.-	855.99	2	114.37	0.89	0.0	128	1/2	
JMFAGNACL10_1B21E3, 1504	- ETLLCATLYALPVPPPGGSSEANK.-	2429.77	3	311.90	1 54	0.0	188	17/92	
ajrawphagjun20dpi1MNaCl, 1752	-.TGWFGLGSR.-	981.09	2	119 13	0.88	0.0	133	3/8	
ajrawphagactin20, 2726	-.LAQQVREATPSAR.-	1427.59	3	590.43	1 24	0.1	434	17/48	
ajrawmediapbsnocells, 754	- QFFALNGSCRLPLSPSLLVK.-	2191.63	3	389 33	1 54	0.1	108	15/76	
jmbsa250naclrawphag3007,1735-1737	-.PVGKVGGEVKLSISYK.-	1661.97	2	207 05	1.28	0.0	161	4/15	
jmldl150naclrawphag3007, 1592	-.DEKASGPSPAPK.-	1184.28	2	680 72	1.36	0.1	420	13/22	
jmldl150naclrawphag3007, 1870	-.LAQQVREATPSAR.-	1427.59	2	150 81	0.85	0.0	153	1/3	
jmldactinrawphag3007, 3598	-.LNFFIHNLAQMKFTGSDDRLTLSFAPR.-	3141.60	2	159.30	1.03	0.1	75	2/13	

control

similar to Phosphatidylinositol-4-phosphate 3-kinase C2 domain-contain					**1581.74**	38073314 0	12		
FPbeads150_Dec19, 941	-.LRLLFPSSFLPSFPSR.-	1865.21	2	42.73	0.95	0.0	45	2/15	
rawextr_1000_beadigg_Mar04, 1252	-.AVVSTALRLQSLGDGYSDGTWAR.-	2353.58	3	1083.55	1 54	0 2	123	1/4	
rawextr_450beadigg_Mar04, 1718	- LFIMVMHIRGLQPLQDGNDPDPYVK.-	2898.40	3	455.46	1.80	0.0	230	11/48	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphoinositide 3 kinase P110delta [Mus musculus]					8849.02	22758919.0	12		
phagrawFsuc600_dec20, 1028	- MRHEVQEHFPEALAR.-	1851.08	3	351.87	1.61	0.0	215	17/56	3
rawsucrfp_900phagigg_Mar04, 1144	-.GLHEFDSLRDPEVNDFRTK.-	2276.45	2	2156.88	1.84	0.3	179	11/36	3
phagrawFsuc250_dec22, 1213	-.ALNDFVKVSSQKTTK.-	1666.90	2	492.36	1.17	0.2	190	2/7	3
phagrawFsuc150_dec22, 1278	-.FEGSEESFTFQVSTKDMPLALMACALRK.-	3138.63	3	340.59	1.48	0.1	171	17/108	3
phagrawFsuc200_dec22, 1293	- GLHEFDSLRDPEVNDFRTK.-	2276.45	2	475.64	1.26	0.2	83	7/36	3
phagrawF300_dec20, 1295	-.LCFALYAVVEK.-	1256.54	2	210.98	1.06	0.1	167	9/20	3
phagrawFsuc500_dec20, 1612	- SNMAATAAFNKDALLNWLKSK.-	2295.65	3	811.62	1.40	0.1	487	1/4	3
JMMAGNEGB16D3, 2148	-.TKVNWLAHNVSKDNR.-	1782.99	1	118.59	0.83	0.1	88	3/14	3
JMMAGNEGB16D3, 2212	-.PPPIPAKKPSSVSLWSLEQPFSIELIEGR.-	3204.71	2	403.28	1.00	0.2	121	5/28	3
jmrawigg5min150mmnacl, 150	-.DALLNWLK.-	973.15	2	829.28	1.50	0.0	551	5/7	5
ajrawphag1MNaCl20, 410	- GELLNPAGTVR.-	1127.28	3	387.41	1.47	0.0	243	3/8	3
jmfagfrench20minigg1mnackdft, 2352	-.TGLIEVVLHSDTIANIQLNK.-	2179.50	3	361.41	1.21	0.0	298	17/76	3
jmfagtmecon7.5min.1596.1596.3	-.LEFDISVCDLPRMAR -	1766.08	0	267.19	1.35	0.0	186	1/4	3
jmbeads500rawphag3007, 1203	- GLHEFDSLRDPEVNDFRTK.-	2276.45	2	143.64	1.38	0.0	86	1/4	3
jmbeads350rawphag30072nd, 1600	-.LINSQISLLIGK.-	1299.59	2	182.37	0.83	0.0	215	5/11	2
jmbeads150rawphag3007, 1774	-.KVNADERMK.-	1091.27	2	231.81	1.19	0.1	160	7/16	3
AJRAWActinContr_june13, 2760	-.PLWIMYSSEEAGSAGNVGIIFKNGDDLR -	3041.38	2	240.34	1.07	0.1	83	1/6	3
RawPhg2007Etsolutiondigest, 516	-.QRLEFDISVCDLPR.-	1691.93	3	572.72	1.18	0.0	475	19/52	3
jmldl350nacirawphag3007,1668-1668	-.GLHEFDSLRDPEVNDFRTK.-	2276.45	2	271.07	1.62	0.0	162	5/18	3

control

phosphoinositide 3 kinase P110delta [Mus musculus]					1213.99	22758919.0	4		
jmbsa150nacirawphag3007, 1759	-.KPSSVSLWSLEQPFSIELIEGRK.-	2632.01	3	144.54	1.04	0.1	113	15/88	3
rawextr_250beadigg_Mar04, 846	- KVNADERMK.-	1091.27	2	99.28	0.88	0.0	99	3/8	3
rawextr_250bead_Mar04, 858	- FLLGRALANR.-	1131.36	2	466.20	1.27	0.0	355	11/18	3
rawextr_60MeOHbead_Mar04, 878	-.FRGYCERAYTILR.-	1648.91	3	503.97	1.47	0.0	342	5/16	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphoinositide-3-kinase, catalytic, gamma polypeptide; PI3K<gamma>; P					8441.50	9937984.0	9		
phagrawF350_dec20, 920	- KPLWLEFKCADPTVLSNETIGIIFK.-	2864.40	3	349.17	1.42	0.0	240	3/16	2
rawsucrfp_800phagigg_Mar04, 932	- TPSLSSKASAETPGSESK.-	1764.87	2	203.60	1.09	0.0	169	9/34	2
phagrawF350_dec20,1392-1394	- KGQWYEYDRYQVVQTLDCLHYWK.-	3136.53	3	1519.60	2.04	0.2	458	11/48	2
JMMAGTube1B16E3, 408	- AQLLYYVNLLLIDHR.-	1845.18	3	2092.97	1.97	0.1	884	5/14	2
jmfag5minigg300mmnacl, 4050	-.GIDIPVLPRNTDLTVFVEANQHGQQVLCQR.-	3475.97	2	9.76	0.69	0.0	14	1/15	2
jmIgG250rawphag3007, 1448	-.VPYDPGLKAGTLVIEK.-	1701.00	2	133.42	0.89	0.0	150	1/3	2
jmIgG350nacirawphag3007,1667-1669	- AYPKLFSSVKWGQQEIVAK.-	2180.53	3	903.71	1.91	0.1	297	1/4	2
jmrawigg5minbeadsfreezethaw, 2044	- IANNCIFIVIHRGTTSQTIK -	2230.62	3	595.51	1.46	0.0	398	5/19	2
jmIgG400rawphag3007, 2308	-.GTTSQTIKVSADDTPGTILQSFFTK -	2644.92	2	694.38	1.17	0.2	97	1/6	2
jmrawigg5min400mmnaclsd, 2317	- MELENYEQPVVLREDNLRR.-	2404.69	3	909.43	1.43	0.2	274	7/36	2
jmfag5mincon250mmnacl, 846	-.WGQQEIVAK.-	1059.20	3	366.49	1.11	0.0	316	15/32	2
jmbeads350rawphag30072nd, 1832	- KTSPHFQKFQDVCVR.-	1821.10	2	265.11	1.07	0.1	233	9/28	1
jmfagcon5minn800mmnacl, 2515	-.TPSLSSKASAETPGSESKGK.-	1950.10	1	296.06	0.81	0.2	78	7/38	2
AJRAWSoluteContr_june13, 2730	-.ALETSVAAEFYHRLGPDQFLLLYQKK.-	3039.48	2	62.31	1.00	0.0	82	4/25	2

control

phosphoinositide-3-kinase, catalytic, gamma polypeptide; PI3K<gamma>; P					1126.95	9937984.0	19		
FPbeads300_Dec19, 1754	-.YDVSSQVISQLKQK.-	1623.83	2	262.54	1.07	0.1	32	4/13	2
FPbeads500_dec19, 2082	- MAEVAGRDAKLYAMHPWVTSK.-	2362.76	3	216.18	1.18	0.1	157	1/5	2
FPbeads400_Dec19, 2088	-.YQVVQTLDCLHYWKLMHK.-	2306.74	3	405.21	1.35	0.0	279	9/34	2
rawextr_600bead_Mar04, 2808	-.VPYDPGLKAGTLVIEKCK.-	1932.32	3	243.01	1.00	0.1	185	7/34	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides fons	Count
similar to PI 3-kinase enhancer long isoform [Mus musculus]					48087.97	38090993.0		13	
phagrawF150_dec22, 623	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	997.23	1.83	0.0	535	2/7	
rawsucrfp_achinphagigg_Mar04,768-770	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1344.61	2.50	0.1	361	25/84	
rawsucrfp_500phagigg_Mar04,770-772	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	766.43	1.91	0.1	304	5/21	
rawsucrfp_300phagigg_Mar04,771-773	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	844.22	2.15	0.1	205	19/84	
rawsucrfp_350phagigg_Mar04,888-890	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	725.88	1.88	0.1	344	1/4	
rawsucrfp_450phagigg_Mar04,918-920	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	2485.00	2.25	0.3	328	11/42	
rawsucrfp_400phagigg_Mar04,928-930	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	643.37	2.02	0.1	279	1/4	
rawsucrfp_700phagigg_Mar04,928-930	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	395.88	1.70	0.0	230	5/21	
rawsucrfp_1000phagigg_Mar04,1010-1012	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1054.19	1.68	0.1	454	23/84	
jmrawbas5min1mnacl,1286-1288	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	974.85	1.81	0.2	281	1/4	
JMMAGNEGB16D3 614-616	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	976.25	2.11	0.1	327	23/84	
jmfag1mnacl0minigg, 1972	-.KEMLVDGQTHLVLIREEAGAPDAK.-	2622.00	3	375.75	1.63	0.0	229	19/92	
jmfag5minigg150mmnacl, 2678	-.RLSLWAAPPGPPLSGGLSPDSKPGGAPSSSR.-	3001.35	2	108.33	0.82	0.1	55	2/15	
jmrawgg5min400mmnaclsd,499-501	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1332.51	2.00	0.2	389	11/42	
jmrawgg5minbeadsyringdnase,567-569	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1099.22	2.20	0.1	332	23/84	
jmfagfrench20minigg1mnacldtt, 622	-.SGKSSLIHR.-	985.12	2	250.20	1.12	0.1	168	7/16	
jmrawgg5min450mmnaclsd,646-648	-.LKSFGSLRNIYK.-	1426.69	3	265.19	1.45	0.1	139	7/22	
jmrawgg5min450mmnaclsd,670-672	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	2007.43	2.17	0.2	480	2/7	
jmrawgg5min1mnacl,671-673	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	524.72	1.89	0.0	265	5/21	
jmraw5minigg1000mmsd, 836	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1614.20	2.07	0.2	441	2/7	
jmraw5minigg1000mmsd, 840	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1337.37	1.71	0.2	413	2/7	
jmfgG150rawphag3007,1012-1014	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	2234.38	2.14	0.2	446	23/84	
jmraw5minigg500mmnaclsd,1018-1020	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1104.14	1.95	0.2	248	19/84	
jmrawgg5min1mnacl, 1039	-.LHGQLSSLRGEGR.-	1410.56	2	193.46	0.91	0.0	197	1/3	
jmfgG400rawphag3007,1072-1074	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	874.29	2.07	0.1	295	1/4	
jmfgG350naclrawphag3007,1085-1087	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	650.29	1.75	0.1	318	5/21	
jmigg450rawphag3007,1100-1102	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	318.70	1.51	0.0	211	19/84	
jmraw5minigg250mmnaclsyringdnase,1190-1192	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1597.02	2.26	0.2	332	11/42	
jmraw5minigg600mmnaclsd,1196-1198	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	780.00	1.99	0.1	345	23/84	
jmfgG500rawphag3007,1211-1213	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	491.60	1.82	0.0	251	1/4	
jmfgG400rawphag3007, 1398	-.VSDPELQAGIQASLDSVRAR.-	2113.32	3	495.05	1.48	0.1	131	1/4	
jmfag_20_minfrench1mnacldttdpi, 2184	-.GSPGPMSRGAGALQRR.-	1598.82	3	542.77	1.19	0.1	398	1/3	
jmfag5minfrench1mnacldttdpi, 2184	-.GSPGPMSRGAGALQRR.-	1598.82	3	542.77	1.19	0.1	398	1/3	
jmraw5minigg250mmnaclsyringdnase, 2306	-.GSPGPMSRGAGALQRR.-	1598.82	3	407.60	1.11	0.1	327	3/10	
jmfag1mnacl0minigg, 1972	-.KEMLVDGQTHLVLIREEAGAPDAK.-	2622.00	3	375.75	1.63	0.0	229	19/92	
jmfag5minigg150mmnacl, 2678	-.RLSLWAAPPGPPLSGGLSPDSKPGGAPSSSR.-	3001.35	2	108.33	0.82	0.1	55	2/15	
jmfagtimecon2.5min.1412.1412.2	-.TVTTSGAKAGGGK.-	1135.25	0	421.43	1.27	0.0	329	13/24	
jmbeads1000naclrawphag3007,364-366	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	287.72	1.54	0.0	175	17/84	
jmbeads400rawphag3007,573-575	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	3786.65	2.67	0.3	400	1/4	
jmbeads450naclrawphag3007,641-643	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	951.10	2.05	0.1	308	1/4	
jmbeadsactinrawphag3007,699-701	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1589.25	2.19	0.2	495	9/28	
jmbeads500rawphag3007,798-800	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	952.65	2.19	0.1	355	2/7	
jmfag5mincont350, 930	-.SLDLDDWPR.-	1117.19	2	703.93	1.76	0.0	375	9/16	
jmbeads350rawphag30072nd,1160-1162	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	657.25	2.02	0.1	276	23/84	
jmfag5mincont400_030531151834, 1944	-.LESVPPPPPSPSAAAAGAPGARGSEPRDPGSPR.-	3134.41	2	492.33	1.18	0.2	79	5/32	
rawphag2007chfbead2,508-510	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1040.61	2.36	0.1	304	1/4	
rawphag2007chfbead1,1128-1130	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1066.12	2.13	0.1	362	1/4	
rawphag2007chfisol2,1230-1232	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	782.85	1.65	0.1	385	11/42	
RawPhg2007MeEthmeth3digest,1324-1326	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	700.24	2.09	0.1	276	1/4	
jmldl150naclrawphag3007, 1018	-.HLLKPDR.-	879.04	2	173.15	1.00	0.0	157	1/2	
jmldl250naclrawphag3007,1072-1074	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1860.53	1.72	0.3	381	5/21	
jmldl500naclrawphag3007,1155-1157	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	391.62	1.51	0.0	253	3/14	
jmldl150naclrawphag3007,1292-1294	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1415.39	1.77	0.2	493	23/84	

control

similar to PI 3-kinase enhancer long isoform [Mus musculus]					14328.94	38090993.0		7	
jmbsa350naclrawphag3007,565-570	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	867.62	2.00	0.1	339	1/4	
jmbsa500naclrawphag3007,650-652	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	689.66	2.27	0.1	268	17/84	
jmbsa300naclrawphag3007,783-795	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	4478.40	2.98	0.3	626	13/42	
jmbsa450naclrawphag3007,788-790	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1714.10	2.39	0.2	484	2/7	
jmbsa400naclrawphag3007_030802153340,793-795	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	840.83	2.04	0.1	274	11/42	
jmbsa600naclrawphag3007,1082-1084	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	1210.48	2.04	0.1	428	2/7	
jmrawbsa5minlowionic,1092-1094	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	796.51	1.83	0.1	338	11/42	
jmbsa1000naclrawphag3007,1221-1223	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	608.21	1.71	0.1	262	1/4	
jmbsa150naclrawphag3007, 1651	-.ISASSPRVVGDARAR.-	1542.73	2	1160.46	1.38	0.2	252	5/14	
rawextr_250beadigg_Mar04, 578	-.RSGNSLNK.-	875.95	2	660.77	1.48	0.1	383	9/14	
FPbeads250_Dec19,1230-1232	-.LESVPPPPPSPSAAAAGAPGAR.-	1998.23	3	263.48	1.57	0.0	168	17/84	
FPbeads1000_Dec19, 1872	-.ELRAEAAAVAGLSTPGSLHRAAK.-	2277.57	3	366.68	1.48	0.1	131	15/88	
rawextr_300bead_Mar04, 2088	-.LSTPSKTEGSAVQAEAKR.-	1861.05	2	234.78	1.39	0.0	161	4/17	
FPbeads350_Dec19, 2211	-.VSDPELQAGIQASLDSVRAR.-	2113.32	3	286.60	1.22	0.1	195	7/38	
rawextr_actinbead_Mar04, 2854	-.LFHRQDALWISTSSAGTGGAEPPALSPAPASPAR.-	3418.76	2	150.37	0.90	0.1	50	4/33	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides fons	Count
similar to phosphoinositide-3-kinase, class 2, beta polypeptide; PI3K-					6533.84	28482204.0		10	
jmfagtimecon7.5min.1150.1150.2	-.SLESVGISRK.-	1076.23	0	485.75	1.15	0.1	342	5/9	
jmfag5mincont150mmnacl, 335	-.DPSVLSVRENR.-	1272.39	3	689.99	1.23	0.2	324	13/40	
jmbeadsactinrawphag3007, 719	-.SKTMPPQVPPR.-	1238.49	2	592.60	1.30	0.1	237	9/20	
jmbeadsactinrawphag3007, 723	-.SKTMPPQVPPR.-	1238.49	2	293.94	1.18	0.1	212	9/20	
phagrawFsuc150_dec22, 868	-.PHTVANGHELFEVSEER.-	1952.07	3	853.06	1.71	0.0	487	21/64	
phagrawF450_dec20, 1238	-.RISAAPVGSRPHTVANGHELFEVSEER.-	2947.22	3	575.01	1.55	0.2	126	2/13	
phagrawFsuc600_dec20, 1604	-.PHTVANGHELFEVSEER.-	1952.07	3	1153.51	1.85	0.1	424	5/16	
phagrawFsuc300_dec20, 3014	-.VVQSVKAICNALAAVETPEITSALNQLPPCPSR.-	3421.98	2	58.52	0.79	0.0	66	1/8	
phagrawF300_dec20, 3045	-.EPLTFTCNCSSTVDLLIHQTLCYTHDELR.-	3354.78	2	354.57	0.98	0.2	68	1/7	
jmldl150naclrawphag3007, 3150	-.PCGLEEFLQNKHALGSHEYIQYCR.-	2837.19	2	79.94	1.03	0.0	58	3/23	
ajrawmediapbsnocells, 634	-.GWKEGRGPLDFNK.-	1504.68	3	513.01	1.66	0.0	307	1/3	
jmfgG400rawphag3007, 788	-.YANRKNATPGNNR.-	1478.58	3	883.94	1.72	0.2	268	7/24	

control

similar to phosphoinositide-3-kinase, class 2, beta polypeptide; PI3K-					1883.99	28482204.0		11	
rawextr_60MeOHbead_Mar04, 1348	-.ELAMAEALQMEYDALSRLRIHHK.-	2614.00	3	878.19	1.95	0.1	281	19/84	
FPbeads500_Dec19, 2302	-.EPLTFTCNCSSTVDLLIHQTLCYTHDELR.-	3354.78	2	57.06	0.81	0.1	33	3/28	
FPbeads500_dec19, 2540	-.PVARSKTMPPQVPPR.-	1662.00	2	456.93	1.01	0.2	163	9/28	
rawextr_200beadigg_Mar04, 2803	-.AICNALAAVETPEITSALNQLPPCPSRMQPK.-	3265.82	2	491.82	0.96	0.2	111	1/8	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
T42642 phosphoinositide 3-kinase (EC 2.7.1.-) - mouse					**9807.10**	11259849.0	26		
phagrawF350_dec20, 812	-.CSTGCPR -	723.85	2	119.90	0.74	0.1	102	1/2	
phagrawF150_dec22, 1066	-.VGEDLRQDMLALQMIKIMDK -	2348.84	2	224.66	0.96	0.1	36	5/38	1
phagrawF200_dec22, 1323	-.TRNPTFNEMLVYSGYSK -	2008.24	3	185.17	1.20	0.0	148	13/64	1
rawsucrfp_300phagigg_Mar04, 1371	-.PLVSPDMAKLFEKIASTSEFLK.-	2452.90	3	293.76	1.58	0.1	133	1/7	1
jmfag5minigg350mmnacl, 126	- MVIFRCLSTGRDR.-	1554.87	3	1081.94	1.74	0.2	287	1/3	1
jmbeads250rawphag3007, 670	-.QDYDLMVFPELDSQK.-	1829.02	3	783.21	2.01	0.0	389	19/56	
ajrawphagjun20dpi1MNaCl, 710	-.LSIIFPLWK.-	1117.41	2	685.28	1.73	0.1	318	9/16	1
jmfag1mnacl7.5minigg, 734	-.RAVDIDVEKLTQAELEK.-	1958.20	3	736.53	1.86	0.1	240	5/16	
jmfag1mnacl5minigg, 846	-.RAVDIDVEKLTQAELEK.-	1958.20	3	780.80	2.01	0.1	219	19/64	
ajrawphagactin20, 898	-.DRGMVELVPASDTLRK.-	1788.06	3	271.37	1.07	0.0	253	7/30	1
jmrawigg5min350mmnaclsyringednase, 1087	-.VTMVNADPLGEEINVMFKVGEDLR.-	2678.08	3	356.38	1.37	0.1	143	4/23	1
jmfag5minigg300mmnacl, 1280	-.RAVDIDVEKLTQAELEK.-	1958.20	3	520.30	1.42	0.1	235	5/16	
ajrawphagjun20actinDPI, 1282	-.ENFFLGGITLPLK.-	1449.72	2	783.71	1.35	0.2	213	11/24	1
jmraw5minigglowionic, 1603	-.QRELQLSVLSAESLR.-	1729.96	3	470.12	1.43	0.1	245	17/56	1
jmfag1mnacl0minigg, 1862	-.DEKAEGIARSAGAVPFSPTLGQIGGAVK.-	2728.05	3	660.16	2.24	0.0	282	5/27	1
jmrawigg5minbeadsfreezethaw, 1872	-.YEHVLGALLSVGGK.-	1443.67	2	228.54	1.11	0.1	124	9/26	1
jmigg450rawphag3007, 1988	-.AVDQVIKAVR.-	1099.31	2	261.30	1.15	0.0	228	4/9	1
JMFAGNACL15B21E3, 2034	-.VTMVNADPLGEEINVMFK.-	2008.35	3	433.68	1.16	0.1	332	19/68	1
ajrawphagjun20dpi1MNaCl, 2172	-.ELNIKSCSFFSSNAMPLK.-	2017.36	3	378.24	1.25	0.0	286	9/34	1
jmfag5minigg450mmnacl_030527025134, 2650	-.NIIQQDKLETLESDIK.-	1888.11	2	169.32	1.17	0.0	125	3/10	1
jmldl1000naclrawphag3007, 1146	-.YLYQIEK.-	957.11	2	382.73	1.13	0.0	339	5/6	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
T42642 phosphoinositide 3-kinase (EC 2.7.1.-) - mouse					**4453.78**	11259849.0	28		
rawextr_700bead_Mar04, 595	-.IQVEYGVTGSFK.-	1328.50	3	640.05	1.85	0.0	340	4/11	
rawextr_chifbead_Mar04, 1150	-.AVNLPRNK.-	912.07	1	432.41	1.23	0.1	314	9/14	
rawextr_800bead_Mar04, 1390	-.LLYLWTSSHTNSIPGAIPK.-	2099.42	3	661.72	1.69	0.0	374	19/72	
rawextr_450beadigg_Mar04, 1536	-.FPYTDHCTNPGYLLSPVTVQR.-	2409.71	3	624.41	1.64	0.1	236	17/80	
rawextr_250bead_Mar04, 2030	-.LIESSLGSIATKFNFFIHNLAQLR.-	2721.15	3	451.65	1.84	0.1	136	4/23	
rawextr_450bead_Mar04,2322-2324	-.SLSGATVTRSQSLIIRTAQFTK.-	2366.70	3	786.78	1.77	0.1	411	19/84	
rawextr_400bead_Mar04, 2592	-.KVNGKSLSGATVTR.-	1418.63	2	150.20	0.85	0.0	165	4/13	
jmbsaactinrawphag3007, 471	-.PPALPVTPVLSPSFSTQLYLR.-	2284.68	3	170.98	1.09	0.1	107	13/80	
jmraw5minbsafreezthaw, 1626	-.IASTSEFLKNGKAR.-	1522.73	3	275.76	1.21	0.1	118	17/52	1
jmraw5minbsabeads,1712-1714	-.IASTSEFLKNGKAR.-	1522.73	3	259.82	1.96	0.1	107	15/52	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
A55748 protein kinase (EC 2.7.1.37) Sak-a - mouse					**3086.10**	1083471.0	22		
jmraw5minigglowionic, 213	-.IHCQLK.-	741.93	2	580.31	1.12	0.0	517	4/5	5
jmfag1mnacl2.5minigg, 786	-.TGISYNLK.-	896.02	2	184.62	1.13	0.1	132	4/7	3
ajrawphagjun20actinDPI, 1258	-.TGISYNLKNENEVTSLKEEVK.-	2396.64	3	736.82	1.81	0.1	377	21/80	3
jmrawigg5min1mnacl, 2379	-.GFPLADRPPLPTDNISR.-	1867.10	2	256.05	1.15	0.1	147	9/32	1
jmldl400naclrawphag3007_030802153313, 1264	-.HFMHQIITGMLYLHSHGILHR.-	2543.02	3	425.32	1.20	0.0	353	9/40	5
phagrawF400_dec20, 136	-.GFPLADRPPLPTDNISR.-	1867.10	2	200.56	1.03	0.0	193	9/32	1
jmbsa150naclrawphag3007, 1851	-.TKKAVVSILDSEEVCVELLR.-	2232.63	3	702.41	1.66	0.1	394	1/4	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
A55748 protein kinase (EC 2.7.1.37) Sak-a - mouse					**136.73**	1083471.0	11		
FPbeads450_Dec19, 2444	-.VGNLLGKGSFAGVYRAESIHTGLEVAIK.-	2888.31	2	136.73	1.57	0.1	40	1/6	5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
AMP-activated protein kinase, gamma-2 subunit; 5-AMP-activated protein					**3316.59**	21703802.0	8		
ajrawphagjun20actinDPI, 116	-.NPSLKR.-	714.84	2	454.16	1.25	0.1	323	7/10	
jmigg600rawphage3007, 1886	-.TVFPFSYQESPPRSPR.-	1896.10	2	791.75	1.49	0.2	164	3/10	
jmldl600naclrawphag3007, 1228	-.KEVSSPGGSSGKK.-	1248.37	2	264.58	0.96	0.0	271	3/8	
jmldl250naclrawphag3007, 1598	-.GPQPRPSSPVSAPVR.-	1532.73	2	208.95	0.99	0.0	209	5/14	
phagrawFsuc250_dec22, 2013	-.MSFSGIFRSSSKESSPNSNPSTSPGGIR.-	2903.14	3	223.74	1.61	0.1	104	1/6	
phagrawFsuc400_dec20, 3094	-.FCLAFQSPARPPLASPTYHAPLR.-	2541.96	2	193.13	0.85	0.1	39	3/22	1
jmbsa150naclrawphag3007, 1536	- MSFSGIFRSSSK.-	1334.53	2	266.77	1.19	0.1	181	4/11	
jmldl600naclrawphag3007, 1772	-.VHIPDLSSFAMPLLDGDVENSEK.-	2514.79	3	496.64	1.42	0.1	245	19/88	
phagrawFsuc250_dec22, 2013	-.MSFSGIFRSSSKESSPNSNPSTSPGGIR.-	2903.14	3	223.74	1.61	0.1	104	1/6	
phagrawFsuc400_dec20, 3094	-.FCLAFQSPARPPLASPTYHAPLR.-	2541.96	2	193.13	0.85	0.1	39	3/22	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
AMP-activated protein kinase, gamma-2 subunit; 5-AMP-activated protein					**182.04**	21703802.0	9		
FPbeads1000_Dec19,1810-1812	-.GPQPRPSSPVSAPVR.-	1532.73	2	182.04	1.08	0.1	136	2/7	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein kinase [Mus musculus]					**4823.12**	2980671.0	12		
jmfag5minigg600mmnacl, 590	-.KLIVAGKYSK.-	1107.37	2	652.28	1.72	0.0	372	1/2	3
jmrawigg5min150mmnacl, 1110	-.SGAPPPSGSAVSTAPTPKPADK.-	2021.22	3	2089.98	2.27	0.1	741	25/84	
jmraw5minigg250mmnaclsyringdnase, 2904	-.QDITQLEESIRADTPSGDEQEPNGALDSK.-	3145.25	2	483.71	0.90	0.2	174	11/56	3
JMFAGNACL10_2B21E3, 3114	-.PLTENPPNKMTQEKLEESNSIGQDQTLTER.-	3429.72	2	214.61	0.82	0.1	79	4/29	3
rawsucrfp_400phagigg_Mar04, 981	-.LQVKIADLGNACWVHK.-	1796.13	3	615.66	1.66	0.1	265	3/10	3
rawsucrfp_chlfphagigg_Mar04, 1328	-.EDLHNANDCDVHTLK.-	1724.84	3	556.97	1.72	0.1	262	17/56	3
rawsucrfp_250phagigg_Mar04, 1922	-.GGYHLVKIGDLFNGR.-	1646.88	2	209.91	0.85	0.0	245	5/14	3

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein kinase, lysine deficient 1 [Mus musculus]					**5435.59**	38424077.0	29		
jmfag5minigg200mmnacl,224-226	-.APGIDDIK.-	828.93	2	778.45	1.61	0.1	442	11/14	1
jmIgG300rawphag3007, 1078	-.APGIDDIKTLEEK.-	1429.60	3	1200.10	2.15	0.0	551	5/12	1
AJRAWActinIgG_june13,1528-1530	-.EAQEDRSQQQDDIEELETK.-	2292.31	3	620.80	2.02	0.0	290	17/72	
jmfagfrench5minigg1mnacldtt, 1545	-.GKKCIVLVTELMTSGTLK.-	1922.39	2	713.47	1.18	0.2	143	11/34	
jmIgG300rawphag3007, 1632	-.CIVLVTELMTSGTLK.-	1608.99	2	186.00	1.07	0.0	171	5/14	1
rawsucrfp_chlfphagigg_Mar04, 1666	-.PEPNGISISGISLDVPDSTHK.-	2164.36	3	1607.48	2.29	0.1	649	11/40	1
phagrawFsuc350_dec20, 1964	-.GSKGHMNYEGPGMARK.-	1720.96	2	238.82	1.22	0.0	195	1/3	2
phagrawFsuc400_dec20, 3642	-.RTLSPETITVAPAVGPLSTMSSTTVTEAGTR.-	3133.52	2	90.47	0.79	0.1	83	2/15	1

control

protein kinase, lysine deficient 1 [Mus musculus]					**1703.71**	38424077.0	19		
FPbeads150_Dec19, 615	-.TPPIIHR.-	834.00	2	558.68	1.32	0.0	409	2/3	
rawextr_250bead_Mar04, 1646	-.GSKGHMNYEGPGMARK.-	1720.96	2	529.03	1.28	0.2	171	3/10	
rawextr_250bead_Mar04, 2082	-.LGKVPPAVIIPPAAPLSGR.-	1854.27	2	129.80	1.15	0.0	109	2/9	
jmbsa150naclrawphag3007, 869	-.SISNPPGSNLRTT.-	1344.46	3	356.74	1.38	0.0	252	7/24	2
jmraw5minbsafreezthaw, 2990	-.SWCRQILKGLQFLHTR.-	1987.36	1	129.47	0.82	0.1	61	1/6	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein kinase, cGMP-dependent, type II [Mus musculus]					**4662.78**	31982097.0	19		
JMFAGNACL10_1B21E3, 902	-.GAKAGVSAEPTTR.-	1245.37	2	457.58	1.11	0.1	243	5/12	2
jmIgG150rawphag3007, 1354	-.GAKAGVSAEPTTRTYDLNK.-	1980.17	3	547.71	1.58	0.0	344	1/4	2
jmIgG150rawphag3007, 1640	-.RGAKAGVSAEPTTR.-	1401.56	2	335.72	1.29	0.0	260	9/26	2
phagrawFsuc500_dec20, 1250	-.LQDVIHVQGGSPLQASPDK.-	1990.21	3	411.84	1.54	0.0	244	17/72	2
phagrawFsuc60MeOH_dec23, 1286	-.YPPEKGVPPDEMSGWDKDF.-	2195.39	3	587.10	1.78	0.1	301	17/72	2
rawsucrfp_actinphagigg_Mar04, 1958	-.GDYIIREGEEGSTFFILAKGK.-	2331.61	3	1067.09	1.64	0.2	388	19/80	2
phagrawF300_dec20, 2311	-.NLPEDKLTKIIDCLEVEYYDK.-	2542.89	2	150.81	0.87	0.1	22	7/40	2
phagrawFsuc500_dec20, 3636	-.LDPQQIKDMVECMYGRNYQQGSYVIK.-	3108.56	2	1104.92	1.16	0.3	69	4/25	1

control

protein kinase, cGMP-dependent, type II [Mus musculus]					**1059.70**	31982097.0	5		
rawextr_350beadigg2_Mar04, 2196	-.IGSGQKTWTFCGTPEYVAPEVILNK.-	2740.13	3	712.96	2.05	0.1	265	5/24	2
jmbsa350naclrawphag3007, 668	- VKVTQSTEGHDQPQLIKTLQK.-	2379.70	3	82.12	1.07	0.0	67	9/80	2
jmraw5minbsafreezthaw, 1388	-.DMVECMYGR.-	1104.31	2	264.62	1.07	0.0	245	1/2	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
C32571 ribosomal protein S6 kinase II (EC 2.7.-.-) alpha chain homolog (clone Mu7A) -					**6831.28**	91277.0	16		
jmfagfrench5minigg1mnacldtt,605-607	- STLAQRRGIK -	1130.33	2	537.34	1.43	0.0	361	11/18	1
JMFAGNACL5B21E3, 998	- RHSFFSTIDWNKLYR.-	1971.21	3	400.48	1.05	0.1	336	2/7	1
jmfag5minigg200mmnacl, 1116	- RHSFFSTIDWNKLYR -	1971.21	3	842.08	1.29	0.1	289	2/7	1
JMFAGNACL15B21E3, 2622	- FYLAELALALDHLHSLGIIYRDLK.-	2786.28	3	312.52	1.40	0.0	216	4/23	1
jmIdlactinrawphag3007, 976	-.YVYVVTEUMKGGELLDK.-	1958.31	3	294.60	1.03	0.0	279	9/32	1
phagrawF450_dec20, 846	-.PATGRPEDTFYFDPEFTAK.-	2190.35	3	623.37	1.62	0.1	175	1/4	1
rawsucrfp_500phagigg_Mar04, 1278	- IGSGKFSLSGGYWNSVSDTAKDLVSK.-	2704.97	3	3742.01	2.27	0.3	528	6/25	1
phagrawF60MeOH_dec23, 1604	-.RHSFFSTIDWNK.-	1538.69	2	191.55	0.93	0.0	204	7/22	1
phagrawFsuc350_dec20, 2770	- CIHKATNMEFAVK.-	1492.79	2	87.31	0.86	0.0	94	7/24	1

control

C32571 ribosomal protein S6 kinase II (EC 2.7.-.-) alpha chain homolog (clone Mu7A) -					**533.28**	91277.0	4		
rawextr_350beadigg2_Mar04, 1252	-.RHSFFSTIDWNKLYR.-	1971.21	3	436.81	1.36	0.1	245	15/56	1
FPbeads400_Dec19, 1406	-.NPANRLGAGPDGVEEIK.-	1737.90	2	96.46	1.10	0.0	88	1/4	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
DNA-dependent protein kinase catalytic subunit [Mus musculus]					**29405.11**	3241856.0	55		
phagrawF400_dec20, 30	- HGDLSSLGPLR -	1152.29	3	1084.87	1.53	0.2	127	1/4	1
phagrawFsuc150_dec22, 34	- FLMKHVFHPKR -	1440.79	2	313.88	1.21	0.1	233	7/20	1
phagrawFsuc250_dec22, 965	- TAKCKIPALDLLIK -	1527.94	2	143.04	1.25	0.0	112	9/26	1
rawsucrlp_600phagigg_Mar04,1262-1264	- VTELALSASDRQTKVAACELLHSMVMFMLGR -	3410.06	3	373.63	2.13	0.1	149	7/40	1
phagrawF400_dec20, 1388	- TQMTSTVREPK.-	1278.46	2	430.75	1.05	0.1	374	9/20	1
phagrawF300_dec20, 1727	- LLQILRSTRLMDEFK -	1864.25	2	311.75	1.07	0.1	208	5/14	1
phagrawF500_dec20, 1730	- IEERLTAPSGDHSMSVDEDEESIDR -	2818.92	3	217.19	1.24	0.0	171	19/96	1
rawsucrlp_400phagigg_Mar04,2030-2032	- LGLHLKGQAIILLPFFTSLREGSLENLK -	3109.70	2	70.02	1.29	0.0	51	7/54	1
rawsucrlp_350phagigg_Mar04, 2444	- HGDLPDIQIQHSGLITPLQAVAQKDPHAK -	3218.70	2	658.86	1.05	0.2	108	6/29	1
phagrawF200_dec22, 2597	- QERSKLLSILSACK -	1576.89	2	240.97	1.00	0.1	126	4/13	1
phagrawFsuc600_dec20,3824-3826	- WMELAKLYR -	1210.47	2	252.25	0.80	0.0	306	7/16	1
JMMAGNEGB16D3,164-166	- SMEEDPQTSK -	1152.22	2	931.91	2.38	0.1	278	11/18	1
JMMAGTube1B16E3, 168	- SMEEDPQTSK -	1152.22	2	400.11	1.58	0.1	198	1/2	1
jmfag1mnacl5mincon, 186	- EFVKSFGNGGSK -	1257.38	2	356.90	1.34	0.0	266	5/11	3
jmfag1mnacl0minigg,144-146	- SMEEDPQTSK -	1152.22	2	307.11	1.63	0.0	164	1/2	1
jmfag1mnacl7,5minigg, 196	- SMEEDPQTSK -	1152.22	2	468.42	1.50	0.1	204	5/9	1
jmfag1mnacl2,5minigg, 200	- SMEEDPQTSK.-	1152.22	2	479.97	2.00	0.0	218	5/9	1
jmfag1mnacl0minigg, 244	- AEEITGLYLQLK.-	1378.60	3	1796.23	1.94	0.0	917	5/11	1
JMFAGNACL10_2B21E3, 294	- EMHKESK.-	889.01	2	208.19	1.05	0.1	136	2/3	1
jmraw5minggtowionic, 437	-.YVAWDAER -	1010.09	2	138.35	0.84	0.0	150	3/7	1
ajrawphagjun20dpi1MNaCl, 440	- AVQKHQGLK -	1009.19	2	188.95	1.04	0.0	166	7/16	1
jmfag1mnacl7,5minigg, 514	- QSPCVTQLNLLESVYTMFR -	2230.59	3	173.74	1.34	0.0	128	7/36	1
jmfag5minigg250mmnacl, 898	-.SMEEDPQTSK -	1152.22	2	1097.98	1.88	0.2	233	5/9	1
jmfag5minigg400mmnacl, 960	- NLFIFENLIDLKR -	1635.93	3	1901.01	2.56	0.2	462	3/8	1
jm5minggrawtowionic, 1132	-.SMEEDPQTSK.-	1152.22	2	393.57	1.63	0.0	233	1/2	1
jmraw5minigg1000mmsd, 1248	- HKSMELFYK -	1183.41	2	80.91	0.71	0.0	100	1/2	1
jmrawminigg200mmnacisyringdnas, 1670	-.LLEKDLCNTNLMQVLVK -	1975.41	3	189.83	1.01	0.0	183	7/32	1
ajrawphagjun20dpi1MNaCl, 1714	- IDQKVMHYSLDIKNTCTSVYTK -	2588.99	3	300.83	1.16	0.0	255	17/84	1
AJRAWActinIgG_june13, 2394	-.EPSFDWKSFEQTMLR.-	1902.12	1	110.37	0.98	0.0	111	3/14	5
jmfag5minigg300mmnacl, 2692	-.QHQNTMEDKFIVCLNK.-	1949.25	1	209.31	0.86	0.1	82	7/30	1
jmfagtimecon7 5min,1594,1594 3	-.TSAEMEAYPALVVEKMLRALK -	2351.82	0	942.03	1.79	0.1	461	21/80	1
jmfagcon5min1000mmnacl_030601180404, 158	-.SMEEDPQTSK.-	1152.22	2	375.72	1.73	0.0	215	5/9	1
jmfag1mnacl5mincon, 186	- EFVKSFGNGGSK.-	1257.38	2	356.90	1.34	0.0	266	5/11	3
jmfag5mincont150mmnacl, 197	-.SDYCQAAK -	885.97	2	504.41	1.25	0.0	399	9/14	1
jmfagcon5min1000mmnacl_030601180404, 258	- SMEEDPQTSK -	1152.22	2	458.66	1.76	0.0	257	11/18	1
jmfagcon5min1000mmnacl_030601180404, 264	-.SMEEDPQTSK.-	1152.22	2	662.35	1.86	0.1	216	5/9	1
jmbeads300rawphag3007, 298	- AEEITGLYLQLK -	1378.60	3	1408.27	1.59	0.1	853	5/11	1
jmfagcon5minn600mmnacl, 833	-.QHQNTMEDKFIVCLNKIAK.-	2261.65	3	515.23	1.56	0.0	318	5/18	1
jmfagtimecon10min, 860	-.MAEEQTGVR.-	950.05	2	741.01	1.11	0.1	588	5/8	1
jmbeads150rawphag3007, 894	- RCYTFPIEVEVPMER.-	1870.19	3	356.52	1.09	0.0	317	2/7	1
jmfagtimecont0min_030601230741,952-954	-.SMEEDPQTSK.-	1152.22	2	338.98	1.34	0.1	202	1/2	1
jmfagcont5minbead,968-970	-.SMEEDPQTSK.-	1152.22	2	956.21	2.00	0.2	227	5/9	1
jmfagtimecon10min,1060-1062	-.SMEEDPQTSK.-	1152.22	2	569.08	2.10	0.1	239	11/18	1
jmbeads300rawphag3007, 1332	-.TITLLDESDISNYLNK.-	1840.02	3	215.70	1.34	0.0	146	1/5	1
jmbeads350rawphag30072nd, 1354	- RLGAALAFNHIYK.-	1474.74	2	293.58	1.17	0.0	247	5/12	1
jmbeadsactinrawphag3007, 1439	-.LGLPDDEVDNQVK -	1442.55	2	518.45	1.32	0.0	392	1/2	1
jmfag5mincont150mmnacl, 2367	-.LGAALAFNHIYKEFR.-	1751.03	2	111.45	0.87	0.1	58	5/28	1
jmrawgg5miniggfreebead, 736	-.LLSILSACK -	948.21	2	193.50	0.98	0.1	129	7/16	1
jmrawgg5miniggfreebead, 2142	-.SLNHLLYDEFIRSVLK.-	1948.26	2	121.05	0.89	0.1	71	1/5	1
rawphag2007chfbead3, 485	-.FGKEVSVK.-	894.05	2	359.33	0.86	0.0	416	5/7	1
rawphag2007chfbead1,962-964	-.SMEEDPQTSK -	1152.22	2	420.82	1.81	0.0	214	5/9	1
RawPhag200760MeBeadsdigest, 1720	- GFPPLAQRFLNALFFLLPK.-	2177.62	3	218.85	1.46	0.0	141	7/36	1
RawPhag200760MeBeadsdigest, 1760	-.SPVNSKSLFKR -	1263.47	2	449.68	1.26	0.1	291	1/2	1
rawphag2007chlfsol1,1908-1910	-.LLSILSACKQLHK.-	1454.81	2	373.81	1.49	0.1	148	1/3	1
RawPhag200760MeBeadsdigest, 1946	- AQFLKNELEIPGQYDGK -	1951.17	3	370.73	1.24	0.1	228	13/64	3
jmidl400firstnaclrawphag3007, 942	-.SMEEDPQTSK -	1152.22	2	392.54	1.49	0.1	204	4/9	1
jmidl400firstnaclrawphag3007, 950	-.SMEEDPQTSK -	1152.22	2	510.28	1.69	0.1	222	5/9	1
jmidl250naclrawphag3007, 1850	-.LAGANPAVITCDELYLGHEASSAFR -	2606.90	3	787.23	1.60	0.1	465	7/32	4
jmidl450naclrawphag3007, 1854	- IKVVQILGSLGGQINK -	1668.02	2	461.56	1.13	0.2	147	4/15	1
jmidichifsolblerawphag3007, 2290	-.KLAGANPAVITCDELYLGHEASSAFR.-	2735.07	3	179.61	1.28	0.0	134	4/25	4
jmfreebeadsrawphag3007, 1414	- LLSILSACKQLHK -	1454.81	2	688.65	1.35	0.2	217	11/24	1
jmfreebeadsrawphag3007, 2087	-.TLLKLCHDAFTENMVGESQLLEK.-	2621.03	3	722.06	1.73	0.0	410	5/22	1

control

DNA-dependent protein kinase catalytic subunit [Mus musculus]					**3919.51**	3241856.0	16		
jmraw5minbsafreezthaw,1824-1826	- SILQPYYK.-	1012.18	1	57.91	0.69	0.1	41	2/7	1
FPbeads300_Dec19, 394	-.LGLPDDEVDNQVK -	1442.55	2	161.94	1.03	0.0	157	7/24	1
rawextr_700beadigg_Mar04, 740	-.SMEEDPQTSK.-	1152.22	2	379.31	1.87	0.0	225	1/2	1
rawextr_150bead_Mar04,803-805	-.VCLDIVYK.-	953.18	2	253.34	1.16	0.0	207	4/7	1
rawextr_200bead_Mar04, 808	-.SMEEDPQTSK.-	1152.22	2	347.90	1.71	0.0	186	4/9	1
rawextr_600bead_Mar04,812-814	-.SMEEDPQTSK.-	1152.22	2	1353.43	2.00	0.2	400	2/3	1
rawextr_300beadigg_Mar4, 1682	-.PVVLQKDVESRSDNR.-	1742.92	2	359.44	1.53	0.1	172	9/28	1
FPbeads350_Dec19, 2041	-.AHAYMTLVGFCDQQLRK.-	1982.32	3	521.38	1.19	0.1	232	15/64	1
FPbeads300_Dec19, 2068	-.VVQILGSLGGQINKSLVTATSGER.-	2428.77	2	52.22	0.81	0.0	50	7/46	1
rawextr_actinbead_Mar04, 2776	-.MLAVMYSRLLK.-	1326.71	3	292.05	1.14	0.0	235	13/40	1
FPbeads1000_Dec19, 3484	-.KFESQDTVALLEAILDGIVDPVDSTLR.-	2946.30	2	140.60	0.76	0.1	53	7/52	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
homeodomain-interacting protein kinase 2b [Mus musculus]					**4501.44**	12751417.0	12		
jmrawigg5min150mmnacl, 684	-.RVNMYDTVNQSK.-	1455.62	3	890.78	1.44	0.1	591	17/44	6
jmrawigg5minbeadsyringdnase, 1385	-.TQASEVLVECDSLGPAISASHHSSSFK.-	2789.03	3	821.03	1.45	0.2	311	5/26	5
jmIgG300rawphag3007, 2014	-.GGLENHCTGNPR.-	1255.35	2	417.29	1.03	0.1	183	4/11	5
JMFAGNACL10_2B21E3, 2232	-.TGHNGTNTLDTKGGLENHCTGNPR.-	2495.63	3	1704.98	1.44	0.3	478	11/46	5
JMFAGNACL5B21E3, 2406	-.SKQHQSSVRNVSTCEVTSSQAISSPQR.-	2933.17	3	196.90	0.99	0.0	199	9/52	5
phagrawF1000_Dec23, 62	-.PGPHFQQQQPLNLSQAQQHMAADR.-	2728.99	3	429.78	1.18	0.2	92	11/92	5
phagrawF600_dec20, 2808	-.YIFNCLDDMAQVNMTTDLEGSDMLVEKADR.-	3439.86	2	40.68	0.82	0.0	34	3/29	4

control

homeodomain-interacting protein kinase 2b [Mus musculus]					**587.18**	12751417.0	4		
rawextr_1000_beadigg_Mar04, 2285	-.QHQSSVRNVSTCEVTSSQAISSPQR.-	2717.92	3	307.19	1.30	0.1	206	3/16	5
jmrawbsa5minlowionic, 1150	-.VNQYPYI.-	897.01	2	379.99	1.21	0.1	288	3/4	5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
M2-type pyruvate kinase [Mus musculus]					3359827.68	1405933.0	2		
ajrawmediapbsnocells, 1104	-.GADFLVTEVENGGSLGSKK.-	1909.09	3	3756.31	2.18	0.3	526	5/18	3
ajrawmediapbsnocells, 1212	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	19276.64	4.85	0.4	2181	19/46	3
ajrawmediapbsnocells,1326-1328	-.GADFLVTEVENGGSLGSK.-	1780.92	2	8837.82	3.42	0.4	935	1/2	3
jm5miniggrawlowionic, 1738	-.GDLGIEIPAEK.-	1142.29	2	4063.93	2.78	0.3	653	7/10	3
jm5miniggrawlowionic, 1940	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	13555.87	3.48	0.5	905	21/32	3
jm5miniggrawlowionic, 1948	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	12800.68	4.16	0.4	1384	35/92	3
jm5miniggrawlowionic, 1960	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	16931.74	4.81	0.5	1077	31/92	3
jm5miniggrawlowionic, 2136	-.GADFLVTEVENGGSLGSK.-	1780.92	2	18486.87	4.33	0.5	1473	21/34	3
jm5miniggrawlowionic, 2142	-.GADFLVTEVENGGSLGSK.-	1780.92	2	15995.88	3.84	0.5	1433	10/17	3
jm5miniggrawlowionic, 2146	-.EAEAAIYHLQLFEELRR.-	2089.34	3	2815.79	2.19	0.3	603	23/64	3
jm5miniggrawlowionic, 2152	-.EAEAAIYHLQLFEELRR.-	2089.34	3	2757.76	2.22	0.3	226	1/4	3
jm5miniggrawlowionic, 2450	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	4515.57	2.62	0.3	773	13/42	4
jm5miniggrawlowionic, 2456	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	16124.50	3.61	0.5	2126	5/12	4
jm5miniggrawlowionic, 3168	-.FGVEQDVDMVFASFIR.-	1861.11	2	2862.47	2.27	0.3	537	13/30	4
jm5miniggrawlowionic,1614-1616	-.LDIDSAPITAR.-	1172.31	2	6133.17	2.74	0.3	1278	3/4	3
jm5miniggrawlowionic,2166-2168	-.RFDEILEASDGIMVAR.-	1823.06	3	8550.44	3.30	0.4	1270	13/30	6
jm5miniggrawlowionic,2302-2304	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	12362.01	3.73	0.5	857	7/22	4
jmag5mincon500mmnacl, 1688	-.GDLGIEIPAEK.-	1142.29	2	6071.76	2.51	0.4	477	3/5	3
jmag5mincon500mmnacl, 1694	-.GDLGIEIPAEK.-	1142.29	2	4617.12	2.59	0.3	613	3/5	3
jmag5mincon500mmnacl, 1902	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	10987.90	2.65	0.6	519	9/16	3
jmag5mincon500mmnacl, 1910	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	10506.63	2.62	0.6	718	19/32	3
jmag5mincon500mmnacl, 2106	-.GADFLVTEVENGGSLGSK.-	1780.92	2	9283.24	3.66	0.4	1284	21/34	3
jmag5mincon500mmnacl, 2110	-.GADFLVTEVENGGSLGSK.-	1780.92	2	12701.69	3.85	0.4	1858	11/17	3
jmag5mincon500mmnacl, 2274	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	3270.11	1.83	0.4	306	19/88	4
jmag5mincon500mmnacl,1172-1174	-.APIIAVTR.-	841.03	2	6168.66	2.22	0.4	1093	6/7	4
jmfag1mnacl0minigg, 1162	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	17056.73	3.62	0.6	850	5/8	3
jmfag1mnacl0minigg, 1166	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	19540.29	3.89	0.6	946	11/16	3
jmfag1mnacl0minigg, 1226	-.KGDVVIVLTGWRPGSGFTNTMR.-	2392.77	3	8639.69	3.15	0.4	742	25/84	4
jmfag1mnacl0minigg, 1328	-.GADFLVTEVENGGSLGSK.-	1780.92	2	24321.27	4.82	0.5	2132	11/17	3
jmfag1mnacl0minigg, 1336	-.GADFLVTEVENGGSLGSK.-	1780.92	2	20714.14	4.74	0.5	1627	21/34	3
jmfag1mnacl0minigg, 1494	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	4024.89	2.65	0.3	551	3/11	4
jmfag1mnacl0minigg, 370	-.APIIAVTR.-	841.03	2	2784.66	2.07	0.2	866	13/14	4
jmfag1mnacl0minigg,1618-1620	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	33751.41	5.21	0.6	2538	19/42	4
jmfag1mnacl0minigg,886-888	-.LDIDSAPITAR.-	1172.31	2	8008.72	2.79	0.3	1728	17/20	3
jmfag1mnacl2,5minigg, 1028	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	11505.33	3.40	0.5	573	1/2	3
jmfag1mnacl2,5minigg, 1212	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	11179.48	2.79	0.6	477	17/32	3
jmfag1mnacl2,5minigg, 1218	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	17004.50	3.62	0.6	789	5/8	3
jmfag1mnacl2,5minigg, 1274	-.KGDVVIVLTGWRPGSGFTNTMR.-	2392.77	3	10300.08	3.20	0.5	911	1/3	4
jmfag1mnacl2,5minigg, 1380	-.GADFLVTEVENGGSLGSK.-	1780.92	2	22244.13	5.05	0.5	2209	12/17	3
jmfag1mnacl2,5minigg, 1384	-.GADFLVTEVENGGSLGSK.-	1780.92	2	22931.08	5.10	0.5	2312	25/34	3
jmfag1mnacl2,5minigg, 1416	-.RFDEILEASDGIMVAR.-	1823.06	3	7763.13	2.60	0.4	1017	2/5	6
jmfag1mnacl2,5minigg, 1474	-.IYVDDGLISLQVK.-	1463.70	2	17608.82	3.90	0.5	2163	5/8	4
jmfag1mnacl2,5minigg, 1532	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	12983.68	3.88	0.5	887	15/44	4
jmfag1mnacl2,5minigg, 1538	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	7331.44	2.97	0.5	407	23/88	4
jmfag1mnacl2,5minigg, 1658	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	18052.76	4.06	0.5	1709	11/28	4
jmfag1mnacl2,5minigg, 1662	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	5407.32	2.21	0.3	1379	29/84	4
jmfag1mnacl2,5minigg, 434	-.APIIAVTR.-	841.03	2	4134.48	2.48	0.3	686	11/14	4
jmfag1mnacl2,5minigg, 438	-.APIIAVTR.-	841.03	2	3242.75	2.02	0.3	864	5/7	4
jmfag1mnacl2,5minigg, 772	-.GDYPLEAVR.-	1020.12	2	3207.32	1.98	0.3	753	13/16	4
jmfag1mnacl2,5minigg, 878	-.NTGIICTIGPASR.-	1303.52	2	6080.18	2.67	0.3	1128	2/3	4
jmfag1mnacl2,5minigg, 950	-.LDIDSAPITAR.-	1172.31	2	3721.60	2.17	0.3	812	7/10	3
jmfag1mnacl2,5minigg,1038-1040	-.GDLGIEIPAEK.-	1142.29	2	8053.51	3.09	0.4	854	7/10	3
jmfag1mnacl5mincon, 1224	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	18194.50	4.89	0.5	1165	12/17	3
jmfag1mnacl5mincon, 1234	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	14244.16	4.37	0.5	818	21/34	3
jmfag1mnacl5mincon, 132	-.GSGTAEVELK.-	991.08	2	2997.18	2.78	0.2	719	7/9	4
jmfag1mnacl5mincon, 1426	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	18575.96	4.04	0.6	978	21/32	3
jmfag1mnacl5mincon, 1432	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	21595.66	4.43	0.6	967	11/16	3
jmfag1mnacl5mincon, 1594	-.GADFLVTEVENGGSLGSK.-	1780.92	2	16489.82	4.51	0.5	1196	11/17	3
jmfag1mnacl5mincon, 1764	-.EATESFASDPILYRPVAVALDTK.-	2494.78	2	11910.87	3.02	0.6	455	19/44	4
jmfag1mnacl5mincon, 186	-.LNFSHGTHEYHAETIK.-	1885.03	3	17737.75	4.16	0.5	1442	9/20	4
jmfag1mnacl5mincon, 190	-.LNFSHGTHEYHAETIK.-	1885.03	3	20781.21	4.18	0.6	1592	29/60	4
jmfag1mnacl5mincon, 2482	-.FGVEQDVDMVFASFIR.-	1861.11	2	20066.46	4.40	0.6	1261	19/30	4
jmfag1mnacl5mincon, 306	-.PVAVALDTK.-	914.08	2	6408.42	2.17	0.4	1015	7/8	4

jmfag1mnacl5mincon, 312	-.PVAVALDTK.-	914.08	2	5155.84	2.32	0.4	656	13/16	4
jmfag1mnacl5mincon,1134-1136	-.LDIDSAPITAR.-	1172.31	2	5171.51	2.44	0.3	1322	4/5	3
jmfag1mnacl5mincon,1236-1238	-.GDLGIEIPAEK.-	1142.29	2	9727.32	3.15	0.5	1031	17/20	3
jmfag1mnacl5mincon,1758-1760	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	7389.95	2.74	0.5	487	25/88	4
jmfag1mnacl5mincon,1892-1894	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	15693.85	3.61	0.5	1702	8/21	4
jmfag1mnacl5mincon,416-418	-.APIIAVTR.-	841.03	2	4242.40	2.02	0.3	979	13/14	4
jmfag1mnacl5minigg, 1102	-.LDIDSAPITAR.-	1172.31	2	2429.91	1.90	0.2	717	7/10	3
jmfag1mnacl5minigg, 1110	-.LDIDSAPITAR.-	1172.31	2	2547.06	1.65	0.2	1232	4/5	3
jmfag1mnacl5minigg, 1188	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	7537.77	3.66	0.4	627	9/17	3
jmfag1mnacl5minigg, 1398	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	16894.50	3.69	0.6	807	11/16	3
jmfag1mnacl5minigg, 1402	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	15993.16	3.43	0.6	764	5/8	3
jmfag1mnacl5minigg, 1602	-.RFDEILEASDGIMVAR.-	1823.06	2	2755.62	2.14	0.3	489	1/2	6
jmfag1mnacl5minigg, 1656	-.IYVDDGLISLQVK.-	1463.70	2	11731.77	3.35	0.4	2192	5/6	4
jmfag1mnacl5minigg, 1854	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	14792.02	3.87	0.5	1247	8/21	4
jmfag1mnacl5minigg, 912	-.GDYPLEAVR.-	1020.12	2	4874.66	2.45	0.3	824	7/8	4
jmfag1mnacl5minigg,1202-1204	-.GDLGIEIPAEK.-	1142.29	2	7672.34	3.04	0.4	614	7/10	3
jmfag1mnacl5minigg,1562-1564	-.GADFLVTEVENGGSLGSK.-	1780.92	2	25009.25	5.16	0.6	1795	11/17	3
jmfag1mnacl5minigg,1606-1608	-.RFDEILEASDGIMVAR.-	1823.06	3	4005.71	2.21	0.3	1074	11/30	6
jmfag1mnacl5minigg,1726-1728	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	12445.16	3.44	0.6	575	25/88	4
jmfag1mnacl5minigg,314-316	-.PVAVALDTK.-	914.08	2	2607.64	2.27	0.2	911	15/16	4
jmfag1mnacl5minigg,412-414	-.APIIAVTR.-	841.03	2	3289.04	2.35	0.2	911	6/7	4
jmfag1mnacl7,5minigg, 1036	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	16340.71	4.66	0.5	1131	23/34	3
jmfag1mnacl7,5minigg, 1046	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	17367.43	3.79	0.6	1111	23/34	3
jmfag1mnacl7,5minigg, 1446	-.RFDEILEASDGIMVAR.-	1823.06	3	7722.39	3.49	0.3	1298	7/15	6
jmfag1mnacl7,5minigg, 1692	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	26121.34	4.82	0.6	2086	3/7	4
jmfag1mnacl7,5minigg, 1700	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	9554.56	3.15	0.4	1161	31/84	4
jmfag1mnacl7,5minigg, 436	-.APIIAVTR.-	841.03	2	4289.53	2.18	0.3	840	6/7	4
jmfag1mnacl7,5minigg, 444	-.APIIAVTR.-	841.03	2	5062.12	2.29	0.4	918	6/7	4
jmfag1mnacl7,5minigg,1054-1056	-.GDLGIEIPAEK.-	1142.29	2	7520.57	2.94	0.4	1121	9/10	3
jmfag1mnacl7,5minigg,1238-1240	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	23060.66	4.87	0.6	1158	11/16	3
jmfag1mnacl7,5minigg,1404-1406	-.GADFLVTEVENGGSLGSK.-	1780.92	2	28992.65	6.07	0.5	1888	23/34	3
jmfag1mnacl7,5minigg,1438-1440	-.RFDEILEASDGIMVAR.-	1823.06	2	2400.32	2.11	0.3	254	2/5	6
jmfag1mnacl7,5minigg,1558-1560	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	6235.56	2.87	0.4	460	3/11	4
jmfag1mnacl7,5minigg,394-396	-.PVAVALDTK.-	914.08	2	3814.22	2.22	0.3	749	7/8	4
jmfag5minigg1000mmnacl, 1050	-.LDIDSAPITAR.-	1172.31	2	6761.70	2.50	0.4	1171	4/5	3
jmfag5minigg1000mmnacl, 1138	-.GDLGIEIPAEK.-	1142.29	2	12246.10	3.35	0.5	989	17/20	3
jmfag5minigg1000mmnacl, 1142	-.GDLGIEIPAEK.-	1142.29	2	7986.69	2.87	0.4	964	4/5	3
jmfag5minigg1000mmnacl, 1322	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	11618.88	3.25	0.5	731	5/8	3
jmfag5minigg1000mmnacl, 1328	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	17756.26	3.98	0.6	729	5/8	3
jmfag5minigg1000mmnacl, 1486	-.GADFLVTEVENGGSLGSK.-	1780.92	2	11378.20	3.72	0.4	1218	10/17	3
jmfag5minigg1000mmnacl, 1490	-.GADFLVTEVENGGSLGSK.-	1780.92	2	29708.87	4.93	0.6	2737	25/34	3
jmfag5minigg1000mmnacl, 1540	-.RFDEILEASDGIMVAR.-	1823.06	2	14956.78	4.01	0.5	1519	7/10	6
jmfag5minigg1000mmnacl, 1578	-.IYVDDGLISLQVK.-	1463.70	2	8217.47	2.79	0.3	1836	19/24	4
jmfag5minigg1000mmnacl, 1588	-.IYVDDGLISLQVK.-	1463.70	2	14936.28	3.37	0.4	2789	11/12	4
jmfag5minigg1000mmnacl, 316	-.PVAVALDTK.-	914.08	2	2934.54	2.19	0.3	495	13/16	4
jmfag5minigg1000mmnacl, 386	-.APIIAVTR.-	841.03	2	4323.29	2.10	0.3	854	13/14	4
jmfag5minigg1000mmnacl, 780	-.VNLAMDVGK.-	947.14	2	2830.24	1.91	0.2	943	13/16	5
jmfag5minigg1000mmnacl, 848	-.GDYPLEAVR.-	1020.12	2	2861.59	2.03	0.3	528	3/4	4
jmfag5minigg1000mmnacl, 854	-.GDYPLEAVR.-	1020.12	2	2506.90	1.84	0.3	615	3/4	4
jmfag5minigg1000mmnacl,1522-1524	-.RFDEILEASDGIMVAR.-	1823.06	2	5578.49	2.80	0.4	538	1/2	6
jmfag5minigg1000mmnacl,1640-1642	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	13513.72	3.81	0.5	952	31/88	4
jmfag5minigg1000mmnacl,1768-1770	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	20460.82	4.71	0.5	1958	5/12	4
jmfag5minigg150mmnacl, 1352	-.GADFLVTEVENGGSLGSK.-	1780.92	2	7668.11	2.67	0.5	363	9/17	3
jmfag5minigg150mmnacl, 1368	-.GADFLVTEVENGGSLGSK.-	1780.92	2	18631.93	4.77	0.5	1017	9/17	3
jmfag5minigg150mmnacl, 846	-.NTGIICTIGPASR.-	1303.52	2	5462.23	3.04	0.3	913	5/8	4
jmfag5minigg150mmnacl,1010-1012	-.GDLGIEIPAEK.-	1142.29	2	4339.98	2.70	0.3	700	3/4	3
jmfag5minigg150mmnacl,1188-1190	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	32270.50	5.65	0.7	1115	3/4	3
jmfag5minigg150mmnacl,1506-1508	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	4478.76	2.66	0.3	508	3/11	4
jmfag5minigg150mmnacl,1642-1644	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	11295.15	3.38	0.4	1575	8/21	4
jmfag5minigg150mmnacl,998-1000	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	19299.96	4.74	0.6	1018	23/34	3
jmfag5minigg200mmnacl, 1336	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	16845.78	3.30	0.6	924	11/16	3
jmfag5minigg200mmnacl, 1342	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	9156.63	2.94	0.5	636	5/8	3
jmfag5minigg200mmnacl, 1412	-.KGDVVIVLTGWRPGSGFTNTMR.-	2392.77	3	4004.13	2.61	0.3	683	9/28	4
jmfag5minigg200mmnacl, 368	-.APIIAVTR.-	841.03	2	2576.11	1.74	0.3	775	6/7	4
jmfag5minigg200mmnacl, 380	-.APIIAVTR.-	841.03	2	3451.19	2.04	0.3	846	6/7	4
jmfag5minigg200mmnacl,1160-1162	-.GDLGIEIPAEK.-	1142.29	2	2649.50	2.53	0.2	486	13/20	3
jmfag5minigg200mmnacl,1512-1514	-.GADFLVTEVENGGSLGSK.-	1780.92	2	17764.08	4.65	0.5	1741	11/17	3
jmfag5minigg200mmnacl,1658-1660	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	6453.32	3.00	0.4	548	27/88	4
jmfag5minigg200mmnacl,1786-1788	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	12822.04	3.70	0.5	1283	5/14	4
jmfag5minigg250mmnacl, 2274	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	18008.22	4.13	0.5	1516	31/84	4
jmfag5minigg250mmnacl, 2296	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	6193.87	2.83	0.3	1077	29/84	4
jmfag5minigg250mmnacl,1460-1462	-.GDLGIEIPAEK.-	1142.29	2	8096.88	3.20	0.4	659	7/10	3
jmfag5minigg250mmnacl,1702-1704	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	19037.01	3.68	0.7	762	9/16	3
jmfag5minigg250mmnacl,1906-1908	-.GADFLVTEVENGGSLGSK.-	1780.92	2	19256.54	4.64	0.4	2234	12/17	3
jmfag5minigg250mmnacl,996-998	-.APIIAVTR.-	841.03	2	3150.89	2.03	0.3	598	11/14	4
jmfag5minigg300mmnacl, 1534	-.LDIDSAPITAR.-	1172.31	2	4604.56	2.41	0.3	1167	17/20	3
jmfag5minigg300mmnacl, 1898	-.GVNLPGAAVDLPAVSEK.-	1637.86	3	7094.24	2.89	0.4	831	3/8	3
jmfag5minigg300mmnacl, 2240	-.IYVDDGLISLQVK.-	1463.70	2	3545.64	1.86	0.3	1163	5/8	4
jmfag5minigg300mmnacl, 2460	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	17396.07	4.34	0.5	1830	3/7	4
jmfag5minigg300mmnacl,1148-1150	-.APIIAVTR.-	841.03	2	4736.53	2.33	0.3	1055	6/7	4
jmfag5minigg300mmnacl,1652-1654	-.GDLGIEIPAEK.-	1142.29	2	3781.73	2.93	0.2	743	13/20	3
jmfag5minigg300mmnacl,1902-1904	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	13648.97	3.52	0.6	715	19/32	3
jmfag5minigg300mmnacl,2112-2114	-.GADFLVTEVENGGSLGSK.-	1780.92	2	17029.59	4.21	0.5	1783	21/34	3
jmfag5minigg350mmnacl, 1105	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	23481.94	4.47	0.6	1118	23/32	3

jmfag5minigg350mmnacl, 1113	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	15873.77	3.60	0.6	927	11/16	3
jmfag5minigg350mmnacl, 1267	-.GADFLVTEVENGGSLGSK.-	1780.92	2	27929.48	5.26	0.6	2275	13/17	3
jmfag5minigg350mmnacl, 1273	-.GADFLVTEVENGGSLGSK.-	1780.92	2	10236.86	3.71	0.4	1233	1/2	3
jmfag5minigg350mmnacl, 1411	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	4277.29	2.54	0.4	362	5/22	4
jmfag5minigg350mmnacl, 1415	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	4855.46	2.50	0.4	439	25/88	4
jmfag5minigg350mmnacl, 863	-.LDIDSAPITAR.-	1172.31	2	3339.91	1.96	0.3	680	7/10	3
jmfag5minigg350mmnacl, 937	-.GDLGIEIPAEK.-	1142.29	2	3776.61	2.35	0.3	550	13/20	3
jmfag5minigg350mmnacl, 943	-.GDLGIEIPAEK.-	1142.29	2	6965.62	2.90	0.4	662	7/10	3
jmfag5minigg350mmnacl,1535-1537	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	24864.54	4.92	0.5	2067	37/84	4
jmfag5minigg350mmnacl,399-401	-.APIIAVTR.-	841.03	2	5181.48	2.51	0.3	858	6/7	4
jmfag5minigg400mmnacl, 1082	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	7729.82	3.28	0.4	529	9/17	3
jmfag5minigg400mmnacl, 1100	-.GDLGIEIPAEK.-	1142.29	2	5881.46	2.65	0.4	596	13/20	3
jmfag5minigg400mmnacl, 1424	-.GADFLVTEVENGGSLGSK.-	1780.92	2	14439.40	4.15	0.5	1407	10/17	3
jmfag5minigg400mmnacl, 1512	-.IYVDDGLISLQVK.-	1463.70	2	11920.78	3.11	0.4	2236	7/8	4
jmfag5minigg400mmnacl, 1518	-.IYVDDGLISLQVK.-	1463.70	2	5078.71	2.48	0.3	1414	3/4	4
jmfag5minigg400mmnacl, 1572	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	5289.13	2.85	0.4	536	27/88	4
jmfag5minigg400mmnacl, 1700	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	11891.04	3.42	0.4	1945	11/28	4
jmfag5minigg400mmnacl, 1712	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	11466.83	3.14	0.4	2076	17/42	4
jmfag5minigg400mmnacl, 379	-.APIIAVTR.-	841.03	2	2675.51	1.93	0.3	663	5/7	4
jmfag5minigg400mmnacl, 390	-.APIIAVTR.-		2	7313.58	2.58	0.4	1003	13/14	4
jmfag5minigg400mmnacl, 816	-.GDYPLEAVR.-	1020.12	2	4706.87	2.10	0.4	888	13/16	4
jmfag5minigg400mmnacl, 824	-.GDYPLEAVR.-	1020.12	2	3084.02	1.79	0.3	896	7/8	4
jmfag5minigg450mmnacl_030527025134, 1284	-.VNLAMDVGK.-	947.14	2	3756.61	2.18	0.3	652	3/4	5
jmfag5minigg450mmnacl_030527025134, 1290	-.VNLAMDVGK.-	947.14	2	2712.63	1.96	0.3	735	3/4	5
jmfag5minigg450mmnacl_030527025134, 1522	-.LDIDSAPITAR.-	1172.31	2	5910.98	2.19	0.4	740	7/10	3
jmfag5minigg450mmnacl_030527025134, 1526	-.LDIDSAPITAR.-	1172.31	2	2657.69	1.88	0.1	1220	17/20	3
jmfag5minigg450mmnacl_030527025134, 2088	-.GADFLVTEVENGGSLGSK.-	1780.92	2	15557.93	4.26	0.4	1680	21/34	3
jmfag5minigg450mmnacl_030527025134, 2096	-.GADFLVTEVENGGSLGSK.-	1780.92	2	14707.26	4.10	0.5	1490	21/34	3
jmfag5minigg450mmnacl_030527025134, 2196	-.IYVDDGLISLQVK.-	1463.70	2	9106.77	3.19	0.3	1704	3/4	4
jmfag5minigg450mmnacl_030527025134, 2200	-.IYVDDGLISLQVK.-	1463.70	2	12263.95	3.50	0.3	2307	7/8	4
jmfag5minigg450mmnacl_030527025134, 2246	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	3866.85	2.12	0.4	406	21/88	4
jmfag5minigg450mmnacl_030527025134,1646-1648	-.GDLGIEIPAEK.-	1142.29	2	5147.21	2.81	0.3	682	3/5	3
jmfag5minigg450mmnacl_030527025134,1894-1896	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	19768.97	4.28	0.6	891	21/32	3
jmfag5minigg450mmnacl_030527025134,2428-2430	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	19009.39	4.43	0.5	1836	11/28	4
jmfag5minigg500mmnacl, 1242	-.LDIDSAPITAR.-	1172.31	2	5261.79	2.52	0.3	1139	4/5	3
jmfag5minigg500mmnacl, 1246	-.LDIDSAPITAR.-	1172.31	2	4043.38	2.02	0.3	1041	4/5	3
jmfag5minigg500mmnacl, 1380	-.GDLGIEIPAEK.-	1142.29	2	8110.46	2.93	0.5	500	3/5	3
jmfag5minigg500mmnacl, 1602	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	17848.97	3.44	0.7	790	5/8	3
jmfag5minigg500mmnacl, 1606	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	12297.92	3.10	0.6	453	17/32	3
jmfag5minigg500mmnacl, 1666	-.KGDVVIVLTGWRPGSGFTNTMR.-	2392.77	3	2904.37	2.55	0.2	673	25/84	4
jmfag5minigg500mmnacl, 1916	-.IYVDDGLISLQVK.-	1463.70	2	8632.38	2.74	0.4	1907	5/6	4
jmfag5minigg500mmnacl, 1932	-.IYVDDGLISLQVK.-	1463.70	2	3212.04	2.16	0.1	1329	3/4	4
jmfag5minigg500mmnacl, 2152	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	2	3426.44	1.55	0.4	555	8/21	4
jmfag5minigg500mmnacl,1800-1802	-.GADFLVTEVENGGSLGSK.-	1780.92	2	12494.83	3.92	0.5	1146	1/2	3
jmfag5minigg500mmnacl,1972-1974	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	9037.23	3.08	0.5	605	13/44	4
jmfag5minigg500mmnacl,2148-2150	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	22567.87	4.24	0.6	1570	17/42	4
jmfag5minigg600mmnacl, 1440	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	7955.73	3.01	0.5	351	21/88	4
jmfag5minigg600mmnacl, 1446	-.EATESFASDPILYRPVAVALDTK.-	2494.78	2	8239.02	2.82	0.5	244	15/44	4
jmfag5minigg600mmnacl, 1560	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	8880.93	3.40	0.4	997	29/84	4
jmfag5minigg600mmnacl, 1568	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	7857.40	3.00	0.4	891	31/84	4
jmfag5minigg600mmnacl, 2170	-.FGVEQDVDMVFASFIR.-	1861.11	2	11425.47	3.14	0.5	977	17/30	4
jmfag5minigg600mmnacl, 3109	-.FGVEQDVDMVFASFIR.-	1861.11	2	11568.75	3.23	0.5	1009	8/15	4
jmfag5minigg600mmnacl,1130-1132	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	17486.58	4.04	0.6	831	5/8	3
jmfag5minigg600mmnacl,1288-1290	-.GADFLVTEVENGGSLGSK.-	1780.92	2	21481.23	4.98	0.5	1729	11/17	3
jmfag5minigg600mmnacl,1382-1384	-.IYVDDGLISLQVK.-	1463.70	2	18572.03	4.09	0.4	2651	11/12	4
jmfag5minigg600mmnacl,402-404	-.APIIAVTR.-	841.03	2	7493.81	2.76	0.4	1039	6/7	4
jmfag5minigg600mmnacl,960-962	-.GDLGIEIPAEK.-	1142.29	2	8074.29	2.97	0.4	747	3/4	3
jmfag5miniggbead, 1167	-.GADFLVTEVENGGSLGSK.-	1780.92	2	17640.11	3.90	0.5	1976	11/17	3
jmfag5miniggbead, 1177	-.GADFLVTEVENGGSLGSK.-	1780.92	2	7474.79	3.61	0.3	1191	9/17	3
jmfag5miniggbead, 1307	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	4935.78	2.79	0.4	305	21/88	4
jmfag5miniggbead, 1359	-.EAEAAIYHLQLFEELR.-	1933.15	2	3032.41	2.55	0.2	720	8/15	3
jmfag5miniggbead, 1433	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	14451.33	3.78	0.5	1355	11/28	4
jmfag5miniggbead, 363	-.APIIAVTR.-	841.03	2	4861.15	1.98	0.4	1006	6/7	4
jmfag5miniggbead, 853	-.GDLGIEIPAEK.-	1142.29	2	3471.61	2.50	0.3	490	3/5	3
jmfag5miniggbead,1011-1013	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	24754.50	4.59	0.7	888	21/32	3
jmfag5miniggbead_030528200105, 1215	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	14876.35	3.51	0.6	1009	11/16	3
jmfag5miniggbead_030528200105, 1359	-.GADFLVTEVENGGSLGSK.-	1780.92	2	5990.48	2.63	0.4	510	9/17	3
jmfag5miniggbead_030528200105, 1367	-.GADFLVTEVENGGSLGSK.-	1780.92	2	15003.01	3.74	0.5	1516	21/34	3
jmfag5miniggbead_030528200105, 1511	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	6697.64	2.81	0.4	404	3/11	4
jmfag5miniggbead_030528200105, 1521	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	9757.65	3.06	0.5	385	23/88	4
jmfag5miniggbead_030528200105, 1637	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	22496.73	4.47	0.6	1839	5/12	4
jmfag5miniggbead_030528200105, 2147	-.FGVEQDVDMVFASFIR.-	1861.11	2	7142.29	2.74	0.4	853	8/15	4
jmfag5miniggbead_030528200105,1045-1047	-.GDLGIEIPAEK.-	1142.29	2	5830.88	2.86	0.4	479	3/5	3
jmfag5miniggbead_030528200105,1403-1405	-.RFDEILEASDGIMVAR.-	1823.06	2	7411.57	2.58	0.5	625	17/30	6
JMFAGNACL10_1B21E3, 1056	-.SVEMLKEMIK.-	1208.52	3	4039.12	2.43	0.3	649	23/36	5
JMFAGNACL10_1B21E3, 1392	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	14792.77	4.70	0.4	1205	31/92	3
JMFAGNACL10_1B21E3, 1414	-.KGDVVIVLTGWRPGSGFTNTMR.-	2392.77	3	8961.60	3.83	0.4	757	13/42	4
JMFAGNACL10_1B21E3, 1418	-.KGDVVIVLTGWRPGSGFTNTMR.-	2392.77	3	6435.12	3.21	0.4	562	2/7	4
JMFAGNACL10_1B21E3, 1532	-.GADFLVTEVENGGSLGSK.-	1780.92	2	12538.13	3.47	0.5	894	1/2	3
JMFAGNACL10_1B21E3, 378	-.APIIAVTR.-	841.03	2	5091.69	2.14	0.4	993	6/7	4
JMFAGNACL10_1B21E3,280-282	-.APIIAVTRNPQTAR.-	1508.75	3	10931.74	3.08	0.5	1111	6/13	4
JMFAGNACL10_2B21E3, 366	-.APIIAVTRNPQTAR.-	1508.75	3	2787.76	2.22	0.3	531	19/52	4
JMFAGNACL10_2B21E3, 370	-.APIIAVTRNPQTAR.-	1508.75	3	3573.56	2.28	0.3	647	11/26	4
JMFAGNACL15B21E3, 1008	-.NTGNCTIGPASR.-	1303.52	2	6512.59	2.86	0.3	1456	3/4	4
JMFAGNACL15B21E3, 334	-.APIIAVTRNPQTAR.-	1508.75	3	8027.21	3.02	0.4	1094	25/52	4
JMFAGNACL15B21E3, 340	-.APIIAVTRNPQTAR.-	1508.75	3	2790.38	1.73	0.3	452	19/52	4
JMFAGNACL5B21E3, 1222	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	10445.87	2.91	0.6	409	15/32	3
JMFAGNACL5B21E3, 1278	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	22860.04	5.74	0.4	2234	39/92	3
JMFAGNACL5B21E3, 1292	-.KGDVVIVLTGWRPGSGFTNTMR.-	2392.77	3	14351.57	3.85	0.5	1434	31/84	4

JMFAGNACL5B21E3, 1402	-.GADFLVTEVENGGSLGSK.-	1780.92	2	10287.06	3.65	0.4	1171	9/17	3
JMFAGNACL5B21E3, 1460	-.RFDEILEASDGIMVAR -	1823.06	2	11435.61	3.77	0.5	964	2/3	6
JMFAGNACL5B21E3, 1462	-.GVNLPGAAVDLPAVSEKDIQDLK.-	2350.66	2	14156.34	3.40	0.6	553	9/22	3
JMFAGNACL5B21E3, 1498	-.IYVDDGLISLQVK.-	1463.70	2	16605.43	4.13	0.4	2038	5/6	4
JMFAGNACL5B21E3, 1700	- LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	25375.25	4.39	0.6	1860	3/7	4
JMFAGNACL5B21E3, 1706	- LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	15040.71	3.73	0.4	2029	3/7	4
JMFAGNACL5B21E3, 2656	-.FGVEQDVDMVFASFIR.-	1861.11	2	19599.80	3.92	0.6	1598	7/10	4
JMFAGNACL5B21E3, 290	-.LNFSHGTHEYHAETIK.-	1885.03	3	9341.99	3.19	0.4	1061	13/30	4
JMFAGNACL5B21E3, 308	-.LNFSHGTHEYHAETIK.-	1885.03	3	11977.01	3.87	0.4	1583	7/15	4
JMFAGNACL5B21E3, 394	-.APIIAVTR.-	841.03	2	5166.28	2.17	0.4	956	13/14	4
JMFAGNACL5B21E3, 692	-.VNLAMDVGK -	947.14	2	3990.59	2.02	0.3	923	7/8	5
JMFAGNACL5B21E3, 696	-.VNLAMDVGK.-	947.14	2	3276.06	2.07	0.3	579	3/4	5
JMFAGNACL5B21E3,1050-1052	-.GDLGIEIPAEK.-	1142.29	2	7084.77	2.74	0.4	883	4/5	3
JMFAGNACL5B21E3,1454-1456	-.GVNLPGAAVDLPAVSEKDIQDLK.-	2350.66	3	3305.74	2.47	0.3	196	1/4	3
JMFAGNACL5B21E3,1562-1564	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	15320.34	4.12	0.6	683	7/22	4
JMFAGNACL5B21E3,950-952	-.LDIDSAPITAR.-	1172.31	2	3784.25	2.25	0.3	1037	3/4	3
jmfreebeadsrawphag3007, 1096	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	18720.50	4.06	0.6	646	19/32	3
jmfreebeadsrawphag3007, 1152	-.EKGADFLVTEVENGGSLGSK.-	2038.20	3	7678.11	3.28	0.3	1372	7/19	3
jmfreebeadsrawphag3007, 1290	-.RFDEILEASDGIMVAR.-	1823.06	2	5175.46	2.34	0.4	486	8/15	6
jmfreebeadsrawphag3007, 1514	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	18787.66	4.49	0.5	1337	31/84	4
jmfreebeadsrawphag3007,1246-1248	- GADFLVTEVENGGSLGSK.-	1780.92	2	26125.07	5.00	0.5	2449	12/17	3
jmfreebeadsrawphag3007,1300-1302	-.GVNLPGAAVDLPAVSEKDIQDLK.-	2350.66	3	5528.91	3.02	0.4	325	27/88	3
jmfreebeadsrawphag3007,1394-1396	- EATESFASDPILYRPVAVALDTK.-	2494.78	3	5995.99	3.26	0.3	726	13/44	4
jmfreebeadsrawphag3007,1400-1402	-.EATESFASDPILYRPVAVALDTK.-	2494.78	2	13492.71	3.86	0.6	444	5/11	4
jmfreebeadsrawphag3007,932-934	-.GDLGIEIPAEK.-	1142.29	2	4000.42	3.09	0.3	639	7/10	3
jmIgG150rawphag3007, 1768	-.GADFLVTEVENGGSLGSK.-	1780.92	2	3885.91	1.82	0.4	561	13/34	3
jmIgG150rawphag3007, 1808	-.GADFLVTEVENGGSLGSK.-	1780.92	2	10388.24	3.48	0.4	1538	21/34	3
jmIgG150rawphag3007, 1846	-.GVNLPGAAVDLPAVSEKDIQDLK.-	2350.66	3	6180.31	2.54	0.5	257	13/44	3
jmIgG150rawphag3007,1626-1628	- GVNLPGAAVDLPAVSEK.-	1637.86	2	9928.57	2.80	0.5	803	17/32	3
jmIgG150rawphag3007,1654-1656	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	31998.00	5.73	0.6	2452	39/92	3
jmIgG250rawphag3007, 1434	-.GDLGIEIPAEK.-	1142.29	2	9797.17	3.33	0.5	692	3/4	3
jmIgG250rawphag3007, 1440	-.GDLGIEIPAEK.-	1142.29	2	4444.66	2.51	0.3	650	13/20	3
jmIgG250rawphag3007, 1666	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	9694.29	2.87	0.5	798	19/32	3
jmIgG250rawphag3007, 1878	-.GVNLPGAAVDLPAVSEKDIQDLK.-	2350.66	3	4424.71	1.97	0.4	342	27/88	3
jmIgG250rawphag3007,1840-1842	-.GADFLVTEVENGGSLGSK.-	1780.92	2	26517.68	5.10	0.5	2513	12/17	3
jmIgG300rawphag3007, 1446	-.GDLGIEIPAEK.-	1142.29	2	3622.10	2.32	0.3	515	13/20	3
jmIgG300rawphag3007, 1784	-.GADFLVTEVENGGSLGSK.-	1780.92	2	6804.87	2.19	0.5	867	8/17	3
jmIgG300rawphag3007, 1810	-.GADFLVTEVENGGSLGSK.-	1780.92	2	12761.98	3.85	0.4	1431	10/17	3
jmIgG300rawphag3007,1260-1262	-.NTGIICTIGPASR.-	1303.52	2	4135.55	2.70	0.2	1141	17/24	4
jmIgG350nacirawphag3007, 1647	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	12135.73	3.67	0.4	1313	8/23	3
jmidl150nacirawphag3007, 1590	-.LDIDSAPITAR.-	1172.31	2	3367.38	1.93	0.3	733	7/10	3
jmidl150nacirawphag3007, 2050	-.GADFLVTEVENGGSLGSK.-	1780.92	2	3756.91	2.12	0.3	971	9/17	3
jmidl250nacirawphag3007,1350-1352	-.LDIDSAPITAR.-	1172.31	2	3997.73	2.35	0.3	913	3/4	3
JMMAGNEGB16D3, 1034	-.GDLGIEIPAEK.-	1142.29	2	4511.22	2.93	0.3	616	7/10	3
JMMAGTube1B16E3, 104	-.GSGTAEVELKK.-	1119.25	2	5827.20	2.66	0.4	768	3/5	4
JMMAGTube1B16E3, 1042	-.KGVNLPGAAVDLPAVSEK.-	1766.03	2	12803.92	4.30	0.5	605	9/17	3
JMMAGTube1B16E3, 130	-.GSGTAEVELK.-	991.08	2	3603.77	2.41	0.3	848	5/6	4
JMMAGTube1B16E3, 1412	-.GADFLVTEVENGGSLGSK.-	1780.92	2	16663.73	4.40	0.5	1542	10/17	3
JMMAGTube1B16E3, 1420	-.GADFLVTEVENGGSLGSK.-	1780.92	2	12294.90	3.70	0.5	1278	10/17	3
JMMAGTube1B16E3, 1470	-.GVNLPGAAVDLPAVSEKDIQDLK.-	2350.66	2	7339.70	3.05	0.4	576	17/44	3
JMMAGTube1B16E3, 1576	-.EATESFASDPILYRPVAVALDTK.-	2494.78	2	4323.43	2.27	0.4	329	4/11	4
JMMAGTube1B16E3, 880	-.NTGIICTIGPASR.-	1303.52	2	4333.81	2.39	0.3	1144	5/8	4
JMMAGTube1B16E3,1058-1060	-.GDLGIEIPAEK.-	1142.29	2	6067.84	3.05	0.4	767	3/4	3
JMMAGTube1B16E3,1242-1244	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	13616.85	3.18	0.6	829	5/8	3
JMMAGTube1B16E3,1284-1286	- KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	28570.30	6.01	0.5	2138	9/23	3
JMMAGTube1B16E3,1570-1572	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	14257.77	4.29	0.5	587	13/44	4
JMMAGTube1B16E3,1704-1706	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	19798.22	4.28	0.6	1532	17/42	4
JMMAGTube1B16E3,968-970	-.LDIDSAPITAR.-	1172.31	2	4664.59	2.24	0.3	1282	4/5	3
jmraw5minigg250mmnaclsyringdnase, 2172	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	4979.89	2.55	0.4	383	23/88	4
jmraw5minigg250mmnaclsyringdnase, 2180	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	3818.39	2.17	0.4	259	5/22	4
jmraw5minigg250mmnaclsyringdnase,2028-2030	-.GADFLVTEVENGGSLGSK.-	1780.92	2	20551.27	4.87	0.5	1701	11/17	3
jmraw5minigg500mmnaclsd, 1822	-.GADFLVTEVENGGSLGSK.-	1780.92	2	7091.72	2.93	0.4	998	9/17	3
jmrawigg5min150mmnacl, 1082	-.GDLGIEIPAEK.-	1142.29	2	5009.81	2.68	0.4	607	13/20	3
jmrawigg5min150mmnacl, 1254	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	16692.95	3.72	0.6	987	21/32	3
jmrawigg5min150mmnacl,1406-1408	-.GADFLVTEVENGGSLGSK.-	1780.92	2	13177.04	4.08	0.4	1237	19/34	3
jmrawigg5min300mmnaclsyringednase, 1891	-.FGVEQDVDMVFASFIR.-	1861.11	2	13670.53	3.03	0.6	988	17/30	4
jmrawigg5minbeadsfreezethaw, 1200	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	14210.10	3.14	0.6	1016	11/16	3
jmrawigg5minbeadsfreezethaw, 1204	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	9481.26	3.01	0.5	862	5/8	3
jmrawigg5minbeadsfreezethaw, 1514	-.EATESFASDPILYRPVAVALD"K.-	2494.78	3	6081.82	2.75	0.4	372	21/88	4
jmrawigg5minbeadsfreezethaw, 1520	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	14306.81	3.73	0.6	583	7/22	4
jmrawigg5minbeadsfreezethaw, 1638	-.LAPITSDPTEAAAVGAVEASFK -	2146.38	3	13515.82	3.62	0.5	1230	31/84	4
jmrawigg5minbeadsfreezethaw, 846	-.NTGIICTIGPASR.-	1303.52	2	4603.39	1.90	0.4	915	2/3	4
jmrawigg5minbeadsfreezethaw,1018-1020	-.GDLGIEIPAEK.-	1142.29	2	5822.22	2.68	0.4	596	13/20	3
jmrawigg5minbeadsfreezethaw,1242-1244	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	17345.45	4.94	0.4	1685	35/92	3
jmrawigg5minbeadsfreezethaw,1362-1364	-.GADFLVTEVENGGSLGSK.-	1780.92	2	13163.66	4.29	0.4	1495	10/17	3
jmrawigg5minbeadsfreezethaw,1410-1412	-.GVNLPGAAVDLPAVSEKDIQDLK.-	2350.66	3	9689.69	3.35	0.5	446	31/88	3
jmrawigg5miniggfreebead, 1308	-.GADFLVTEVENGGSLGSK.-	1780.92	2	12526.52	3.72	0.5	995	19/34	3
jmrawigg5miniggfreebead, 2060	-.QAHLYRGIFPVLCKDAVLNAWAEDVDLR.-	3214.69	2	135.05	0.92	0.1	118	1/6	4
jmrawigg5miniggfreebead,1448-1450	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	6818.47	2.96	0.4	563	25/88	4
jmrawigg5miniggfreebead,384-386	-.APIIAVTR.-	841.03	2	411.58	1.32	0.1	251	9/14	4
jmrawrminigg200mmnaclsyringdnas, 1462	-.GDLGIEIPAEK.-	1142.29	2	2837.45	2.24	0.3	478	3/5	3
jmrawrminigg200mmnaclsyringdnas, 1466	-.GDLGIEIPAEK.-	1142.29	2	5295.43	2.54	0.4	725	13/20	3
jmrawrminigg200mmnaclsyringdnas, 1666	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	2862.54	1.68	0.4	292	13/32	3
jmrawrminigg200mmnaclsyringdnas, 1872	-.KGVNLPGAAVDLPAVSEKDIQDLK.-	2478.83	3	9682.29	3.36	0.4	1108	8/23	3
jmrawrminigg200mmnaclsyringdnas, 2010	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	3568.92	2.47	0.3	370	1/4	4
jmrawrminigg200mmnaclsyringdnas, 2018	-.EATESFASDPILYRPVAVALDTK.-	2494.78	3	5848.43	2.75	0.4	368	1/4	4
jmrawrminigg200mmnaclsyringdnas,1858-1860	-.GADFLVTEVENGGSLGSK.-	1780.92	2	15975.61	5.02	0.4	1591	21/34	3
jmrawrminigg200mmnaclsyringdnas,2180-2182	-.LAPITSDPTEAAAVGAVEASFK.-	2146.38	3	19910.40	4.47	0.5	1716	17/42	4

control

M2-type pyruvate kinase [Mus musculus] musculus]					**24951.66**	1405933.0	15		
FPbeads700_Dec19, 1103	-.GADFLVTEVENGGSLGSKK.-	1909.09	3	779.32	1.45	0.0	531	23/72	3
rawextr_700beadigg_Mar04, 1246	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	1398.25	1.69	0.2	230	5/16	3
FPbeads800_Dec19, 3608	-.LDIDSAPITARNTGIICTIGPASRSVEMLK.-	3144.66	2	82.56	0.90	0.1	59	9/58	3
jmraw5minbsaresebeads, 1488	- GDLGIEIPAEK.-	1142.29	2	1730.86	2.02	0.2	454	7/10	3
jmraw5minbsaresebeads, 1666	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	12871.25	2.97	0.8	660	17/32	3
jmraw5minbsaresebeads, 1670	-.GVNLPGAAVDLPAVSEK.-	1637.86	2	8089.43	2.41	0.5	516	1/2	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Pyruvate kinase 3 [Mus musculus] mest					7936.48	38075009.0	12		
ajrawphagjun20dpi1MNaCl, 656	-.VLGEKGKNINIISK.-	1513.81	3	1188.38	1.55	0.1	656	19/52	1
JMFAGNACL10_1B21E3, 830	-.CNQAGKLVK.-	961.17	2	422.15	0.95	0.1	418	5/8	
jmfag5minigg150mmnacl,968-970	-.SVEMLKEMIKSR.-	1451.78	2	164.42	1.16	0.0	137	9/22	
jmfag5minigg350mmnacl, 1165	-.VENGASLGSK.-	962.04	2	279.61	0.97	0.0	263	4/9	
jmlgG250rawphag3007, 1626	-.GATLKITLNKAFMK.-	1536.91	2	1317.30	1.54	0.3	163	9/26	
jmfag5minigg600mmnacl, 1902	-.ACNTGIICTIGPASRSVEMLK.-	2165.59	3	223.88	1.18	0.1	160	1/5	
jmfagfrench20minigg1mnacldtt, 28	-.VNLTMDVGK.-	977.16	3	152.56	0.87	0.0	175	5/16	
ajrawphag1MNaCl20, 808	-.VNLTMDVGK.-	977.16	3	271.09	1.05	0.0	259	3/8	
jmfag5minigg250mmnacl, 900	-.SVEMLKEMNK.-	1209.46	3	1052.29	1.30	0.1	628	17/36	
jmrawgg5min300mmnaclsyringednase, 1583	-.TGLIKGSGIAEVELKK.-	1643.95	2	893.07	1.51	0.0	580	13/30	
jmfag5minigg350mmnacl, 1839	-.SADFQVTGVENSSSLVSK.-	1855.98	2	263.79	1.11	0.0	229	11/34	
ajrawphag1MNaCl20,2884-2886	-.TGLIKGSGIAEVELKK.-	1643.95	2	272.46	1.35	0.0	195	11/30	
jmraw5minbsafreezthaw, 1718	-.LVKCATQMLESIVK.-	1563.95	2	125.99	0.98	0.0	125	4/13	
ajrawmediapbsnocells,1902-1904	-.EATESFASDSILYRPIVVALDTK.-	2526.82	3	1309.50	1.98	0.2	430	5/22	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
HXK1_MOUSE Hexokinase, type I (HK I) (Hexokinase, tumor isozyme)					5510.52	30316354.0	27		
jmfag5minigg1000mmnacl, 508	-.TVCGVVSK.-	792.97	2	774.30	1.39	0.0	546	11/14	2
jmfag1mnacl7.5minigg,1438-1440	- QCSHHLYTMGQNCQRGQAVDVEPK -	2731.05	3	378.70	2.39	0.0	158	17/92	1
jmlggachnrawphag3007, 1618	-.TLRRLVPDSDVR.-	1427.64	2	179.83	1.41	0.0	126	7/22	2
jmfag5minigg600mmnacl, 1778	-.QSGSENPASEDR.-	1277.24	2	183.99	0.88	0.0	186	4/11	1
rawsucrfp_600phagigg_Mar04, 740	-.LSDEILIDILTRFK.-	1676.98	3	310.50	1.67	0.0	173	1/4	2
rawsucrfp_250phagigg_Mar04, 746	- LSDEILIDILTRFK.-	1676.98	3	1108.67	1.70	0.2	366	17/52	2
rawsucrfp_350phagigg_Mar04, 1018	-.FEKMISGMYLGEIVR.-	1774.14	3	1540.63	2.28	0.1	485	23/58	4
phagrawF200_dec22, 1565	-.LVPDSDVRFLLSESGSGK.-	1907.12	2	41.89	0.99	0.0	42	7/34	2
rawsucrfp_150phagigg_Mar04, 2087	-.CTVSFLLSEDGSGKGAALITAVGVR.-	2452.81	3	482.70	1.28	0.0	364	11/48	2
rawsucrfp_350phagigg_Mar04, 2586	- SANLVAATLGAILNR.-	1484.73	2	213.99	0.75	0.1	167	9/28	2
ajrawmediapbsnocells, 1788	- CTVSFLLSEDGSGKGAALITAVGVRLR.-	2722.16	3	295.33	1.70	0.1	138	9/52	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein kinase JNK2 beta 2 [Mus musculus] lus]					4061.58	4558397.0	12		
jmfag5minigg450mmnacl_030527025134, 866	-.AXEVILGMGYK.-	1194.47	3	517.81	1.62	0.1	154	7/20	
jmraw5minigg500mmnaclsd, 1684	-.SDCTLKILDFGLARTACTNFMMTPYVVTR.-	3269.87	3	654.78	2.29	0.1	183	9/56	6
phagrawFsuc250_dec22, 865	-.MSDSKSDGQFYSVQVADSTFTVLK.-	2641.89	3	1744.75	2.07	0.3	206	5/23	6
phagrawFchlfbead_dec23, 913	-.MSYLLYQMLCGIKHLHSAGIIHR.-	2686.26	3	1079.98	1.86	0.2	292	21/88	16
phagrawFsuc300_dec20, 3732	-.VLFPGRDYIDQWNKVIEQLGTPSAEFMK.-	3283.75	2	64.26	0.90	0.0	71	4/27	3

control

protein kinase JNK2 beta 2 [Mus musculus] lus]					809.69	4558397.0	13		
rawextr_300beadigg_Mar4, 1030	-.DLKPSNIVVK.-	1113.33	2	517.44	1.39	0.0	373	5/9	16
jmraw5minbsafreezthaw, 2458	-.MSDSKSDGQFYSVQVADSTFTVLKR.-	2798.08	3	292.25	1.55	0.0	188	19/96	6

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Wiskott-Aldrich syndrome protein interacting protein; WASP interacting					6762.08	23346579.0	1		
JMFAGNACL10_2B21E3,436-438	- SGPLPPPPSER.-	1134.27	2	820.74	1.17	0.2	205	9/20	
jmfag5miniggbead, 1865	- PVPSSLHNRGSPAGLGAPRPPFPGNR.-	2636.96	3	1045.54	1.55	0.2	357	21/100	
jmfag5minigg200mmnacl, 2286	- PDSLPPPVPNTPR.-	1387.57	2	65.43	0.80	0.0	65	5/24	
JMMAGTube1B16E3, 2294	-.GSPAGLGAPRPPFPGNRGAAFGAGSAR.-	2494.76	3	1293.26	1.78	0.1	695	3/13	
jmrawgg5minbeadsfreezethaw,778-780	-.DNDSGGSRPPILPPGGR.-	1692.82	3	1052.39	1.79	0.2	272	19/64	
jmfag5mincon450mmnacl, 1772	- PDSLPPPVPNTPR.-	1387.57	2	500.44	1.11	0.2	188	1/2	
rawphag2007chfbead2,470-472	- GSPAGLGAPR.-	882.99	2	176.70	1.17	0.0	142	4/9	
phagrawFsucchfbead_dec23, 1628	-.PPVPSTPRPGLGSQAPPPPPPPSR.-	2384.72	3	233.86	1.23	0.1	114	4/23	
phagrawF250_dec22,1719-1721	-.PPFPGNRGAAFGAGSARQNPSGSSSPFPR.-	2873.10	3	229.66	1.87	0.0	122	1/7	
phagrawF200_dec22,2009-2011	-.PPFPGNRGAAFGAGSARQNPSGSSSPFPR.-	2873.10	3	618.33	2.25	0.1	175	19/112	
phagrawFsuc450_dec20, 2694	-.QNPSGSSSPFPR.-	1261.33	2	725.72	1.33	0.2	313	5/11	

control

Wiskott-Aldrich syndrome protein interacting protein; WASP interacting					2551.31	23346579.0	14		
rawextr_150bead_Mar04, 825	-.DNDSGGSRPPILPPGGR.-	1692.82	3	203.42	1.29	0.0	153	1/4	
rawextr_350beadigg2_Mar04, 1064	-.DNDSGGSRPPILPPGGR.-	1692.82	3	481.59	1.81	0.1	240	5/16	
rawextr_200bead_Mar04, 1090	- DNDSGGSRPPILPPGGR -	1692.82	3	488.05	1.69	0.1	88	15/64	
rawextr_60MeOHbead_Mar04, 1542	-.PPFPGNRGAAFGAGSAR.-	1630.79	2	378.95	1.47	0.1	115	9/32	
rawextr_chlfbeadIgG_Mar04, 1592	-.MPVPPPPAPPPPPTFALANTEKPTLNK.-	2821.33	3	413.14	1.65	0.1	224	5/26	
rawextr_1000_beadigg_Mar04, 2067	- QNPSGSSSPFPRPPLPPTPSRALDDK.-	2747.02	2	292.33	0.79	0.2	88	9/50	
jmraw5minbsareebeads, 1068	-.GSPAGLGAPR.-	882.99	2	293.85	1.13	0.0	245	5/9	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
WASP family 1 [Mus musculus]					**3697.82**	13994209.0	7		
jmfag1mnacl0minigg, 634	-.QKNLDRPHEPEK.-	1491.64	2	740.94	1.66	0.1	343	1/2	2
AJRAWActinIgG_june13, 984	-.YAEDIFGELFNEAHSFSFR.-	2280.44	3	979.81	1.69	0.1	377	17/72	2
jmfagcon5minn600mmnacl, 729	-.NIDPRHLCHTALPR.-	1643.90	3	1396.37	1.62	0.0	840	11/26	2
jmfagcon5min1000mmnacl_030601180404, 1084	-.QLSSLSKYAEDIFGELFNEAHSFSFR.-	3024.29	3	152.26	1.01	0.1	110	13/100	2
jmldi500naclrawphag3007, 1315	-.TPVFVSPTSPPPPPPLPSALSTSSLR.-	2631.02	3	428.44	1.32	0.1	174	1/5	

control

WASP family 1 [Mus musculus]					**485.54**	13994209.0	4		
rawextr_actinbead_Mar04, 480	-.KGIQLR.-	714.88	2	268.41	1.06	0.0	252	3/5	2
rawextr_900bead_Mar04,1316-1318	-.PTPTCISSATGLIENRPQSPAAGR.-	2425.71	2	217.23	1.29	0.1	56	4/23	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Wasp-binding protein [Mus musculus]					**3377.69**	37537556.0	9		
JMMAGNEGB16D3, 1520	-.GSSGGYGPGAAALQPK.-	1418.54	1	392.17	1.39	0.0	258	1/3	
jmfag5minigg1000mmnacl, 1702	-.GSSGGYGPGAAALQPK.-	1418.54	2	270.73	1.37	0.0	184	1/3	
jmfag5minigg1000mmnacl, 2078	-.PPPPAREPPSRGAAPPPPPPMIR.-	2383.80	3	408.47	1.37	0.1	227	5/22	
JMFAGNACL15B21E3,2110-2112	-.ASLPELPRMQR.-	1298.54	2	242.48	1.09	0.1	181	2/5	
jmIgG150rawphag3007, 1148	-.SAPVIEKPRGSSGGYGPGAAALQPK.-	2396.69	3	342.33	1.62	0.0	205	3/16	
jmIgG400rawphag3007, 1596	-.GLAPPPPTSATPSLLSNR.-	1777.02	2	358.51	1.22	0.0	293	11/34	
jmfagtimecon2.5min.1826.1826.2	-.EPPSRGAAPPPPPPMIR.-	1768.08	0	301.99	1.07	0.0	276	11/32	
jmfagtimecon5min, 717	-.EKPLPPTPGQR.-	1220.40	2	78.10	0.85	0.0	83	3/10	
jmfagcon5min1000mmnacl_030601180404,1876-1878	-.KTPGPVRGLAPPPPTSATPSLLSNR.-	2512.89	3	564.15	1.89	0.0	286	7/32	
rawsucrfp_chlfphagigg_Mar04, 1370	-.TPAGPPPPPPPPLRNGHR.-	1856.12	2	211.64	1.45	0.1	73	7/34	
RawPhg2007MeEthmeth3digest, 3474	-.AARGAPPLPPILR.-	1329.62	2	62.35	0.70	0.0	89	5/24	
rawsucrfp_actinphagigg_Mar04, 1324	-.PPGSAASGRPHDDTDSNR.-	1837.85	2	144.76	1.04	0.1	67	7/34	

control

Wasp-binding protein [Mus musculus]					**515.28**	37537556.0	10		
FPbeads600_Dec19, 696	-.DAPPPPPPYR.-	1107.24	2	321.47	1.05	0.1	225	4/9	
FPbeads800_Dec19, 2024	-.YSFHPVEDFPAPEEYKHLQR.-	2490.71	2	193.81	1.09	0.1	40	4/19	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
cyclin-dependent kinase inhibitor 1B (P27) [Mus musculus]					**5325.61**	31542372.0	6		
jmIgG400rawphag3007, 1286	-.KWNFDFQNHK.-	1364.49	2	612.31	1.55	0.1	311	4/9	1
JMFAGNACL15B21E3, 2018	-.NLFGPVNHEELTRDLEK.-	2012.21	3	417.84	1.33	0.0	313	17/64	1
jmfag5minigg1000mmnacl, 2368	-.VLAQESQDVSGSRQAVPLIGSQANSEDR.-	2943.13	3	212.01	1.14	0.0	163	4/27	1
jmldi1000naclrawphag3007,1494-1496	-.KWNFDFQNHK.-	1364.49	2	1280.51	1.82	0.0	700	11/18	1
jmldi300naclrawphag3007, 1498	-.KWNFDFQNHK.-	1364.49	2	896.44	1.37	0.2	349	1/2	1
rawsucrfp_800phagigg_Mar04, 1150	-.PPKSACKVLAQESQDVSGSR.-	2088.33	3	317.86	1.37	0.1	193	1/4	1
rawsucrfp_1000phagigg_Mar04, 1211	-.KWNFDFQNHK.-	1364.49	2	1434.66	1.58	0.2	538	5/9	1
phagrawFsuc300_dec20, 2564	-.HLVDQMPDSSDNPAGLAEQCPGMR.-	2569.84	2	154.00	0.90	0.1	60	9/46	

control

cyclin-dependent kinase inhibitor 1B (P27) [Mus musculus]					**207.64**	31542372.0	6		
jmbsa250naclrawphag3007, 893	-.MSNVRVSNGSPSLERMDAR.-	2107.36	3	207.64	1.24	0.0	166	17/72	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
polynucleotide kinase 3'- phosphatase; polynucleotide kinase 3'-phosph					**2972.92**	10946988.0	10		
JMFAGNACL10_1B21E3, 740	-.LQEHLDPALQRLYR.-	1753.00	3	186.58	1.37	0.0	136	1/4	1
jmrawgg5min1mnacl, 951	-.KLLVFTASGVK.-	1163.44	2	2013.28	1.51	0.3	447	11/20	1
jmigg800rawphage3007, 2016	-.LVIFNQMGIGR.-	1248.52	2	169.50	1.13	0.0	140	9/20	
jmldiacinrawphag3007, 2766	-.ARILYPEIPK.-	1200.46	2	277.75	0.84	0.2	67	2/9	
phagrawFsuc400_dec20, 2258	-.CFNFCATEQARHNNR.-	1925.15	2	325.81	1.07	0.1	80	4/15	1

control

polynucleotide kinase 3'- phosphatase; polynucleotide kinase 3'-phosph					**847.96**	10946988.0	5		
rawextr_400beadgg_Mar04, 1698	-.DFSCADRLFALNVGLPFATPEEFFLK.-	2949.37	3	268.17	0.92	0.0	288	9/50	1
rawextr_800beadgg_Mar04, 2322	-.NQVELIADPESRTVAVKQLGVNPSTVGVQELK.-	3420.88	2	159.37	0.87	0.1	115	5/31	
jmraw5minbsaleezthaw, 2064	-.PRARILYPEIPK.-	1453.76	2	392.44	1.00	0.0	394	1/2	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 [Mus					10742.03	21704000.0	20		
jmrawgg5minbeadsyringdnase, 971	- RLNITTEPLTR.-	1314.52	1	380.01	1.36	0.1	132	9/20	1
jmrawgg5min400mmnaclsd,1021-1023	- RLNITTEPLTR.-	1314.52	1	1086.79	1.25	0.3	90	7/20	1
jmfag5minigg200mmnacl, 1052	-.VLPLTPEQALK.-	1209.46	2	178.60	1.00	0.0	168	7/20	1
jmrawgg5min450mmnaclsd,1236-1238	-.RLNITTEPLTR.-	1314.52	1	123.77	1.01	0.0	115	2/5	1
jmfag5minigg1000mmnacl, 1554	-.PSKVLPLTPEQALK.-	1521.83	2	66.68	0.97	0.0	48	3/13	1
jmgg450rawphag3007,1640-1642	-.RLNITTEPLTR.-	1314.52	1	1272.64	1.66	0.2	199	1/2	1
jmIgG150rawphag3007, 1662	- RLNITTEPLTR.-	1314.52	1	65.67	0.96	0.0	64	3/10	1
jmIgG300rawphag3007, 1678	- RLNITTEPLTR.-	1314.52	1	191.57	1.25	0.1	114	2/5	1
jmIgG300rawphag3007, 1684	- RLNITTEPLTR.-	1314.52	1	1848.20	1.49	0.3	146	2/5	1
jmIgG250rawphag3007, 1690	-.RLNITTEPLTR.-	1314.52	1	71.12	0.87	0.0	73	7/20	1
jmIgG400rawphag3007, 1770	-.IIGKGSFGQVARVYDHK.-	1876.15	3	636.96	1.26	0.0	482	9/32	1
jmraw5minigg600mmnaclsd,1816-1818	- RLNITTEPLTR.-	1314.52	1	158.52	1.27	0.0	102	2/5	1
jmfag5minigg450mmnacl_030527025134, 1920	- GLPRYCSVSTQTDGRVVLLGGR.-	2335.67	3	732.04	1.61	0.1	389	19/84	1
jmIgG1000naclrawphag3007,2036-2038	- RLNITTEPLTR.-	1314.52	1	425.48	1.28	0.2	105	2/5	1
jmIgG250rawphag3007, 3632	- LNITTEPLTRGHTQHFVNGSEMK.-	2611.92	2	59.15	0.79	0.0	52	3/22	1
jmidl150naclrawphag3007,914-916	- KDAALPGAGLPPQQR.-	1519.73	3	389.80	1.38	0.1	235	9/28	
jmidl400firstnaclrawphag3007,1622-1624	- RLNITTEPLTR.-	1314.52	1	318.69	1.13	0.1	251	1/2	1
jmidl300naclrawphag3007,1832-1834	- RLNITTEPLTR.-	1314.52	2	510.82	1.30	0.0	392	11/20	1
jmidl300naclrawphag3007, 1836	- RLNITTEPLTR.-	1314.52	1	218.62	1.30	0.1	129	9/20	1
jmidl300naclrawphag3007, 1840	- RLNITTEPLTR.-	1314.52	1	520.20	1.08	0.2	183	2/5	1
phagrawF400_dec20, 1132	-.RLNITTEPLTR.-	1314.52	1	99.24	0.85	0.1	90	2/5	1
rawsucrfp_500phagigg_Mar04, 1222	- RLNITTEPLTR.-	1314.52	2	311.12	1.07	0.0	279	9/20	1
rawsucrfp_actinphagigg_Mar04, 1242	-.RLNITTEPLTR.-	1314.52	1	146.34	0.89	0.1	134	9/20	1
phagrawFsuc200_dec22, 1243	-.RLNITTEPLTR.-	1314.52	1	464.31	1.18	0.2	56	3/10	1
rawsucrfp_800phagigg_Mar04, 1318	-.IIGKGSFGQVARVYDHK.-	1876.15	2	353.76	1.15	0.0	291	3/8	1
phagrawF300_dec20,1339-1341	- RLNITTEPLTR.-	1314.52	1	203.84	1.41	0.1	82	7/20	1
rawsucrfp_450phagigg_Mar04, 2218	-.SNTLQSDGISNSEKSSPASQGKSSESLSAVK.-	3112.26	2	108.29	1.02	0.1	61	3/20	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 [Mus					6764.05	21704000.0	7		
FPbeads150_Dec19, 1223	- RLNITTEPLTR.-	1314.52	2	738.94	1.21	0.2	234	2/5	1
FPbeads150_Dec19, 1225	- RLNITTEPLTR.-	1314.52	1	165.09	1.11	0.0	146	9/20	1
rawextr_300beadigg_Mar4, 2838	-.RGPPGSKDWATALK.-	1484.69	2	132.54	0.90	0.0	146	4/13	1
jmbsa250naclrawphag3007,1045-1047	- RLNITTEPLTR.-	1314.52	1	1610.62	1.65	0.3	213	11/20	1
jmbsa400naclrawphag3007_030802135631,1053-1055	- RLNITTEPLTR.-	1314.52	1	1920.53	1.68	0.3	149	9/20	1
jmbsa350naclrawphag3007,1059-1061	- RLNITTEPLTR.-	1314.52	2	207.73	1.13	0.1	147	3/10	1
jmbsa350naclrawphag3007,1067-1073	- RLNITTEPLTR.-	1314.52	1	189.87	1.82	0.0	104	2/5	1
jmbsa500naclrawphag3007, 1114	- RLNITTEPLTR.-	1314.52	1	396.34	1.32	0.1	212	1/2	1
jmbsa150naclrawphag3007,1257-1259	-.RLNITTEPLTR.-	1314.52	1	294.62	1.13	0.0	261	11/20	1
jmbsa300naclrawphag3007,1286-1288	- RLNITTEPLTR.-	1314.52	1	159.19	1.19	0.0	117	9/20	1
jmbsa1000naclrawphag3007,1805-1807	- RLNITTEPLTR.-	1314.52	1	689.53	1.41	0.2	125	2/5	1
jmraw5minbsalfreezthaw, 1966	- RVVNPTNAFQGLGSKLPPVVGIASK.-	2550.99	3	259.05	1.94	0.0	133	1/6	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
mKIAA0617 protein [Mus musculus] e 5-kinase; phos					2613.07	39104526.0	18		
JMFAGNACL10_1B21E3, 320	-.FLPSPVVIKKR.-	1284.62	3	433.34	1.35	0.0	309	7/20	2
jmigg450rawphag3007, 1138	-.CNIPPAPR.-	868.04	1	78.29	0.82	0.0	91	3/7	1
jmfag5minigg200mmnacl,1236-1238	-.IRAFPMTMDEK.-	1339.61	2	1420.87	1.68	0.2	224	9/20	1
jmfag1mnacl2,5minigg, 2092	-.NPVDYIQGLLDLK.-	1488.71	2	329.56	1.13	0.0	282	1/2	1
jmrawigg5min300mmnacleyringednase, 2795	-.LEGMFR.-	752.91	1	166.89	0.90	0.1	105	1/2	7
jmraw5minigg600mmnaclsd, 3002	-.FYLAKHSGRQLTLQHHMGSADLNATFYGPVK.-	3489.95	2	184.12	0.82	0.1	35	7/60	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
NIMA-related expressed kinase 9 [Mus musculus]					3488.76	21553095.0	22		
jmfag5minigg350mmnacl, 1319	-.PRSSTVTEAPIAVVTSR.-	1772.00	3	1379.38	1.87	0.2	498	9/32	
jmIgG300rawphag3007, 1336	-.LEGGQQVGMHSR.-	1299.44	2	441.66	1.49	0.0	291	5/11	1
jmrawgg5minbeadsfreezethaw, 1496	-.HCDSINSDFGSESGGGGDSGPGPSAVPGPR.-	2801.86	3	427.63	1.64	0.1	198	17/116	
JMFAGNACL10_2B21E3, 1978	-.ALTSAACACSALQVEVDR.-	1809.06	2	552.05	1.18	0.1	420	13/34	1
jmIgG500rawphag3007, 2211	-.LDPAVPCVGKALTSAACACSALQVEVDR.-	2789.25	3	568.39	1.70	0.1	230	5/27	1
phagrawFsuc250_dec22, 1709	-.TFDATNPLNLCVK.-	1436.66	2	119.64	0.91	0.0	131	1/3	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
NIMA-related expressed kinase 9 [Mus musculus]					672.83	21553095.0	9		
rawextr_actinbeadigg_Mar04, 1375	-.EVDLTRLSEKER.-	1475.63	2	423.37	1.08	0.1	357	9/22	
rawextr_700beadigg_Mar04, 2020	-.LDVIKSGCSARQVCAGNTHFAVVTVEK.-	2834.27	2	52.40	0.98	0.0	37	7/52	
jmbsa150naclrawphag3007, 1697	-.PDLDSESWCLLGTDSCR.-	1898.06	2	197.05	1.20	0.1	134	9/32	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
unnamed protein product [Mus musculus] kinase 14					4030.70	26338994.0	17		
jmfagfrench20minigg1mnacldtt, 942	-.WIFSKFSSSAKDEVK.-	1759.98	3	1635.36	1.52	0.2	598	19/56	2
AJRAWActinIgG_june13,1072-1074	-.QEGACCLGLLCASLSYEAEK.-	2089.40	3	971.80	2.29	0.0	423	21/76	2
jmfag1mnacl7,5minigg, 1778	-.HDDTRGHADIQNDEK.-	1751.75	2	223.56	1.34	0.0	166	2/7	2
phagrawF350_dec20, 792	-.KIPEPTGK.-	870.03	2	593.27	1.28	0.0	440	9/14	
rawsucrfp_350phagigg_Mar04, 966	-.KIPEPTGK.-	870.03	2	606.71	1.34	0.0	452	5/7	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
polo-like kinase 2; serum-inducible kinase [Mus musculus]					**2759.74**	22779889.0	21		
jmfag5minigg600mmnacl, 914	-.SGTSAVENKQQIGDAIRMIVR.-	2274.59	3	533.14	1.47	0.0	344	9/40	1
ajrawphagjun20actinDPI, 1430	-.VSITQQPSKHR -	1281.45	3	651.34	1.01	0.2	418	2/5	1
ajrawphagjun20actinDPI, 1754	-.MCEQALGKACGGDSKK.-	1626.91	2	426.26	0.96	0.2	183	1/3	1
JMFAGNACL15B21E3, 2018	- YYLRQIVSGLK -	1340.60	2	253.95	1.16	0.1	129	7/20	1
jmfag1mnacl5minigg,2132-2134	- ARKVLTEPEVR -	1298.52	2	156.60	1.16	0.0	133	3/10	1
jmfag5minigg1000mmnacl, 2920	- GTLGSCSSSSECLEDSTMGSVADTVARVLR -	3020.32	2	124.22	1.05	0.0	109	5/29	1
rawsucrfp_400phagigg_Mar04,1227-1229	- IIPHSRVAKPHQR -	1539.81	2	396.26	1.44	0.0	250	3/8	1
ajrawmediapbsnocells, 1426	-.VSITQQPSKHR -	1281.45	3	217.96	0.82	0.0	266	13/40	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Falz protein [Mus musculus] t kinase 6 [Mus muscul					**3838.83**	27370657.0	19		
ajrawphagjun20actinDPI,494-496	-.LEKSNGEVSESPGAGK.-	1589.69	2	674.44	1.73	0.1	214	1/3	2
jmrawigg5min350mmnaclsynngednase, 687	-.SPEGCLSETHDSSSMAEKK.-	2024.18	3	327.49	1.15	0.0	283	19/72	1
jmfag1mnacl2,5minigg, 1082	-.DAEKSREEAEDPSADK.-	1777.78	3	591.76	1.35	0.0	433	7/20	2
jmIgG350naclrawphag3007, 1173	-.EFALALAILECAVK.-	1491.82	3	614.12	1.38	0.1	336	19/52	2
ajrawphag1MNaCl20,1292-1294	-.PREFALALAILECAVK.-	1745.12	3	482.05	1.41	0.0	331	17/60	2
jmIgG400rawphag3007, 1394	-.GTSGSTRIITR.-	1149.28	2	273.58	1.25	0.0	213	9/20	2
jmfag5minigg1000mmnacl, 2094	-.EGKEVLVVNSQGEVSRLSTK.-	2160.42	3	624.18	1.17	0.2	237	15/76	2
jmfag5minigg300mmnacl, 2640	-.GYWEAELCRVLEDIR.-	1853.09	2	161.62	0.89	0.0	179	2/7	2
jmfag5minigg450mmnacl_030527025134, 3306	-.VYHNQYSTNSFALNKHQHREDHDK.-	2970.13	2	89.59	1.27	0.0	68	4/23	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
adenylate kinase 2 [Mus musculus]					**2709.93**	34328230.0	5		
JMFAGNACL5B21E3, 866	-.TRLEAYHTQTTPLVEYYR.-	2242.48	3	2072.77	2.41	0.2	595	23/68	1
rawsucrfp_800phagigg_Mar04, 660	-.ITGRLIHPKSGR.-	1335.58	3	148.98	1.28	0.0	117	13/44	1
ajrawmediapbsnocells, 1022	-.LIHPKSGRSYHEEFNPPK.-	2137.39	3	488.18	1.35	0.0	362	4/17	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
vaccinia related kinase 2; vaccinia virus BIR kinase related kinase 2					**2791.14**	21312468.0	11		
JMFAGNACL15B21E3, 152	-.AANLLLDFTNPDR.-	1460.62	3	672.20	1.55	0.1	391	17/48	2
jmrawigg5min450mmnaclsd, 786	-.VYLADYGLSYR.-	1320.48	2	122.50	0.90	0.0	122	3/10	2
jmfag5minigg500mmnacl, 1588	-.LDYLGIPVFYGFGLTDFKGR.-	2279.62	3	86.65	1.19	0.0	69	7/38	4
jmfag5minigg150mmnacl, 2148	-.LPWEAKLDDPVAVQTAK.-	1882.15	1	674.31	1.05	0.2	184	5/16	2
ajrawmediapbsnocells, 472	-.LDDPVAVQTAK.-	1157.30	2	623.57	1.49	0.1	266	9/20	2
ajrawmediapbsnocells, 1622	-.AANLLLDFTNPDRVYLADYGLSYR.-	2762.07	3	611.91	1.55	0.1	249	5/23	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
vaccinia related kinase 2; vaccinia virus BIR kinase related kinase 2					**976.25**	21312468.0	11		
jmbsa1000naclrawphag3007, 1091	-.TPAQQKVDSPKATR.-	1527.71	3	891.64	1.43	0.0	623	19/52	1
jmbsa500naclrawphag3007,1351-1353	-.FMVMERLGIDLQKLLDQNGGFK.-	2554.03	2	84.61	1.16	0.0	73	5/21	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
unnamed protein product [Mus musculus] nase PAK 6					**24988.60**	26337801.0	6		
phagrawF500_dec20, 1488	-.DSCGPDPGVRGLR.-	1329.47	2	613.70	0.93	0.2	207	3/8	
phagrawFsuc200_dec22, 1827	-.TELGSFFTEYLQNQLLTKGMVILR.-	2803.27	3	233.51	1.13	0.1	107	7/46	3
jmrawigg5min150mmnacl, 330	-.GTAKANVGAGK.-	974.10	2	594.05	1.21	0.1	462	11/20	9
jmfag1mnacl5minigg, 1098	-.QMVIDVLHPGK.-	1237.50	2	1214.64	1.30	0.2	356	9/20	10
ajrawphagjun20dpi1MNaCl, 1136	-.QMVIDVLHPGKATVPK.-	1734.10	2	397.35	1.27	0.0	310	11/30	9
jmfag5minigg350mmnacl, 1375	-.TTGFGMIYDSLDYAK.-	1682.88	2	13442.36	3.37	0.6	824	17/28	8
jmfag5minigg400mmnacl, 1542	-.TTGFGMIYDSLDYAK.-	1682.88	2	6611.32	2.58	0.5	333	13/28	8
jmfag5minigg200mmnacl, 1628	-.TTGFGMIYDSLDYAK.-	1682.88	2	1607.01	1.69	0.2	644	15/28	8
jmfagtimecon7.5min.2160.2160.2	-.YLIESSKEMTPLK.-	1539.82	0	138.40	1.18	0.0	92	3/8	
jmfag5mincont350, 1542	-.YLIESSKEMTPLK.-	1539.82	2	138.26	1.05	0.1	101	1/3	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to protein kinase nek1 (EC 2.7.1.-) - mouse [Rattus norvegicus					**4832.71**	34878053.0	14		
jmfag5minigg150mmnacl, 236	-.AEDNEAR.-	804.79	2	743.30	1.47	0.1	481	2/3	1
jmfag5minigg400mmnacl, 381	-.DRPSVNSILEK.-	1258.41	2	327.51	0.89	0.1	207	7/20	3
JMFAGNACL15B21E3, 534	-.EEEVYLAR.-	1009.10	2	403.55	1.31	0.0	306	4/7	
jmfag5minigg350mmnacl, 655	-.PASGQGVSSFVPAQKITK.-	1803.05	3	725.92	1.23	0.1	426	21/68	2
jmrawigg5min350mmnaclsyringednase, 1253	-.DGTVQLGDFGIARVLNSTVELAR.-	2432.72	3	340.23	1.38	0.0	232	17/88	3
jmfag5minigg300mmnacl, 1972	- PASGQGVSSFVPAQK.-	1460.62	2	216.68	0.85	0.1	224	5/14	2
jmldl60MeOHrawphag3007, 1842	- PSVNSILEKGFIAKR.-	1659.96	2	219.39	0.89	0.1	117	1/4	3
rawsucrfp_450phagigg_Mar04, 1304	-.PSSSRGGKPR.-	1029.14	1	220.31	0.88	0.1	206	4/9	
phagrawF150_dec22, 1568	-.REVAVLANMKHPNIVQYK.-	2111.50	2	606.44	1.07	0.2	178	9/34	3
jmrawbas5min1mnacl, 1214	-.PSVNSILEKGFIAK.-	1503.77	3	1029.38	1.63	0.1	567	19/52	3

control

similar to protein kinase nek1 (EC 2.7.1.-) - mouse [Rattus norvegicus					**245.18**	34878053.0	10		
FPbeads600_Dec19, 950	- EINISRMSDKER.-	1478.66	3	245.18	1.00	0.0	228	3/11	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
DnaJ (Hsp40) homolog, subfamily C, member 3; protein kinase, interfero					**4479.39**	31542563.0	17		
jmfag5minigg150mmnacl, 360	-.LIESAEELIRDGR.-	1501.67	3	846.61	1.57	0.1	510	19/48	
JMFAGNACL15B21E3, 776	-.VIALKMDFTAAR.-	1336.63	3	1028.56	1.53	0.2	442	17/44	
jmrawrminigg200mmnaclsyringdnas, 912	-.QGKLDEAEDDFKK.-	1523.63	3	455.84	1.10	0.0	410	3/8	
jm5miniggrawlowionic, 934	-.AALPDLTKVIALK.-	1353.68	3	1408.78	1.38	0.1	921	19/48	
jmfag5minigg600mmnacl, 950	-.ERICHCFSKDEK.-	1495.71	2	189.75	0.90	0.0	211	4/11	
jmIgG350naclrawphag3007, 1173	-.GHLLLKQGK.-	994.22	2	549.85	1.37	0.0	394	5/8	

control

DnaJ (Hsp40) homolog, subfamily C, member 3; protein kinase, interfero					**467.85**	31542563.0	6		
rawextr_700beadigg_Mar04, 682	-.EVLSDPEMR.-	1076.21	3	467.85	1.59	0.1	252	3/8	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
sterile-alpha motif and leucine zipper containing kinase AZK; MLK-like					**4723.55**	30017393.0	2		
jmrawigg5minbeadsfreezethaw, 1122	-.EVPFKGLEGLQVAWLVVEK.-	2142.53	3	1317.73	1.82	0.2	351	23/72	
jmfagtrench5minigg1mnacldtt,287-289	-.GSVSLNSSPK.-	976.07	2	2008.32	2.47	0.1	740	13/18	
ajrawphagjun20actinDPI, 748	-.GSVSLNSSPKGRYGGK.-	1594.76	3	915.10	1.63	0.2	111	1/4	
jm5miniggrawlowionic, 1776	- IVNLELVFGFHLK.-	1529.85	2	101.18	1.04	0.0	86	7/24	
jmfag5minigg350mmnacl, 2451	-.TQTPVKYQQITPSINPSRSSSPTQYGLSR.-	3223.54	2	152.68	0.96	0.1	46	3/28	
ajrawphagactin20, 2676	-.PGTGPQDCK.-	903.00	2	228.54	0.84	0.1	239	1/2	

control

sterile-alpha motif and leucine zipper containing kinase AZK; MLK-like					**1712.06**	30017393.0	3		
rawextr_150beadigg2_Mar04, 128	- SRNVVIAADGVLK.-	1342.57	2	875.26	1.50	0.1	508	7/12	2
rawextr_1000_beadigg_Mar04, 1196	- MSSLGASFVQIK.-	1268.51	2	213.57	1.19	0.0	160	4/11	2
FPbeads500_dec19, 1562	-.LLLLEEEDLKDMGIVSK.-	1946.30	3	388.76	1.34	0.1	150	11/64	
rawextr_500beadigg_Mar04, 2287	-.LPQSALNTHQSPDFK.-	1683.85	2	234.47	1.07	0.0	218	9/28	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
choline/ethanolamine kinase [Mus musculus]					**3100.60**	6671748.0	8		
ajrawphagjun20dpi1MNaCl, 412	-.GEILSEEEQKK.-	1290.40	3	499.80	1.51	0.1	157	3/10	
jmfag5minigg350mmnacl, 783	-.CPEPIPNRRR.-	1238.45	2	496.95	1.06	0.2	233	4/9	
ajrawphagactin20, 1096	-.HYLAEVQKGEILSEEEQKK.-	2259.50	3	753.28	1.84	0.0	387	1/4	
phagrawF150_dec22,1744-1746	-.PTDYPTREQQLHFIRHYLAEVQK.-	2871.20	2	461.78	1.70	0.1	167	13/44	
phagrawFsuc60MeOH_dec23, 1924	-.PTDYPTREQQLHFIRHYLAEVQK.-	2871.20	2	169.72	1.01	0.0	158	3/11	
phagrawF300_dec20, 2019	-.PTDYPTREQQLHFIRHYLAEVQK.-	2871.20	2	338.68	1.32	0.1	65	2/11	
phagrawFsuc300_dec20, 2484	-.YLKQIQDLPSTSLPQMNLVEMYSLK.-	2941.46	2	380.40	1.08	0.2	87	3/16	

control

choline/ethanolamine kinase [Mus musculus]					**1151.63**	6671748.0	6		
rawextr_250beadigg_Mar04, 1690	-.DPVLSGAIATRMARFHGMEMPFTK.-	2665.16	3	864.25	1.78	0.1	433	21/92	
jmraw5minbsabeads, 1260	-.GEILSEEEQKK.-	1290.40	3	287.38	1.12	0.1	79	9/40	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phosphorylase kinase alpha 2 [Mus musculus]					**4071.07**	27370156.0	17		
jmfagfrench20minigg1mnackdlt, 462	-.QLTVGLPPEPR.-	1207.41	3	609.43	1.56	0.0	378	17/40	1
jmrawigg5min150mmnacl,1030-1032	-.DILSVMAKAK.-	1076.34	2	381.23	1.19	0.1	294	5/9	1
jmfag1mnacl0minigg, 1198	-.TNQGIPELNASSVGVAK.-	1685.86	2	142.51	1.15	0.0	122	9/32	2
jmfag5minigg600mmnacl, 2884	-.SLNCSGKEASESLMNLSPFDMKSLLHHILSGK.-	3476.01	2	21.41	0.79	0.0	27	7/62	1
jmigg450rawphag3007, 2968	-.AKAYELEQNVVK.-	1392.58	2	275.64	1.29	0.1	95	7/22	3
jmrawigg5miniggfreebead, 794	-.LDGYARLVQQTILCYQNPVTGLLSASHDQK.-	3333.76	2	39.72	0.84	0.1	18	5/58	3
jmldl600naclrawphag3007, 2606	-.PIHSSMSSPAISIHEVGHTGATKTERSGITR.-	3246.61	3	126.45	1.43	0.0	80	13/120	1
phagrawF350_dec20, 273	-.HIGVLGTSKLYVIR.-	1556.88	3	394.17	1.57	0.0	239	1/4	2
phagrawFsuc200_dec22,865-867	-.DGIHLVPELYAIPPDKVDEEYK.-	2541.84	3	498.47	1.47	0.1	306	17/84	2
rawsucrfp_60MeOHphagigg_MAr04, 1238	-.VDEEYKNPHTVDRVPLGK.-	2097.32	3	727.06	1.73	0.0	398	1/4	2
phagrawFsuc350_dec20, 1842	-.SLNCSGKEASESLMNLSPFDMK.-	2389.71	3	349.93	1.43	0.1	156	1/6	1
rawsucrfp_350phagigg_Mar04, 2010	-.PIHSSMSSPAISIHEVGHTGATKTERSGITR.-	3246.61	3	505.05	1.45	0.1	240	23/120	1

control

phosphorylase kinase alpha 2 [Mus musculus]					**248.02**	27370156.0	11		
FPbeads400_Dec19, 2822	-.GLLKEHGMTVQSIADVHPIRVQPGR.-	2740.18	2	95.19	0.90	0.0	96	3/16	2
jmbsa150naclrawphag3007,1063-1065	-.DILSVMAKAK.-	1076.34	2	152.83	0.98	0.1	84	1/3	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ProSAPiP2 protein [Mus musculus]					**4760.12**	37674212.0	16		
JMFAGNACL10_1B21E3, 624	-.ELSSLQGR.-	889.98	2	228.39	1.31	0.0	173	9/14	
jmrawrminigg200mmnaclsyringdnas, 1244	-.SPVPPSCQSPSPQR.-	1467.63	2	413.93	1.06	0.1	305	11/26	
jmIgG150rawphag3007, 1462	-.SCPLCQLGFPVGYPDDALIK.-	2137.51	3	747.64	1.23	0.1	409	5/19	
jmigg600rawphage3007, 2128	-.SPVPPSCPAPQPRPPPPPGER.-	2161.47	2	70.87	1.00	0.0	54	7/40	
jmbeadsactinrawphag3007, 425	-.LGGLERENATLR.-	1329.49	3	1157.32	1.87	0.1	542	9/22	
jmbeads350rawphag30072nd, 1156	-.SPASPSCPSPVPQRR.-	1566.77	2	252.49	1.13	0.0	218	5/14	
jmbeads150rawphag3007, 1984	-.HIDSHLENSKI.-	1293.41	1	438.65	1.18	0.1	245	9/20	
RawPhag200760MeBeadsdigest,1340-1342	-.RSPASPSCPSPVPQRR.-	1722.96	3	280.05	1.46	0.0	188	4/15	
rawsucrfp_60MeOHphagigg_MAr04, 1910	-.PPPCAPCPSPQQRRSPASPSCPSPVPQR.-	2926.35	3	292.45	1.35	0.1	130	17/108	
jmldl1000naclrawphag3007, 1754	-.HSPAPACPSPSPPAR.-	1472.66	2	93.34	0.82	0.0	113	1/4	
phagrawFsuc250_dec22, 1273	-.VSLQQRLNQFQHELQKSK.-	2212.50	3	492.54	1.52	0.1	221	7/34	
rawsucrfp_60MeOHphagigg_MAr04, 1910	-.PPPCAPCPSPQQRRSPASPSCPSPVPQR.-	2926.35	3	292.45	1.35	0.1	130	17/108	

control

ProSAPiP2 protein [Mus musculus]					**1249.96**	37674212.0	18		
rawextr_200bead_Mar04, 846	-.ILRTLLQEQARNAGQR.-	1868.14	3	871.99	1.78	0.1	328	3/10	
rawextr_450beadigg_Mar04, 1366	-.HSPLSQRHSPAPACPSPSPPAR.-	2278.54	2	108.99	0.85	0.0	128	3/14	
rawextr_500bead_Mar04, 2158	-.SPVPPSCPAPQPRPPPPPGER.-	2161.47	2	180.66	1.27	0.1	97	9/40	
FPbeads500_dec19, 2730	-.SPVPPSCPAPQPRPPPPPGER.-	2161.47	2	88.32	1.06	0.0	83	9/40	

APPENDIX B – LIPASE SUMMATION OF IONS

The summation of peptides from Lipases found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PA2Z_MOUSE Group XIII secretory phospholipase A2 precursor (Phosphatidylcholi					**4658.97**	20178006.0	4		
jmfag5minigg150mmnacl, 426	- WCLHSICSDLK.-	1305.55	3	722.42	1.58	0.1	379	3/8	1
jmfag5minigg150mmnacl, 432	-.WCLHSICSDLK. -	1305.55	3	1359.26	1.93	0.1	623	9/20	1
JMFAGNACL10_2B21E3, 1448	- QLRGSFESVNSYVDSFMELLGGK.-	2564.86	3	702.79	1.53	0.1	367	19/88	1
ajrawphag1MNaCl20, 1548	- APMPRPGYK.-	1017.23	2	172.25	1.11	0.0	155	3/8	1
jmbeads250rawphag3007, 1662	-.QLRGSFESVNSYVDSFMELLGGK.-	2564.86	3	131.35	1.27	0.1	57	13/88	1
jmkdlactmrawphag3007, 1576	-.RAELSYAFYGCHCGLGGKGSPK.-	2302.62	3	468.98	1.84	0.0	238	19/84	1
phagrawFchfbead_dec23, 1471	- MKLLCGFFLLWLGLVGNLAQSDPSPK -	2849.45	3	934.69	1.62	0.2	322	21/100	1
phagrawF150_dec22, 1508	- MKLLCGFFLLWLGLVGNLAQSDPSPK.-	2849.45	3	167.33	1.12	0.0	147	3/20	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PA2Z_MOUSE Group XIII secretory phospholipase A2 precursor (Phosphatidylcholi					**248.68**	20178006.0	2		
rawextr_400bead_Mar04, 1391	-.PFMNSQRAACICAEEEKEEL.-	2299.59	3	248.68	1.14	0.0	209	15/76	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase A2, group IB, pancreas, receptor; PLA2-I receptor [Mus mu					**2675.25**	6679365.0	2		
jmraw5minbsabeads, 2038	-.VVKEVWIGLNQLDEK.-	1771.05	2	966.74	1.38	0.2	203	9/28	1
jmrawf5minbsareebeads, 2896	-.QIHRWIAYTSSGGDICEHPSRDLYTLK -	3148.50	2	130.41	0.81	0.1	42	3/26	1
JMFAGNACL15B21E3, 348	-.HGRFCYK.-	911.07	2	345.18	1.07	0.0	299	2/3	1
jmfag1mnacl7.5minigg, 858	-.KMIEGPLQYKVQVK.-	1662.03	3	455.61	1.62	0.1	176	9/26	1
ajrawphagjun20dpi1MNaCl, 1084	- WIAYTSSGGDICEHPSR.-	1880.03	3	312.83	1.39	0.1	178	15/64	1
ajrawphagjun20actinDPI, 1230	-.VQVKSDNTVVAR.-	1316.49	2	170.64	0.89	0.1	150	7/22	1
ajrawphagjun20dpi1MNaCl, 1874	- AGQVPADEQSGCPAGWERHGR.-	2209.35	3	236.35	1.11	0.1	164	17/80	1
jmrawigg5minbeadsyringdnase, 2659	-.IPVSFEWSSGSSVIFTNWYPLEPR.-	2800.12	2	57.48	0.84	0.0	46	7/46	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase A2, group IB, pancreas, receptor; PLA2-I receptor [Mus mu					**918.13**	6679365.0	16		
rawextr_150bead_Mar04, 1447	-.DQIQWSNGSPVIFQNWDK -	2163.34	3	422.24	1.28	0.1	158	15/68	
rawextr_150bead_Mar04, 1499	-.DQIQWSNGSPVIFQNWDK.-	2163.34	3	392.59	1.27	0.0	305	1/4	
FPbeads150_Dec19, 2397	-.WEVKDCSDFKAMSLCK.-	1891.23	2	103.30	1.01	0.0	60	7/30	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase A2, group VI; 85 kDa calcium-independent phospholipase A2					**15926.97**	8393978.0	2		
jmkdl250nacirawphag3007, 900	- PKVMLTGTLSDR.-	1318.57	3	708.12	1.64	0.1	397	15/44	2
jmkdl150nacirawphag3007, 1022	- PKVMLTGTLSDR.-	1318.57	3	499.58	1.49	0.0	327	7/22	2
jmkdl250nacirawphag3007, 1270	-.KPAFILSSMR.-	1150.42	2	230.22	1.05	0.0	197	1/2	2
rawsucrfp_800phagigg_Mar04,914-916	-.GCDVDSTSSSGNTALHVAVMRNR.-	2378.59	3	516.09	2.13	0.0	237	5/22	2
rawsucrfp_450phagigg_Mar04, 978	-.MVVDCCTDPDGRAVDR.-	1752.98	2	112.69	1.24	0.0	88	4/15	2
rawsucrfp_600phagigg_Mar04, 1022	-.GCDVDSTSSSGNTALHVAVMRNR.-	2378.59	3	679.58	1.72	0.1	243	21/88	2
rawsucrfp_450phagigg_Mar04,1038-1038	-.GCDVDSTSSSGNTALHVAVMRNR.-	2378.59	3	364.09	1.93	0.0	177	17/88	2
rawsucrfp_1000phagigg_Mar04,1141-1143	-.GCDVDSTSSSGNTALHVAVMRNR.-	2378.59	3	853.75	2.16	0.1	277	23/88	2
rawsucrfp_800phagigg_Mar04, 1504	-.SMAYMRGVYFRMK.-	1641.02	2	281.17	0.87	0.1	191	1/3	2
JMFAGNACL10_2B21E3, 766	- EEGQLILLQNVSNR.-	1613.80	3	742.37	1.62	0.0	455	17/52	2
jmrawigg5min350mmnaclsyringednase, 933	-.PKVMLTGTLSDRQPAELHLFR.-	2410.83	3	785.01	1.45	0.0	542	11/40	2
JMFAGNACL5B21E3,950-952	-.ISKQLQDLMPISRAR.-	1757.10	3	868.41	1.82	0.0	365	5/14	1
jmfag1mnacl5minigg, 1110	-.ISKQLQDLMPISRAR.-	1757.10	3	817.62	1.80	0.1	359	9/28	1
jmrawigg5minbeadstreszethaw, 1212	-.ISKQLQDLMPISRAR.-	1757.10	3	1958.87	1.91	0.3	244	2/7	1
jmfag5minigg150mmnacl, 1214	-.ISKQLQDLMPISRAR.-	1757.10	3	643.22	1.55	0.0	401	19/56	1
jmfag5minigg200mmnacl,1364-1366	-.ISKQLQDLMPISRAR.-	1757.10	3	959.88	1.73	0.1	481	3/8	1
jmfag5minigg400mmnacl, 2856	-.KPAFILSSMR.-	1150.42	2	318.14	0.96	0.1	217	7/18	2
jmag5mincon500mmnacl, 3596	-.ASGVATKDLFDWVAGTSTGGILALAILHSK -	3001.43	2	204.39	1.11	0.1	83	4/29	
jmfagtmecon7 5min,1514,1514.3	-.ISKQLQDLMPISRAR.-	1757.10	0	837.28	1.75	0.1	341	5/14	1
jmfag5mincont400_030531151834, 480	- ELGKMVVDCCTDPDGR.-	1738.99	3	298.59	1.43	0.0	209	4/15	2
jmfag5mincont200mmnacl, 1364	-.ISKQLQDLMPISRAR.-	1757.10	3	1295.02	1.63	0.0	786	23/56	1
jmfag5mincont200mmnacl, 1366	-.ISKQLQDLMPISRAR.-	1757.10	3	434.19	1.57	0.0	271	17/56	1
jmfag5mincon450mmnacl,1714-1716	-.ISKQLQDLMPISRAR.-	1757.10	3	901.34	2.19	0.0	411	17/56	1
jmfagcont5minbead, 1776	-.ISKQLQDLMPISRAR.-	1757.10	3	404.73	1.25	0.0	323	17/56	1
jmag5mincon500mmnacl, 3598	-.ASGVATKDLFDWVAGTSTGGILALAILHSK.-	3001.43	2	204.39	1.11	0.1	83	4/29	2
RawPhg2007MeEthmeth3digest, 1760	-.YGASPLHWAKNAEMARMLLK.-	2288.73	3	399.33	1.43	0.1	251	9/38	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase A2, group VI; 85 kDa calcium-independent phospholipase A2					**991.79**	8393978.0	14		
rawextr_1000bead_Mar04, 748	-.KPAFILSSMR.-	1150.42	2	197.38	1.03	0.0	191	7/18	2
rawextr_400beadigg_Mar04, 1270	-.YGASPLHWAKNAEMARMLLK.-	2288.73	2	210.53	1.51	0.1	100	9/38	2
jmfreebeadsrawphag3007, 1112	-.ISKQLQDLMPISRAR.-	1757.10	3	583.88	1.45	0.1	331	2/7	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Calcium-dependent phospholipase A2 precursor (Phosphatidylc					**2404.52**	38079191 0	2		
jmidichlfsolblerawphag3007, 2256	- HQVGSCVASIGYLSLSFR -	1925 20	2	187.61	0 93	0 1	111	7/34	
phagrawFsuc250_dec22, 809	- PGYEGLKK -	892 04	2	197 03	0 97	0 1	91	1/2	
phagrawFsuc150_dec22, 1346	- NYGFYGCYCGWGGRGTPKDGTDW.-	2561 75	2	217 08	0 85	0 1	55	3/22	
phagrawF400_dec20, 1528	-.PSLEPGGVRTGLGSDNLR.-	1826.01	2	167 12	1 35	0 0	123	9/34	
phagrawFsuc800_dec23, 1738	-.HQVGSCVASIGYLSLSFR.-	1925 20	2	1635 69	1 42	0 3	169	11/34	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase A2, group IVB (cytosolic) [Mus musculus]					**4523.75**	38075595.0	8		
jmfag5minigg400mmnacl, 1074	-.RALQEFPAAAR.-	1230.40	2	1150.10	1.46	0.2	206	2/5	
jmraw5minigg500mmnaclsd,1380-1382	-.YSYFQLMDTLTRATGLD -	1996.23	3	214.45	1.29	0.1	120	13/64	
rawphag2007chfbead3, 1047	-.RALQEFPAAAR.-	1230 40	2	406.62	1.51	0.0	247	1/2	
phagrawF400_dec20, 644	-.RALQEFPAAAR.-	1230.40	2	63.56	0.92	0.0	68	1/4	
jmbeads150rawphag3007, 1850	-.RALQEFPAAAR.-	1230.40	2	176.52	0.97	0 1	117	3/10	
jmrawigg5min1mnacl, 347	-.QVVAAALK -	799.98	2	265.33	1.19	0.0	222	4/7	
ajrawphag1MNaCl20, 1520	-.EAMHQAVQR.-	1070.21	2	400.84	1.14	0.0	349	9/16	1
jmIgG350naclrawphag3007, 1889	-.YGAFISSELFGSEFFMGRLVK.-	2386 75	3	610.92	1.51	0 0	388	17/80	1
ajrawphag1MNaCl20.2086-2088	-.SKLGALAPSQLWRYR.-	1747.04	2	284.24	1.13	0.1	193	5/14	1
RawPhag200760MeBeadsdigest, 1310	-.WLAGKGLPLLGAILLR.-	1692.13	3	493.57	1.30	0.1	272	1/4	
jmag5mincon500mmnacl, 434	-.QVVAAALK.-	799.98	2	253.22	0.92	0.0	269	4/7	
phagrawFsuc400_dec20, 2060	-.YGAYVPTELFGSEFFMGRLLHFWPEPR.-	3248.70	3	204.39	1.16	0.1	149	2/13	

control

phospholipase A2, group IVB (cytosolic) [Mus musculus]					**1357.49**	38075595.0	2		
FPbeads200_Dec19,1123-1125	-.RALQEFPAAARDLNVPR.-	1925.19	3	170.79	1.25	0.0	117	15/64	
rawextr_200bead_Mar04, 1456	-.RALQEFPAAARDLNVPR.-	1925.19	3	322.27	1.35	0.1	112	1/4	
rawextr_600bead_Mar04, 1806	-.YGAYVPTELFGSEFFMGRLLHFWPEPR.-	3248.70	3	864.43	1.86	0.2	89	2/13	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase C, beta 3 [Mus musculus]					**8916.15**	31982122.0	1		
ajrawphag1MNaCl20, 1344	-.LAMNILAQNASR.-	1302.53	3	288.35	1.32	0.0	207	3/11	2
jmfag5minfrench1mnacldttdpi, 1782	-.IAAFEEGGKFVGHRILPVSAIR.-	2368.77	3	316.74	1.15	0.0	258	3/14	1
jmfag_20_minfrench1mnacldttdpi, 1782	-.IAAFEEGGKFVGHRILPVSAIR.-	2368.77	3	316.74	1.15	0.0	258	3/14	1
rawsucrfp_300phagigg_Mar04,1147-1149	-.EVELTEINRR.-	1259.40	2	362.78	1.05	0.1	258	1/2	2
phagrawF400_dec20, 1418	-.PGVHALQLEPPTVVETLRRGSK.-	2385.75	2	137.09	1.07	0.0	126	5/21	
phagrawFchlf_dec23, 1698	-.PDKSFDPFTEVIVDGIVANALRVK.-	2632.01	3	388.56	1.37	0.1	173	9/46	1
phagrawFsuc700_dec23, 1781	-.IAAFEEGGKFVGHRILPVSAIR.-	2368.77	3	307.06	1.34	0.0	213	5/28	1
phagrawF250_dec22, 2221	-.FVGHRILPVSAIR.-	1465.77	2	83.40	0.92	0.0	89	1/4	1
phagrawFsuc350_dec20, 3382	-.VISGQFLSDKKVGIYVEVDMFGLPVDTR.-	3114.61	2	137.02	1.03	0.1	41	4/27	1
jmfag1mnacl7,5minigg,122-124	-.RHITESVNSIRR.-	1468.65	3	345.50	1.58	0.1	126	15/44	2
jmfag1mnacl0minigg, 756	-.VWSEELFKLAMNILAQNASR.-	2321.69	3	650.98	1.42	0.1	349	5/19	2
jmfag1mnacl7,5minigg, 1006	-.DPRLNEVLYPPLRSSQAR.-	2112.38	3	197.92	1.47	0.0	126	15/68	1
jmfag5minigg1000mmnacl, 1146	-.SFDPFTEVIVDGIVANALR.-	2064.33	3	774.52	1.41	0.1	335	17/72	1
ajrawphag1MNaCl20, 1344	-.LAMNILAQNASR.-	1302.53	3	288.35	1.32	0.0	207	3/11	2
JMFAGNACL10_1B21E3, 1988	-.PSPSALGKATNSEDVK.-	1601.74	2	291.85	0.97	0.1	210	1/3	2
jmfag5mincon450mmnacl, 782	-.RHITESVNSIRR.-	1468.65	3	277.38	1.49	0.0	164	4/11	2
jmbeads150rawphag3007, 788	-.RHITESVNSIR.-	1312.46	2	279.98	1.04	0.0	252	9/20	2
jmag5mincon500mmnacl, 844	-.KAVALTR.-	758.93	2	1983.97	1.96	0.0	1003	11/12	2
jmfagcon5minn600mmnacl, 2879	-.ILPVSAIRSGYHYVCLR.-	1948.33	2	134.08	0.92	0.0	145	1/4	1
jmfag1mnacl7,5minigg,122-124	-.RHITESVNSIRR.-	1468.65	3	345.50	1.58	0.1	126	15/44	
jmfag5miniggbead, 1037	-.VKVISGQFLSDKK.-	1449.72	2	76.53	0.85	0.0	77	3/8	
rawphag2007chfbead3, 631	-.VETALESCGLNFNRVESIR.-	2138.39	2	126.12	0.90	0.0	134	2/9	
rawphag2007chlfsol3, 1189	-.ILLEIGAKGKPYLTLEQLMDFINQK.-	2877.44	3	399.51	1.30	0.1	167	3/16	1
phagrawFchlf_dec23, 1698	-.PDKSFDPFTEVIVDGIVANALRVK.-	2632.01	3	388.56	1.37	0.1	173	9/46	1
rawphag2007chlfsol2, 2338	-.DVLEAIAEAAFKTSPYPVILSFENHVDSAK.-	3263.64	2	17.69	0.76	0.0	21	5/58	1

control

phospholipase C, beta 3 [Mus musculus]					**790.84**	31982122.0	14		
rawextr_700bead_Mar04,621-623	-.LKEVVLDTHTTQFK.-	1659.91	3	147.22	1.45	0.0	91	11/52	2
rawextr_1000bead_Mar04, 1866	-.DQMSMEGFSR.-	1188.32	2	152.92	0.77	0.0	174	1/3	1
jmrawf5minbsareebeads, 2106	-.IAAFEEGGKFVGHRILPVSAIR.-	2368.77	3	490.69	1.18	0.2	88	13/84	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase C beta 4 [Mus musculus]					**9857.93**	29293803.0	14		
jmfag5minigg600mmnacl, 1796	-.EMDQLKKVQLEHLEFLEK.-	2258.62	2	120.52	1.06	0.0	113	4/17	
jmfag5minigg250mmnacl, 1904	-.GLISSDGFCRYLMSDENAPVFLDR.-	2707.04	3	835.27	1.83	0.1	297	19/92	1
JMMAGTube1B16E3, 3118	-.VKEIVAQHTKEWSEMINTHSAEEQEIR.-	3224.55	2	255.47	0.82	0.2	37	7/52	1
jmldactinrawphag3007, 908	-.LAFLTNTTGKIPVR.-	1531.83	3	846.37	1.39	0.0	586	5/13	1
jmldl500naclrawphag3007, 1109	-.ADQMRAMGIETSDIADVPSDTSKNDK.-	2797.03	3	279.07	1.31	0.1	162	1/5	1
phagrawFsuc150_dec22, 166	-.ETEIKIQTLTTDHK.-	1657.85	2	392.82	1.15	0.0	329	11/26	1
phagrawFsuc800_dec23, 1864	-.QWVEGLRSIIHNFRANNVSPMTCLK.-	2915.39	3	1453.86	1.90	0.2	302	7/32	1
phagrawFsuc60MeOH_dec23, 1992	-.KINGDKTDYLTVDQLVSFLNEHQR.-	2835.12	3	288.06	1.31	0.0	205	4/23	1
phagrawFsuc250_dec22, 2299	-.INGDKTDYLTVDQLVSFLNEHQR.-	2706.95	3	403.31	1.28	0.0	310	19/88	1
phagrawFsucchlfbead_dec23, 2316	-.ADQMRAMGIETSDIADVPSDTSKNDK.-	2797.03	2	102.95	0.84	0.0	109	1/5	1
jmfagtimecon2.5min.1762.1762.2	-.TEKVIFQALKELGLPSGK.-	1959.32	0	138.78	1.47	0.0	94	4/17	1
jmfag5mincont400_030531151834, 600	-.LHCTQVDK.-	944.09	2	222.15	1.33	0.1	141	1/2	1
jmfag5mincont350, 940	-.TDIEDLFKK.-	1109.26	2	684.51	1.32	0.1	380	11/16	1
jmfagtimecon10min,2180-2182	-.AMQIIEMYEPDEELKK.-	1968.28	3	361.80	1.03	0.1	169	1/4	1
jmfagcont5minbead, 3358	-.FQGFHVAEERNIHYNMSSFNESVGLGYLK.-	3375.72	2	62.13	0.80	0.0	56	3/28	
jmfagfrench5minigg1mnacldtt, 395	-.IVAQYDKEKSTHEK.-	1676.85	3	355.58	1.32	0.1	229	4/13	1
jmIgG350naclrawphag3007, 947	-.PTTTAALGSGQEAKK.-	1460.62	3	1137.53	2.26	0.0	483	11/28	1
jmraw5minigg250mmnaclsyringdnase, 1376	-.PTTTAALGSGQEAK.-	1332.44	2	376.94	1.03	0.0	359	6/13	1
ajrawphagjun20actinDPI, 1648	-.VILPDLAVLR.-	1109.39	2	183.84	0.92	0.0	199	4/9	1
jmrawigg5min150mmnacl, 1716	-.VILPDLAVLR.-	1109.39	2	203.58	1.00	0.0	201	4/9	1
jmfagfrench20minigg1mnacldtt,1738-1740	-.VILPDLAVLR.-	1109.39	2	597.30	1.25	0.2	92	7/18	1
jmfag5minigg600mmnacl, 1796	-.EMDQLKKVQLEHLEFLEK.-	2258.62	2	120.52	1.06	0.0	113	4/17	
ajrawphagjun20dpi1MNaCl, 1846	-.VILPDLAVLR.-	1109.39	2	332.61	1.29	0.1	208	1/2	1
phagrawFsucchlfbead_dec23, 2316	-.ADQMRAMGIETSDIADVPSDTSKNDK.-	2797.03	2	102.95	0.84	0.0	109	1/5	1

control

phospholipase C beta 4 [Mus musculus]					**997.97**	29293803.0	15		
rawextr_1000bead_Mar04, 736	-.IAVYDDNNK.-	1052.12	2	180.96	1.03	0.1	105	3/8	1
rawextr_500beadigg_Mar04, 904	-.PTTTAALGSGQEAKK.-	1460.62	2	348.01	1.52	0.0	219	9/28	1
FPbeads200_Dec19, 1728	-.ANPAKANVTPQSSSELR.-	1770.93	2	125.86	0.93	0.0	134	7/32	1
rawextr_60MeOHbead_Mar04, 2546	-.VKEIVAQHTKEWSEMINTHSAEEQEIR.-	3224.55	2	46.63	0.89	0.0	52	7/52	1
jmbsa1000naclrawphag3007, 1391	-.PTTTAALGSGQEAK.-	1332.44	2	296.51	1.21	0.0	231	9/26	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase C, epsilon [Mus musculus]					**11725.24**	23956100.0	4		
jmldl500naclrawphag3007, 1755	-.DIFDIYSVPCNR.-	1442.62	2	423.72	1.02	0.1	370	5/11	2
jmldl150naclrawphag3007, 1880	-.ELCEVLDGASGLLKLCPR.-	1917.28	2	216.46	1.08	0.0	199	5/17	
rawsucrfp_350phagigg_Mar04, 710	-.VLPMDYLCFLTRDLSSPECQR.-	2487.91	2	289.72	1.21	0.1	178	1/4	1
phagrawFsuc800_dec23, 1310	-.FPGLSTLNSSGSSRGKER.-	1881.04	2	123.88	0.99	0.0	120	4/17	2
phagrawFsuc700_dec23, 1403	-.CCWNMGNYNAVMEFLAGLRSRK.-	2565.02	2	141.09	0.90	0.1	79	3/14	
rawsucrfp_600phagigg_Mar04, 1568	-.DIFDIYSVPCNR.-	1442.62	2	499.29	1.01	0.1	301	9/22	2
rawsucrfp_500phagigg_Mar04, 1808	-.DIFDIYSVPCNR.-	1442.62	2	436.86	1.03	0.1	202	7/22	2
phagrawFsuc150_dec22, 1844	-.AYSLTTAGSPNLATGMSSPISAWSSSSWHGR.-	3169.43	2	37.29	0.81	0.0	41	1/10	1
phagrawFsuc60MeOH_dec23, 1902	-.KAGLLWPCGNVMGTLSAMDIR.-	2234.70	3	1113.75	1.51	0.1	600	11/40	
rawsucrfp_450phagigg_Mar04, 1970	-.DIFDIYSVPCNR.-	1442.62	2	517.40	1.02	0.2	249	9/22	2
phagrawFsuc150_dec22, 1994	-.KVLPGIQLEMEDSPMDVSPAGSQPR.-	2683.06	2	107.15	0.95	0.1	57	7/48	
phagrawFsuc450_dec20,2238-2240	-.DIFDIYSVPCNR.-	1442.62	2	221.91	1.27	0.0	166	7/22	2
phagrawFchlfbead_dec23, 2553	-.QGALIPPTISQWNKHK.-	1819.10	2	102.85	0.96	0.0	92	7/30	
phagrawFsuc350_dec20, 3016	-.DIFDIYSVPCNR.-	1442.62	2	413.36	1.32	0.0	291	5/11	2
phagrawFsuc350_dec20, 3158	-.DIFDIYSVPCNR.-	1442.62	2	96.67	0.92	0.0	100	3/11	2
jmfag5minigg350mmnacl, 281	-.MSPGETAPFNR.-	1207.34	3	593.70	1.37	0.0	433	2/5	3
ajrawphagjun20dpi1MNaCl, 706	-.IMESSGPHSDR.-	1216.31	2	305.21	1.08	0.0	277	9/20	
AJRAWActinIgG_june13, 922	-.EEKPVGALSSSDTVGYQQ.-	1896.00	3	819.74	1.49	0.1	362	9/34	2
jmfag1mnacl7.5minigg, 1618	-.NGQVQCEHCTSLR.-	1475.64	2	246.31	1.25	0.0	192	5/12	
jmfagfrench5minigg1mnacldtt, 1697	-.NCMAYACKLVELTR.-	1615.97	2	136.90	0.92	0.1	110	3/13	
jmIgG250rawphag3007, 1928	-.KESRQIAPELSDLVIYCQAVK.-	2391.77	3	1400.38	2.12	0.1	436	1/4	2
jmIgG400rawphag3007, 2256	-.LSSMLLSETGVTLLYGLQTTDNR.-	2513.85	3	573.59	1.88	0.0	297	9/44	1
jmfag5mincon250mmnacl, 328	-.RGISFASELK.-	1108.27	3	385.35	1.23	0.1	157	5/18	2
jmfag5mincont200mmnacl, 650	-.ALHIPGCK.-	839.04	2	359.55	1.09	0.1	304	4/7	
jmfag5mincont200mmnacl, 1012	-.QYVSLYQEDGRYEGPTLAHAVELFGGR.-	3057.32	3	156.97	1.27	0.0	109	15/104	1
jmfagtimecont0min_030601230741, 1144	-.IKKADNSSGNK.-	1162.28	3	762.24	1.58	0.0	465	3/8	2
jmbeads350rawphag30072nd, 1396	-.SAFITSDLPIIISIENHCSLPQQR.-	2684.06	3	522.02	1.74	0.1	255	19/92	2
jmbeadsactinrawphag3007, 1549	-.IVLKPQQETLEEK.-	1555.80	1	500.98	1.20	0.2	113	1/3	3
rawphag2007chlfsol3, 2091	-.HTAEMLFSGLLELTTAVR.-	1990.31	1	34.77	0.63	0.0	53	3/17	1
phagrawFchlfbead_dec23, 2553	-.QGALIPPTISQWNKHK.-	1819.10	2	102.85	0.96	0.0	92	7/30	
jmrawbas5min1mnacl, 2454	-.GLPSPPQLVASESVQSKEEK.-	2111.34	2	83.30	0.72	0.0	116	4/19	3

control

phospholipase C, epsilon [Mus musculus]					**4251.91**	23956100.0	35		
rawextr_chlfbeadIgG_Mar04, 790	-.TSIAQYITGSLLEATTSLGAR.-	2154.41	3	316.83	1.88	0.1	133	19/80	1
rawextr_300bead_Mar04, 1314	-.DNFASKNDESR.-	1283.29	2	287.44	0.98	0.0	290	1/2	2
rawextr_800bead_Mar04, 1514	-.DIFDIYSVPCNR.-	1442.62	2	261.41	1.20	0.1	157	7/22	2
rawextr_800bead_Mar04, 1656	-.DIFDIYSVPCNR.-	1442.62	2	273.32	1.05	0.1	233	7/22	2
rawextr_350bead_Mar04, 1662	-.QIAPELSDLVIYCQAVKFPGLSTLNSSGSSRGK.-	3467.94	3	305.47	1.31	0.1	149	17/128	2
rawextr_60MeOHbeadIgg_Mar04, 2004	-.ILLDQECVFQAQSK.-	1622.87	2	88.04	0.82	0.0	99	7/26	3
FPbeads600_Dec19, 2090	-.PVGALSSSDTVGYQQ.-	1509.60	2	256.00	0.68	0.0	376	13/28	2
rawextr_chlfbeadIgG_Mar04, 2156	-.AKQLLQQVLAVDQDTKCTATDYFLMEEK.-	3231.69	3	295.74	1.53	0.0	179	19/108	3
rawextr_400beadigg_Mar04, 2360	-.VHFEDLVFLRFAVVENNSSAITAQR.-	2864.21	3	516.24	1.50	0.0	343	5/24	3
rawextr_60MeOHbead_Mar04, 2378	-.EEKPVGALSSSDTVGYQQ.-	1896.00	2	445.91	1.31	0.1	305	6/17	2
rawextr_350beadigg2_Mar04, 2394	-.NPSPGMSAKNAEK.-	1331.48	2	373.52	1.21	0.1	244	5/12	1
rawextr_350beadigg2_Mar04, 2468	-.GSCEGMRHTWEESSPLSPSTSLSAIIR.-	2920.23	3	245.33	1.54	0.1	96	7/52	3
rawextr_600beadigg_Mar04, 2484	-.ELIDLQPLIQFPEEVASILTEQEQNIYR.-	3330.73	2	36.49	0.89	0.0	39	4/27	1
FPbeads300_Dec19, 2978	-.DIFDIYSVPCNR.-	1442.62	2	288.79	1.03	0.0	269	9/22	2
jmbsa150naclrawphag3007, 1912	-.KMAEIFK.-	867.09	1	261.38	0.91	0.0	284	7/12	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Ina protein [Mus musculus] phospholipase C zeta [M					**39887.76**	17390900.0	12		
jmfagtimecon2.5min.1102.1102.2	-.EYQDLLNVK.-	1122.25	0	1086.09	1.57	0.2	353	9/16	17
jmfagtimecon2.5min.1108.1108.2	-.EYQDLLNVK.-	1122.25	0	3039.14	2.25	0.3	497	11/16	17
jmfagtimecon7.5min.1574.1574.2	-.EYQDLLNVK.-	1122.25	0	1245.64	2.03	0.1	430	5/8	17
jmfagtimecon7.5min.1570.1570.2	-.EYQDLLNVK.-	1122.25	0	2639.20	1.94	0.3	533	11/16	17
AJRAWActinContr_june13, 832	-.HLREYQDLLNVK.-	1528.74	3	10209.72	3.47	0.3	1740	27/44	9
jmbeads250rawphag3007, 904	-.EYQDLLNVK.-	1122.25	2	788.25	1.79	0.1	378	9/16	17
jmbeads300rawphag3007,904-906	-.EYQDLLNVK.-	1122.25	2	2850.32	2.35	0.3	505	11/16	17
jmfagcon5min1000mmnacl_030601180404,908-910	-.EYQDLLNVK.-	1122.25	2	2567.00	1.96	0.3	638	3/4	17
jmfagcon5minn600mmnacl,1201-1203	-.EYQDLLNVK.-	1122.25	2	1923.93	2.22	0.2	476	11/16	17
jmfagtimecont0min_030601230741, 1458	-.EYQDLLNVK.-	1122.25	2	2879.72	1.97	0.3	400	5/8	17
jmfagcont5minbead,1478-1480	-.EYQDLLNVK.-	1122.25	2	2205.86	2.02	0.3	429	5/8	17
jmbeads350rawphag30072nd, 1494	-.EYQDLLNVK.-	1122.25	2	864.45	1.52	0.2	341	1/2	17
jmag5mincon500mmnacl, 1634	-.EYQDLLNVK.-	1122.25	2	608.14	1.48	0.0	407	9/16	17
jmag5mincon500mmnacl, 1638	-.EYQDLLNVK.-	1122.25	2	2756.41	1.66	0.3	456	5/8	17
jmfagtimecon10min,1660-1662	-.EYQDLLNVK.-	1122.25	2	1453.86	1.88	0.2	455	5/8	17
jmfagtimecont10min_030601202502, 1678	-.EYQDLLNVK.-	1122.25	2	1801.61	1.90	0.2	422	5/8	17
AJRAWActinContr_june13, 2130	-.QLQARTIEIEGLR.-	1527.75	2	968.42	1.77	0.0	536	1/2	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase C-like 2 [Mus musculus] ulus] inal					**4064.26**	38082546.0	6		
jmfag5mincont350,702-704	-.PEAAAAGTRGR.-	1057.15	2	699.39	1.51	0.1	404	11/20	
rawphag2007chfbead2, 648	-.LTPLSSLSPRPRQDPR.-	1821.08	3	940.63	1.60	0.1	402	3/10	
rawphag2007chfbead2, 656	-.LTPLSSLSPRPRQDPR.-	1821.08	3	1137.74	1.55	0.1	589	7/20	
ajrawphagactin20, 560	-.VPAAGAPPPK.-	905.08	3	304.68	1.08	0.0	265	1/3	
jmfag5minigg400mmnacl, 698	-.ESDHNR.-	757.73	2	270.68	0.97	0.0	277	7/10	
jmIgG350naclrawphag3007,819-821	-.IGFCMGNGFAPLRK.-	1511.84	3	547.47	1.62	0.1	293	9/26	
ajrawphagactin20, 898	-.AGSFIACFCGSK.-	1191.41	2	163.66	0.95	0.0	154	7/22	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase C-like 2 [Mus musculus] [Mus musc					**419.85**	38082546.0	7		
rawextr_150beadigg_Mar04, 618	-.GAPMAECGR.-	892.04	2	182.77	1.19	0.0	147	1/2	
rawextr_500beadigg_Mar04, 1480	-.ARSPDGSPRPVGGSAK.-	1539.68	2	237.08	1.23	0.1	119	1/3	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Nck, Ash and phospholipase C binding protein; SH2 domain containing SO					**2869.04**	20149738.0	10		
phagrawFsuc60MeOH_dec23, 1206	-.ALPPGLALER.-	1037.24	2	183.85	0.91	0.1	131	7/18	
phagrawFsuc300_dec20, 1610	- RPSGDLAASAASLTDMGGSAVR.-	2091 29	3	472.66	1 10	0 0	428	5/21	
phagrawFsuc350_dec20, 1660	-.FEDRCQSVVEFK.-	1600.82	2	526.32	1.27	0.1	372	5/12	
JMFAGNACL10_2821E3, 478	- ALPPGLALER.-	1037.24	2	816.17	1 31	0.1	580	11/18	
jmrawigg5minbeadsfreezethaw, 1264	- CALDPKALPPGLALER.-	1665 00	2	454 01	1.58	0.1	218	1/3	
jmfag5minigg600mmnacl, 1530	-.EAQLISKQKQEVEPST.-	1816.00	3	416.03	1.16	0.2	126	11/60	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase C-L2 [Mus musculus] beta binding pro					**6065.06**	**6705987.0**			
jmkdl250naclrawphag3007, 1732	-.GAAGGALPTSPSPALGAKGALK.-	1893.18	2	518.01	1.71	0.1	182	11/42	2
jmraw5minbsabeads, 3722	-.TRPEIYFLLVQFSSNK.-	1943.24	1	29.32	0.76	0.0	36	1/6	
rawsucrfp_450phagigg_Mar04,586-588	-.PGTENSEAQK.-	1061.09	3	192.39	1.07	0.1	98	1/4	3
phagrawFsuc350_dec20, 1586	-.FLARVFPSPMRIDSSNMNPQDFWK.-	2885.32	3	93.14	0.97	0.0	95	3/23	3
phagrawFsuc350_dec20, 2526	-.ARYDSGGVSNGDCSLGVSGDEAR.-	2273.34	3	600.73	1.61	0.0	371	1/4	2
jmfag5minigg150mmnacl, 162	-.EVRTGKNTDIFR.-	1436.60	3	145.36	1.07	0.0	136	13/44	2
jmfag1mnacl5minigg, 462	-.GQADLLKYAKNETLENLK.-	2049.31	3	553.72	1.61	0.1	176	15/68	3
jmrawigg5min300mmnaclsyringednase, 503	-.KKTVSFSSMPTEK.-	1470.72	3	265.98	1.06	0.0	250	5/16	2
JMMAGNEGB16D3, 590	-.AGAGEGGGGGGGGR.-	1017.00	2	467.72	1.51	0.0	309	1/2	
jmrawigg5minbeadsyringdnase, 673	-.ENVEQPNHVPVKR.-	1546.71	3	251.12	1.32	0.0	190	7/24	3
jm5miniggrawlowionic, 1010	-.ENVEQPNHVPVKR.-	1546.71	3	169.63	1.30	0.0	119	13/48	3
jmrawigg5min400mmnaclsd,1119-1121	-.GAAGGALPTSPSPALGAKGALK.-	1893.18	2	662.61	2.16	0.1	198	11/42	2
jmfagfrench5minigg1mnacldtt, 1365	-.ENMQNAVVSFK.-	1267.44	2	148.82	1.07	0.0	138	3/10	3
jmIgG350naclrawphag3007, 2421	-.ENVEQPNHVPVKRFQLCK.-	2166.49	3	161.93	1.10	0.1	122	15/68	3
JMFAGNACL15B21E3, 3086	-.LYTTSPNMEESYLPSPDVLKGKILIK.-	2938.43	2	72.40	0.89	0.0	74	4/25	3
jmfagtimecon2.5min.1208 1208.1	-.KTVSFSSMPTEK.-	1342.54	0	156.63	1.25	0.0	122	7/22	2
jmfagtimecon7.5min.1596.1596.2	-.SKDKAGTEITK.-	1178.32	0	450.10	1.12	0.1	222	9/20	3
jmfagtimecon10min, 264	-.NLNPGLKTSK.-	1072.24	3	282.25	1.20	0.0	224	11/36	3
jmbeads500rawphag3007, 1279	-.GAAGGALPTSPSPALGAK.-	1523.72	2	546.81	1.13	0.2	195	5/17	2
jmfag1mnacl5mincon, 3048	-.MAECGRGAAGGALPTSPSPALGAKGALK.-	2540.95	3	296.39	1.41	0.0	204	7/36	1

control

phospholipase C-L2 [Mus musculus] beta binding pro					**1060.73**	**6705987.0**	**22**		
rawextr_200bead_Mar04, 54	-.TSPGRGPLGVALAR.-	1352.57	2	98.54	0.83	0.0	119	7/26	2
rawextr_900bead_Mar04, 906	-.TLWIKTVDEVFK.-	1479.75	3	294.17	1.24	0.0	236	1/4	3
rawextr_1000bead_Mar04, 1124	-.GAAGGALPTSPSPALGAKGALK.-	1893.18	3	192.77	1.17	0.0	145	5/21	2
rawextr_150bead_Mar04,1475-1477	-.AGTEITKEEFIEVFHELR.-	2149.39	3	281.64	1.33	0.1	170	4/17	
rawextr_350bead_Mar04, 1638	-.LQKAVESFTWNITILK.-	1892.23	2	131.75	1.33	0.0	90	7/30	3
FPbeads1000_Dec19, 2378	-.YAKNETLENLKQIHFAAVSCGLNK.-	2693.08	2	61.86	0.80	0.1	51	3/23	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
phospholipase C, delta; phospholipase C delta-1; PLC-delta 1 [Mus muscu					**6458.61**	**9790167.0**	**12**		
rawsucrfp_1000phagigg_Mar04,1403-1405	-.SVHFGGFSSPSTSGGAFYEMASFSESRALR.-	3229.49	3	553.67	1.76	0.2	75	4/29	7
rawsucrfp_400phagigg_Mar04, 1653	-.EEEAGPALALSLIERYEPSETAK.-	2504.73	3	214.45	1.44	0.0	149	7/44	6
jmfag5minigg1000mmnacl, 1680	-.LRVWIISGGQLPKVNK.-	1880.27	3	141.53	1.02	0.1	89	11/60	7
jmigg450rawphag3007, 1222	-.NKDNKMNFK.-	1139.31	2	213.12	1.01	0.1	158	9/16	7
AJRAWActnIgG_june13,1480-1482	-.QTAVITNNGFNPR.-	1432.57	3	498.30	1.77	0.1	201	7/24	6
jmraw5minigg600mmnaclsd, 1546	-.QTAVITNNGFNPR.-	1432.57	3	415.60	1.33	0.2	61	3/16	5
jm5miniggrawlowionic,1644-1646	-.QTAVITNNGFNPR.-	1432.57	3	238.25	1.39	0.0	171	7/24	7
jmfag5minigg1000mmnacl, 1680	-.LRVWIISGGQLPKVNK.-	1880.27	3	141.53	1.02	0.1	89	11/60	7
jmIgG250rawphag3007, 3278	-.NGDLHPSATLFVKISIQD.-	1956.19	1	1019.40	1.03	0.3	52	7/34	7
jmraw5minbsabeads, 3722	-.TRPEIYFLLVQFSSNK.-	1943.24	1	29.32	0.76	0.0	36	1/6	
jmkdl150naclrawphag3007, 1440	-.HNVGHLSRIYPAGWR.-	1763.99	2	704.03	1.50	0.2	160	9/28	1
jmfagtimecon10min, 982	-.MNFKEVKDFLK.-	1399.68	3	1784.29	1.76	0.1	957	11/20	1
jmbeads1000naclrawphag3007, 1229	-.QTAVITNNGFNPR.-	1432.57	3	208.94	1.35	0.1	104	11/48	1
jmfag5mincont200mmnacl, 1780	-.MDSGRDFLTLHGLQDDPDLQALLK.-	2700.02	2	298.17	0.96	0.2	66	7/46	1

control

phospholipase C, delta; phospholipase C delta-1; PLC-delta 1 [Mus muscu					**532.04**	**9790167.0**	**7**		
rawextr_600bead_Mar04,1200-1202	-.QTAVITNNGFNPR.-	1432.57	3	166.64	1.42	0.0	113	1/4	1
rawextr_1000_beadigg_Mar04,1350-1352	-.AFAEAAGSAETLSVEKLVTFLQHQQR.-	2833.15	3	173.31	1.55	0.1	73	4/25	1
rawextr_700bead_Mar04, 1560	-.ELNVQVDDSYARKIFR.-	1954.18	2	83.59	0.80	0.0	89	7/30	1
jmbsa1000naclrawphag3007, 1527	-.QTAVITNNGFNPR.-	1432.57	3	108.50	1.05	0.0	102	1/4	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dJ511B24.2.5 (phospholipase C, gamma 1 (formerly subtype 148) (1-Phosph					**6001.40**	**41393059.0**	**1**	**0**	
aj1MNaClphagIgGDPIRJun18, 1342	-.FCWNLLGGSVWARQAAEAS*S*S*QHR.-	2902.93	2	351.42	1.06	0.1	108	9/46	Peptides Ions
ajactinphagIgGDPIPJun18, 1330	-.DLKNMLSQVNYR.-	1481.70	2	196.94	1.51	0.1	89	9/22	1
jmraw5minbsafreezthaw, 2648	-.NGRGIVCPFVEIEVAGAEYDSTKQK.-	2712.03	3	426.47	1.85	0.0	212	3/16	
JMMAGTube1B16E3, 1870	-.LSEPVPQTNAHESK.-	1537.86	2	147.19	0.89	0.0	165	7/26	
jmfag5minigg400mmnacl, 2302	-.LAEGSAYEEVPTSVMYSENDISNSIK.-	2835.05	2	403.90	1.00	0.2	108	4/25	
rawsucrfp_250phagigg_Mar04, 1068	-.NNYSEDLELASLLIK.-	1722.92	3	347.40	1.85	0.0	188	17/56	
rawsucrfp_500phagigg_Mar04, 1276	-.ESETFVGDYTLSFWR.-	1837.97	3	288.61	1.15	0.1	145	11/56	
rawsucrfp_600phagigg_Mar04, 1652	-.NPGFYVEANPMPTFK.-	1712.95	2	579.61	1.24	0.1	321	5/14	
jmrawigg5min400mmnaclsd, 261	-.EWYHASLTR.-	1183.27	3	221.34	0.85	0.0	258	11/32	
jmrawigg5min400mmnaclsd, 389	-.IGTERACYR.-	1069.22	2	129.59	0.81	0.0	159	3/8	1
jmIgG150rawphag3007, 1390	-.PDQSHCFVILYGMEFR.-	1943.24	3	626.97	1.48	0.0	424	7/20	
jmraw5miniggiowionic,1523-1525	-.VPNMRFLR.-	1033.28	2	433.79	1.02	0.0	422	9/14	
jmrawigg5minbeadsfreezethaw, 2798	-.YQQPFEDFRISQEHLADHFDSR.-	2786.92	3	168.83	1.08	0.0	151	13/84	
jmbeads1000naclrawphag3007, 344	-.PVDIAADGLPSPNQLRR.-	1820.04	3	101.25	1.12	0.0	90	11/64	
jmfagcon5minn600mmnacl, 1129	-.HPLYRK.-	813.97	2	978.09	1.57	0.2	329	7/10	
jmfag5mincon450mmnacl, 3136	-.EASSSTELHSSEK.-	1392.41	2	174.28	1.21	0.0	140	1/3	
RawPhg2007MeEthmeth3digest,2194-2196	-.EDELTFTK.-	983.06	2	425.93	1.13	0.0	370	9/14	

control

phospholipase C, gamma 1; 1-phosphatidylinositol-4,5-bisphosphate phos					**956.88**	**41393059.0**	**7**		
rawextr_450bead_Mar04, 990	-.NNYSEDLELASLLIKIDIFPAK.-	2507.86	3	584.37	1.84	0.1	228	19/84	
rawextr_250bead_Mar04, 1316	-.VPRDGAFLVRK.-	1258.50	2	372.51	1.09	0.1	242	2/5	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Sec23-interacting protein p125; phospholipase [Mus musculus					**2739.70**	38087445.0		10	
jmfag5minigg bead_030528200105, 1061	- SPGSVAVSNGVIKHSQFQEK -	2100.32	3	447.97	1.56	0.0	286	5/19	1
jmfag5minigg600mmnacl, 2144	- NPNFKGKVSVAGHSLGSLILFDILSNQR.-	3013.44	2	129.51	0.90	0.1	114	1/6	1
rawsucrfp_800phagigg_Mar04, 1350	- PPATLAFTTGSQDALSAFPPSVSK.-	2391.66	3	240.21	1.14	0.0	211	19/92	1
rawphag2007chfbead2, 476	- NIKKITLPSIGR.-	1340.64	3	499.62	1.63	0.0	305	17/44	1
rawphag2007chfsol1, 1296	-.TKEMASPSSESNESK.-	1612.70	3	1422.40	1.67	0.1	737	11/28	1
similar to Sec23-interacting protein p125; phospholipase [Mus musculus					**118.23**	38087445.0		8	
FPbeads300_Dec19, 2364	-.VSRVEFLPVHWHSALGGHATGVDR -	2628.93	2	118.23	0.91	0.1	78	4/23	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
LIPS_MOUSE Hormone sensitive lipase (HSL)					**5901.00**	1708847.0		10	
jmag5mincon500mmnacl,1424-1426	-.AFWNITEIEVLSSLANMASTTVR.-	2554.90	3	277.65	2.14	0.0	107	2/11	3
jmfag1mnacl5minigg, 2494	-.AFWNITEIEVLSSLANMASTTVRVSR.-	2897.30	2	233.15	0.83	0.2	45	7/50	3
jmldl1000naclrawphag3007, 2230	-.ICLAGDSAGGNLCITVSLRAAAYGVR.-	2552.96	3	349.52	1.81	0.0	185	19/100	3
jmldl300naclrawphag3007, 2240	-.TLPPVHLVACALDPMLDDSVMFAR.-	2613.12	3	330.27	1.19	0.0	273	5/23	2
phagrawF350_dec20, 229	-.SHEPYLK.-	873.98	2	160.83	1.15	0.0	138	1/2	3
phagrawFsuc600_dec20, 1222	-.LGASSWLNSFPELSGRK.-	1850.07	3	497.63	1.57	0.1	151	17/64	
rawsucrfp_150phagigg_Mar04, 2327	-.TLPPVHLVACALDPMLDDSVMFAR.-	2613.12	3	391.65	1.51	0.1	219	4/23	2
jmraw5minigg250mmnacisyringdnase, 196	-.KSIFFR.-	797.97	2	187.10	0.94	0.1	167	3/5	3
jmrawgg5minbeadsyringdnase,1263-1265	-.LILTPPAAPLN.-	1120.37	2	211.36	1.19	0.0	165	2/5	2
jmIgG350naclrawphag3007, 2063	-.ICLAGDSAGGNLCITVSLRAAAYGVR.-	2552.96	2	91.33	0.92	0.1	35	3/25	3
ajrawphagjun20dpi1MNaCl, 2066	-.DEVRPMDGVPRVR.-	1526.75	2	362.92	0.93	0.1	225	3/8	2
jmIgG1000naclrawphag3007, 2438	-.ICLAGDSAGGNLCITVSLRAAAYGVR.-	2552.96	3	306.73	1.73	0.0	170	4/25	3
jmfag1mnacl5minigg, 2494	-.AFWNITEIEVLSSLANMASTTVRVSR.-	2897.30	2	233.15	0.83	0.2	45	7/50	3
jmbeads400rawphag3007, 1279	-.ICLAGDSAGGNLCITVSLRAAAYGVR.-	2552.96	3	867.55	2.12	0.1	291	23/100	3
jmag5mincon500mmnacl,1424-1426	-.AFWNITEIEVLSSLANMASTTVR.-	2554.90	3	277.65	2.14	0.0	107	2/11	3
jmfagtimecont0min_030601230741, 1710	-.SVSEAALAQPEGLLGTDTLK.-	2001.23	3	479.66	1.25	0.1	291	17/76	2
rawphag2007chfbead3, 929	-.RSSQGVLHMPLYTSPIVK.-	2014.38	3	642.85	1.25	0.0	513	19/68	2
LIPS_MOUSE Hormone sensitive lipase (HSL)					**2632.22**	1708847.0		14	
rawextr_150beadigg2_Mar04, 96	-.SEGPRLDVRPR.-	1282.44	3	249.37	1.15	0.0	209	3/8	
rawextr_60MeOHbead_Mar04, 512	-.VLNSLAKSEGPR.-	1271.45	3	422.51	1.20	0.1	227	13/44	3
rawextr_60MeOHbead_Mar04, 998	-.GAEFER.-	708.74	1	557.71	1.17	0.1	284	7/10	3
rawextr_900bead_Mar04, 1396	-.AFWNITEIEVLSSLANMASTTVR.-	2554.90	2	55.90	0.89	0.0	59	2/11	3
FPbeads250_Dec19, 1406	-.CVSAYSGTEAEDHFDSDQK.-	2090.13	3	752.52	1.30	0.1	485	7/24	3
FPbeads450_Dec19, 2028	-.ICLAGDSAGGNLCITVSLRAAAYGVR.-	2552.96	2	264.03	1.18	0.1	73	1/5	3
rawextr_250bead_Mar04, 2102	-.ICLAGDSAGGNLCITVSLR.-	1864.18	2	330.19	1.23	0.1	217	13/36	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
lipase, member H; lipase H [Mus musculus]					**4022.93**	23510279.0		5	
phagrawF200_dec22, 968	-.NGKCVSCGAGQIVPCPR.-	1690.01	3	413.95	1.17	0.1	314	1/4	2
phagrawF600_dec20, 1400	-.GFITIKLRGEDGNITESK.-	1979.22	2	152.77	1.36	0.0	94	9/34	2
jm5miniggrawlowionic,2656-2658	-.VTGLDPAGPLFNGRPPEER.-	2023.24	3	706.94	2.09	0.1	302	2/9	2
jmIgG150rawphag3007, 3004	-.GASLDNIYMIGVSLGAHIAGFVGESYEGKLGR.-	3283.70	2	152.94	0.89	0.1	54	7/62	2
jmfag5minigg400mmnacl, 770	-.CVSCGAGQIVPCPR.-	1390.68	2	1027.29	1.21	0.2	349	1/2	2
jmfag5minigg500mmnacl,1152-1154	-.VAEISLLFSTGSVVGPK.-	1704.99	2	513.37	1.75	0.0	277	13/32	1
JMFAGNACL15B21E3, 1700	-.PPEERLDPSDALFVDVIHSDTDGIKYFK.-	3205.52	2	87.69	0.91	0.0	84	1/6	
jm5miniggrawlowionic,2656-2658	-.VTGLDPAGPLFNGRPPEER.-	2023.24	3	706.94	2.09	0.1	302	2/9	2
JMFAGNACL10_1B21E3, 3026	-.SDTDETCPSFTRLSFHSAVVGTGLSVR.-	2871.13	2	261.04	1.17	0.1	136	5/26	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
lipase, member H; lipase H [Mus musculus]					**227.10**	23510279.0		2	
FPbeads350_Dec19, 1393	-.GFITIKLRGEDGNITESK.-	1979.22	2	227.10	1.26	0.1	95	4/17	2

APPENDIX C – CDC SUMMATION OF IONS

The summation of peptides from CDC's found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to CDC42-binding protein kinase alpha; mytonic dystrophy kinas					5418.65	38085310.0	10		
jmfag5minigg350mmnacl, 221	- FPGCGSR.-	723.82	2	378.31	1.02	0.0	372	7/12	
jmfag5minigg450mmnacl_030527025134, 278	- FPGCGSR.-	723.82	2	219.86	0.94	0.0	217	1/2	
jmfag5minigg450mmnacl_030527025134, 396	- FPGCGSR -	723.82	2	153.56	0.67	0.1	162	5/12	
jmfag5minigg250mmnacl,608-610	- FPGCGSR -	723.82	2	476.26	1.11	0.1	327	2/3	
jmraw5minigg500mmnaclsd, 746	- FPGCGSR -	723.82	2	780.28	0.96	0.2	304	7/12	
jmfag5minigg150mmnacl, 1180	- DGGLEVERSSPGR -	1359.43	2	123.71	0.93	0.0	126	7/24	
JMFAGNACL5B21E3, 2046	- GTVAQFPARASPSQPVPHPSRPGGPR.-	2652.96	3	863.96	2.03	0.2	177	1/5	
jmigG400rawphag3007, 2024	- LFPMSALDGRETDFYKLAETK.-	2433.77	3	1229.17	1.67	0.2	389	17/80	
JMFAGNACL5B21E3, 2036	- KELHDSEGQQLALNK.-	1710.87	2	273.64	1.12	0.1	178	2/7	
jmidl450naclrawphag3007,1288-1290	- NADKVFAMKILNK.-	1492.81	3	920.09	1.87	0.1	449	19/48	1

similar to CDC42-binding protein kinase alpha; mytonic dystrophy kinas					1498.84	38073634.0	23		
rawextr_500beadigg_Mar04,714-716	- ELEVHTEALIAEASK -	1640.82	3	917.62	1.65	0.2	187	2/7	
rawextr_200bead_Mar04, 2322	-.CSILMLADSENERSKWVGVLSELHK -	2846.28	3	405.31	1.45	0.1	248	1/8	
FPbeads250_Dec19,2940-2942	-.GVGTAYEGHVRIPK.-	1484.69	2	175.90	0.92	0.1	130	9/26	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Cdc42 binding protein kinase beta [Mus musculus]					4021.91	33942081.0	18		
jmrawigg5min400mmnaclsd, 861	-.RLGQNGIEDFKK.-	1405.59	2	580.26	1.52	0.1	224	5/11	
jmIgG300rawphag3007, 980	- TLDPLWK.-	873.03	2	530.60	1.11	0.1	450	2/3	
jmraw5minigg500mmnaclsd, 1140	-.EELHKQLVEASERLK.-	1810.05	3	730.87	1.37	0.1	444	2/7	
jmIgG150rawphag3007, 1640	-.DMQLHREDFEIIKVIGR.-	2100.43	3	757.35	1.82	0.0	414	17/64	
ajrawphagjun20actinDPI, 1734	-.DIKPDNVLLDVNGHIRLADFGSCLK.-	2754.16	3	605.04	1.41	0.1	330	3/16	
jmrawminigg200mmnaclsyringdnas, 2066	-.QLEDTVTLRQEHEDSTHRLK.-	2436.63	3	390.60	1.80	0.0	212	4/19	
jmfagfrench5minigg1mnackltt, 2099	-.KLQESTQTVQSLHGSTRALGNSNR.-	2613.83	3	427.19	1.16	0.2	102	7/46	

control

Cdc42 binding protein kinase beta [Mus musculus]					1649.73	33942081.0	21		
FPbeads400_Dec19, 1094	-.VKQGGRGPGAASEHQQEISK.-	2065.24	3	231.97	1.31	0.1	74	7/38	
rawextr_1000_beadigg_Mar04, 1474	-.GPGAASEHQQEISKIR.-	1708.86	3	692.36	1.88	0.1	336	3/10	
rawextr_900bead_Mar04, 1574	-.GSLKSMTQSNTLTK.-	1496.71	2	125.40	0.82	0.0	151	9/26	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Cdc42 GTPase-activating protein [Mus musculus]					8568.58	9938022.0	11		
jmrawigg5min400mmnaclsd,935-937	-.EVYLQDIHCVGSLCK.-	1708.00	3	645.32	1.84	0.1	311	17/56	
jmrawigg5min350mmnaclsyringednase, 1139	-.EVYLQDIHCVGSLCK.-	1708.00	3	497.81	1.95	0.0	251	2/7	
jmIgG350naclrawphag3007, 1631	-.SLTLPALSLPMK.-	1271.60	2	406.89	0.94	0.2	199	4/11	
jmIgG1000naclrawphag3007, 2152	-.QEFGSDQCPDLTR.-	1496.59	2	425.30	0.90	0.1	430	11/24	
jmfag5minigg450mmnacl_030527025134, 1726	-.ATIRPAKSMDSLCSVPVEGK.-	2090.46	3	269.67	1.30	0.0	183	17/75	
phagrawF300_dec20, 1397	-.EVYLQDIHCVGSLCK.-	1708.00	3	967.42	1.60	0.1	381	19/56	
jmfagtrmecon7.5min.1692.1692.3	-.EVYLQDIHCVGSLCK.-	1708.00	0	908.10	1.74	0.1	444	9/28	
jmfagtrmecon7.5min.1696.1696.3	-.EVYLQDIHCVGSLCK.-	1708.00	0	650.51	1.65	0.0	387	9/28	
jmfag5mincont200mmnacl, 466	-.NKGAKQK.-	773.91	2	600.05	1.18	0.0	507	5/6	
AJRAWSoluteContr_june13, 964	-.EVYLQDIHCVGSLCK.-	1708.00	3	2099.09	2.06	0.1	851	23/56	
jmbeads450naclrawphag3007, 1404	-.LRQEFGSDQCPDLTR.-	1765.93	2	96.30	0.84	0.1	86	1/4	
jmbeadsactinrawphag3007, 2658	-.KIEATICNGDAAFLAVR.-	1793.08	2	1002.13	1.38	0.2	350	3/8	

control

Cdc42 GTPase-activating protein [Mus musculus]					1110.57	9938022.0	4		
rawextr_700bead_Mar04, 879	-.EVYLQDIHCVGSLCK.-	1708.00	3	1110.57	2.13	0.1	479	3/8	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
sorting nexin 26; TC10/CDC42 GTPase-activating protein [Mus musculus]					**3838.02**	30142699.0	11		
jmigg450rawphag3007, 1098	- LYFRELPNPLLTYQLYGK -	2229.61	3	304.11	1.15	0.0	243	15/68	1
jmraw5minigg600mmnaclsd,2116-2118	APPQPSGSR -	896.97	2	313.61	0.98	0.1	232	1/2	1
jmfag1mnacl5mincon, 1940	- SEESLSSQASGAGLQR -	1607.66	2	569.37	1.93	0.1	228	11/30	1
jmfag5minigg400mmnacl, 2034	- PLPWLGGSRAPPQPSGSR -	1861.10	2	347.34	1.07	0.1	105	4/17	1
jmfag5miniggbead, 2497	- PTRPEPLYVNLALGPRGPSPASSSSSSPPAHPR -	3381.75	2	46.79	0.76	0.0	60	1/8	1
rawsucrfp_60MeOHphagigg_Mar04, 1184	- PGGSSWKTFFALGRGPSIPR -	2119.41	3	431.27	1.36	0.1	239	4/19	1
phagrawFsuc450_dec20, 2702	- APWGPHTPHRVPGPWGSPEPFLLYR -	2853.23	2	341.68	0.97	0.1	145	11/48	1
jmfagtmecont10min_030601202502, 1514	- LARRPTR.-	870.04	2	386.77	1.02	0.1	331	2/3	1
jmbeadsactinrawphag3007, 1565	- CIFDRRFSCLPELPPPPEGTR -	2431.82	3	259.16	1.21	0.0	213	7/40	
rawsucrfp_60MeOHphagigg_Mar04, 1184	- PGGSSWKTFFALGRGPSIPR -	2119.41	3	431.27	1.36	0.1	239	4/19	1
rawphag2007chlfsol1, 2138	- PAPPSYGRGGEVRGSLYR.-	1920.12	2	406.66	1.21	0.1	137	9/34	1

sorting nexin 26; TC10/CDC42 GTPase-activating protein [Mus musculus]					**1838.90**	30142699.0	19		
rawextr_actinbeadigg_Mar04,509-511	- GPSIPRK.-	754.90	2	123.41	1.21	0.0	94	1/2	1
FPbeads700_Dec19, 1167	- LGTPTEPTTPKTPASPVER -	1980.21	3	259.26	1.12	0.0	213	13/72	1
rawextr_400beadigg_Mar04, 1768	- PSEAMSVPGEEER -	1468.57	2	398.21	1.01	0.1	367	5/12	1
jmbsa400nacirawphag3007_030802153340, 1455	- AQQVAEQQSQQEQGGTPPAPHSPFRR.-	2861.04	3	747.36	1.39	0.2	212	3/20	1
jmbsa1000nacirawphag3007, 1693	- CCSEFIEAHGVVDGIYR.-	1899.14	2	310.66	0.98	0.1	104	9/32	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
cell cycle p34 CDC2 kinase protein [Mus musculus]					**2668.32**	20066967.0	11		
JMFAGNACL15B21E3, 946	-.AFGIPIRVYTHEVVTLWYR.-	2321.71	3	288.15	1.42	0.0	195	5/24	4
jmfag5minigg350mmnacl, 1057	-.KPLFHGDSEIDQLFR.-	1803.01	3	1249.46	1.66	0.0	751	23/56	4
jmfag5minigg600mmnacl, 1644	-.KPLFHGDSEIDQLFRIFR.-	2219.53	3	197.05	1.16	0.0	169	13/68	4
jmIgG350naclrawphag3007, 1709	-.ISGKMALKHPYFDDLDNQIK.-	2334.68	3	165.23	0.94	0.0	152	15/76	5
JMFAGNACL10_1B21E3, 2322	-.LADFGLARAFGIPIR.-	1617.92	2	172.70	1.23	0.0	128	9/28	5
jmfagfrench5minigg1mnacldtt, 2339	-.LADFGLARAFGIPIR.-	1617.92	3	595.73	1.40	0.1	295	9/28	5

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
p34 cdc2 kinase [Mus musculus] musculus] mify membe					**3022.15**	1575290.0	5		
jmfag5minigg1000mmnacl, 320	-.HRVTGQIVAMKK.-	1368.68	3	202.05	1.19	0.1	94	13/44	4
jmfag5minigg1000mmnacl, 1448	-.MEDYIKIEK.-	1169.37	1	787.34	1.54	0.0	510	9/16	3
jmfag1mnacl0minigg, 1624	-.LYLIFEFLSMDLKK.-	1761.16	2	966.94	2.04	0.1	360	11/26	4
jmfag5minfrench1mnacldttdpi,2200-2202	-.LYLIFEFLSMDLKK.-	1761.16	2	532.91	1.87	0.1	210	9/26	4
jmfag_20_minfrench1mnacldttdpi,2200-2202	-.LYLIFEFLSMDLKK.-	1761.16	2	532.91	1.87	0.1	210	9/26	4

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
CDC2-related protein kinase 7; protein kinase for splicing component [					**4269.32**	30794424.0	25		
ajrawphagjun20actinDPI, 394	-.NNSPAPPQPAPVK.-	1317.48	2	1081.50	1.59	0.1	506	1/2	1
jmrawgg5min150mmnacl, 1792	-.NFLHQDIKCSNILVNNSGQIR.-	2414.73	2	58.39	1.07	0.0	43	7/40	
jmfag1mnacl0minigg, 1832	-.FDIIGIIGEGTYGQVYKAKDK.-	2316.64	3	980.05	1.60	0.2	307	9/40	2
ajrawphagactin20, 1950	- STPDTELVTVAHSNPEVKHCLDTGK -	2679.95	3	362.96	1.26	0.1	246	3/16	1
jmfagfrench5minigg1mnacldtt, 2103	-.TQEPAGNLEENTNDKNSGPQGPRR.-	2610.70	3	226.42	1.24	0.0	179	17/92	1
jmrawgg5min1mnacl, 2217	-.ETTSGTTAEPVK.-	1221.30	1	173.60	1.11	0.0	155	4/11	1
jmfag5minigg400mmnacl, 2938	- EQRTRHLLTDLPLPPELPGGDPSPPDSPEPK.-	3387.75	2	267.88	0.91	0.2	24	1/10	1
jmfag1mnacl0minigg, 3060	- DVKPVAPKEVIVTSK -	1610.92	2	1118.52	1.13	0.3	237	5/14	1

control

CDC2-related protein kinase 7; protein kinase for splicing component [					**1835.76**	30794424.0	14		
rawextr_300bead_Mar04, 1374	-.ETTSGTTAEPVKNNSPAPPQPAPVK.-	2519.75	2	679.04	1.58	0.2	124	5/24	
rawextr_300bead_Mar04, 1600	- SFMKQLMEGLDYCHK.-	1831.17	2	173.09	1.19	0.0	145	2/7	
FPbeads150_Dec19, 1747	-.PIFQANLELAQLELISR -	1956.28	2	428.44	1.18	0.1	150	1/4	
rawextr_250bead_Mar04, 2012	-.STPDTELVTVAHSNPEVKHCLDTGK.-	2679.95	3	555.18	1.56	0.1	253	11/48	

APPENDIX D – RECEPTORS SUMMATION OF IONS

The summation of peptides from receptors found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
CD36_MOUSE Platelet glycoprotein IV (GPIV) (GPIIIB) (CD36 antigen) (PAS IV) (PA					**3309.04**	729081.0		14	
JMFAGNACL10_1821E3, 1526	-.VFNGKDNISKVAIIESYK.-	2026.32	3	211.06	1.51	0.0	139	19/68	1
AJRAWActinIgG_june13, 1962	- FVLPANAFASPLQNPDNHCFCTEK -	2665.00	3	523.74	1.66	0.0	313	5/23	1
jmIgG400rawphag3007, 2340	-.PYIVPILWLNETGTIGDEKAEMFK.-	2766.21	3	1388.59	1.50	0.3	211	4/23	2
jmfag5minigg1000mmnacl, 2802	-.NCGLIAGAVIGAVLAVFGGILMPVGDMLIEK.-	3043.74	2	213.44	1.01	0.1	104	3/20	
jmfag5minigg450mmnacl_030527025134, 2818	- IKLLGMVEMALLGIGVVMFVAFMISYCACKSK.-	3468.43	2	84.29	0.80	0.1	45	7/62	2
jmbeads300rawphag3007, 886	- TIKREVVLEEGTTAFK.-	1822.10	3	457.11	1.43	0.0	319	17/60	1
jmfreebeadsrawphag3007, 1158-1160	-.SIYAVFGSEIDLK.-	1442.84	2	302.43	1.49	0.0	190	7/24	1
phagrawFActin_dec23, 914	-.LQVNILVKPAR.-	1251.55	3	128.38	0.84	0.0	146	3/10	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
CD36_MOUSE Platelet glycoprotein IV (GPIV) (GPIIIB) (CD36 antigen) (PAS IV) (PA					**1353.63**	729081.0		2	
rawextr_400bead_Mar04,571-573	- FFSSDICR.-	975.10	1	320.73	1.17	0.0	273	1/2	1
rawextr_450bead_Mar04,676-678	-.FFSSDICR.-	975.10	1	730.46	1.38	0.1	417	9/14	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulin-like growth factor binding protein 7 [Mus musculus]					**4620.89**	6679869.0		9	
jmrawigg5minbeadsfreazethaw, 1204	- GEKAITQVSKGTCEQGPSIVTPPK.-	2456.80	3	288.10	1.60	0.0	170	9/46	1
jmfag5minigg200mmnacl,1376-1378	-.EDAGEYECHASNSQGQASAAAK.-	2225.25	3	1009.66	1.90	0.0	513	23/84	2
ajrawphagjun20actinDPI, 1572	-.GTCEQGPSIVTPPK.-	1414.61	2	179.22	0.86	0.1	114	5/13	2
jmkdl250naclrawphag3007, 1584	-.ENLAIQTRGGPEKHEVTGWVLVSPLSK.-	2947.34	3	619.88	1.45	0.1	271	19/104	2
jmkdl250naclrawphag3007, 1594	-.TELLPGDRENLAIQTRGGPEK.-	2295.54	3	760.29	1.62	0.1	321	19/80	2
jmkdl150naclrawphag3007, 1762	-.KGKAGAAAGGPATLAVCVCK.-	1774.15	2	146.31	0.99	0.1	100	6/19	1
AJRAWSoluteContr_june13, 1236	-.KGKAGAAAGGPATLAVCVCK.-	1774.15	2	464.61	1.21	0.0	377	6/19	1
jmfagtimecont0min_030601230741, 1748	-.GEKAITQVSKGTCEQGPSIVTPPK.-	2456.80	3	1152.82	2.20	0.1	329	13/46	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulin-like growth factor binding protein 7 [Mus musculus]					**1835.57**	6679869.0		4	
rawextr_800bead_Mar04, 868	-.ITVVDALHEIPLK.-	1448.73	2	501.67	1.67	0.1	271	3/8	2
rawextr_800beadigg_Mar04, 1700	-.KGKAGAAAGGPATLAVCVCK.-	1774.15	2	837.16	1.55	0.2	171	5/19	1
jmbsa250naclrawphag3007,587-589	-.ITVVDALHEIPLKKGEGAQL.-	2132.49	3	496.74	1.49	0.0	333	4/19	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Insulin degrading enzyme [Mus musculus] n [Mus mus					**3375.75**	27371196.0		8	
jmfag5minigg400mmnacl, 1212	-.FEIIKEAYMR.-	1300.55	2	745.69	1.15	0.2	232	4/9	1
jmag5mincon500mmnacl, 2374	-.LRAEGPQEWVFQECKDLNAVAFR.-	2708.05	3	227.91	1.39	0.0	162	15/88	1
ajrawphagjun20dpi1MNaCl, 1142	-.SILGARPPPAK.-	1107.33	2	179.58	0.95	0.1	156	2/5	1
jmIgG400rawphag3007, 1738	- DATPYPALIKDTAMSK.-	1722.99	2	150.18	1.16	0.1	88	1/5	2
jmIgG1000naclrawphag3007, 1816	-.DREVNAVDSEHEKNVMNDAWR.-	2515.66	3	291.01	1.51	0.1	91	7/40	1
jmIgG1000naclrawphag3007, 1816	-.DREVNAVDSEHEKNVMNDAWR.-	2515.66	3	291.01	1.51	0.1	91	7/40	1
jmkdl1000naclrawphag3007, 1956	-.QEAIPEDIIQKWQNADLNGKFK.-	2586.89	3	627.22	1.58	0.1	236	4/21	
jmrawigg5miniggfreebead, 2146	-.TLTKDDIIRFYQEMLAVDAPR.-	2496.87	3	431.98	1.28	0.1	193	3/16	1
jmkdl150naclrawphag3007, 2790	-.RYNDKQPILLK.-	1388.64	2	431.16	1.26	0.1	313	9/20	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Insulin degrading enzyme [Mus musculus] containing					**476.82**	27371196.0		9	
rawextr_450bead_Mar04, 1542	-.FHSTYYSSNLMAICVLGRESLDDLTNLVVK.-	3390.88	3	150.98	0.99	0.1	90	7/58	1
rawphag2007chlfsol1, 1588	-.NGLVWLLHPALPGTLRSILGARPPPAK.-	2846.41	3	61.21	1.26	0.0	37	17/104	1
FPbeads1000_Dec19, 2730	-.TDRTEQWYGTQYKQEAIPEDIIQK.-	2942.19	2	264.63	0.96	0.1	131	9/46	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulinoma-associated 1; insulinoma-associated protein (IA-1) [Mus musc					7882.34	8393617.0	17		
jmraw5minigglowonic, 385	- SARSCGRR -	893.01	2	630.82	1.20	0.0	505	9/14	
JMFAGNACL10_1B21E3, 426	- APSAKKPK -	827.01	2	891.00	1.26	0.0	702	5/7	
JMFAGNACL5B21E3, 482	- ALLLSPGCGGAR.-	1115.33	2	424.64	1.40	0.1	120	9/22	
jmfag1mnacl7.5minigg, 622	- IRIRLR -	827.06	2	150.99	1.04	0.0	126	3/5	
jmIgG250rawphag3007, 1370	- LHFEDEVTTSPVLGLKIKEGPLEAPR.-	2877.28	3	361.67	1.74	0.0	206	9/50	
jmraw5minigg250mmnaclsyringdnase,1540-1542	- LHFEDEVTTSPVLGLKIKEGPLEAPR.-	2877.28	3	450.97	1.92	0.0	230	19/100	
ajrawphagjun20dpi1MNaCl, 1662	- PVSREHEKHK.-	1247.39	1	370.76	1.27	0.1	75	1/3	
jmfag5minigbead_030528200105, 801	- APSAKKPK.-	827.01	2	195.55	0.73	0.1	118	3/7	
jmldlactinrawphag3007,828-830	- APSAKKPK.-	827.01	2	482.83	1.33	0.0	347	4/7	
jmldi350naclrawphag3007, 1338	- LHFEDEVTTSPVLGLKIKEGPLEAPR -	2877.28	3	293.41	1.55	0.0	170	3/20	
phagrawF450_dec20, 912	- LHFEDEVTTSPVLGLKIKEGPLEAPR -	2877.28	3	801.29	2.00	0.1	251	9/50	
phagrawFsuc450_dec20, 1734	- LHFEDEVTTSPVLGLKIKEGPLEAPR -	2877.28	3	495.04	1.67	0.1	255	1/5	
jmbeads1000naclrawphag3007, 146	- KSTPVSYRVR.-	1193.38	3	518.80	1.45	0.1	215	13/36	
jmbeadsactinrawphag3007, 1193	- GRAGGAARPLGEFICQLCK -	1948.31	3	452.67	1.46	0.1	284	7/24	
jmfag5mincon300mmnacl, 2310	- CPECAKVFSCPANLASHR.-	1934.26	3	1361.90	1.56	0.1	848	25/68	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulin receptor substrate 1 [Mus musculus]					10649.26	29825829.0	18		
rawsucrfp_1000phagigg_Mar04, 1315	- AGNTVPFGAGAAVGGSGGGGGGGSEDVK.-	2291.38	3	2450.19	2.41	0.2	454	25/108	1
jmrawf5minbsareebeads, 1486	- PTFVHILDRIQDELR -	1853.12	3	671.74	1.56	0.1	336	5/14	
JMMAGTube1B16E3,612-614	- AASEAGGPAR.-	886.93	2	888.18	1.46	0.2	234	5/9	1
JMFAGNACL10_1B21E3, 536	- RSSEDLSNYASISFQK.-	1832.95	3	572.28	1.58	0.1	312	3/10	1
jmfag5minigg350mmnacl, 567	- AASEAGGPAR -	886.93	2	493.80	1.19	0.1	218	4/9	1
jmfag5minigg150mmnacl,580-582	- AASEAGGPAR.-	886.93	2	207.44	0.98	0.1	187	7/18	1
jmrawgg5min450mmnaclsd, 662	- AASEAGGPAR.-	886.93	2	82.38	0.95	0.0	86	4/9	1
jmfagfrench5minigg1mnacldtt, 693	- LSSSSGRLR.-	963.08	2	397.53	1.37	0.0	288	1/2	1
ajrawphagjun20dpi1MNaCl, 728	- AASEAGGPAR -	886.93	2	188.27	0.92	0.0	194	4/9	1
jmfagfrench20minigg1mnacldtt,732-734	- AASEAGGPAR -	886.93	2	537.49	1.39	0.1	199	4/9	1
jmIgG150rawphag3007, 990	-.AASEAGGPAR -	886.93	2	161.36	1.03	0.0	141	1/3	1
jmrawrminigg200mmnaclsyringdnas, 1018	-.AASEAGGPAR.-	886.93	2	516.35	1.10	0.2	111	7/18	1
ajrawphagactin20, 1392	-.AGNTVPFGAGAAVGGSGGGGGGGSEDVK.-	2291.38	3	1274.26	1.65	0.2	236	25/108	1
jmfag5minigg200mmnacl, 1456	-.VNLSPNHNQSAKVIR -	1677.89	2	158.27	0.88	0.0	175	2/7	1
jmrawrminigg200mmnaclsyringdnas, 1848	-.VDTAAQTNSRLAR.-	1403.53	2	115.82	0.86	0.0	126	1/3	1
ajrawphag1MNaCl20, 2134	-.VREQQQQQQSSLHPPEPK.-	2145.32	3	136.99	1.12	0.0	122	15/68	1
JMFAGNACL15B21E3, 2240	- YIPGANLGTSPALPGDEAAGAADLDNR.-	2627.81	3	611.21	1.34	0.1	358	5/28	1
jmfag5minigg500mmnacl, 3714	-.LSSSSGRLRYTATAEDSSSSTSSDSLGGGYCGAR.-	3375.50	2	72.37	0.81	0.1	54	4/33	1
rawphag2007chlfbead3, 689	-.AASEAGGPAR.-	886.93	2	427.27	1.12	0.1	223	4/9	1
rawsucrfp_60MeOHphagigg_MAr04, 854	-.EVWQVILKPK.-	1240.52	2	183.96	0.85	0.0	216	4/9	1
RawPhg2007MeEthmeth3digest, 1486	-.ASSDGEGTMSR.-	1098.13	2	282.41	1.18	0.1	203	9/20	1
jmldi150naclrawphag3007, 1278	-.AASEAGGPAR.-	886.93	2	130.67	1.00	0.0	123	1/3	1
rawphag2007chlfsol2, 2406	- SIPMPSSR -	875.03	1	87.03	1.05	0.0	82	3/7	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulin receptor substrate 1 [Mus musculus]					7257.97	29825829.0	13		
rawextr_350beadigg2_Mar04, 330	-.LARPTR.-	713.85	2	138.92	0.79	0.0	172	3/5	1
rawextr_chlfbeadIgG_Mar04, 686	-.AASEAGGPAR.-	886.93	2	443.36	1.16	0.1	284	1/2	1
rawextr_700beadigg_Mar04,808-810	- AASEAGGPAR.-	886.93	2	359.68	1.30	0.1	251	5/9	1
rawextr_60MeOHbeadigg_Mar04, 850	-.AASEAGGPAR.-	886.93	2	277.18	1.12	0.1	194	4/9	1
rawextr_350beadigg2_Mar04, 924	- AASEAGGPAR.-	886.93	2	253.75	1.08	0.1	190	4/9	1
rawextr_350beadigg_Mar04,936-938	-.AASEAGGPAR.-	886.93	2	406.15	1.28	0.1	253	4/9	1
jmrawgg5minigfreebead,972-974	-.EVWQVILK.-	1015.23	2	296.30	1.58	0.0	174	5/7	1
rawextr_350beadigg2_Mar04,1318-1320	-.AGNTVPFGAGAAVGGSGGGGGGGSEDVK.-	2291.38	3	1717.45	2.26	0.1	672	7/27	1
rawextr_450beadigg_Mar04, 1322	- AGNTVPFGAGAAVGGSGGGGGGGSEDVK.-	2291.38	3	794.52	2.01	0.0	392	2/9	1
rawextr_300beadigg_Mar4, 1772	- SPGEYVNIEFGSGQPGYLAGPATSR -	2555.74	2	356.69	1.61	0.1	53	3/16	1
FPbeads500_dec19, 2026	- AGNTVPFGAGAAVGGSGGGGGGGSEDVK.-	2291.38	2	788.39	1.23	0.2	199	2/9	1
FPbeads800_Dec19, 2518	- SSFRSVTPDSLGHTPPARGEEELSNYICMGGK.-	3424.77	3	467.20	1.19	0.0	389	23/124	1
rawextr_300beadigg_Mar4, 2760	-.AGNTVPFGAGAAVGGSGGGGGGGSEDVK.-	2291.38	3	958.37	1.39	0.1	632	1/4	1
rawextr_700bead_Mar04, 611	-.AASEAGGPAR.-	886.93	2	349.01	1.34	0.1	235	1/2	1
rawextr_150bead_Mar04, 697	-.PASVDGSPVSPSTNR.-	1471.56	3	645.36	1.34	0.0	481	19/56	1
rawextr_chlfbead_Mar04, 886	-.AASEAGGPAR.-	886.93	2	262.22	1.29	0.1	134	1/3	1
rawextr_450bead_Mar04, 2258	-.HOHLRLSSSSGRLR.-	1634.83	2	206.35	1.06	0.1	168	4/13	1
rawextr_250bead_Mar04, 2736	-.ESAPVCGAAGGLEKSLNYIDLDLAKER.-	2821.16	2	140.64	0.86	0.1	56	7/52	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
IRS2_MOUSE INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS)					**8423.91**	3024044.0	1		
jmraw5minbsareebeads, 844	-.LCLSARTIGFVK.-	1308.62	3	477.18	1.77	0.0	269	4/11	1
JMMAGTube1B18E3, 128	-.LCLSARTIGFVK.-	1308.62	3	316.51	1.34	0.0	230	15/44	1
jmfag5minigg1000mmnacl, 522	-.RVSGDGAQDLDR.-	1289.34	3	265.38	1.72	0.0	153	13/44	1
jmfag5minigg400mmnacl, 704	-.ADPQGGRRR.-	1013.10	2	154.59	1.06	0.0	144	7/16	2
jm5minggrawlowionic, 978	-.LCLSARTIGFVK.-	1308.62	3	994.64	1.74	0.1	420	21/44	1
JMFAGNACL5B21E3, 1578	-.RFFVLRGPGTGGDEASAAGGSPPQPPR.-	2682.94	3	348.77	1.90	0.0	173	19/104	1
jmfag5minigg150mmnacl, 1616	-.LCLSARTIGFVK.-	1308.62	2	162.74	0.94	0.0	164	4/11	1
ajrawphagjun20dpr1MNaCl, 1752	-.VIALDCCLNINKR.-	1475.81	3	248.02	1.32	0.0	182	1/4	1
jmigg600rawphage3007, 1912	-.MWCGSKLSMENPDPK.-	1724.02	2	71.80	1.00	0.0	72	2/7	2
jmraw5minigglowionic, 2231	-.QVPQPSSASLDEYTLMRATFSGSSGR.-	2774.02	3	641.36	1.43	0.1	357	1/5	1
JMFAGNACL10_1B21E3, 2738	-.QILQPRLAAALPPSGAAVPAPPSGVGR.-	2593.02	3	1186.34	1.57	0.1	638	25/104	2
jmfagtimecon2.5min 3096.3096.2	-.SPKPSTRSGDTVGSMDGLLSPEASSPYPPLPPR.-	3382.75	0	257.19	0.90	0.1	146	5/32	2
jmfag5mincont350, 140	-.LCLSARTIGFVK.-	1308.62	3	419.08	1.55	0.1	237	9/22	1
jmfag5mincont350, 472	-.LSMENPDPK.-	1031.17	2	214.96	1.27	0.0	158	1/2	2
jmfagcont5minbead, 878	-.LCLSARTIGFVK.-	1308.62	3	517.93	1.34	0.1	258	4/11	1
AJRAWpellet1_contr_jun13, 1054	-.HKYLIALYTK.-	1250.52	2	272.99	0.88	0.1	158	4/9	1
jmfag5mincont200mmnacl, 2894	-.SKSQSSGSSATHPISVPGAR.-	1942.08	2	129.53	0.90	0.0	142	9/38	1
phagrawFsuc200_dec22, 1169	-.PEGFLGQRCRAVR.-	1489.73	3	785.61	1.36	0.0	568	3/8	2
phagrawFsuc700_dec23, 1209	-.PEGFLGQRCR.-	1163.34	2	142.42	0.98	0.0	131	1/3	2
phagrawF200_dec22, 1243	-.SDDYMPMSPTSVSAPK.-	1713.91	2	122.10	0.74	0.1	130	4/15	2
phagrawF250_dec22, 2577	-.SQSSGSSATHPISVPGAR.-	1726.83	2	694.78	1.16	0.2	147	4/17	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
IRS2_MOUSE INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS)					**2538.66**	3024044.0	16		
rawextr_actinbeadigg_Mar04, 1139	-.DGSGGELYGYMSMDRPLSHCGR.-	2389.64	3	797.39	1.93	0.0	389	5/21	1
rawextr_450beadigg_Mar04, 2220	-.SRTDSLAATPPAAKCTSCR.-	1937.19	3	612.29	1.46	0.1	282	1/4	1
rawextr_1000_beadigg_Mar04, 2549	-.TASEGDGGAAGGAGTAGGRPMSVAGSPLSPGPVR.-	2954.18	2	232.32	1.12	0.1	54	5/33	1
rawextr_chlfbead_Mar04, 1702	-.ETSVGFQNGLNYIAIDVR.-	1997.20	3	376.09	1.28	0.1	261	4/17	2
rawextr_actinbead_Mar04, 2760	-.TASEGDGGAAGGAGTAGGR.-	1520.50	2	520.57	1.26	0.1	254	11/36	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulin receptor substrate 4 [Mus musculus]					**10812.64**	6754372.0	12		
jmfreebeadsrawphag3007, 606	-.DVWQVVVKPRGLGHR.-	1747.04	3	3366.48	2.23	0.4	198	15/56	
JMFAGNACL10_1B21E3, 1106	-.DVWQVVVKPRGLGHR.-	1747.04	3	621.59	1.44	0.1	405	17/56	
jmfag5minigg350mmnacl, 1871	-.PGDGHGSGGGKNSGSGKNSDDGDR.-	2216.14	3	387.18	1.43	0.0	254	5/23	
jmrawigg5min300mmnaclsyringednase, 519	-.ALCADEYRAR.-	1168.31	2	492.64	1.18	0.1	286	11/18	
JMFAGNACL10_1B21E3, 1106	-.DVWQVVVKPRGLGHR.-	1747.04	3	621.59	1.44	0.1	405	17/56	
jmfag5minfrench1mnacldttdpi, 1256	-.NSGSGKNSDDGDR.-	1309.24	2	374.39	0.97	0.1	249	3/8	
jmfag_20_minfrench1mnacldttdpi, 1256	-.NSGSGKNSDDGDR.-	1309.24	2	374.39	0.97	0.1	249	3/8	
jmraw5minigg600mmnaclsd, 1266	-.ALCADEYRAR.-	1168.31	2	213.38	1.34	0.0	154	1/2	
jmrawgg5minbeadsfreezethaw, 1408	-.RCGTLGALPDGEPAALAAAAAAEPPFYK.-	2730.09	3	1022.80	1.51	0.2	271	11/54	
jmfag5minigg350mmnacl, 1871	-.PGDGHGSGGGKNSGSGKNSDDGDR.-	2216.14	3	387.18	1.43	0.0	254	5/23	
jmrawigg5minbeadsfreezethaw, 3014	-.ALAVVSALAAAPSIGDVFAGFRAAAGVDSASAR.-	3061.44	2	70.41	0.67	0.0	94	9/64	1
jmfagtimecon7.5min.1294.1294.3	-.DVWQVVVKPRGLGHR.-	1747.04	0	323.30	1.57	0.0	186	1/4	
jmfagtimecon7.5min.1230.1232.2	-.FRHSVR.-	801.92	0	68.28	0.81	0.0	59	3/5	
jmfagcon5minn600mmnacl, 375	-.EPPPPFR.-	839.96	2	197.67	0.89	0.0	207	2/3	
AJRAWSoluteContr_june13, 872	-.PKPLNPTQERR.-	1336.53	2	221.12	1.21	0.0	180	1/2	1
jmfagcont5minbead,996-998	-.RAASVPPSLFR.-	1201.40	2	258.39	1.30	0.1	74	7/20	
jmbeads600naclrawphage3007, 1359	-.AREASGSSSGNTEEK.-	1510.50	2	236.96	1.41	0.1	137	5/14	
phagrawFsuc1000_dec23, 1009	-.MASCSFSGHQALRRLR.-	1821.13	2	162.40	0.97	0.1	80	1/5	
phagrawF250_dec22, 1469	-.IPQPEDVPNDRAR.-	1507.63	2	189.55	0.94	0.0	202	3/8	
phagrawFsuc450_dec20, 1754	-.AAAGVDSASARGFQPVAGAQAVR.-	2158.36	2	122.37	0.97	0.0	126	5/22	1
phagrawF450_dec20, 1952	-.GDCIPMNNWGSGNGRGSGGGRGSSGQGSSSQGSGGR.-	3327.41	2	14.82	0.67	0.0	21	3/35	
phagrawF400_dec20, 1990	-.AAVSAFPTDSLDRDFPAASAVIAAPAEAPLLAVSR.-	3469.89	2	229.65	0.88	0.1	96	5/34	1
phagrawFsuc300_dec20, 2618	-.RCGTLGALPDGEPAALAAAAAAEPPFYK.-	2730.09	3	221.47	1.40	0.0	157	7/36	
phagrawFsuc300_dec20, 2768	-.APDTNKGDDSKDNDSDSDYMFMAPGAGAIPK.-	3232.42	2	634.62	1.10	0.2	118	1/6	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulin receptor substrate 4 [Mus musculus]					**4159.47**	6754372.0	18		
rawextr_150beadigg2_Mar04, 232	-.RYGLEQFCRLR.-	1441.69	2	467.26	1.48	0.1	210	2/5	
rawextr_actinbeadigg_Mar04, 559	-.PLNPTQERR.-	1111.24	3	441.92	1.50	0.1	264	13/32	1
rawextr_chlfbeadIgG_Mar04, 782	-.GSSGQGSSSQGSGGR.-	1296.24	2	422.46	0.95	0.1	310	11/28	
rawextr_chlfbeadIgG_Mar04, 2198	-.AFDEDEDDPYVPMR.-	1699.78	2	111.11	1.02	0.1	71	5/26	
rawextr_800bead_Mar04, 724	-.ALCADEYRAR.-	1168.31	2	465.54	1.40	0.0	330	5/9	
rawextr_200bead_Mar04, 2396	-.SQSLFASTRAAVSAFPTDSLDR.-	2328.52	3	716.42	1.71	0.1	255	3/14	1
jmbsa150naclrawphag3007,1175-1177	-.RLRASAAAAASAALAAVATTPFLSSGTR.-	2661.01	3	1117.82	2.26	0.2	202	11/54	
jmbsa600naclrawphag3007, 1538	-.YGLEQFCRLRAIR.-	1625.92	2	92.30	0.81	0.0	112	1/4	
jmbsa300naclrawphag3007, 1564	-.RVIILYQCFSVSQR.-	1713.04	2	129.52	1.16	0.1	65	3/13	
jmbsa350naclrawphag3007, 1850	-.IPQPEDVPNDRAREASGSSSGNTEEK.-	2771.85	3	195.13	1.02	0.0	177	3/20	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Insulin receptor-related receptor [Mus musculus]					**5279.32**	6754362.0	21		
jmfag5minigg250mmnacl, 746	- TLRFVFNLTEEDR.-	1640.82	3	211.15	1.19	0.0	178	7/24	1
jmfag1mnacl0minigg, 938	-.VEFLKEASVMK.-	1281.55	2	179.89	0.82	0.1	104	3/10	
jmIgG350naclrawphag3007, 1773	-.TNGDRAACQTR.-	1193.28	2	92.94	0.83	0.0	90	1/4	1
AJRAWActinIgG_june13, 1938	-.KFENFLHHAITIPK.-	1695.99	2	350.53	1.31	0.1	218	9/26	
jmraw5minigg500mmnaclsd, 2908	-.LENCSVVEGHLQILLMFAATGEDFRGLSFPR.-	3451.96	2	230.53	0.83	0.1	79	3/20	1
JMFAGNACL10_1B21E3, 2984	-.DVGLPSLGAVLRGAVRVEK -	1937.28	1	30.75	0.73	0.0	35	1/6	1
jmfag1mnacl5minigg, 3048	-.LFLGYALIIFEMPHLRDVGLPSLGAVLR -	3112.77	2	50.07	0.79	0.0	40	7/54	1
JMFAGNACL15B21E3, 3110	-.IDIHACNHAAHTVGCSAATFVFARTMPHR.-	3136.59	2	72.27	0.74	0.0	97	9/56	
phagrawF600_dec20, 499	-.LGEEATVLCVSR.-	1277.47	3	137.42	1.34	0.0	98	5/22	
phagrawFsuc250_dec22, 2629	-.GMACTAGGDCCHSECLGGCSQPEDPR.-	2585.86	3	572.61	1.40	0.0	399	23/100	1
rawsucrfp_700phagigg_Mar04, 2879	- ACVACRHLYFQGVCLRACPPGTYQYESGR.-	3250.75	2	21.61	0.77	0.0	28	5/56	
phagrawFsuc400_dec20, 3424	- DVGLPSLGAVLRGAVR.-	1580.86	2	1999.03	1.54	0.3	221	3/10	1
jmfagtimecon2.5min.1128.1128.3	-.KFENFLHHAITIPK.-	1695.99	0	961.62	1.83	0.1	484	9/26	
jmfag5mincont150mmnacl, 393	- NNSDFEIQEDK.-	1339.35	3	368.91	1.19	0.0	309	7/20	

control

Insulin receptor-related receptor [Mus musculus]					**1082.56**	6754362.0	9		
rawextr_900bead_Mar04,982-984	-.HRREAGLLR.-	1108.28	1	241.14	1.09	0.1	177	7/16	
rawextr_chlfbead_Mar04, 1800	- DVGLPSLGAVLRGAVRVEK.-	1937.28	2	161.07	1.01	0.1	134	2/9	1
rawextr_chlfbead_Mar04, 1940	-.LRYAKVGGVHLALLPPGNYSAK.-	2325.74	3	680.36	1.38	0.1	455	11/42	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Insulin-like growth factor binding protein 6 [Mus musculus]					**2926.88**	6680387.0	1		
jmraw5minbsareebeads, 2936	-.RGPCWCVDPMGQPLPVSPDGQGSTQCSARSSG -	3262.63	2	147.17	0.83	0.1	26	3/31	1
JMMAGTube1B16E3, 842	-.ENEETPLRALLIGQGR -	1797.01	3	232.12	1.34	0.0	172	17/60	
AJRAWActinIgG_june13, 1308	- ENEETPLRALLIGQGR.-	1797.01	3	420.11	1.59	0.1	209	4/15	
jmraw5minigg500mmnaclsd, 2112	- GPCWCVDPMGQPLPVSPDGQGSTQCSAR.-	2875.24	3	1282.12	1.86	0.2	360	7/36	1
ajrawmediapbsnocells, 618	- ENEETPLR.-	988.04	2	585.31	1.21	0.2	114	4/7	
jmbeads600naclrawphage3007,979-981	-.ENEETPLRALLIGQGR.-	1797.01	3	260.04	1.48	0.1	136	7/30	

control

Insulin-like growth factor binding protein 6 [Mus musculus]					**1141.87**	6680387.0	4		
rawextr_450beadigg_Mar04, 950	- ENEETPLRALLIGQGR -	1797.01	3	684.65	1.62	0.2	142	7/30	
FPbeads250_Dec19, 1392	- ENEETPLRALLIGQGR -	1797.01	3	457.22	1.52	0.1	174	4/15	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulinoma-associated 2; mit 1 gene; mit 1 [Mus musculus]					**5150.44**	9938006.0	14		
jmfreebeadsrawphag3007, 942	-.RGKGAPICASAPAAVR.-	1525.81	2	315.35	1.02	0.0	307	2/5	
jmrawgg5min150mmnacl, 1148	-.GKGAPICASAPAAVRK.-	1497.79	2	70.81	0.77	0.0	74	7/30	
jmfag5minigg350mmnacl, 1155	-.CPECDKVFSCPANLASHR.-	1978.27	3	787.41	1.33	0.2	184	7/34	
jmIggactinrawphag3007, 1202	-.PTPACAASK.-	845.99	2	104.46	0.85	0.1	94	3/8	
jmraw5minigglowionic,1639-1641	-.IKEEEPGAPAR.-	1197.32	2	462.89	1.22	0.1	325	9/20	
ajrawphagactin20,2534-2536	-.IKEEEPGAPAR.-	1197.32	2	382.53	1.00	0.0	381	1/2	
jmldl400naclrawphag3007_030802153313, 1940	-.EEEPGAPARALGGVR.-	1509.65	2	182.70	0.90	0.1	117	1/4	
phagrawFsuc400_dec20, 1300	-.CPECDKVFSCPANLASHR.-	1978.27	3	969.31	1.47	0.2	347	9/34	
rawsucrfp_300phagigg_Mar04,1537-1539	-.IKEEEPGAPAR.-	1197.32	2	431.84	1.01	0.1	331	11/20	
phagrawF1000_Dec23, 1914	-.HGPGSSGASAGATSEVFVCPYCHKKFR.-	2782.11	3	360.62	1.46	0.1	198	19/104	
phagrawF300_dec20, 2045	-.TPLGEFICQLCKHQYADPFALAQHR.-	2888.32	3	515.52	1.53	0.0	333	3/16	
phagrawFsuc250_dec22, 2497	-.GLLGSPCLAPPQDDAEWGAGGGDGPGPSPAK.-	2876.11	3	397.96	1.50	0.0	264	7/40	
phagrawFsuc600_dec20, 3640	-.EELLLPALVGAPSEAGPGGASDGSAQQIFSCK.-	3101.44	2	169.04	0.92	0.1	54	5/31	

control

insulinoma-associated 2; mit 1 gene; mit 1 [Mus musculus]					**801.78**	9938006.0	6		
FPbeads250_Dec19, 1318	-.PGLQALVYPEAAR.-	1385.59	2	352.25	1.29	0.0	271	3/8	
rawextr_1000_beadigg_Mar04, 1530	- IKEEEPGAPAR.-	1197.32	2	196.60	0.98	0.0	193	9/20	
jmbsa300naclrawphag3007, 119	- GFLVKRTK.-	949.18	3	252.94	1.63	0.0	155	5/14	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulin-like growth factor I receptor [Mus musculus]					**4293.95**	33859572.0	24		
JMFAGNACL15B21E3, 324	-.ANERALPLPQSSTC.-	1487.67	3	597.09	1.35	0.1	371	17/52	
ajrawphagjun20actinDPI,554-556	-.HSHALVSLSFLK.-	1339.57	2	454.66	1.34	0.1	130	7/22	
jmfag5minigg250mmnacl, 2134	-.NCMVAEDFTVK.-	1257.46	2	295.13	1.02	0.0	288	2/5	
jmiggactinrawphag3007, 2260	-.RLENCTVIEGFLHILLISKAEDYR.-	2834.29	3	222.03	1.43	0.1	117	9/46	
ajrawphagactin20, 2260	- ERTVISNLRPFTLYR.-	1866.16	2	142.84	1.28	0.0	92	2/7	
jmraw5minigg250mmnaclsyringdnase, 2794	-.TMPAEGADDIPGPVTWEPRPENSIFLK.-	2989.32	2	111.91	0.84	0.1	77	2/13	
jmag5mincon500mmnacl, 776	- EGEPGILLHGLK.-	1263.47	3	270.40	1.41	0.0	188	17/44	
ajrawmediapbsnocells, 1786	-.PEVEQNNLVLIPPSLSK.-	1878.16	2	505.99	1.19	0.2	197	11/32	
rawsucrfp_400phagigg_Mar04, 1721	-.YRPPDYRDLISFTVYYK.-	2197.48	3	578.07	1.57	0.1	244	1/4	
jmbeads400rawphag3007, 1233	- NLTVRSGKMYFAFNPK.-	1874.20	2	172.54	1.09	0.0	158	4/15	
AJRAWActinContr_june13, 2856	-.NVTEYDGQDACGSNSWNMVDVDLPPNK.-	2970.16	2	246.21	0.99	0.1	68	2/13	
jmfagcont5minbead, 3640	-.PFTLYRIDIHSCNHEAEKLGCSASNFVFAR.-	3427.86	2	597.09	1.07	0.2	64	7/56	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
insulin-like growth factor I receptor [Mus musculus]					**1976.75**	33859572.0	6		
rawextr_60MeOHbead_Mar04, 1002	-.ELGQGSFGMVYEGVAKGVVK.-	2056.37	3	359.10	1.65	0.1	177	15/76	
rawextr_60MeOHbead_Mar04, 2462	-.TIDSVTSAQMLQGCTILKGNLLINIRR.-	2960.51	2	83.33	0.81	0.0	102	2/13	
FPbeads600_Dec19, 898	-.GPCCACPKTEAEK.-	1337.57	2	548.99	1.17	0.2	143	3/8	
rawextr_450beadigg_Mar04, 1810	-.GNNIASELENFMGLIEVVTGYVK.-	2498.84	3	631.07	1.84	0.0	341	9/44	
jmbsaactinrawphag3007, 1510	-.FVMEGGLLDKPDNCPDMLFELMR.-	2672.16	3	354.26	1.32	0.0	269	17/88	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
BMX non-receptor tyrosine kinase [Mus musculus]					**4673.75**	6753196.0	12		
jmfag5minigg1000mmnacl, 1844	-.LLKIPRAVPVLK.-	1347.76	2	219.45	1.33	0.1	124	5/11	1
jmraw5minigg250mmnaclsyringdnase, 1898	-.QPYDLYDNSEVVVKVSQGHR.-	2334.53	3	276.72	1.24	0.0	224	9/38	
jmraw5minigg500mmnaclsd, 1952	-.VPVSVALGSGIWELKR.-	1712.03	2	828.75	1.30	0.2	160	1/3	
jmfag5mincont150mmnacl, 111	-.LRHPVSTKANK.-	1251.46	3	578.97	1.60	0.0	355	7/20	
jmfagtimecont0min_030601230741, 1212	-.GNPHLLIK.-	892.08	2	559.52	1.44	0.1	359	9/14	1
jmfagtimecont0min_030601230741, 3302	-.MSWGFPESSSSEEEENLHAYDWFAGNISR.-	3364.52	2	275.58	0.88	0.2	56	1/7	1
rawsucrfp_chlfphagigg_Mar04, 2128	-.FYGVCSKKYPIYIVTEYITNGCLLNYLK.-	3307.91	3	96.43	0.95	0.1	71	11/108	
phagrawFchlf_dec23,2322-2324	-.VPVSVALGSGIWELKR.-	1712.03	2	167.68	1.13	0.0	146	7/30	
jmidl350nacirawphag3007, 1690	-.VPVSVALGSGIWELKR.-	1712.03	2	632.03	1.17	0.2	213	1/3	
phagrawF600_dec20, 972	-.QPYDLYDNSEVVVK.-	1689.81	2	269.29	0.86	0.1	276	9/26	
rawsucrfp_actinphagigg_Mar04, 1140	-.GKEGAFMVRNSSQMGMYTVSLFSK.-	2657.09	3	129.82	1.43	0.0	91	7/46	
rawsucrfp_800phagigg_Mar04, 1458	-.VPVSVALGSGIWELKR.-	1712.03	2	250.35	1.18	0.1	122	1/3	
rawsucrfp_700phagigg_Mar04, 1486	-.VPVSVALGSGIWELKR.-	1712.03	2	96.68	0.93	0.0	98	1/3	
rawsucrfp_actinphagigg_Mar04, 1796	-.VPVSVALGSGIWELKR.-	1712.03	2	292.47	1.02	0.1	85	1/5	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
BMX non-receptor tyrosine kinase [Mus musculus]					**639.39**	6753196.0	10		
rawextr_700bead_Mar04, 1209	-.VPVSVALGSGIWELKR.-	1712.03	2	317.68	1.59	0.1	154	2/5	
FPbeads300_Dec19, 1516	-.MSPNNYKER.-	1139.27	1	321.70	0.92	0.0	340	1/2	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
endothelial-specific receptor tyrosine kinase [Mus musculus]					**2611.93**	8567412.0	3		
jmfagfrench5minigg1mnacldtt, 1895	-.YLDILEVHLPHAQPQDAGVYSAR.-	2593.88	3	932.75	1.52	0.1	395	5/22	
jmfag1mnacl2,5minigg, 2344	-.YLDILEVHLPHAQPQDAGVYSAR.-	2593.88	3	1015.98	1.84	0.1	421	1/4	
jmfagtimecon10min, 1668	-.QQYSSTLSSQQLLHFAADVAR.-	2351.56	3	387.32	1.51	0.0	251	19/80	
jmidl250nacirawphag3007,1096-1098	-.GYLYLAIEYAPHGNLLDFLGK.-	2368.72	3	275.87	1.49	0.0	185	21/80	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
receptor tyrosine kinase EphA1 [Mus musculus] eras					**2572.06**	10047365.0	8		
jmfag1mnacl5mincon, 188	-.NCWAYDRAR.-	1155.27	3	915.10	1.64	0.1	465	7/16	1
jmfag1mnacl0minigg, 1952	-.PYGEMSNQEVMKSIEDGYR.-	2234.45	2	169.69	1.20	0.1	101	2/9	1
rawsucrfp_chlfphagigg_Mar04, 2512	-.PHFLQLQAHLEQLLTDPHSLRTIANFDPR.-	3409.85	2	255.58	0.92	0.1	60	1/7	1
phagrawFsuc400_dec20, 2980	-.SQNRVSGLDSSSPSSASLSINMGHAESLSGLSLK.-	3405.70	2	245.25	0.90	0.1	75	1/6	1
phagrawFsuc350_dec20, 3128	-.RGLYLAFHNPGSCVALVSVRVFYQR.-	2854.33	2	986.44	1.12	0.3	66	1/6	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
receptor tyrosine kinase EphA1 [Mus musculus] LE1					**406.84**	10047365.0	6		
rawextr_900beadigg_Mar04, 1326	-.LPSLSGSDGIPYR.-	1362.51	3	406.84	1.12	0.0	358	7/24	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Fc receptor, IgE, high affinity I, alpha polypeptide [Mus musculus]					**3517.37**	6753828.0	7		
jm5miniggrawlowonic, 1316	-.YICQKQGLFKSK.-	1443.74	2	367.93	1.40	0.0	247	4/11	
jmigg600rawphag3007, 1516	-.KVIYYRNDHAFNYSYESPVSIR.-	2723.00	3	1149.52	1.41	0.2	454	23/84	
ajrawphagactin20, 2226	-.IAVVKAYK.-	892.12	2	55.96	0.81	0.0	69	3/7	
jmld250nactrawphag3007, 1344	-.YICQKQGLFK.-	1228.49	2	886.41	1.26	0.1	647	11/18	
phagrawFsuc200_dec22, 1327	-.WIHNGTVSEVNSSHLVIVSATVQDSGK.-	2866.14	3	315.49	1.48	0.1	151	17/104	
rawsucrfp_400phagigg_Mar04, 1758	-.WIHNGTVSEVNSSHLVIVSATVQDSGK.-	2866.14	3	742.06	1.54	0.2	216	19/104	

control

Fc receptor, IgE, high affinity I, alpha polypeptide [Mus musculus]					**672.99**	6753828.0	2		
rawextr_chlbeadIgG_Mar04, 2098	-.WIHNGTVSEVNSSHLVIVSATVQDSGK.-	2866.14	3	327.35	1.32	0.1	199	17/104	
FPbeads450_Dec19, 2464	-.EATLNDSGTYHCKGYLRQVEYESDK.-	2908.11	3	345.64	1.12	0.1	195	17/96	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
high affinity immunoglobulin gamma Fc receptor I [Mus musculus molossinus					**2283.71**	4973138.0	3		
jmlagtranch5miniggtrmnacldlt, 124	-.HRYTSAGVSITVK.-	1419.81	3	1145.31	1.87	0.0	611	19/48	6
jmlgG400rawphag3007, 1530	-.ILEYRNTSSEYHIARAER.-	2209.41	3	195.23	1.23	0.0	158	13/68	3
phagrawF250_dec22, 1237	-.IALKTNLSHSGIYHCSGMGRHR.-	2552.97	2	201.91	0.88	0.1	55	9/44	1
phagrawF500_dec20, 1360	-.SFKPSSGSKIALK.-	1513.81	2	169.45	1.04	0.0	155	4/13	1
RawPhag2007E1Beadsdigest_030718152503, 2482	-.MILTSFGDDMWLLTTLLLWVPVGGEVVNATK.-	3422.06	2	248.40	0.89	0.1	82	3/20	5
phagrawFsuc800_dec23, 1112	-.EDAGFYWCEVATEDSSVLKR.-	2306.49	3	323.42	1.45	0.0	211	9/38	4

control

high affinity immunoglobulin gamma Fc receptor I [Mus musculus molossinus					**575.15**	4973138.0	3		
FPbeads400_Dec19, 1264	-.PGLQLHFSFYVGSKILEYRNTSSEYHIAR.-	3414.82	3	575.15	2.08	0.1	88	9/56	1

APPENDIX E – GTPase SUMMATION OF IONS

The summation of peptides from GTPases found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
I48310 kinase-related protein ros - mouse					**9764.98**	2117869.0	30		
jmrawigg5minbeadsfreezethaw, 136	-.KGSTDQEK.-	892.94	2	611.17	1.23	0.0	472	5/7	1
jmrawigg5min350mmnaclsyringednase, 554	-.ANSSDRRHK.-	1071.13	2	375.96	1.02	0.2	123	1/2	1
jmfag1mnacl5minigg, 898	-.KGSTDQEKIEFLK.-	1523.71	3	314.45	1.54	0.0	191	17/48	1
jmrawigg5min300mmnaclsyringednase,923-925	-.DTKAVRIVESGTLK.-	1517.75	2	670.95	1.80	0.1	198	9/26	1
jmIgG150rawphag3007, 1046	-.DFAVKPQSK.-	1020.17	2	1091.21	1.86	0.1	431	9/16	1
jmrawigg5min450mmnaclsd,1136-1138	-.DTKAVRIVESGTLK.-	1517.75	2	436.85	1.73	0.0	236	6/13	1
ajrawphagjun20dpi1MNaCl, 1382	-.VIAVDWIARHLYFALK.-	1916.30	3	137.10	0.98	0.0	139	11/60	
ajrawphag1MNaCl20,2000-2002	-.DTKAVRIVESGTLK.-	1517.75	2	1700.42	2.07	0.3	183	5/13	1
jmrawigg5minbeadsyringdnase, 2065	-.QLGVCLLGEPQYILELMEGGDLLSYLR.-	3137.70	2	509.46	0.83	0.2	69	4/27	1
jmIgG150rawphag3007, 2140	- APESVPSAPENPRIFILSSGRYTK.-	2617.94	3	3818.51	2.09	0.4	475	11/46	
jmrawigg5min400mmnaclsd, 2721	-.ASNQHGRSQCSCNVTESELSGAMTVDTSDPDR.-	3384.55	2	32.19	0.85	0.0	34	7/62	1
jmIgG300rawphag3007, 3228	-.HKMLESQENVARIEGLQPFSMYMIQIAVK.-	3393.00	2	66.72	0.76	0.0	78	9/56	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
I48310 kinase-related protein ros - mouse					**3491.61**	2117869.0	24		
rawextr_1000_beadigg_Mar04, 1074	-.DTKAVRIVESGTLK.-	1517.75	2	213.04	1.65	0.0	121	9/26	
rawextr_400bead_Mar04, 1133	-.DTKAVRIVESGTLK.-	1517.75	2	467.11	1.44	0.2	83	4/13	
rawextr_500beadigg_Mar04, 1144	-.DTKAVRIVESGTLK.-	1517.75	2	632.36	1.52	0.2	116	9/26	
rawextr_150bead_Mar04, 1261	-.PLPGNFSSTPKVIPDPVQESSFR.-	2500.79	3	1729.62	1.86	0.3	119	17/88	
rawextr_450bead_Mar04, 2432	-.ASQNGTQIFNVDLEHK.-	1801.94	2	449.48	1.05	0.2	131	4/15	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rho-associated coiled-coil forming kinase 1 [Mus musculus]					**16083.11**	6677759.0	20		
jmrawigg5min350mmnaclsyringednase,807-809	- SLQESLQKTIYK.-	1438.65	3	290.22	1.56	0.0	186	13/44	
jmIgG300rawphag3007, 914	- GAFGEVQLVRHK.-	1341.54	3	456.78	1.30	0.0	340	15/44	
jmfag1mnacl5minigg, 584	-.PDNMLLDK -	946.10	2	1062.23	1.71	0.1	577	11/14	2
JMFAGNACL10_1B21E3, 986	-.YLPSANASENR.-	1222.29	2	378.03	1.17	0.0	306	9/20	1
jmfag5minigg250mmnacl, 1478	-.ILFYNDEQDK -	1285.39	2	1319.23	1.96	0.0	664	13/18	1
JMMAGNEGB16D3, 1548	- DMLLLACSQDEQKKWVTHLVK.-	2486.94	3	307.55	1.49	0.1	144	17/80	1
jmrawigg5min300mmnaclsyringednase, 1395	- IMNHKNSLTFPDDNDISKEAK.-	2418.67	3	1565.28	1.51	0.3	322	19/80	2
jmfag5minigg250mmnacl, 1478	- ILFYNDEQDK.-	1285.39	2	1319.23	1.96	0.0	664	13/18	1
jmIgG1000naclrawphag3007,1638-1640	- SLQESLQKTIYK.-	1438.65	3	801.67	1.80	0.1	324	4/11	
ajrawphag1MNaCl20, 1754	- KDIEVEPVQQGEK.-	1499.65	2	97.96	0.74	0.0	131	1/3	1
jmfag5minigg1000mmnacl, 1928	-.ILENSKSQADKDYYQLQAVLEAER.-	2813.07	3	1208.66	2.07	0.2	337	19/92	1
JMFAGNACL15B21E3, 3458	-.DRGHDSEMIGDLQARITSLQEEVK.-	2728.98	3	309.13	1.20	0.1	69	11/92	1
jmldl150naclrawphag3007, 894	- PVTQGDVYR.-	1035.14	3	774.15	1.40	0.2	236	3/8	1
jmldl450naclrawphag3007, 2082	- GILEEQYFELTQESK.-	1814.97	2	134.35	0.96	0.0	124	1/4	1
jmrawigg5miniggfreebead, 1574	- QEITDKDHTVSR.-	1429.52	2	327.98	1.11	0.0	286	5/11	1
jmfagcon5minn600mmnacl, 911	- IPKNPPSGFVRASPR.-	1623.88	3	621.41	1.38	0.1	315	17/56	1
jmbeads500rawphag3007, 1179	-.IMNHKNSLTFPDDNDISK.-	2090.30	3	955.78	1.21	0.2	357	1/4	2
jmbeads150rawphag3007, 2332	-.SGHLKLADFGTCMK.-	1508.79	1	581.47	1.86	0.1	251	5/13	2
jmfagtmecont0min_030601230741, 3214	-.DRGHDSEMIGDLQAR.-	1700.82	2	214.43	1.05	0.0	204	9/28	1
rawphag2007chfbead3, 118	-.DVKPDNMLLDK.-	1288.50	3	344.90	1.34	0.1	113	13/40	2
rawphag2007chfisol2, 1216	-.TQAFEADNLKGLEK.-	1564.72	3	745.70	1.37	0.1	472	9/26	1
phagrawFsuc700_dec23,1043-1045	-.NIDNFLSRYKDTINK -	1842.05	2	389.96	1.25	0.1	269	5/14	1
phagrawF800_Dec23,1136-1138	-.QCSMLDVDLKQSQQKLEHLTENK.-	2717.07	3	445.07	1.48	0.0	294	9/44	1
phagrawF400_dec20, 1210	-.LFHVRPVTQGDVYRAETEEIPK.-	2585.90	3	394.97	1.59	0.0	234	1/4	1
rawsucrfp_actinphagigg_Mar04, 1240	-.VEGERKEAQDMLNHSEK.-	2001.17	3	256.31	1.25	0.0	199	15/64	1
phagrawF250_dec22, 1467	- DRGHDSEMIGDLQARITSLQEEVK -	2728.98	2	90.01	1.00	0.0	73	4/23	1
rawsucrfp_600phagigg_Mar04, 1494	-.NSLTFPDDNDISK.-	1466.53	3	228.94	1.19	0.0	180	13/48	2
phagrawF250_dec22, 1647	-.AFVGNQLPFVGFTYYSNRR.-	2237.50	3	347.10	1.31	0.0	261	1/4	2
phagrawFsuc400_dec20, 3934	-.HQKELNDMQAQLVEECTHRNELQMQLASK.-	3453.88	2	114.62	0.86	0.1	52	1/8	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rho-associated coiled-coil forming kinase 1 [Mus musculus]					**3003.23**	6677759.0	26		
rawextr_350bead_Mar04, 862	-.NKNIDNFLSR.-	1221.35	2	204.62	1.12	0.0	172	4/9	
FPbeads400_Dec19, 1180	-.KWVTHLVKK.-	1139.42	2	323.19	1.07	0.1	253	7/16	
rawextr_400bead_Mar04, 1213	-.LLSKFEMIKR.-	1265.59	2	348.53	1.30	0.0	264	1/2	
rawextr_800bead_Mar04, 1244	-.YLPSANASENRSSSNVDKSLQESLQK.-	2854.04	3	977.81	2.02	0.2	134	9/50	
jmbsa150naclrawphag3007, 143	-.ILENSKSQADK.-	1233.35	2	495.73	1.31	0.1	312	2/5	1
jmbsaactinrawphag3007, 2261	-.VVKNTSGK.-	832.97	1	186.57	0.74	0.1	189	3/7	1
jmraw5minbsafreezthaw, 1184	-.LGRNGVEEIK.-	1115.27	3	335.02	1.39	0.0	230	5/12	2
jmraw5minbsabeads, 1628	-.VEGERKEAQDMLNHSEK.-	2001.17	3	117.20	1.05	0.0	90	5/32	1
jmrawbsa5minlowionic, 1996	-.PVTQGDVYR.-	1035.14	2	34.56	0.68	0.0	30	3/16	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rho GDP dissociation inhibitor (GDI) alpha; RhoGDI-1 [Mus musculus]					**38494.87**	31982030.0	4		
JMMAGTube1B16E3, 876	- SIQEIQELDKDDESLRK.-	2047.21	3	7960.38	3.06	0.4	721	23/64	2
jmrawggs5minbeadsfreezethaw, 980	- SIQEIQELDKDDESLR.-	1919.04	3	5330.23	2.47	0.4	670	2/5	2
jm5miniggrawlowionic, 1662	- SIQEIQELDKDDESLR.-	1919.04	2	6703.47	2.74	0.4	894	1/2	2
jmbeads300rawphag3007,948-950	- VAVSADPNVPNVIVTR -	1651.89	2	5317.03	2.95	0.4	506	7/15	2
ajrawmediapbsnocells, 948	- SIQEIQELDKDDESLR.-	1919.04	3	5311.54	2.48	0.4	460	1/3	2
ajrawmediapbsnocells, 1288	- AEEYEFLTPMEEAPK -	1784.97	2	1874.04	1.54	0.2	865	15/28	2
jmfag5miniggbead_030528200105, 881	- SIQEIQELDKDDESLRK -	2047.21	3	1909.31	2.06	0.2	323	17/64	2
jmfag5miniggi1000mmnacl, 1442	- AEEYEFLTPMEEAPK -	1784.97	2	1138.40	1.76	0.1	437	3/7	2
jmfag5mincont200mmnacl, 684	- DDESLRK.-	862.91	2	227.74	1.07	0.0	212	7/12	2
jmfag5mincont200mmnacl, 1150	- SIQEIQELDKDDESLR -	1919.04	3	2036.26	1.84	0.2	501	23/60	2
phagrawF250_dec22, 1147	- YKEALLGRVAVSADPNVPNVIVTR.-	2582.98	3	588.89	1.50	0.0	376	5/23	1
phagrawFsuc150_dec22, 1566	- EIVSGMKYIQHTYRK -	1854.17	2	97.58	1.08	0.0	73	1/4	2
Rho GDP dissociation inhibitor (GDI) alpha; RhoGDI-1 [Mus musculus]					**2782.68**	31982030.0	3		
rawextr_60MeOHbead_Mar04, 2084	- SRFTDDDKTDHLSWEWNLTIK -	2608.80	3	2782.68	2.37	0.2	613	11/40	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rho, GDP dissociation inhibitor (GDI) beta [Mus musculus]					**59520.62**	33563236.0	3		
jmfag1mnacl7,5minigg, 1534	- ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	6133.48	2.86	0.4	736	1/4	
jmfag1mnacl5mincon, 1736	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	4234.02	2.55	0.3	472	6/25	
jmfreebeadsrawphag3007, 1372	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	6060.11	2.81	0.4	529	6/25	
jmfag5mincont350, 1458	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	3910.51	2.59	0.3	375	11/50	
jmfag5mincont200mmnacl,1678-1678	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	7352.35	3.45	0.4	400	11/50	
jmfag5mincon250mmnacl, 2004	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	7932.51	3.22	0.4	669	1/4	
jmfag1mnacl2,5minigg, 1510	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	1427.28	2.52	0.2	277	11/50	
jmfag5minfrench1mnacldttdpi, 730	-.VNKDIVSGLK.-	1073.27	2	158.99	0.88	0.1	150	4/9	
jmfag_20_minfrench1mnacldttdpi, 730	-.VNKDIVSGLK.-	1073.27	2	158.99	0.88	0.1	150	4/9	
jmfagfrench20minigg1mnacldtt, 1274	-.ATFMVGSYGPR.-	1186.37	2	140.67	0.78	0.0	169	7/20	
jmrawggs5minbeadsfreezethaw, 1492	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	2020.07	1.89	0.3	250	21/100	
jmfag1mnacl2,5minigg, 1510	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	1427.28	2.52	0.2	277	11/50	
jmfag1mnacl7,5minigg, 1534	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	6133.48	2.86	0.4	736	1/4	
jmrawggs5minbeadsfreezethaw, 2364	-.DAQPQLEEADDDLDSKLNYKPPPQK.-	2856.05	2	197.08	0.92	0.1	80	5/24	
jmbeads250rawphag3007, 916	-.YVQHTYRTGMRVDK.-	1755.00	2	389.65	1.48	0.1	234	9/26	
jmbeads300rawphag3007, 920	-.YVQHTYRTGMRVDK.-	1755.00	2	368.60	1.45	0.0	248	9/26	
jmfag5mincont350, 1458	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	3910.51	2.59	0.3	375	11/50	
jmfag5mincont200mmnacl,1676-1678	-.ATFMVGSYGPRPEEYEFLTPVEEAPK.-	2946.28	3	7352.35	3.45	0.4	400	11/50	
phagrawF60MeOH_dec23, 304	-.KTLLGDVPVVADPTVPNVTVTR.-	2292.66	3	212.71	1.29	0.0	164	3/14	

control

Rho, GDP dissociation inhibitor (GDI) beta [Mus musculus]					**253.83**	33563236.0	7		
rawextr_900beadigg_Mar04, 260	-.VNKDIVSGLK.-	1073.27	3	226.77	1.20	0.0	178	1/4	
rawextr_200bead_Mar04, 2430	-.DAQPQLEEADDDLDSKLNYK.-	2308.40	2	27.06	0.78	0.0	34	5/38	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to RhoGEF glutamate transport modulator GTRAP48 [Mus musculus]					**6734.76**	38077561.0	1		
ajrawmediapbsnocells, 1002	-.SRSDVDMDAAAEATR.-	1595.68	3	1059.58	1.75	0.0	603	5/14	
JMFAGNACL15B21E3, 232	-.VTQLQLK -	830.01	2	593.32	1.17	0.0	504	2/3	
jmrawggs5min150mmnacl, 392	-.SESLKGREEMK -	1294.46	2	135.58	0.90	0.0	150	7/20	
jmiggactinrawphag3007, 1028	-.LDATALERASNPLAAEFK.-	1918.14	3	464.81	1.45	0.0	314	5/17	
jmfag5minigg250mmnacl, 1520	-.PKSSSQSIKPGNVR.-	1485.67	3	261.71	1.48	0.0	162	15/52	
jm5miniggrawlowionic, 1842	-.QPSDTSETTGLVQR.-	1519.60	2	506.20	1.25	0.0	385	5/13	
jmIgG350nacirawphag3007, 1903	-.QTFSPVLKLNAVLIR.-	1700.06	2	60.97	0.89	0.0	68	2/7	
jmfag5minigg300mmnacl, 2092	-.QEVINELFVTEASHLR.-	1886.10	3	550.48	1.18	0.1	409	17/60	
jmag5mincon500mmnacl, 2224	-.FQLFMQEAESHPQCRR.-	2008.27	2	307.67	1.34	0.0	227	1/3	
jmfag5minigg150mmnacl, 3058	-.NSVLSDPGLDSPQTSPVILARVGQHHR.-	2882.19	2	379.13	0.90	0.2	71	2/13	
jmfag5minigg450mmnacl_030527025134, 4020	-.SALYEAQEAVMPEIQEQINDYRSKR.-	2970.26	2	44.82	0.93	0.0	47	1/8	
jmfagtimecon7.5min.2084.2084.2	-.FPSISESLVNR.-	1249.40	0	468.75	1.31	0.1	300	1/2	
jmfagtimecon7.5min.122.122.2	-.DISDLMLAR.-	1034.21	0	838.59	1.28	0.1	302	1/2	
jmfagtimecont10min_030601202502, 990	-.TLRVLDLIFYQR.-	1537.83	3	562.63	1.59	0.0	342	7/22	
jmfag5mincont200mmnacl, 1646	-.FQLFMQEAESHPQCRR.-	2008.27	2	784.58	1.31	0.2	223	3/10	
jmag5mincon500mmnacl, 2224	-.FQLFMQEAESHPQCRR.-	2008.27	2	307.67	1.34	0.0	227	1/3	
RawPhag200760MeBeadsdigest,1278-1280	-.IVLVQSVRPGGAAMR.-	1554.89	3	818.09	1.54	0.1	500	9/28	
jmraw5minbsabeads, 2238	-.VKIPEMLQAEIDLRLR.-	1925.33	2	202.61	1.43	0.0	135	4/15	
jmraw5minbsafreezthaw, 2298	-.SHPAYLVVFLR.-	1302.55	2	95.26	0.95	0.0	100	3/10	
jmbsaactinrawphag3007,2747-2749	-.HRLEGYQKR.-	1187.34	2	0.00			25	1/8	
phagrawFsuc700_dec23, 1517	-.DMGVIFHTIEQLTVK.-	1732.04	2	345.50	0.97	0.2	118	2/7	1
phagrawFsuc1000_dec23, 2243	-.KEKDALEDK.-	1076.18	2	146.91	0.89	0.0	149	3/8	

control

similar to RhoGEF glutamate transport modulator GTRAP48 [Mus musculus]					**3462.87**	38077561.0	15		
jmbsa250nacirawpnag3007, 855	-.KPSEGPGPEQR.-	1182.27	2	272.80	1.01	0.0	264	9/20	1
rawextr_chlbeadIgG_Mar04, 518	-.QLAALGDILSKYEEDR.-	1822.01	2	1055.87	2.35	0.1	324	11/30	
rawextr_500beadigg_Mar04, 968	-.NPASLLEEQIEGARRR.-	1840.04	3	653.21	1.37	0.0	475	3/10	
FPbeads150_Dec19, 1063	-.PKSSSQSIKPGNVR.-	1485.67	3	614.49	1.81	0.1	220	15/52	
FPbeads250_Dec19, 1472	-.LSVDSQEADSGLDSGTER.-	1866.88	3	523.81	1.64	0.1	282	4/17	
rawextr_300beadigg_Mar4, 2528	-.VNPMIPPPPPPPPLPPPQHITGPK.-	2517.03	3	342.69	1.57	0.0	217	4/23	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions
similar to Rho guanine nucleotide exchange factor (GEF) 17; Rho-specif					12540.05	38087045.0		24
ajrawphagjun20dpi1MNaCl, 384	- SARPLSGPGIEGR -	1297.45	3	654.84	1.15	0.1	455	17/48
jmfag_20_minfrench1mnacldttdpi, 850	- GPVGTARPLR.-	1024.20	2	210.66	0.81	0.0	257	7/18
jmfag5minfrench1mnacldttdpi, 850	- GPVGTARPLR -	1024.20	2	210.66	0.81	0.0	257	7/18
jmfagfrench5minigg1mnacldtt, 1079	- VSKLASGPPAAPAQPR -	1547.79	2	301.81	1.36	0.1	156	3/10
jmfggactinrawphag3007,1208-1210	- PAAAVPGQPSRRVSK	1521.75	3	609.24	1.59	0.0	383	2/7
jmfgG350nacirawphag3007, 2003	-.SSVGWGVYRSPSFGTGDGLLLR.-	2312.57	3	252.32	1.27	0.0	174	5/21
jmfgG300rawphag3007, 2088	- PSGGPGNR -	741.78	1	147.49	0.70	0.1	118	3/7
jm5minggrawlowionic, 2352	- ALVSPETPPTPGALRRR.-	1819.10	2	409.23	1.45	0.0	281	5/18
jmfagtrnecon2 5min 2596 2596 3	- PMSDTGGAPFRVAKVSFPAYLASPAGSR -	2639.22	0	600.56	1.53	0.1	319	5/27
jmfag5mincont200mmnacl,894-896	- PMSDTGGAPFRVAK.-	1434.85	3	811.57	1.99	0.0	401	9/26
jmbeads350rawphag30072nd, 1614	-.LLERWSGGPGPREEDADTPGLR.-	2409.60	3	323.43	1.42	0.0	223	3/14
jmfag5mincont200mmnacl, 3194	-.VPPSGPNGTELSNGEASEAYRSLSDPIPQR.-	3127.33	2	107.33	0.93	0.0	104	4/29
rawphag2007chflsol1, 960	- SLSDPIPQR.-	1013.13	2	585.92	1.62	0.0	356	11/18
rawphag2007chflsol2,1046-1048	-.SLSDPIPQR.-	1013.13	2	1331.72	1.89	0.2	386	11/18
rawsucrfp_chflphagigg_Mar04, 1514	-.LFGGPSSRRPSMDSEALGSTSPDR.-	2508.71	3	1038.20	1.46	0.2	413	1/4
rawphag2007chflsol2, 2996	-.TGLPVTPAMDEGLTSGHSDWSVVSEENK.-	2945.17	2	893.68	1.17	0.3	115	5/27
jmldichflsolblarawphag3007, 1738	-.DSPSAGSPMEQSESTLSQSPTSPTTR.-	2666.77	3	650.67	1.67	0.1	319	11/50
jmldl400nacirawphag3007_030802153313,1836-1838	- VSKLASGPPAAPAQPR.-	1547.79	2	273.18	0.84	0.0	302	2/5
ajrawmediapbanocells,146-148	-.ATPDEPAPASKCCSK.-	1505.70	3	854.00	1.72	0.1	349	17/56
rawsucrfp_450phagigg_Mar04, 630	- LFGGPSSRR -	977.10	2	151.81	0.99	0.0	150	3/8
rawsucrfp_400phagigg_Mar04,1301-1303	- SLSDPIPQRHR.-	1306.46	2	1038.64	1.37	0.3	119	7/20
rawsucrfp_chflphagigg_Mar04, 1514	-.LFGGPSSRRPSMDSEALGSTSPDR.-	2508.71	3	1038.20	1.46	0.2	413	1/4
phagrawFsuc450_dec20, 3434	- RYMLTLHSGDVPAPGPVDLPCLPPSAPPSTETK -	3445.96	2	44.89	0.87	0.0	62	1/8

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions
similar to Rho guanine nucleotide exchange factor (GEF) 17; Rho-specif					2129.10	38087045.0		17
rawextr_actinbead_Mar04, 902	-.LLERWSGGPGPREEDADTPGLR -	2409.60	3	848.49	1.81	0.1	423	1/4
rawextr_1000bead_Mar04, 970	- RPARSSHQELR -	1337.47	3	533.20	1.31	0.2	136	13/40
FPbeads150_Dec19, 1167	-.VAKVSFPAYLASPAGSR.-	1721.98	2	747.41	1.28	0.1	370	13/32

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
FGD1_MOUSE Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (					3860.79	1706790.0		25	
JMFAGNACL15B21E3, 462	-.RAPTPIREK.-	1058.26	2	187.20	0.96	0.1	110	1/2	2
jmfag5minigg600mmnacl, 606	-.LLGQKFTVRAR.-	1289.58	3	821.81	1.54	0.2	222	3/10	
jmfgG300rawphag3007, 1240	- YULFNDR.-	1054.22	2	982.68	1.32	0.1	587	5/7	2
jMFAGNACL10_2B21E3, 1830	- GDTFCPGPTLSEDK.-	1487.58	2	67.87	0.76	0.0	76	3/13	2
jmfgG300rawphag3007, 2118	-.VIIHEVQKEEACR.-	1554.80	2	267.27	1.61	0.0	161	3/8	
jmrawf5minbsareebeads, 924	- WMAVLGR.-	833.04	2	390.40	1.22	0.0	320	2/3	2
jmrawf5minbsareebeads,1396-1398	-.ELIKEGHILK.-	1180.42	3	307.26	1.84	0.1	155	7/16	2
jmbeads400rawphag3007, 1099	-.HVFKITQSHLSWYFSPETEELQR.-	2884.16	3	1439.71	2.12	0.2	299	19/88	2
jmfagtrnecon10min, 3294	-.YLILFNDRLLYCVPR.-	1899.29	2	95.39	0.84	0.1	60	5/28	2
jmrawgg5minigghrawbead, 534	-.LLEEARNR.-	1001.12	2	1367.65	1.53	0.0	892	11/14	1
jmbsa450nacirawphag3007, 1255	-.HHCKACGHVVCGK.-	1379.86	2	269.34	0.89	0.1	131	1/3	2
jmrawbas5min1mnacl,1952-1954	-.AVELVNTWTER.-	1318.46	2	151.33	0.97	0.0	154	9/20	1
rawsucrfp_800phagigg_Mar04,634-636	- PSPLKRAPGPK.-	1148.38	3	60.52	1.02	0.0	59	1/4	1
phagrawF500_dec20, 815	-.YPRIGDILQKLAPFLK.-	1873.27	3	504.94	1.45	0.0	348	17/60	1
rawsucrfp_450phagigg_Mar04, 1424	- SAANTPGAAPLACADSDPGALEPGLPVSR.-	2706.97	2	163.46	1.68	0.0	106	5/26	1
phagrawF150_dec22, 1450	- GLVPRAEASTSSAAVSSLIEKFER.-	2506.80	3	696.55	1.72	0.1	364	21/92	1
phagrawF1000_Dec23,1844-1846	- SAANTPGAAPLACADSDPGALEPGLPVSR.-	2706.97	3	804.20	2.09	0.1	208	19/112	1
phagrawFsuc300_dec20, 1884	- AVELVNTWTER.-	1318.46	2	296.54	1.12	0.0	180	7/20	1
phagrawF800_Dec23, 3096	-.PQVPPKPSYLQMPRVLPPPEPIPPPPSR.-	3113.71	2	56.87	0.88	0.1	32	5/54	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
FGD1_MOUSE Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (					1551.80	1706790.0		18	
rawextr_190bead_Mar04, 137	- LSAKNGTTQDR.-	1191.28	3	231.89	1.25	0.0	165	13/40	4
rawextr_900bead_Mar04,1202-1204	- SAANTPGAAPLACADSDPGALEPGLPVSR.-	2706.97	3	709.21	2.20	0.0	316	23/112	1
rawextr_200bead_Mar04, 1497	-.ALRFSYHLEGSQPRPGLHQGNR.-	2521.78	3	388.39	1.42	0.0	272	19/84	1
rawextr_150bead_Mar04, 2271	-.WMAVLGRAGRGDTFCPGPTLSEDK.-	2565.91	2	73.09	0.81	0.0	87	4/23	2
rawextr_800bead_Mar04, 2738	-.PAPGPCPVPPEPAMLPQPPPQPTGSQLPEGEASR.-	3428.88	2	150.22	1.12	0.1	50	1/11	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rho guanine nucleotide exchange factor (GEF) 1; lymphoid blast crisis l					6214.75	6678668.0		9	
jmfag5minigg150mmnacl, 1554	-.APGPVHTQEIEENLLSLEVAIR.-	2416.72	3	1775.26	2.05	0.2	447	2/7	1
jmfag1mnacl7,5minigg,1606-1608	-.APGPVHTQEIEENLLSLEVAIR.-	2416.72	3	1632.43	2.35	0.2	332	1/4	1
JMMAGTube1B16E3, 1622	-.APGPVHTQEIEENLLSLEVAIR.-	2416.72	3	618.51	2.05	0.1	216	17/84	1
jmfag5minigg450mmnacl_030527025134, 1632	-.GEPSAPDCRHLK.-	1310.47	3	1022.20	1.49	0.2	107	1/4	1
jmrawgg5minbeadsfreezethaw,1550-1552	-.APGPVHTQEIEENLLSLEVAIR.-	2416.72	3	1034.26	2.06	0.2	273	3/14	1
phagrawFsuc1000_dec23, 505	-.DRGNYEAR.-	981.01	3	132.09	1.09	0.1	72	1/4	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rho guanine nucleotide exchange factor (GEF) 1; lymphoid blast crisis l					2438.48	6678668.0		8	
rawextr_500bead_Mar04, 1274	-.ELVPPDTLLSLPKSQVKR.-	2021.39	3	165.50	1.18	0.0	119	13/68	1
rawextr_60MeOHbeadlgg_Mar04,1320-1322	-.LTKYPLLLQSIGQNTEESTER.-	2421.69	3	2272.98	2.35	0.2	402	1/4	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rho guanine nucleotide exchange factor (GEF) 5 [Mus musculus]					**9087.43**	38083968.0	21		
jmrawgg5min1mnacl, 973	- EVEERRVATQYTENQR -	2009.13	3	388.56	1.27	0.0	306	4/15	
jmigG350nacirawphag3007, 1215	- TIPEGIMRSSQIPALDPEAQEDR -	2554.82	3	349.06	1.52	0.0	220	19/88	
jmigg450rawphag3007, 1328	- THNSQQEEFR.-	1276.30	2	289.52	0.97	0.1	180	7/18	
jmrawgg5min300mmnaclsyringednase, 1409	- TSESSSEQVVLGQVPNK.-	1789.92	2	1044.42	2.01	0.1	410	13/32	
jmrawgg5min1mnacl,1613-1615	- TSESSSEQVVLGQVPNK.-	1789.92	2	721.09	1.59	0.1	281	5/16	
jmrawgg5min450mmnaclsd, 1616	-.TSESSSEQVVLGQVPNK.-	1789.92	2	515.27	1.63	0.1	275	3/8	
jmrawgg5min450mmnaclsd, 1620	- TSESSSEQVVLGQVPNK -	1789.92	2	976.91	1.65	0.1	386	3/8	
jmrawgg5min150mmnacl, 1658	- TSESSSEQVVLGQVPNK.-	1789.92	2	387.36	1.36	0.1	252	5/16	
jmigG350naclrawphag3007, 1991	-.LDSLAEPHGLSSPRHRR -	1929.13	3	684.52	2.01	0.0	341	21/64	
JMFAGNACL15B21E3, 2932	- EKEEEETSPDTSIPRGSWPPCK.-	2503.69	2	864.35	1.47	0.2	114	3/14	
AJRAWActinIgG_june13, 3580	-.SRDGIVFSDSSTALFALKQDSEEFTSNPER.-	3335.54	2	128.29	0.71	0.1	63	9/58	
jmfagtimecon10min, 2688	-.THPGETEQTQGSGSELLR -	1928.01	2	342.11	1.33	0.1	214	5/17	
rawphag2007chfbead1, 2096	- TSESSSEQVVLGQVPNK.-	1789.92	2	1013.58	1.90	0.2	275	11/32	
rawphag2007chfsol1, 3302	- HSHPPPLTLSSGLHRSSK.-	1939.17	1	106.30	0.71	0.1	92	4/17	
jmkl600naclrawphag3007, 1980	- TSESSSEQVVLGQVPNK.-	1789.92	2	336.41	1.11	0.1	254	11/32	
jmraw5minbsafreezthaw, 1934	- DPSYKWTDGHR.-	1362.43	2	92.39	0.84	0.0	110	7/20	
rawsucrfp_400phagigg_Mar04, 1330	- PLPSTPESPNHTQTSIPSRLR.-	2316.56	3	466.12	1.88	0.0	239	1/5	
phagrawF500_dec20, 1454	- NPAAGRLPGSSDSVVFR.-	1730.91	2	140.20	0.76	0.1	146	1/4	
phagrawFsuc250_dec22, 1973	-.TEQTPDSLGMSLSFSHLELPQR.-	2474.73	2	240.99	1.01	0.1	63	4/21	

control

Rho guanine nucleotide exchange factor (GEF) 5 [Mus musculus]					**375.57**	38083968.0	8		
rawextr_150bead_Mar04,1311-1313	- RHSHPPPLTLSSGLHRSSK -	2095.36	3	375.57	1.43	0.1	216	17/72	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rho-GTPase-activating protein PS-GAP-b [Mus musculus]					**7705.17**	37730280.0	12		
jmiggactinrawphag3007, 1418	-.MCNELDLENSADWEVKTVTSALKQYLR.-	3158.55	3	2544.27	2.26	0.3	344	23/104	4
jmigG350naclrawphag3007, 1507	-.EMLDILVK.-	961.20	2	1284.33	1.90	0.0	671	5/7	4
jmfag1mnacl5minigg, 2296	-.NLEEQREIVALSVTETLIKPLEK.-	2654.05	3	990.75	1.38	0.2	152	2/11	
JMFAGNACL10_1B21E3, 1194	-.VNAIHFLVHKLPEKNK.-	1888.25	3	675.87	1.43	0.1	364	19/60	4
jmfag5minigg150mmnacl, 1734	-.PGVPLTVQAFSEEERK.-	1788.00	2	251.47	1.12	0.0	221	3/10	4
jmfag5mincon450mmnacl, 530	-.HLTNVSSHSK.-	1110.21	3	184.12	1.19	0.0	154	5/18	4
jmfagtimecon10min, 1326	-.AHEAELER.-	955.01	2	474.93	1.38	0.1	284	1/2	5
jmbeads450naclrawphag3007, 1561	-.FQNIVVEILIENHEK.-	1826.09	2	146.87	1.05	0.0	139	2/7	3
rawphag2007chfbead2, 1370	-.KQWLEALGGKEALFHTFNR.-	2246.56	3	364.22	1.49	0.0	244	17/72	2
rawphag2007chfbead1, 2284	-.TVTSALKQYLRSLPEPLMTYELHR.-	2848.31	3	277.55	1.35	0.0	198	15/92	4
RawPhag200760MeBeadsdigest, 2310	-.RASQFTAEGYLYVQEK.-	1891.07	2	179.61	1.32	0.1	45	7/30	4
rawphag2007chfbead3, 2625	-.FCFDIEAADRPGVPLTVQAFSEEERK.-	2956.28	2	331.17	1.06	0.1	154	1/5	4

control

Rho-GTPase-activating protein PS-GAP-b [Mus musculus]					**295.08**	37730280.0	7		
rawextr_150bead_Mar04, 437	-.LPEKNK.-	728.86	2	295.08	1.77	0.0	165	3/5	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	
Rho GTPase-activating protein; GAB-associated CDC42; rac GTPase activa					**8123.67**	28893539.0	33		
JMFAGNACL5B21E3, 114	-.SRPTKQK.-	844.98	2	425.25	1.47	0.1	219	2/3	
jmrawgg5minbeadsfreezethaw, 238	-.QLCESK.-	707.82	2	554.16	1.26	0.0	440	4/5	
jmfag1mnacl5minigg, 358	-.SSSVSKRK.-	879.00	2	287.75	1.14	0.0	232	1/2	
JMFAGNACL10_1B21E3, 490	-.PSLPQKQSSLRNR.-	1511.71	3	1087.52	1.76	0.0	614	5/12	
ajrawmediapbsnocells, 1164	-.ELPNPLLTYQLYEK.-	1721.98	2	637.16	1.23	0.1	372	11/26	
ajrawmediapbsnocells,1356-1358	-.HLSLLADYCSITNMHAK.-	1918.23	2	207.30	1.24	0.1	74	1/4	
jmigG150rawphag3007, 1372	-.SSKPSSFTEKVVYAFSPK.-	1990.25	3	540.50	1.46	0.2	138	4/17	
jmigG400rawphag3007, 1588	-.SEESLTSLHAVDGDSKLFR.-	2092.25	3	669.01	1.27	0.2	260	1/4	
jmrawgg5minbeadsfreezethaw, 1758	-.DKAHHPLSGSPEENSSTATMAYMMATPAR.-	3090.42	2	57.57	0.94	0.0	52	1/8	
jmraw5minigg250mmnaclsyringdnase, 2184	- HTYTSWDLEDMEKYRMQSIR.-	2590.88	3	596.93	1.68	0.0	353	4/19	
ajrawphag1MNaCl20, 2520	- PKSLLVSSPSTK.-	1244.46	1	189.31	0.88	0.0	207	1/2	
AJRAWActinContr_june13, 812	-.TQAQVSSPIVTENK.-	1502.65	3	169.05	1.28	0.0	116	3/13	
jmfag5mincont400_030531151834, 980	-.KSPVGSWRSFFNLGK.-	1710.96	2	128.99	0.99	0.0	129	2/7	
jmfagcon5minn600mmnacl, 1223	-.SEESLTSLHAVDGDSKLFRPR.-	2345.55	2	220.39	1.00	0.1	111	1/4	
jmfag5mincon250mmnacl, 1508	-.LSGVASNIQRLR.-	1314.52	2	499.83	1.21	0.2	166	4/11	
jmfag5mincont350, 2408	-.TQAQVSSPIVTENKYIEVGEGPAALQGK.-	2916.23	2	144.07	0.84	0.1	48	7/54	
jmfagtimecom0min_030601230741, 2414	-.ELPNPLLTYQLYEKFSDAVSAATDEER.-	3101.37	2	44.90	0.74	0.0	41	3/26	
jmbeads250rawphag3007, 2532	- PQSVPPHHNKLEPHQVYGAR.-	2292.54	3	683.74	1.39	0.1	274	1/4	
jmfag5mincont200mmnacl, 3268	- LSPSKKDAEAGGSQSQTPGSTASSEPVSPVQEK.-	3273.47	2	209.80	0.95	0.1	71	5/32	
ajrawmediapbsnocells,1356-1358	-.HLSLLADYCSITNMHAK -	1918.23	2	207.30	1.24	0.1	74	1/4	
rawsucrfp_800phagigg_Mar04, 14	-.VKGPIMSQYDNMTPAVQEDLGGIYVIHLR.-	3248.75	2	110.14	0.80	0.1	60	1/8	
phagrawF250_dec22, 925	- AESECLESGASFLDSLGYTRDK -	2379.54	3	193.44	1.18	0.1	129	13/84	
phagrawF600_dec20, 1932	-.TQAQVSSPIVTENKYIEVGEGPAALQGK.-	2916.23	2	259.55	1.00	0.1	73	1/6	

control

Rho GTPase-activating protein; GAB-associated CDC42; rac GTPase activa					**2417.66**	28893539.0	24		
FPbeads400_Dec19, 1178	-.KSPVGSWRSFFNLGK.-	1710.96	2	559.97	1.52	0.2	97	3/14	
rawextr_200bead_Mar04, 1194	-.NESEPSEMK.-	1051.11	2	553.94	1.06	0.1	384	5/8	
rawextr_60MeOHbeadigg_Mar04, 2334	-.PHHSSELTDKSPMPSTLPRDK.-	2361.62	3	193.42	1.32	0.0	147	1/5	
rawextr_700bead_Mar04, 2564	-.ELPNPLLTYQLYEKFSDAVSAATDEERLIK.-	3455.88	2	59.87	0.82	0.1	39	3/29	
rawextr_chfbeadIgG_Mar04, 2698	-.SVPISRTEVPPDDEPAYCPRPVYQYK.-	3008.35	2	1050.46	1.31	0.3	132	1/5	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
brain stress early protein Gbi; rho GTPase activating protein 14; EST					7211.53	27597098.0	12		
jmfag1mnacl0minigg, 406	- MFPNSSSDK.-	1013.11	2	646.08	1.35	0.0	469	5/8	1
jmfag5minigg1000mmnacl, 444	-.DPDAAMRR.-	932.04	3	469.55	1.18	0.0	380	13/28	1
jmfag1mnacl7.5minigg, 502	- MFPNSSSDK.-	1013.11	2	248.58	0.90	0.1	185	1/2	1
jmrawigg5min350mmnaclsyringednase, 580	-.PVRPVVQHR.-	1088.29	3	352.82	1.03	0.0	336	7/16	1
jmag5mincon500mmnacl, 786	-.HSSLGDHK -	880.93	2	633.44	1.24	0.1	324	4/7	1
jmrawigg5minbeadsfreezethaw, 976	-.DEGVFSLKSLNQGSGGK.-	1723.87	3	228.69	1.51	0.0	150	17/64	
jmiggactinrawphag3007, 1044	-.SDGAAIPRRR.-	1099.23	3	660.10	1.71	0.0	384	17/36	1
jmiggactinrawphag3007, 1050	-.SDGAAIPRRR.-	1099.23	3	773.46	1.92	0.1	373	17/36	1
ajrawphagjun20dpi1MNaCl, 2412	- SSSSSSSGVGSPAVTPTEK.-	1752.82	2	391.68	1.27	0.1	191	1/3	1
phagrawF300_dec20, 1055	- RMATFGSAGSINYPDKK -	1644.09	3	718.38	1.53	0.1	390	17/64	1
jmfagtimecon7 5min.1440.1440.2	-.SGGDTHSPPR -	1011.03	0	286.27	1.03	0.0	270	1/2	1
jmag5mincon500mmnacl, 786	- HSSLGDHK.-	880.93	2	633.44	1.24	0.1	324	4/7	1
jmag5mincon500mmnacl, 622	-.IPKERK.-	770.94	2	364.99	0.91	0.2	170	1/2	
jmfagtimecon10min, 812	- KGLYPMK.-	837.07	2	91.74	1.02	0.0	89	5/12	
jmfag5mincont400_030531151834, 2964	-.RHGCRGHIVTWYLVIIEWPAHIHLER.-	3193.73	2	39.30	0.76	0.0	52	3/25	
RawPhg2007Etsoluhondigest, 653	-.MATFGSAGSINYPDKK -	1687.90	3	673.01	1.55	0.1	378	3/10	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
brain stress early protein Gbi; rho GTPase activating protein 14; EST					632.62	27597098.0	5		
rawextr_250bead_Mar04, 2112	-.QTLGEGERAECGTTRPPCLPPK -	2341.66	3	632.62	1.31	0.1	276	17/84	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
T-cell activation Rho GTPase-activating protein [Mus musculus]					$740.19	22165374.0	14		
jmrawigg5minbeadsfreezethaw, 368	- NDQSLSFQAQK.-	1266.34	3	453.18	1.24	0.1	259	2/5	
jmraw5minigg600mmnaclsd, 986	- QVAGGLPR.-	797.93	2	715.57	1.33	0.2	273	1/2	
AJRAWActinIgG_june13, 2106	-.PSTAVPPVPSHHGGDLSEGTPGGHR -	2447.61	2	391.31	0.92	0.2	73	3/16	1
ajrawphagactin20, 2156	-.VLSWPSLMRK.-	1217.51	3	185.20	0.94	0.1	98	2/9	
jmfag1mnacl7.5minigg, 356	- DTCESSSESSVSMVVRLK.-	1945.18	2	104.42	0.83	0.0	121	4/17	1
jmfag5minigg450mmnacl_030527025134, 730	- QVAGGLPR.-	797.93	2	327.64	0.98	0.1	309	4/7	
phagrawFsucchifbead_dec23, 800	- ILVEFLIDNCFEIFGENIRTR -	2542.94	3	236.88	1.19	0.0	198	1/5	1
rawsucrtp_350phagigg_Mar04, 1336	- LLSCDLFEDWMGALEKPTEEDRIEALK.-	3153.57	3	239.52	1.44	0.0	165	19/104	
phagrawFsuc150_dec22, 1462	- SELHQLRTVSESMQKAK.-	1973.25	3	439.25	1.22	0.1	169	13/64	1
rawsucrtp_60MeOHphagigg_MAr04, 1986	-.AKLDCLGPQHSHLVFEADQLCCARESYI.-	3148.59	2	101.32	0.96	0.0	97	1/6	1
jmbeads600nacirawphage3007, 104	-.QVAGGLPR.-	797.93	2	117.08	0.80	0.0	138	1/2	
jmfag5mincon450mmnacl, 196	- QVAGGLPR.-	797.93	2	133.54	0.92	0.0	121	3/7	
jmbeadsactinrawphag3007, 250	-.QVAGGLPR.-	797.93	2	1179.82	1.55	0.1	556	11/14	
jmfag1mnacl7.5minigg, 356	-.DTCESSSESSVSMVVRLK.-	1945.18	2	104.42	0.83	0.0	121	4/17	1
AJRAWpellet1_contr_jun13, 622	- TVSESMQKAK.-	1109.28	2	680.29	1.23	0.2	168	7/18	1
jmfagcon5minn600mmnacl, 2475	-.PNLLLLRHLLYVLHLISKNAEVNK -	2812.39	2	153.04	0.87	0.1	89	9/46	
jmfag5mincon450mmnacl, 3190	-.SRMFKPSTAVPPVPSHHGGDLSEQTPGGHR.-	3097.42	2	45.16	0.82	0.0	49	7/58	1
RawPhg2007MeEthmeth3digest, 2330	-.QLPVHLLAVVFK.-	1364.70	2	132.56	1.08	0.0	116	9/22	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
T-cell activation Rho GTPase-activating protein [Mus musculus]					278.82	22165374.0	5		
rawextr_actinbead_Mar04, 2196	-.ELKEGLNCGVSVNLKQLPVHLLAVVFK.-	2949.55	2	278.82	1.33	0.1	160	11/52	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ARH7_MOUSE Rho guanine nucleotide exchange factor 7 (PAK-interacting exchange					3003.03	18202873.0	5		
jmraw5minigg1000mmsd, 1078	-.TPKPWSLSWLRPAPPLR.-	2003.38	3	606.04	1.30	0.1	255	7/32	
jmIgG250rawphag3007, 2974	-.SNGQTVIEEKSLVDTVYALKDEVQELR.-	3065.38	2	139.78	0.82	0.1	57	2/13	5
jmfag5minigg150mmnacl.910-912	- SRKESAPQVLLPEEEK.-	1841.06	3	1192.47	2.04	0.1	407	3/10	2
jmfag5minigbead_030528200106, 2599	-.IIVEETKSNGQTVIEEK.-	1918.14	2	690.90	1.27	0.1	431	3/8	5
AJRAWActinContr_june13, 924	-.PSVMLSPSPRMSGFIYQGK.-	2053.46	3	373.85	1.16	0.0	301	17/72	4

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ARH7_MOUSE Rho guanine nucleotide exchange factor 7 (PAK-interacting exchange					1182.67	18202873.0	5		
jmbsaactinrawphag3007, 824	-.NERYLLLFPKPSVMLSPSPR.-	2345.79	2	1182.67	1.30	0.3	31	7/38	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Cdc42/Rac effector kinase; PAK-3 [Mus musculus] [M					5646.82	3420949.0	5		
jmfag5miniggbead, 1619	-.SIYTRSVVESIASPAAPNK.-	1991.24	3	202.18	1.07	0.1	113	11/72	4
JMFAGNACL10_2B21E3, 2552	-.LTDFGFCAQITPEQSKR.-	1942.19	3	322.30	0.94	0.0	341	15/64	8
jmfag5mincon300mmnacl, 166	-.SIFPGGGDKTNK.-	1221.35	3	279.30	1.12	0.0	231	3/11	4
jmbeadsactinrawphag3007,246-248	-.QMNLQQQPKK.-	1243.46	3	3133.37	3.01	0.1	997	7/12	5
jmfreebeadsrawphag3007, 178	-.SDNILLGMDGSVK.-	1349.54	3	402.94	1.63	0.0	227	5/16	5
rawphag2007chifbead3, 997	-.LRSIFPGGGDKTNK.-	1490.89	3	697.42	1.33	0.0	525	21/52	4
rawsucrtp_60MeOHphagigg_MAr04,1096-1098	-.LTDFGFCAQITPEQSKR.-	1942.19	3	237.52	1.43	0.0	167	13/64	8
phagrawFsuc200_dec22, 1553	-.PLPMAPEEK.-	1012.21	2	281.80	0.92	0.2	52	5/16	4
phagrawFsuc600_dec20, 3082	-.ETVNNQKYMSFTSGDKSAHGYIAAHQSNTK.-	3316.56	2	89.99	0.88	0.1	49	7/58	4

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Cdc42/Rac effector kinase; PAK-3 [Mus musculus] ua					604.70	3420949.0	10		
rawextr_150bead_Mar04, 1613	-.CLEMDVDRRGSAK.-	1480.70	2	428.18	1.00	0.1	219	5/12	4
FPbeads300_Dec19, 1952	-.ELIINEILVMRENK.-	1715.05	2	176.51	1.28	0.0	127	4/13	5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rac GTPase-activating protein 1 [Mus musculus]					5356.45	6755266.0	4		
jmkdl500nacrawphag3007, 1129	-.TVPLLSKVDDIHVICSLLK.-	2094.55	3	471.97	1.15	0.1	365	17/72	
jmfag1mnacl0minigg, 1090	-.TTVTVPSDGGPIEAVSTIETLPSWTR.-	2715.99	3	904.74	1.71	0.0	531	21/100	
JMMAGNEGB16D3, 1784	-.PLEPRTDTDNLGTPQNTGGMR.-	2271.46	3	271.34	1.29	0.0	211	1/5	
jmrawigg5min350mmnaclsyringednase, 651	-.DFEDFRK.-	957.02	2	261.68	0.90	0.0	292	7/12	
jmrawmnigg200mmnaclsynngdnas, 1216	-.AETGRSALDVK.-	1147.27	2	319.60	1.34	0.0	224	1/2	
jm5miniggrawlowionic, 1522	-.NQVDVEIKR.-	1101.24	2	365.29	1.34	0.1	244	1/2	
jmigg600rawphage3007, 1702	-.TVIKPESCVPCGKR.-	1517.84	2	463.70	0.95	0.1	374	5/13	
jmfagfrench5minigg1mnackdtt, 2237	-.NLKEPLLTFWLSK.-	1589.90	2	312.64	0.95	0.1	152	1/3	
jmfagcont5minbead, 696	-.GNGNSTPRTPDVK.-	1343.43	3	1435.60	1.43	0.3	138	1/4	
jmfag5mincont400_030531151834, 850	-.NQVDVEIKR.-	1101.24	2	364.17	1.35	0.0	263	9/16	
rawphag2007chfbead2, 66	-.DLLLKAETGRSALDVK.-	1730.00	3	185.70	1.02	0.0	158	11/60	

control

Rac GTPase-activating protein 1 [Mus musculus]					299.62	6755266.0	9		
rawextr_250bead_Mar04,784-786	-.LHDFVSK.-	845.97	2	135.14	1.16	0.0	117	1/2	
FPbeads800_Dec19, 2908	-.TPDVKVSLLGPVTTPEFQLVKTPLSSSLSQR.-	3326.83	2	164.48	0.96	0.1	38	2/15	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
GDIB_MOUSE RAB GDP dissociation inhibitor beta (RAB GDI beta) (GDI-2)					21477.00	13638229.0	7		
JMMAGNEGB16D3,1300-1302	-.PALELLEPIEQK.-	1380.81	2	1598.93	1.84	0.1	691	7/11	5
JMFAGNACL5B21E3, 2084	-.IYKVPSTEAEALASSLMGLFEK.-	2385.76	3	5562.29	2.90	0.3	770	25/84	6
jmfag1mnacl5mincon, 2454	-.VPSTEAEALASSLMGLFEK.-	1981.26	3	4204.23	2.06	0.4	742	13/36	6
JMFAGNACL10_1B21E3, 2814	-.MNEEYDVIVLGHTGTECILSGIMSVNGK.-	3011.44	2	239.99	0.95	0.1	57	4/27	
jmrawigg5min400mmnaclsd, 2165	-.TYDATTHFETTCDDIKDIYKR.-	2537.74	3	398.10	1.21	0.1	292	19/80	2
jmrawigg5min150mmnacl, 2202	-.CKQLICDPSYVK.-	1397.69	2	48.90	0.68	0.0	51	5/22	5
jmraw5minigg1000mmsd, 3244	-.VICILSHPIKNTNDANSCQIIIPQNQVNR.-	3247.74	2	294.21	0.91	0.1	107	9/56	5
jmfag1mnacl5mincon, 2454	-.VPSTEAEALASSLMGLFEK.-	1981.26	3	4204.23	2.06	0.4	742	13/36	6
jmrawigg5min400mmnaclsd, 2165	-.TYDATTHFETTCDDIKDIYKR.-	2537.74	3	398.10	1.21	0.1	292	19/80	2
jmrawigg5min150mmnacl, 2202	-.CKQLICDPSYVK.-	1397.69	2	48.90	0.68	0.0	51	5/22	5
rawsucrfp_400phagigg_Mar04, 54	-.PIEEIIMQNGKVIGVKSEGEIAR.-	2511.92	3	286.92	1.12	0.1	158	7/44	2
phagrawF450_dec20, 288	-.PALELLEPIEQK.-	1380.81	3	473.04	1.38	0.1	172	13/44	5
rawsucrfp_600phagigg_Mar04, 690	-.PALELLEPIEQK.-	1380.81	3	229.77	1.43	0.0	156	13/44	5
rawsucrfp_600phagigg_Mar04, 1268	-.IPGAPPASMGRGRDWNVDLIPK.-	2348.71	3	3382.03	2.32	0.3	512	23/84	2
phagrawF800_Dec23, 2332	-.PALELLEPIEQKFVSISDLLVPK.-	2580.08	2	111.36	0.85	0.0	114	5/22	2

control

GDIB_MOUSE RAB GDP dissociation inhibitor beta (RAB GDI beta) (GDI-2)					698.58	13638229.0	7		
rawextr_250beadigg_Mar04, 278	-.TFEGIDPKK.-	1035.18	3	131.61	1.26	0.0	90	9/32	2
rawextr_500beadigg_Mar04, 1474	-.VPSTEAEALASSLMGLFEKRR.-	2293.63	2	242.20	1.07	0.1	112	9/40	6
FPbeads500_dec19, 2650	-.FKIPGAPPASMGRGR.-	1542.84	2	324.77	1.10	0.1	174	11/28	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
rab effector MYRIP [Mus musculus] g factor I recep					5468.55	21218142.0	13		
jmfagfrench20minigg1mnackdtt, 710	-.RRCGECK.-	852.02	2	148.58	1.22	0.0	120	7/12	3
jmigg600rawphage3007, 1006	-.NRLYELAMK.-	1138.37	2	186.58	0.97	0.1	130	3/8	3
jmIgG150rawphag3007, 1224	-.IEASSVTPIK.-	1045.21	2	357.13	1.17	0.0	303	5/9	3
jmraw5minigglowionic, 1423	-.SQSAFSFTMEDALKSGSAEAAPRSPK.-	2701.95	3	2402.55	2.02	0.3	505	6/25	2
jmraw5minigg250mmnaclsyringdnase, 2032	-.KLPAPPVK.-	850.08	1	182.39	0.92	0.0	193	1/2	3
JMFAGNACL10_1B21E3,122-124	-.NRLYELAMK.-	1138.37	2	213.90	1.11	0.0	192	7/16	3
jmfag5minigg600mmnacl, 260	-.VGPEESNR.-	887.92	2	1219.91	1.60	0.0	760	11/14	3
jmfag5minigg400mmnacl, 1058	-.KKCSAVSLCNISTEVLK.-	1824.20	2	757.50	1.44	0.2	266	11/32	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rab6-interacting protein 2 [Mus musculus]					**8788.25**	30017397.0	1		
jmrawf5minbsareebeads, 2012	-.GLSAKATEEDHER.-	1443.50	3	280.53	1.21	0.0	232	1/3	3
JMMAGTube1B16E3, 1524	-.ENNMLREEMHR.-	1459.64	2	192.56	1.38	0.0	120	2/5	2
jmigg450rawphag3007,900-902	-.QMEVYR.-	825.96	2	551.66	1.15	0.1	442	4/5	2
jmrawigg5min1mnacl, 2997	-.VVQEENQHMQMTIQALQDELRIQR.-	2939.32	2	97.27	0.93	0.1	59	4/23	3
jmraw5minigg250mmnaclsyringednase, 1570	-.PSPDQIIQPLLELDQNRSK.-	2192.46	3	343.48	1.57	0.0	198	17/72	
ajrawphagactin20,1602-1604	-.RAAGLQSEIGQVK.-	1357.54	2	284.92	1.35	0.1	104	1/3	1
jmfagtimecon7.5min.2210.2210.3	-.MACVKQLQLLPAVHMCAAPRVK.-	2409.05	0	839.09	1.46	0.1	532	2/7	
jmfag5mincon450mmnacl, 1962	-.ENNMLREEMHR.-	1459.64	2	529.13	1.34	0.2	170	9/20	2
jmfag5mincont400_030531151834, 2766	-.LETLTNQFSDSKQHIEVLKESLTAK.-	2861.20	2	86.53	0.90	0.1	50	1/8	2
rawsucrfp_60MeOHphagigg_MAr04, 1394	-.VEQLKEELSSKDAQGEELK.-	2161.35	2	1002.02	1.61	0.2	243	1/3	1
JMFAGNACL15B21E3, 534	-.QEEIDTYKKDLK.-	1510.67	3	1640.32	1.82	0.0	892	5/11	1
jmfag5minigg1000mmnacl, 608	-.LLEMLQSK.-	962.19	2	627.75	1.50	0.0	417	9/14	5
jmigg450rawphag3007,900-902	-.QMEVYR.-	825.96	2	551.66	1.15	0.1	442	4/5	2
phagrawF300_dec20, 1131	-.EHASSLASSGLKK.-	1315.46	2	520.25	1.05	0.2	184	1/3	1
rawsucrfp_actinphagigg_Mar04, 1142	-.SNQTNHKPSPDQIIQPLLELDQNR.-	2787.04	3	239.07	1.83	0.0	128	9/46	
rawsucrfp_60MeOHphagigg_MAr04, 1394	-.VEQLKEELSSKDAQGEELK.-	2161.35	2	1002.02	1.61	0.2	243	1/3	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rab6-interacting protein 2 [Mus musculus]					**3067.60**	30017397.0	5		
FPbeads150_Dec19, 877	-.DLEEEIQMLK.-	1248.43	2	142.42	0.94	0.0	150	7/18	2
rawextr_60MeOHbeadigg_Mar04, 1056	-.QELSRKDTELLALQTK.-	1874.13	3	667.75	1.33	0.1	382	17/60	2
rawextr_400beadigg_Mar04,365-367	-.KVNVLQK.-	829.02	2	137.73	1.32	0.0	104	7/12	1
rawextr_300beadigg_Mar4, 1432	-.EHASSLASSGLKK.-	1315.46	2	316.24	1.04	0.0	300	11/24	1
rawextr_350bead_Mar04, 1780	-.VEPSSQSPGRSPRLPR.-	1750.94	2	672.58	1.60	0.2	188	1/3	2
rawextr_900beadigg_Mar04, 1792	-.EELSSKDAQGEELKK.-	1691.82	2	172.65	1.00	0.0	167	9/28	1
rawextr_300beadigg_Mar4, 1846	-.TNAEKQVEELLMAMEK.-	1865.16	2	522.78	1.81	0.1	200	3/10	
rawextr_200beadigg_Mar04, 2259	-.SLQADTTNTDTALTTLEEALADKER.-	2708.87	3	435.45	1.68	0.1	127	17/96	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rab11-FIP4-like [Mus musculus]					**8256.50**	28202067.0	12		
jmfag5miniggbead_030528200105, 1233	-.INLLNDLEAR.-	1171.33	2	970.97	1.70	0.0	547	2/3	
JMFAGNACL15B21E3, 3002	-.VHELEEMVKDQETTAEQALEEEAR.-	2816.01	2	88.89	0.86	0.0	104	9/46	
jmrawbsa5minlowionic, 2326	-.LEDTSLR.-	833.91	2	1228.91	1.35	0.2	464	2/3	1
jmbeads350rawphag30072nd, 1006	-.QENMQLVHR.-	1155.31	2	551.41	1.61	0.1	258	1/2	
jmrawigg5min300mmnaclsyringednase, 689	-.INLLNDLEAR.-	1171.33	2	617.38	1.31	0.1	335	11/18	
jmIgG150rawphag3007, 1334	-.SKLKQENMQLVHR.-	1611.90	3	571.78	1.46	0.1	349	1/3	
rawphag2007chifsol2, 1522	-.KINLLNDLEAR.-	1299.50	2	799.38	1.51	0.1	482	11/20	
phagrawF400_dec20, 906	-.KINLLNDLEAR.-	1299.50	2	1691.99	1.57	0.0	1060	7/10	
rawsucrfp_600phagigg_Mar04, 1322	-.ILAILDHNPSILEIK.-	1803.18	3	80.60	0.91	0.0	76	3/20	1
phagrawFsuc300_dec20, 1778	-.KINLLNDLEAR.-	1299.50	2	1327.40	1.55	0.1	742	13/20	
jmfreebeadsrawphag3007, 608	-.INLLNDLEARLK.-	1412.66	2	327.80	1.10	0.1	183	4/11	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rab11-FIP4-like [Mus musculus]					**895.74**	28202067.0	9		
FPbeads600_Dec19, 810	-.DEMDLYKRMMDK.-	1575.86	3	402.40	1.34	0.1	265	15/44	1
rawextr_450bead_Mar04, 1216	-.LRDQNDDLNGQILSLSLYEAKNLFATQTK.-	3310.66	3	214.05	1.11	0.0	189	5/28	1
FPbeads600_Dec19, 1262	-.NLKANSPNRK.-	1142.30	2	279.30	1.09	0.1	178	4/9	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
hypothetical protein ((NM_017382) RAB11a, member RAS oncogene family					**2429.55**	32414965.0	4		
phagrawF600_dec20, 1286	-.STIGVEFATRSIQVDSK.-	1839.04	3	404.23	1.43	0.1	181	15/64	
rawsucrfp_350phagigg_Mar04,1884-1886	-.GAVGALLVYDISKGVTFENVNR.-	2323.83	3	355.27	1.65	0.0	215	3/14	
phagrawFsuc500_dec20, 1986	-.STIGVEFATRSIQVDSK.-	1839.04	3	963.26	2.22	0.0	424	17/64	
phagrawF800_Dec23, 2098	-.STIGVEFATRSIQVDSK.-	1839.04	3	594.75	1.76	0.1	311	9/32	
RawPhg2007MeEthmeth3digest, 3164	-.AITSAYYRGAVGALLVYDISKGVTFENVNR.-	3249.67	2	112.04	0.97	0.1	39	7/58	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind					**3713.70**	5803135.0	6		
JMFAGNACL10_1B21E3, 132	-.IRTVEINGEK.-	1159.32	3	902.49	1.58	0.0	570	4/9	
jmfag5minigg1000mmnacl, 1158	-.LLIIGDSGVGK.-	1072.28	2	955.70	1.59	0.0	581	13/20	
jmfag1mnacl5mincon, 1250	-.LLIIGDSGVGK.-	1072.28	2	1800.81	1.45	0.2	919	4/5	
AJRAWActinContr_june13, 236	-.KVVETEDAYK.-	1182.31	2	54.70	0.76	0.0	69	5/18	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind					**1729.25**	5803135.0	4		
rawextr_800bead_Mar04,1032-1034	-.GTHGVIVVYDVTSAESFVNVKR.-	2378.67	3	1729.25	1.90	0.2	599	1/4	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAB GTPase activating protein 1; rab6 GTPase activating protein (GAP a					**4006.06**	22122645 0		2	
jmldl600naclrawphag3007, 1346	- RLEEESAQLKEMCR -	1722.97	2	736 51	1 45	0 2	128	4/13	1
jmfag5minigg350mmnacl, 409	- ADALNKELLMTK -	1347 61	3	205 29	1 52	0.0	134	7/22	1
jmfag5minigg250mmnacl, 1984	- EGRVKGISSAK -	1132 30	2	313.66	0.94	0 1	236	1/2	1
jmrawgg5min300mmnaclsynngednase, 949	- IQDLEHHLGLALSEVQAAK -	2073.34	3	294 21	1 12	0 1	195	2/9	1
jmlgG400rawphag3007, 1178	ADALNKELLMTK.-	1347.61	3	261 66	1 07	0.0	243	13/44	1
jmfagtrench5minigg1mnacldtt, 1395	- GISSAKGVSDEDTDEEK -	1767.79	2	230 94	1 17	0 1	143	1/4	1
jmraw5minigglowionic, 1739	- NQLREMELELAQTKLQLVEAECK.-	2718 15	2	66 18	0 93	0.0	61	7/44	1
jmfreebeadsrawphag3007, 390	- ENRRLQEANMR.-	1417 58	3	518 15	1 71	0.1	270	13/40	1
jmfag5mincon300mmnacl, 1060	- RELDKAESEIK.-	1318.46	3	817 85	1 36	0.1	470	7/20	1
jmfag5mincont400_030531151834, 1624	- AESEIKKNSSIIGDYK.-	1782.97	3	279 30	1 34	0.0	208	1/4	1
jmfagtimecont0min_030601230741, 2608	-.GISSAKGVSDEDTDEEK -	1767 79	2	282 32	1.09	0 1	171	5/16	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAB guanine nucleotide exchange factor (GEF) 1; Ras negative regulator					3146.41	9910316.0		10	
jmfag5minigg350mmnacl, 933	- HIFNAIKITK.-	1185.44	2	233 07	1 17	0.1	166	4/9	
jmrawgg5min150mmnacl, 1392	- YMSGQTSPRKQESESWPPEACLGVK.-	2797.12	3	631.35	1.82	0.1	292	19/96	
jmfag5minigg200mmnacl, 2480	-.LDAQSLNLSQEDFDRYMSGQTSPRK.-	2888.12	2	55.88	0.82	0.0	57	7/48	
ajrawphagactin20, 2624	-.LDAQSLNLSQEDFDR.-	1751 83	2	376.81	1.09	0.1	294	11/28	
jmfagtimecon7 5min.966.966.2	- HIFNAIKITK.-	1185.44	0	421 71	1.00	0.1	271	4/9	
jmbeads450naclrawphag3007, 1941	-.TGQEVYKQTKMFLEAMPYK.-	2293.69	2	372 82	1 01	0.2	69	7/36	
rawphag2007chfbead3, 671	-.QIQEDWELAERLQR.-	1814.98	3	354 65	1 32	0.0	249	9/26	
phagrawFchff_dec23, 1898	-.NLDLLSQLNER.-	1315 46	2	284 36	1 15	0.0	238	2/5	
phagrawF60MeOH_dec23,1988-1990	- RIRALHWVTPQMLCVPVNEEIPEVSDMVVK.-	3491.15	3	415.78	1.64	0.1	94	4/29	

control

RAB guanine nucleotide exchange factor (GEF) 1; Ras negative regulator					**879.22**	9910316.0		10	
rawextr_60MeOHbead_Mar04, 682	- NLDLLSQLNER.-	1315.46	3	418.73	1.31	0.0	317	7/20	
rawextr_1000bead_Mar04, 1318	-.LQREEEEAFASSQSSQGAQSLTFSKFEEK.-	3280.46	3	299.16	1.22	0.1	214	9/56	
rawextr_200beadigg_Mar04, 2593	-.LQREEEEAFASSQSSQGAQSLTFSKFEEK.-	3280 46	2	161.33	0.87	0.1	40	1/8	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAB2, member RAS oncogene family-like; ral guanine nucleotide dissociat					**2900.86**	6677737.0		10	
jmfag5minigg400mmnacl,470-472	-.EGVVGGSADLIRNLR.-	1556 75	3	576.23	1 81	0.1	293	17/56	1
JMFAGNACL10_2821E3, 1074	-.GGGVVPYLGTFLK.-	1308.55	2	323.83	1 35	0.0	238	1/3	1
jmfag5minigg500mmnacl, 1552	-.LESFLLRTGYAAREGVVGGSADLIR.-	2652.00	3	293.22	1.49	0.0	184	5/24	1
phagrawFsuc200_dec22, 1825	- SAGCGGGVSGPGSSDCR.-	1454.53	2	408.11	1 15	0.1	220	3/8	1
phagrawF60MeOH_dec23, 1830	- VAGAVVSSVLGATSIGEGPREVTVR.-	2412.73	3	117 05	1.21	0.1	71	13/96	1
phagrawF800_Dec23, 2316	-.DSLRVFSSLCQIFSEEDNYSQSR -	2711.90	3	377.86	1.27	0.0	283	17/88	1
rawsucrtp_chlphagigg_Mar04, 2456	-.IIRVQMELGEDGSVYKSILVTSQDK.-	2810.22	3	380.00	1.32	0.0	287	5/24	2
phagrawFsuc450_dec20,2846-2848	-.SAGCGGGVSGPGSSDCR.-	1454 53	2	424.54	1 87	0.0	227	11/32	1

control

RAB2, member RAS oncogene family-like; ral guanine nucleotide dissociat					**682.88**	6677737.0		2	
jmbsa1000naclrawphag3007, 1621	-.MLPRPLRLLLDTTPPGGVVLSSFR.-	2637.18	3	682 88	1.50	0.1	409	21/92	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
regulating synaptic membrane exocytosis 2; Rab3 interacting protein 1;					**2757.02**	16716607.0		12	
jmldl250naclrawphag3007, 1286	-.SASQLSQTEGGGKKLR.-	1647.82	2	825.80	1.31	0.1	408	13/30	1
jmldl300naclrawphag3007,1290-1292	-.NVEQGHRGTR.-	1154.22	2	541.93	1.68	0.1	294	5/9	1
jmldl150naclrawphag3007, 1386	-.EEEKEQSVLK.-	1219.32	2	1011.53	1.56	0.2	247	1/2	
jmldl600naclrawphag3007, 1812	-.VLQIIVWGDYGRMDHK.-	1931.25	3	302.52	1.14	0.0	250	4/15	2
jmldlactinrawphag3007, 1824	-.VPRGLRNEEAPQEK.-	1623.80	2	75.23	0.81	0.0	70	5/26	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ras homolog gene family, member U; Wnt1 responsive Cdc42 homolog [Mus					**6217.52**	19923060.0		3	
rawsucrfp_500phagigg_Mar04,580-582	- HCPKAPIILVGTQSDLR -	1849.19	3	401.87	1.78	0.0	212	17/64	
rawsucrfp_600phagigg_Mar04, 686	- APIILVGTQSDLR.-	1363.62	3	1544.07	1.78	0.0	852	11/24	
JMMAGNEGB16D3,810-812	-.GPGVSGGRGR.-	899.98	2	855.05	1.14	0.0	568	11/18	
jmigg450rawphag3007, 928	- APIILVGTQSDLR.-	1363.62	3	501.14	1.40	0.1	319	5/16	
jmigg600rawphage3007, 994	-.APIILVGTQSDLR.-	1363.62	3	776.24	1.38	0.0	557	17/48	
jm5miniggrawlowionc, 3342	- EVFDAAIVAGIQHSDSQLQPKKSK.-	2597.91	2	80.83	0.90	0.1	34	3/23	
AJRAWActinContr_june13, 156	- PVRLQLCDTAGQDEFDK.-	1936.14	3	185.43	0.91	0.0	181	15/64	
jmfagcont5minbead, 890	-.APIILVGTQSDLR.-	1363.62	3	584.57	1.49	0.0	393	17/48	
jmbeads400rawphag3007, 1069	-.VLIELDKCKEK.-	1318.61	2	606.19	1.03	0.1	526	11/20	
jmfagtimecont0min_030601230741, 2738	-.PVRLQLCDTAGQDEFDK.-	1936.14	1	22.96	0.73	0.0	30	5/32	
rawphag2007chfbead1, 868	- HCPKAPIILVGTQSDLR.-	1849.19	3	879.19	1.95	0.1	353	19/64	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ras homolog gene family, member U; Wnt1 responsive Cdc42 homolog [Mus					**1773.06**	19923060.0		6	
rawextr_900bead_Mar04, 384	-.HCPKAPIILVGTQSDLR -	1849.19	3	780.21	1.64	0.1	438	11/32	
rawextr_300bead_Mar04,409-411	- APIILVGTQSDLR.-	1363.62	3	992.85	2.05	0.1	361	1/3	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to ras-GTPase-activating protein SH3-domain binding protein [M					**7237.55**	38077047.0		9	
jmrawigg5minbeadsfreezethaw, 330	- PIREAGK -	770.90	2	758.53	1.39	0.0	544	5/6	
jmigG400rawphag3007, 2118	- VPASQPCPESKPDSQIPPQRPQR -	2543.85	3	514.68	1.63	0.0	309	5/22	
ajrawphagjun20dp1MNaCl, 2666	-.HPDSHQLFIGNLPHETVDKSELK.-	2642.91	3	579.62	1.45	0.1	221	17/88	
jmfag5miniggbead_030528200105, 436	- TRTAREGDR.-	1062.12	3	659.78	1.15	0.1	405	15/32	
jmrawigg5miniggfreebead,2118-2120	- PGDVEPRRMVR -	1312.53	2	512.64	1.61	0.0	315	11/20	
phagrawFsuc200_dec22, 1657	- SELKNFFQNVGNVVELRINSGGK.-	2550.86	3	273.84	1.30	0.0	200	15/88	
phagrawF60MeOH_dec23, 2468	-.SELKNFFQNVGNVVELRINSGGK.-	2550.86	3	311.74	1.40	0.1	112	2/11	
phagrawF600_dec20, 605	- PSPLLVRR.-	938.15	2	49.60	0.76	0.0	53	2/7	
jmfagcon5minn600mmnacl, 135	-.LWGPGGPGDGSSGGIR.-	1470.57	3	1876.60	1.71	0.1	1068	2/5	
jmfagcont5minbead, 2518	-.YFVRQYCTLLNQAPDILHR.-	2351.72	2	450.89	1.37	0.1	157	11/36	
jmfagtimecon7.5min.2512.2512.2	- DNRLQGPGGPRGGPSGGMR.-	1867.04	0	533.65	1.60	0.1	291	13/36	
jmfagcon5minn600mmnacl, 2811	- RFMQTFVLAPEGSAANKFYVHNDIFR.-	3060.48	2	404.24	0.92	0.2	108	9/50	
phagrawF60MeOH_dec23, 2468	- SELKNFFQNVGNVVELRINSGGK.-	2550.86	3	311.74	1.40	0.1	112	2/11	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to ras-GTPase-activating protein SH3-domain binding protein [M					**293.53**	38089608.0		2	
rawextr_60MeOHbead_Mar04, 614	-.YQDEVFGGFVTEPQK.-	1744.88	3	293.53	1.43	0.0	203	15/56	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ras-GTPase-activating protein SH3-domain binding protein [Mus musculus]					**2573.89**	1698657.0		13	
jmraw5miniigg250mmnaclsynngdnase, 242	-.GIVGGGMMRDR.-	1149.37	3	273.26	1.23	0.1	184	3/10	2
jmrawigg5minbeadsynngdnase,541-543	-.ETRGGGDDR.-	962.95	2	660.10	1.17	0.2	204	1/2	2
jmfagfrench5minigg1mnackdtt, 1581	-.ILIAKPIMFRGEVR.-	1644.06	2	249.63	1.28	0.0	196	4/13	2
jmfag1mnacl2,5minigg, 1700	-.LGSGRGTGQMEGTLHR.-	1657.84	2	226.25	0.89	0.0	252	11/30	
jmrawigg5minbeadsfreezethaw, 2032	-.IIRYPDSHQLFVGNLPHDIDENELK.-	2964.28	2	446.22	1.25	0.1	183	5/24	2
jmfagtimecon7.5min,2176.2176.2	-.PIMFRGEVRLNVEEK.-	1818.13	0	459.47	1.40	0.0	319	9/28	2
rawphag2007chlfsol2,2072-2074	-.PIMFRGEVRLNVEEK.-	1818.13	2	195.38	1.40	0.0	121	2/7	2
rawphag2007chlfsol2, 2620	-.RIIRYPDSHQLFVGNLPHDIDENELK.-	3120.47	2	63.58	0.92	0.0	68	4/25	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ras-GTPase-activating protein SH3-domain binding protein [Mus musculus]					**1073.66**	1698657.0		10	
rawextr_800beadigg_Mar04, 718	- PSPLLVGR -	839.02	2	77.42	1.02	0.0	72	3/7	4
rawextr_250beadigg_Mar04, 1456	-.PGRGDMEQNDSDNR.-	1591.60	3	369.43	1.39	0.1	227	17/52	2
rawextr_350beadigg2_Mar04, 1560	- SATPPPAEPASLPQEPPKPR.-	2068.32	3	626.81	1.19	0.0	523	1/4	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAS p21 protein activator 3; GAPIII activator 3; Ras GTPase-activating					**9598.83**	7110713.0		25	
jmfag1mnacl7,5minigg, 592	- FGMKNFKK -	1000.24	2	343.04	0.98	0.0	337	4/7	3
jmraw5miniigg1000mmad, 1062	- PTIEEICQSHK -	1285.45	2	231.73	1.27	0.1	123	9/20	2
jmraw5miniigg250mmnaclsynngdnase, 1300	- PTIEEICQSHKSCEIDPVK.-	2157.46	3	1511.49	1.70	0.2	604	5/18	2
jmrawigg5min1mnacl, 1571	- SIEQPILLKEGFMIKR.-	1903.32	2	234.28	1.87	0.1	93	4/15	3
jmiggactinrawphag3007, 2110	-.ILRHSSSYEAWYFLQPR.-	2154.42	3	586.81	1.71	0.0	310	5/16	2
jmiggactinrawphag3007, 2120	-.ILRHSSSYEAWYFLQPR.-	2154.42	3	1019.11	2.12	0.1	314	5/16	2
rawsucrfp_600phagigg_Mar04, 874	-.VVPFISAIASAEVKRTQDPNTIFR.-	2661.05	3	1340.36	2.04	0.2	113	5/23	2
rawsucrfp_150phagigg_Mar04, 1531	-.YADAVKNFLDLISSSGR.-	1857.06	2	399.51	1.69	0.1	193	9/32	3
phagrawFsuc600_dec20,1736-1738	- SFQNYIRQQSEISTHSI.-	2039.19	3	1095.12	1.74	0.2	200	7/32	3
phagrawFsuc300_dec20, 3844	- IFECQGLPIVNGQCDPYATVTLAGPFR.-	2911.35	2	122.61	1.09	0.1	69	2/13	2
jmfagtimecon2.5min.2842.2842.3	-.DLLLKSADVEPVSASAAHILGEVCRDK.-	2838.23	0	220.66	1.13	0.1	155	15/104	2
jmbeads450nacirawphag3007, 1475	-.YADAVKNFLDLISSSGR.-	1857.06	2	1409.59	1.29	0.3	263	5/16	3
jmfag5mincon300mmnacl, 2300	-.VDLWNASNLKFGDEFLGELR.-	2324.58	3	405.81	1.60	0.1	222	17/76	2
jmfag5mincont150mmnacl, 2817	-.LNVVYTEDHVFSSEYYSPLRDLLLK.-	3002.37	2	59.30	0.73	0.0	55	1/8	2
jmfreebeadarawphag3007, 1980	-.CIDETMKLAGMHYLHVTLKPTIEEICQSHK.-	3471.10	3	638.44	1.32	0.1	263	19/116	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAS p21 protein activator 2 [Mus musculus]					7208.47	16716601 0	20		
JMFAGNACL5B21E3, 502	-.IYSIFTLSLLKLQK.-	1668.06	3	534.20	1.40	0.1	220	15/52	
jmfag1mnacl5minigg, 816	-.YGSKENPIVGK.-	1192.35	2	232.08	0.90	0.1	161	9/20	
jmigg600rawphage3007,1782-1784	-.LVPFITAVAELDLK.-	1529.85	2	740.29	1.48	0.1	323	5/13	
jmfag5minigg1000mmnacl, 1886	-.FPNHPHVQYSAVSSFVFLR.-	2233.52	3	291.67	1.11	0.0	262	1/4	
jmldl400firstnaclrawphag3007, 972	-.DCFCTINLDQEEVYR.-	1849.04	3	1378.93	2.06	0.1	626	3/8	
jmldl150naclrawphag3007, 2960	-.MAAAAPAAAAASPEAPAVSGSADPETGDEDSR.-	2943.06	2	340.36	1.01	0.1	144	11/62	
ajrawmediapbsnocells, 1394	-.DCFCTINLDQEEVYR.-	1849.04	2	1396.22	1.78	0.3	157	2/7	
phagrawF150_dec22,1248-1250	-.YGSKENPIVGKIS.-	1392.58	2	130.34	1.17	0.0	102	1/3	
rawsucrfp_250phagrgg_Mar04, 1320	-.TLTLISKTIQIIGNWGCQSR.-	2233.62	3	1090.51	1.57	0.2	437	1/4	
phagrawFsuc250_dec22, 1915	-.KFLDEISSTETKESSGTSEPVHLK.-	2650.88	3	263.90	1.32	0.0	200	5/23	
phagrawFsuc600_dec20, 2510	-.LVPFITAVAELDLK.-	1529.85	2	288.90	1.00	0.1	241	11/26	
phagrawFsucchifbead_dec23, 2934	-.LEIRIDLWNNENLVQDVFLGEIK.-	2772.15	3	135.11	0.96	0.0	133	13/88	
jmfag5mincont200mmnacl, 1992	-.KFLDEISSTETKESSGTSEPVHLK.-	2650.88	3	385.99	1.20	0.1	139	15/92	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAS p21 protein activator 2 [Mus musculus]					417.19	16716601.0	7		
rawextr_400bead_Mar04, 1549	-.EPGYSKFTIEDSVATFKTIQQIK.-	2631.96	3	306.68	1.39	0.0	200	2/11	
jmbsaactinrawphag3007,2747-2749	-.LDEPHEKYR.-	1187.29	2	0.00			25	1/8	
jmraw5minbsafreezthaw, 2756	-.FFAVAILSPHAFHLRPHYPDTQTVR.-	2922.34	3	110.52	1.70	0.0	65	1/8	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAS p21 protein activator 1; p120-rasGAP; GTPase-activating protein [M					11271.47	21703900.0	15		
phagrawFsuc200_dec22,703-705	-.QVSSLVLHIEEAHKLPVK.-	2028.39	3	260.53	1.22	0.0	196	15/68	
phagrawF400_dec20, 1026	-.YIYGCLQKSVQHK.-	1567.84	2	221.94	1.26	0.0	175	3/8	
phagrawFsuc200_dec22,1147-1149	-.YIYGCLQKSVQHK.-	1567.84	2	588.85	1.77	0.0	332	1/2	
phagrawFsuc400_dec20,1706-1708	-.YIYGCLQKSVQHK.-	1567.84	2	594.58	1.71	0.1	234	5/12	
phagrawFsuc350_dec20, 1726	-.YIYGCLQKSVQHK.-	1567.84	2	344.35	1.20	0.1	254	5/12	
phagrawFsuc350_dec20, 1732	-.YIYGCLQKSVQHK.-	1567.84	2	557.51	1.52	0.1	261	5/12	
phagrawFsuc450_dec20, 3222	-.SNKHRMIMFLDELGNVPELPDTTEHSR.-	3168.55	2	703.51	1.00	0.3	66	2/13	
jmfag5minigbead, 1311	-.KSKDPDILFMR.-	1350.61	2	67.02	0.89	0.0	75	2/5	
jmfag1mnacl7.5minigg, 2540	-.PSDNTPGDYSLYFRTNENIQRFK.-	2763.96	3	908.25	1.66	0.2	254	5/22	
jmfag5minfrench1mnacldttdpi, 1154	-.EPVPMQDQGQVLNDTVDGK.-	2071.26	3	784.62	1.65	0.0	475	19/72	
jmfag_20_minfrench1mnacldttdpi, 1154	-.EPVPMQDQGQVLNDTVDGK.-	2071.26	3	784.62	1.65	0.0	475	19/72	
jmIgG500rawphag3007, 1659	-.YIYGCLQKSVQHK.-	1567.84	2	338.13	1.51	0.0	218	3/8	
jmrawgg5min350mmnaclsyringednase, 2345	-.YYNSIGDIIDHYRK.-	1757.93	2	92.39	0.81	0.0	112	7/28	
jmfag1mnacl7.5minigg, 2540	-.PSDNTPGDYSLYFRTNENIQRFK.-	2763.96	3	908.25	1.66	0.2	254	5/22	
jmIgG300rawphag3007, 2544	-.GEKLLYPVAPPEPVEDR.-	1910.16	2	202.65	1.08	0.0	184	9/32	
jmrawgg5minbeadsyringdnase, 2751	-.WKNLYFILEGSDAQLIYFESEKR.-	2851.21	2	96.76	0.71	0.0	121	9/44	
jmfag5mincont400_030531151834, 886	-.SKDPDILFMR.-	1222.44	2	481.54	0.97	0.1	380	1/2	
jmbeads500rawphag3007,1193-1195	-.YIYGCLQKSVQHK.-	1567.84	2	796.10	1.87	0.1	301	11/24	
jmbeads1000naclrawphag3007,1369-1371	-.YIYGCLQKSVQHK.-	1567.84	2	818.84	1.92	0.1	343	11/24	
jmbeads350rawphag30072nd,1588-1590	-.YIYGCLQKSVQHK.-	1567.84	2	552.76	1.72	0.0	322	5/12	
jmfag5mincon300mmnacl, 2020	-.ATKPKGLIDLSVCSVYVVHDSLFGR.-	2706.16	3	289.38	1.63	0.1	131	3/16	
rawphag2007chifsolt, 1072	-.TKDAFYKNIVK.-	1327.55	3	878.88	1.99	0.0	441	3/8	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
glutamate receptor, ionotropic, AMPA3 (alpha 3); cAMP-dependent Rap1 g					5235.53	8393313.0	15		
jmIgG300rawphag3007, 754	-.GSALGTPVNLAVLK.-	1340.59	3	730.50	1.36	0.0	532	19/52	
jmfag1mnacl2.5minigg, 940	-.DIQEFRRIIEEMDR.-	1851.08	3	677.05	1.55	0.1	294	7/28	
jmraw5minigg500mmnaclsd, 1088	-.GAILSLLGYYK.-	1198.44	2	66.48	0.90	0.0	49	7/20	
jmfagfrench20minigg1mnacldtt, 2408	-.LSIVGDGKYGARDPETK.-	1807.00	2	251.36	1.16	0.1	191	9/32	
jmfag5mincont400_030531151834, 764	-.INTILEQVVILGKHSR.-	1821.18	3	439.49	1.49	0.0	294	3/10	
AJRAWpellet: _contr_jun13, 1296	-.YGARDPETKIWNGMVGELVYGR.-	2512.83	3	739.74	1.13	0.0	641	11/42	
AJRAWActinContr_june13, 1500	-.GFSILQAIMEAAVQNNWQVTAR.-	2448.79	2	55.15	1.06	0.0	52	3/14	
jmbeads1000naclrawphag3007, 1999	-.NAPLKYTSALTHDAILVIAEAFR.-	2515.89	3	404.80	1.23	0.1	236	19/88	
jmfag5mincont200mmnacl, 2878	-.NTVQEHSAFRFAVQLYNTNQNTTEK.-	2942.15	2	69.11	0.87	0.1	37	5/48	
jmldl250naclrawphag3007, 1278	-.GYGVATPKGSALGTPVNLAVLK.-	2114.47	3	1801.85	1.92	0.2	390	19/84	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAP1, GTP-GDP dissociation stimulator 1; cDNA sequence BC011279 [Mus m					3104.99	21704072.0	6		
JMFAGNACL10_1B21E3, 832	-.SEMPPVQFKLLGTLRMLIDAQAEAAEQLGK.-	3255.86	3	501.17	1.70	0.1	267	21/116	1
JMFAGNACL5B21E3, 840	-.NAKLVERLVEWCEAK.-	1789.09	3	280.58	1.34	0.0	209	13/56	1
ajrawphag1MNaC20, 498	-.LLSALIRHSK.-	1138.39	3	580.47	1.50	0.1	266	4/9	1
ajrawphagactin20, 842	-.LLSALIRHSK.-	1138.39	3	274.88	1.31	0.0	198	5/12	1
jmfagfrench20minigg1mnacldtt, 2050	-.EDDVAELKTASDLMVLLLLGDESMQKLFEGGK.-	3496.99	2	360.51	1.13	0.1	112	5/31	1
jmbeads300rawphag3007, 2678	-.SEMPPVQFKLLGTLRMLIDAQAEAAEQLGK.-	3286.86	2	113.27	1.06	0.1	55	4/29	1
rawphag2007chifbead3, 110	-.NLAIPVVNKAK.-	1167.43	3	994.12	1.68	0.2	191	13/40	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAP1, GTP-GDP dissociation stimulator 1; cDNA sequence BC011279 [Mus m					892.70	21704072.0	11		
rawextr_450bead_Mar04, 532	-.NLAIPVVNKAK.-	1167.43	3	238.14	0.98	0.0	232	7/20	1
rawextr_300bead_Mar04, 782	-.SEMPPVQFKLLGTLRMLIDAQAEAAEQLGK.-	3286.86	3	211.35	1.32	0.0	152	15/116	1
rawextr_900beadigg_Mar04, 1044	-.DVIKTIVQSGGIK.-	1358.61	2	443.22	1.08	0.1	199	5/12	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rap1 guanine-nucleotide-exchange factor directly activated by cAMP; ex				**2658.92**	**21450061.0**		**13**	
ajrawphag1MNaCl20, 600	-.QDFNRIIK -	1034 19	3	233.62	1.06	0.1	196	5/14
jmfag5minigg200mmnacl,1762-1764	-.NRYTVMSGTPEKILELLLEAMR.-	2566.04	3	1165.51	2.30	0.2	174	3/14
jmfag5minigg200mmnacl, 2184	-.TMRLEEHGKVVLVLER.-	1910.28	2	291.62	1.00	0.1	155	3/10
jmfagcont5minbead, 1964	-.TDEELDLIFEELLHIK.-	1958.20	3	762.28	1.59	0.2	165	7/30
phagrawFsuc200_dec22, 1323	-.VSLEQATTEHVHKAGK.-	1735.92	2	205.88	0.93	0.1	161	4/15

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Rap1 guanine-nucleotide-exchange factor directly activated by cAMP; ex				**800.14**	**21450061.0**		**6**	
rawextr_200bead_Mar04, 1636	-.RPSCIQGLRWTPLTNSEDSLDFR.-	2692.99	3	800.14	1.87	0.1	227	17/88

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				**63109.41**	**4506413.0**		**4**	
AJRAWActinIgG_june13, 1198	-.LVVLGSGGVGK.-	986.19	2	3058.54	2.25	0.2	749	13/20	1
rawphag2007chlfsol3, 561	-.LVVLGSGGVGK.-	986.19	2	2855.44	1.65	0.3	786	7/10	1
rawphag2007chfbead3, 717	-.LVVLGSGGVGK.-	986.19	2	5984.80	2.63	0.4	887	3/4	1
AJRAWActinContr_june13, 558	-.LVVLGSGGVGK.-	986.19	2	2104.65	2.08	0.2	528	13/20	1
jmfagcon5minn600mmnacl, 601	-.LVVLGSGGVGK.-	986.19	2	4575.36	2.51	0.3	772	3/4	1
jmfagcon5minn600mmnacl, 642	-.LVVLGSGGVGK.-	986.19	2	1656.87	2.13	0.2	528	11/20	1
jmbeads40rawphag3007, 969	-.VVGKEQGQNLAR.-	1299.48	2	188.46	1.16	0.0	145	4/11	2
AJRAWActinContr_june13, 1478	-.SKINVNEIFYDLVR.-	1710.98	3	14301.19	3.90	0.4	2088	7/13	2
jmfagcon5min1000mmnacl_030601180404, 1740	-.INVNEIFYDLVR.-	1495.71	2	12278.96	3.75	0.4	1368	9/11	2
AJRAWActinContr_june13, 1794	-.INVNEIFYDLVR.-	1495.71	2	16225.16	4.13	0.5	1464	10/11	2

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				**24733.93**	**4506413.0**		**4**	
rawextr_1000bead_Mar04, 884	-.LVVLGSGGVGK.-	986.19	2	5412.29	2.32	0.4	687	13/20	1
rawextr_800beadigg_Mar04, 1764	-.INVNEIFYDLVR.-	1495.71	2	8246.88	3.14	0.4	1127	17/22	2
FPbeads450_Dec19, 2472	-.INVNEIFYDLVR.-	1495.71	2	10664.13	3.34	0.4	1174	19/22	2
rawextr_actinbeadigg_Mar04, 1733	-.DTEDVPMILVGNKCDLEDERVVQK.-	2678.02	3	410.83	1.44	0.1	251	19/92	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to IQ motif containing GTPase activating protein 3 [Mus muscul				**9048.40**	**38077593.0**		**3**	
jmkd400nacirawphag3007_030802153313,1064-1066	-.EGKAAQTER.-	990.05	2	270.43	1.26	0.0	209	1/2
jmkd300nacirawphag3007,1072-1074	-.EGKAAQTER.-	990.05	2	334.83	1.53	0.0	217	1/2
jmbaa1000nacirawphag3007,1049-1051	-.EGKAAQTER.-	990.05	2	303.91	1.40	0.1	173	7/18
jmfag5minigg600mmnacl, 1456	-.LQHFKANLDAIIK.-	1511.79	2	133.46	0.97	0.0	138	1/3
JMFAGNACL5B21E3, 1816	-.EEIQAGVAVANEK.-	1358.48	2	202.91	0.81	0.1	214	1/3
jmigG150rawphag3007, 824	-.EGKAAQTER.-	990.05	2	297.57	1.16	0.1	135	3/8
jmrawigg5min400mmnaclad, 1067	-.EQKSQELGLVRLLEK.-	1771.05	2	126.92	0.95	0.0	119	3/14
jmigG300rawphag3007, 1812	-.PMVYITVGELIGTHR.-	1687.00	2	240.81	1.22	0.0	191	9/28
ajrawphagjun20actinDPI, 1862	-.YFQKNVDSVVKIQAFFR.-	2090.41	3	977.39	1.77	0.2	264	17/64
phagrawF300_dec20, 64	-.SQLLSPFSSLDFSPLPLVHFQRHR.-	2810.21	3	213.84	1.30	0.1	119	13/92
phagrawF600_dec20, 958	-.AAQTERVLRNPNVALR.-	1809.07	3	345.05	1.41	0.1	162	7/30
phagrawF350_dec20, 1218	-.FAHLLNQSQEDFSAESELLK.-	2307.50	2	510.85	1.21	0.2	145	5/19
phagrawFsuc60MeOH_dec23, 1264	-.FAHLLNQSQEDFSAESELLK.-	2307.50	3	1725.77	2.03	0.2	469	11/38
phagrawFsuc400_dec20, 1746	-.EQLSDMMILDKQKGLK.-	1878.25	3	161.59	1.00	0.0	139	7/30
phagrawFsuc500_dec20, 1826	-.KDLCGLPVGKTCSPVHSWMEVCLK.-	2632.19	2	100.70	1.06	0.0	95	9/48
phagrawFsuc450_dec20, 3450	-.IGGILANEFSADEAAVHAAILAINDAVER.-	2952.27	2	25.85	0.69	0.0	36	3/28
jmfag5mincont200mmnacl, 414	-.RHHSLMAHSLLSLSEK.-	1847.14	3	939.91	1.92	0.0	474	3/10
jmfagcon5minn600mmnacl, 1133	-.NVDSVVKIQAFFR.-	1523.78	2	381.09	1.11	0.1	236	5/12
jmfag5mincon450mmnacl, 3226	-.TLSALLLPAAGLEDVSLHVAPRYHLLLVAAK.-	3253.87	2	49.78	0.77	0.0	63	2/15
phagrawFsuc60MeOH_dec23, 1264	-.FAHLLNQSQEDFSAESELLK.-	2307.50	3	1725.77	2.03	0.2	469	11/38

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to IQ motif containing GTPase activating protein 3 [Mus muscul				**2314.34**	**38077593.0**		**27**	
rawextr_900beadigg_Mar04, 370	-.LDISLR.-	716.85	2	225.08	1.06	0.0	198	1/2
rawextr_150beadigg_Mar04, 748	-.ANEDTSTAQR.-	1093.09	2	283.80	1.40	0.0	202	1/2
rawextr_60MeOHbead_Mar04, 1258	-.ASDCYQGLVDELAKDICNQRR.-	2398.66	3	409.05	1.60	0.0	253	9/40
FPbeads600_Dec19, 1556	-.FFVNAKFLGVDMEK.-	1645.95	2	162.96	1.07	0.1	118	7/26
rawextr_60MeOHbeadigg_Mar04, 2834	-.VIQDVLEDRSVSIHTDPVHIYK.-	2564.88	3	297.56	1.19	0.0	238	4/21
jmbaa1000nacirawphag3007,1049-1051	-.EGKAAQTER.-	990.05	2	303.91	1.40	0.1	173	7/18
FPbeads500_dec19, 2930	-.VTGDPGAVLWLEEIRQGVARANEDTSTAQR.-	3241.52	3	812.07	1.38	0.1	280	11/58

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to SREBP cleavage activating protein [Mus musculus]				**3645.31**	**23593606.0**		**3**	
jmrawbas5min1minacl, 1896	-.APEVTWGPEDEELWRK.-	1943.11	3	518.38	1.26	0.0	404	3/10	
jmrawbas5min1minacl, 2374	-.SLEEVCLQVTDLLPGLR.-	1886.20	3	596.77	1.38	0.1	303	15/64	
JMFAGNACL10_1B21E3, 1598	-.PPSPGPPLPQASQEEGTAPEK.-	2115.29	3	508.78	1.41	0.1	257	9/40	1
jmrawigg5minbeadsfreezethaw, 964	-.RLRVIYFLAR.-	1307.62	2	198.09	0.75	0.0	243	4/9	
AJRAWActinIgG_june13, 1980	-.DSGGGGAFETQENWERLSDGGK.-	2344.42	3	766.29	1.61	0.2	229	4/21	1
rawsucrfp_900phagigg_Mar04,1074-1076	-.RLPPESCLPSAKPVGR.-	1708.02	2	187.33	1.45	0.0	129	1/3	
jmfagtimecont10min_030601202502, 1020	-.VLCPRNYGQPGGGGPGRR.-	1785.03	3	293.86	1.41	0.1	178	17/64	1
AJRAWpellet2_contr_jun13, 1543	-.VYQEEGLAAMRMPALR.-	1836.17	2	575.80	1.07	0.2	192	1/3	1

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to SREBP cleavage activating protein [Mus musculus]				**671.78**	**23593606.0**		**7**	
rawextr_450bead_Mar04, 1020	-.PGPRRDSCGGGAFETQENWER.-	2350.47	3	391.00	1.34	0.0	286	9/40	1
rawextr_450bead_Mar04, 2082	-.KLRSLLPEHGCLLLSPGNFWQNDWER.-	3110.54	2	480.78	1.21	0.2	85	7/50	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ARG1_MOUSE ADP-ribosylation factor GTPase activating protein 1 (ADP-ribosylat					**6347.77**	27923732.0	7		
jmfag5minigg350mmnacl, 411	- EGATKFGSQASQK -	1339.44	3	642.79	1.26	0.1	232	17/48	3
JMMAGTube1816E3, 822	- IFDDVSSGVSQLASKVQGVGSK.-	2209.44	3	733.87	1.69	0.0	429	11/42	1
jmrawigg5min450mmnaclsd, 138	- EGATKFGSQASQK.-	1339.44	3	332.01	1.26	0.0	241	17/48	3
ajrawphagjun20dpi1MNaCl, 508	- PAQEKVKEGR -	1142.29	2	525.39	1.34	0.0	374	5/9	1
jmIgG150rawphag3007, 1418	- YVGFGKTVPPQKR.-	1477.74	2	311.89	1.27	0.0	234	3/8	
jm5miniggrawlowionic, 1668	- SPSSDSWTCADASTGRR.-	1784.85	3	297.68	1.17	0.0	254	15/64	3
phagrawFsuc250_dec22, 1387	- SPSSDSWTCADASTGRR.-	1784.85	2	549.45	1.07	0.1	387	11/32	3
phagrawFchlfbead_dec23, 1393	- ASELGHSLNENVLKPAQEK.-	2065.27	3	683.22	1.26	0.2	311	1/4	3
phagrawFsucchlf_dec23, 1850	- SVTMDKWKDIELEK -	1722.99	2	336.89	1.21	0.1	185	11/26	3
jmbeadsactinrawphag3007, 284	- AGGNAKFR.-	820.92	2	260.43	1.03	0.0	252	4/7	3
jmfag5mincon300mmnacl, 1202	- ASELGHSLNENVLKPAQEK.-	2065.27	3	495.22	1.40	0.1	326	5/18	3
jmfag5mincon250mmnacl, 1708	- SPSSDSWTCADASTGR -	1628.66	2	158.82	1.19	0.0	124	3/10	3
phagrawFchlfbead_dec23, 1393	- ASELGHSLNENVLKPAQEK.-	2065.27	3	683.22	1.26	0.2	311	1/4	3
phagrawFsucchlf_dec23, 1850	- SVTMDKWKDIELEK.-	1722.99	2	336.89	1.21	0.1	185	11/26	3

control

ARG1_MOUSE ADP-ribosylation factor GTPase activating protein 1 (ADP-ribosylat					**533.27**	27923732.0	5		
rawextr_500beadigg_Mar04, 1977	- GLGVHLSFVRSVTMDK.-	1747.06	2	533.27	1.47	0.1	144	3/10	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ADP-ribosylation factor GTPase activating protein 3; ADP-ribosylation					**10013.42**	30841021.0	15		
jmfag5minigg200mmnacl, 260	-.QGVRSVAGK.-	902.03	2	1224.06	1.19	0.1	953	13/16	2
jmfag5minigg200mmnacl, 282	-.QGVRSVAGK.-	902.03	2	977.67	1.47	0.0	647	11/16	2
JMFAGNACL10_1B21E3, 398	-.QAQAVDKRK.-	1044.19	2	205.61	1.16	0.0	177	1/2	2
jmfag5minigg150mmnacl, 670	-.DERLNLSGQK.-	1160.26	3	908.82	1.69	0.0	525	4/9	2
jmfag1mnacl7.5minigg, 1072	-.LTNTSFTEIEK.-	1283.41	2	895.06	1.08	0.2	259	2/5	2
JMFAGNACL10_2B21E3, 1136	-.PNQAKKGLGAK.-	1112.31	2	169.44	0.95	0.0	163	2/5	2
jmfag5minigg450mmnacl_030527025134, 1366	-.LSVFANGVMTSIQDRYGS.-	1946.18	3	645.37	1.31	0.1	453	19/68	2
jmfag5minigg200mmnacl, 2168	-.LSTSSSISSADLFDEQRK -	1972.10	1	152.23	0.97	0.1	93	7/34	2
jmfreebeadsrawphag3007, 2191	-.DSSRDPEPAMRSTGSSDR -	1952.01	2	308.63	1.22	0.1	182	5/17	2
jmldl150naclrawphag3007,2844-2846	- QTAGNYNLSNVLPNAPDMAQFKQGVR.-	2835.15	3	249.31	1.68	0.1	108	4/25	2
ajrawphagjun20actinDPI, 590	-.EKIKTLATQATR.-	1360.59	2	239.87	1.07	0.1	126	9/22	2
jmrawigg5min450mmnaclsd, 1126	-.NPSWASISYGVFLCIDCSGSHR.-	2400.68	3	473.70	1.52	0.1	284	19/84	2
jmfag5minfrench1mnacldttdpi, 1910	- SGISHSVTSDMQTIEQESPTLAK.-	2447.66	2	167.35	1.05	0.1	115	5/22	2
jmfag_20_minfrench1mnacldttdpi, 1910	- SGISHSVTSDMQTIEQESPTLAK.-	2447.66	2	167.35	1.05	0.1	115	5/22	2
jmIgG300rawphag3007, 2040	- DSSRDPEPAMRSTGSSDR.-	1952.01	2	101.22	0.88	0.1	69	7/34	2
jmraw5minigg250mmnaclsyringdnase, 2178	-.HEGGPGQGPSVEGLNTPGKAAPEVSSIIK.-	2815.09	3	175.39	1.34	0.0	131	3/16	1
rawsucrfp_chlfphagigg_Mar04, 1482	-.GAPKEESIVSSLRLAYK.-	1849.12	2	355.15	1.17	0.1	263	11/32	2
phagrawFsuc150_dec22, 2094	-.YNSRAAQLYR.-	1242.37	2	1265.11	1.16	0.3	256	4/9	2
jmfagtimecon2.5min.446.446.3	-.DSSRDPEPAMRSTGSSDR.-	1952.01	0	446.78	1.35	0.0	328	4/17	2
jmbeads250rawphag3007, 174	-.PEYEPIGSTDEAQKKFGNVK.-	2238.44	3	387.48	1.69	0.1	196	4/19	2
jmfag5mincont200mmnacl, 714	-.EQEDLARGAPK.-	1214.31	2	281.01	0.88	0.0	311	11/20	2
jmfag5mincont400_030531151834, 2202	-.KYQEDPEDSYFSSSSKWSEQSSSR.-	2845.88	3	216.81	1.28	0.0	167	9/46	1

control

ADP-ribosylation factor GTPase activating protein 3; ADP-ribosylation					**300.68**	30841021.0	8		
FPbeads300_Dec19, 1534	-.LERLSTSSSISSADLFDEQR.-	2242.39	3	300.68	1.60	0.0	186	4/19	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
4833420I20Rik protein [Mus musculus] or (GEF) 1; R					**18301.20**	20987708.0	5		
jmfag5minigg600mmnacl, 174	-.FMSVQR.-	767.92	2	39.02	0.82	0.0	43	1/2	5
jmfag1mnacl0minigg, 1614	-.ITGEAFVQFASQELAEK.-	1869.06	2	17625.46	4.58	0.5	1495	19/32	5
jmrawigg5minbeadsyringdnase, 1759	-.TEMDWVLKHSGPNSADSANDGFVR.-	2634.82	3	636.72	1.74	0.1	280	19/92	4

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Vav2 protein [Mus musculus] tumor virus] sculus]					**6016.02**	31418561.0	5		
phagrawFsuc250_dec22, 1809	-.MWSYGFYLIHLQGKQGFQFFCKTEDMK.-	3334.88	3	2413.57	1.90	0.3	251	5/26	
JMFAGNACL15B21E3, 2372	-.GQVQLCCSRHAGAVTARR.-	1914.21	1	111.31	0.89	0.0	121	9/34	
rawsucrfp_150phagigg_Mar04, 1706	-.PQMSQVISAVSRLSLHSIAQSKGIR.-	2695.14	3	514.34	2.11	0.0	243	17/96	
phagrawFsuc250_dec22, 1809	-.MWSYGFYLIHLQGKQGFQFFCKTEDMK.-	3334.88	3	2413.57	1.90	0.3	251	5/26	
phagrawFsuc400_dec20, 3122	-.GQVQLCCSRHAGAVTARR.-	1914.21	3	409.03	1.47	0.0	270	4/17	
phagrawFchlf_dec23, 3290	-.LQAVGHYTQVPLQVSGANHQQGLKPVSSFLR.-	3361.80	2	154.21	0.91	0.1	90	1/6	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Vav2 oncogene [Mus musculus]					**10446.42**	6678555.0	1		
jmraw5minbsareebeads, 968	-.HIKVVEK.-	853.05	2	288.74	0.86	0.1	284	7/12	1
JMMAGTube1B16E3, 76	-.GTFYQGYLCTR.-	1309.48	2	161.32	1.02	0.0	158	7/20	1
JMMAGNEGB16D3, 240	- TFLKVCHDK -	1091.31	2	1213.11	1.66	0.2	471	5/8	
jmrawigg5min1mnacl, 777	- RSCCLLEIQETEAK.-	1623.88	2	411.29	1.09	0.1	283	5/13	1
ajrawphagjun20dpi1MNaCl, 1028	-.QQLKEALEAMQDLAMYINEVKR.-	2623.05	3	894.65	1.93	0.1	255	17/84	1
ajrawphag1MNaCl20, 1060	-.FAISIKFNDEVK.-	1411.63	3	766.50	1.43	0.0	528	17/44	1
jmfagfrench5minigg1mnackdtt, 2407	-.CGVGAHKECLEVIPPCKMSSPADVDAPGAGPGPK.-	3319.85	2	43.78	0.74	0.1	26	1/11	1
jmfagtimecont10min_030601202502, 836	-.VCHDKFGLR.-	1075.27	3	671.34	1.73	0.1	333	3/8	
jmbeadsactinrawphag3007, 837	-.EVIELLFHKMTDDPMHNKDIK.-	2554.97	3	662.38	2.02	0.1	201	17/80	1
jmfagcon5min1000mmnacl_030601180404, 1506	-.PAEAERFAISIK -	1332.53	2	173.53	0.74	0.1	137	7/22	1
jmbeads450naclrawphag3007, 1643	-.DIKKWSYGFYLIHLQGK.-	2097.45	3	159.05	1.11	0.0	133	11/64	
jmfag5mincon300mmnacl, 1664	-.QDRYLFLFDK.-	1345.53	2	668.62	1.06	0.2	306	1/2	1
jmfag5mincon250mmnacl, 2628	-.QQTDNLLKSHASGTYLIRER.-	2331.58	2	97.99	1.12	0.0	83	9/38	1
rawphag2007chlfsol2, 814	-.ERTTSR.-	749.80	2	52.87	0.68	0.0	76	2/5	
rawphag2007chlfsol1, 898	-.WLIDCKVLPPNHR.-	1591.91	3	497.80	1.02	0.2	177	11/48	1
rawsucrfp_chlfphagigg_Mar04, 2062	-.VLKYHLLLKELLSHSADR.-	2136.53	3	603.73	1.57	0.1	332	4/17	1
jmidlactinrawphag3007, 2584	-.PDKANANHHSFQMYTFDK.-	2152.34	3	451.52	1.18	0.1	354	5/17	1
jmbsaactinrawphag3007, 2385	-.GYSYELKEVIELLFHK.-	1969.27	3	340.42	1.41	0.1	139	13/60	1
rawsucrfp_chlfphagigg_Mar04, 2062	-.VLKYHLLLKELLSHSADR.-	2136.53	3	603.73	1.57	0.1	332	4/17	1
phagrawF150_dec22, 2518	-.FGLRNSELFDPFDLFDVRDFGK.-	2635.91	3	1684.05	1.84	0.3	283	17/84	

control

Vav2 oncogene [Mus musculus]					**548.21**	6678555.0	13		
FPbeads350_Dec19, 871	-.YHLLLKELLSHSADR.-	1796.06	3	250.87	1.05	0.1	122	11/56	1
rawextr_600bead_Mar04, 1228	-.DGVLLCQLLHNLSPGSIDLKDINFR.-	2782.21	3	297.34	1.56	0.0	174	17/96	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Vav 3 oncogene [Mus musculus]					**5071.99**	30931094.0	4		
ajrawphagactin20, 1214	-.TKESGEYAISIK.-	1326.48	2	204.15	1.10	0.1	134	4/11	4
jmfagcon5min1000mmnacl_030601180404, 235	-.GDNYEMK.-	856.92	2	68.52	0.78	0.0	87	5/12	3
jmfag5mincont200mmnacl, 514	-.SCCLAEIRQTEEK.-	1510.72	3	580.22	1.52	0.1	322	5/16	3
jmfag1mnacl5mincon, 1128	-.DMRELSLLK.-	1105.33	1	306.47	1.13	0.0	247	7/16	2
jmfagcont5minbead, 1664	-.VGWFPSTYVEEDE.-	1558.63	3	711.36	1.35	0.1	321	17/48	2
jmfag5mincont350, 1712	-.EIKQFQLSIENLNQPVLLFGR.-	2487.88	3	673.23	1.66	0.0	381	1/4	3
jmbeads600naclrawphage3007, 1716	-.TPIALATGIRPFPTEESINDEDIYK.-	2792.09	3	703.10	1.52	0.2	225	11/48	3
AJRAWSoluteContr_june13, 1742	-.WLEQFEMALSNIRPDYADSNFHDFK.-	3075.36	2	61.65	0.87	0.0	69	1/6	3
phagrawFsucchlfbead_dec23, 1196	-.ESGEYAISIKYNNEAKHIK.-	2195.42	3	306.58	1.22	0.1	208	2/9	4
phagrawFchlfbead_dec23, 1719	-.DDQNLYQVFINYK.-	1660.81	2	339.42	1.14	0.1	179	1/3	3
jmidl400naclrawphag3007_030802153313, 1568	-.VCQMLLRGTFYQGYLCFKCGAK.-	2531.08	3	673.59	1.56	0.1	210	5/28	3
jmidl150naclrawphag3007, 1992	-.YDFCARDMRELSLLK.-	1861.18	2	144.58	1.02	0.1	91	2/7	2
jmraw5minbsabeads, 1460	-.YNNEAK.-	738.77	1	299.12	0.93	0.1	184	1/2	4

control

Vav 3 oncogene [Mus musculus]					**995.83**	30931094.0	25		
rawextr_60MeOHbeadIgg_Mar04, 730	-.QVDPGLPKMQVIR.-	1481.79	3	335.73	1.61	0.0	202	7/24	4
rawextr_250bead_Mar04, 1818	-.KSELFEAFDLFDVRDFGK.-	2164.40	3	268.15	1.40	0.0	180	7/34	3
rawextr_150bead_Mar04, 2345	-.YNNEAKHIKILTR.-	1600.85	2	391.95	1.24	0.1	222	5/12	4

APPENDIX F – G-PROTEIN SUMMATION OF IONS

The summation of peptides from G-proteins found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor, family C, group 2, member A [Mus musculus]					**3892.80**	20892429.0		8	
jmfag5minigg bead, 909	- QPAFGISFVLCISCILVK.-	1939.42	3	1280.46	1.41	0.2	573	21/68	6
jmfag5minigg300mmnacl, 1222	- DCQAGTR -	750.81	2	110.68	0.87	0.1	47	1/2	6
jmfag5minigg300mmnacl, 1842	-.TNRVLLVFEAKIPTSFHR -	2129.49	3	358.01	1.37	0.1	212	4/17	6
ajrawphag1MNaCl20, 716	-.GLFTNGSCADIK.-	1226.39	3	266.00	1.13	0.0	233	13/44	5
jmigg600rawphage3007, 1512	- LLNSSTAFR.-	1009.14	2	131.77	0.77	0.0	170	1/2	5
jmfag5minfrench1mnacldttdpi, 1552	- SFVISGGGSSVTENILHS.-	1791.94	2	282.61	1.10	0.1	120	9/34	3
jmfag_20_minfrench1mnacldttdpi, 1552	-.SFVISGGGSSVTENILHS.-	1791.94	2	282.61	1.10	0.1	120	9/34	3
jm5minggrawlowionic, 1670	-.EVPFSNCSR.-	1039.15	2	121.88	0.90	0.1	68	9/16	5
jmidl450naclrawphag3007, 1442	- VIVVFSSGPDLEPLIKEIVRR -	2367.82	3	678.22	1.34	0.1	475	1/4	5
phagrawFsuc200_dec22, 2311	-.EVPFSNCSRDCQAGTRK.-	1899.10	2	420.57	0.95	0.2	118	1/4	5

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor, family C, group 2, member A [Mus musculus]					**852.11**	20892429.0		11	
FPbeads150_Dec19, 1349	- VYILFKPSR.-	1236.53	2	394.82	1.24	0.0	303	1/2	4
rawextr_450beadigg_Mar04, 1356	- LFINEGKILWSGFSREVPFSNCSR -	2788.18	3	457.29	1.91	0.1	195	4/23	5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor, family C, group 2, member A, related seque					**3984.06**	38086653.0		8	
JMMAGNEGB1603, 934	- NILYHAFNWHTGKIK.-	1843.12	3	684.26	1.45	0.0	467	9/28	
JMFAGNACL15B21E3, 1478	-.IPQLTFGQFDSILNDRGQFNSLYQMAPK.-	3230.64	3	610.06	1.48	0.1	381	23/108	
rawphag2007chfbead1, 2056	-.KSPVVLTGPSWSASAHIGTFLQLYK.-	2689.11	3	117.35	1.16	0.0	100	5/32	
jmfagtimecon2.5min 2112.2112.3	-.YPEDAYLPKFWHLFFKCSFSK.-	2655.07	0	506.31	1.59	0.1	241	9/40	
AJRAWSoluteContr_june13, 944	-.GEEMVFFQWQTPQSVCSK.-	2132.41	3	642.32	1.36	0.2	237	7/34	
jmidlactinrawphag3007, 2432	-.AFAYQSALVLHKR.-	1504.76	3	799.90	1.57	0.1	419	1/3	
phagrawF350_dec20, 766	-.AFSQQSHLRIHER.-	1609.78	3	432.55	1.26	0.0	337	7/24	
rawsucrfp_700phagigg_Mar04, 1572	-.FLSFSMQEEFRTR.-	1678.89	2	191.32	1.20	0.1	112	1/3	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor, family C, group 2, member A, related seque					**1497.84**	38086651.0		3	
rawextr_800bead_Mar04, 1408	-.CPESHYANSEKSHCLQK.-	1962.16	2	172.09	0.96	0.0	171	11/32	1
rawextr_450bead_Mar04, 1732	-.WSWVGLIIPDDHRGTQILSDLR.-	2578.91	3	939.15	2.31	0.1	283	17/84	1
FPbeads700_Dec19, 1557	-.IPQVTFGPFDSILNDR.-	1820.04	2	338.69	1.23	0.1	189	1/3	
rawextr_450beadigg_Mar04, 2678	-.KSPAILTGPSWSTSAHIGTFLQLYK.-	2705.10	2	47.91	0.67	0.0	58	7/48	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein pathway suppressor 2 [Mus musculus]					**3036.86**	31980980.0		1	
jmbsa150naclrawphag3007, 350	-.LQEKLSALQEEK.-	1416.60	2	1148.66	2.00	0.0	566	13/22	2
rawsucrfp_chlfphagigg_Mar04, 562	-.MPALLERPK.-	1055.32	3	190.35	1.00	0.1	142	5/16	2
jmfag5minigg200mmnacl, 1184	-.HQLFLQLKKVLHEEEK.-	2020.36	3	1697.85	2.19	0.1	712	7/20	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor 4 [Mus musculus]					**4926.37**	28316758.0		2	
jmrawigg5minigg freebead, 2072	-.IKRLALSLIAIVLVCFAPYHALLLSR.-	2895.63	3	3964.05	2.21	0.3	689	1/4	1
JMMAGTube1B16E3, 1936	-.STTGKSSGAVWAVPPTAQGDQVPLK.-	2483.76	3	255.12	1.23	0.0	198	3/16	
jmfag5mincont200mmnacl, 2386	-.RSTTGKSSGAVWAVPPTAQGDQVPLK.-	2639.95	3	707.21	1.51	0.1	339	19/100	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
regulator of G-protein signaling 19 interacting protein 3; PDZ-domain					**3260.68**	22507363.0	7		
jmfagtimecon7.5min.897 897 3	-.RAFDMIGQRSR.-	1337.54	0	209.18	1.30	0.1	132	3/8	
AJRAWpellet1_contr_jun13, 618	- RAFDMIGQR.-	1094.27	2	203.75	1.02	0.0	177	7/18	
jmbeads350rawphag30072nd, 2238	- ELYAKIAEAFGIAPTEILFCTLNSHK -	2881.34	3	1057.07	1.88	0.2	274	1/5	
jmfagtimecont10min_030601202502, 3028	-.LVFRTQLAHGSPTGRIEGFTNVR.-	2557.90	3	1790.68	1.52	0.3	178	2/11	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor 22 [Mus musculus]					**3689.49**	30424810.0	7		
jmfagfrench20minigg1mnacldtt, 486	-.IGTRFSTGQK.-	1095.24	3	388.11	1.37	0.1	145	11/36	1
jmrawigg5min350mmnaclsyringednase, 885	-.VTYEDSEIR.-	1112.17	2	445.55	1.02	0.1	341	9/18	1
jm5miniggrawlowionic, 1364	-.IGTRFSTGQK.-	1095.24	3	133.57	1.18	0.0	93	5/18	1
jmfagfrench5minigg1mnacldtt, 2737	-.LRLCFLVMAYGTTIFHPLLYAFTRQK.-	3104.77	2	497.46	1.00	0.2	101	4/25	1
jmrawbas5min1mnacl, 1020	-.ILQALNIR.-	941.15	3	673.26	1.54	0.2	156	9/28	1
jmfagfrench20minigg1mnacldtt, 486	-.IGTRFSTGQK.-	1095.24	3	388.11	1.37	0.1	145	11/36	1
jmfag5minigg200mmnacl, 494	-.PANRILTMGR.-	1129.36	2	86.86	0.87	0.0	94	7/18	2
jmrawigg5min350mmnaclsyringednase, 885	-.VTYEDSEIR.-	1112.17	2	445.55	1.02	0.1	341	9/18	1
jm5miniggrawlowionic, 1364	-.IGTRFSTGQK.-	1095.24	3	133.57	1.18	0.0	93	5/18	1
jmfagfrench5minigg1mnacldtt, 2737	-.LRLCFLVMAYGTTIFHPLLYAFTRQK.-	3104.77	2	497.46	1.00	0.2	101	4/25	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor 37-like 1; G protein-coupled receptor 37-lk					**3897.75**	30794242.0	7		
jmfag5mincon450mmnacl, 756	-.VRGPPGRK.-	867.04	2	261.38	0.88	0.1	254	1/2	2
jmfagcon5minn600mmnacl, 937	-.QTLDLLGLINQFSTFFK.-	1986.30	3	462.61	1.20	0.1	306	19/64	2
jmbeads350rawphag30072nd, 1108	- PRESPPLLPLGTPC.-	1477.76	2	299.11	1.02	0.0	293	11/26	1
jmfagtimecont0min_030601230741, 2760	- PLGQAFLDCCCCCCCEECGGASDSSATVSADSK.-	3265.87	2	88.16	0.89	0.0	88	5/32	2
rawsucrfp_250phagigg_Mar04, 826	- QTLDLLGLINQFSTFFK.-	1986.30	3	1866.56	2.19	0.2	247	9/32	2
jmrawigg5minbeadsfreezethaw, 802	- QTLDLLGLINQFSTFFK.-	1986.30	3	534.36	1.42	0.1	332	17/64	2
jmfag5minigg450mmnacl_030527025134, 1200	- QTLDLLGLINQFSTFFK.-	1986.30	3	385.58	1.36	0.0	278	1/4	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor 39 [Mus musculus]					**2890.26**	21492622.0	2		
rawphag2007chfbead3, 553	-.RIMAAAKPK.-	986.26	2	580.73	1.35	0.0	425	5/8	
jmag5mincon500mmnacl, 880	-.PQPLSPESPQTGSETK.-	1683.80	3	527.13	1.26	0.1	381	19/60	
jmfagtimecon10min, 898	-.PQPLSPESPQTGSETK.-	1683.80	3	1782.40	2.07	0.1	790	7/20	

control

G protein-coupled receptor 39 [Mus musculus]					**720.13**	21492622.0	2		
jmbsa250naclrawphag3007, 901	-.DSTSSARSPLIFLASR.-	1708.90	2	720.13	1.08	0.2	265	1/3	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor 124 [Mus musculus]					**3164.66**	16905079.0	18		
phagrawFsuc1000_dec23, 1517	-.APPPPCKLTNLQVAQSQVCEASVAAR.-	2680.10	3	154.07	1.05	0.0	143	7/50	
phagrawFsuc600_dec20, 1764	-.DNLKGSGSALERESK.-	1591.71	2	202.25	1.03	0.1	148	2/7	
jmrawigg5minbeadsfreezethaw, 214	-.VTNNRGDFR.-	1079.15	3	596.98	1.51	0.1	349	3/8	
jmrawigg5min300mmnaclsyringednase, 677	-.SHVAQNPKQGNRISLEPGEELR.-	2460.69	3	239.69	1.49	0.0	152	5/28	
jmraw5minigg1000mmsd,726-728	-.AGETGGKSR.-	862.91	2	109.89	1.31	0.0	76	7/16	
ajrawphagactin20,1248-1250	-.DNLKGSGSALER.-	1247.34	2	723.00	1.56	0.2	132	1/2	
jmigg600rawphage3007, 1516	-.ISLEPGEELRGSTRLR.-	1814.04	2	399.45	1.10	0.1	230	1/3	
jmIggactinrawphag3007, 1788	-.GDGEPEPTGSRGSLAPR.-	1683.76	3	562.60	1.58	0.1	291	9/32	
jmfagcont5minbead, 3368	-.IGGAALSPHAQHISVNSR.-	1816.02	2	176.73	0.96	0.1	141	4/17	

control

G protein-coupled receptor 124 [Mus musculus]					**1156.18**	16905079.0	17		
FPbeads400_Dec19, 1458	-.YEDASVTGAEAIAGGSMKTGLWK.-	2343.60	2	399.20	0.99	0.2	87	1/4	
rawextr_actinbeadigg_Mar04, 1857	-.CSGERPKGLSGGAHNPAR.-	1794.98	2	332.92	1.07	0.1	212	5/17	
rawextr_250bead_Mar04, 1860	-.SNVISTVQPGAFLGLGELKRLDLSNNR.-	2900.28	3	424.05	1.80	0.1	178	19/104	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor 128 [Mus musculus]					**5606.10**	27370236.0		1	
ajrawmediapbsnocells, 956	-.PMPSITPLK.-	984.24	2	290.24	0.91	0.0	304	1/2	
rawsucrfp_250phagigg_Mar04,1048-1050	-.LRVRMYNMLR.-	1352.70	2	459.62	1.46	0.0	306	5/9	
rawsucrfp_800phagigg_Mar04, 2664	-.QMENYSYSQGDQTVVEPNIAIQSVTR.-	2959.20	2	128.15	1.07	0.1	75	4/25	
JMFAGNACL15B21E3, 558	-.VLWKNNQNLTSTK.-	1546.75	3	585.71	1.36	0.0	425	1/3	
ajrawphagactin20, 1368	-.VFQSEASKILKSLSSSFDR.-	2130.39	3	1023.68	1.58	0.2	245	19/72	
ajrawphag1MNaCl20,1476-1478	-.NNQNLTSTKKVSSLK.-	1662.87	2	395.95	1.27	0.1	148	9/28	
ajrawphagjun20dpi1MNaCl,1594-1596	-.VLWKNNQNLTSTKK.-	1674.93	3	482.69	1.72	0.1	104	5/26	
jmfag5miniggbead_030528200105, 308	-.TKVFQSEASKILK.-	1479.75	3	973.11	1.62	0.0	583	17/48	
JMFAGNACL15B21E3, 558	-.VLWKNNQNLTSTK.-	1546.75	3	585.71	1.36	0.0	425	1/3	
rawphag2007chfbead3, 2099	-.TAIATVSQILDASEDVFQKAAEMDNSK.-	2884.17	3	107.01	1.35	0.0	75	2/13	
jmfag5mincont150mmnacl, 1113	-.LCNVSEFGNIELQNVTK.-	1909.15	3	574.25	1.24	0.0	464	17/64	

control

G protein-coupled receptor 128 [Mus musculus]					**371.76**	27370236.0		6	
rawextr_350beadigg2_Mar04, 1848	-.SLPSLNERFRLLEPSGMTEETSLS.-	2695.00	3	371.76	1.70	0.0	212	17/92	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor 135 [Mus musculus]					**3459.07**	32306524.0		3	
phagrawFsucchlfbead_dec23, 2772	-.LGACSRMPSSNPASGSGGEVVMWAR.-	2508.84	3	863.35	1.41	0.2	162	5/32	
jmfag5mincont350, 204	-.VLRFFSEVR.-	1153.36	3	850.43	2.05	0.0	414	7/16	
jmfag1mnacl5mincon, 1322	-.TRNMDAFLPSQGLGFQAR.-	2010.27	3	998.95	1.78	0.1	527	11/34	
jmfag5mincon300mmnaci, 2270	-.LGACSRMPSSNPASGSGGEVVMWAR.-	2508.84	3	746.34	1.16	0.1	468	23/96	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor 156; GABAB-related G-protein coupled recept					**8664.17**	40254201.0		2	
jmraw5minbsareebeads, 856	-.PVVNFKDDLK.-	1175.36	3	128.99	0.85	0.0	147	5/18	1
jmfagtmecon7.5min.428 428.3	- PVVNFKDDLK.-	1175.36	0	265.20	1.31	0.0	201	1/3	1
jmfag1mnacl5mincon, 816	-.DEKSCMERLLTEK.-	1582.83	3	779.70	1.71	0.2	194	5/16	1
jmfag5mincont150mmnacl, 1747	- SCMERLLTEKNAVIESLQEQVSNAK.-	2822.21	3	707.49	1.88	0.1	265	11/48	1
ajrawmediapbsnocells,1034-1036	-.QWKAFEGENQTMR -	1625.79	2	174.44	1.19	0.0	129	1/3	1
jmraw5minbsabeads, 1130	-.PVVNFKDDLK.-	1175.36	3	364.80	1.03	0.1	304	7/18	1
jmrawbsa5minlowionic, 1196	- PVVNFKDDLK.-	1175.36	3	418.24	1.12	0.1	334	5/12	1
phagrawF700_Dec23, 1496	-.QYCDHLDTGCNQK -	1525.65	2	87.20	0.80	0.1	67	5/24	1
phagrawFchlf_dec23, 2000	- LLTEKNAVIESLQEQVSNAK -	2215.49	3	210.75	1.17	0.0	178	4/19	1
JMFAGNACL10_1B21E3, 320	- QSPEGLPK.-	855.96	2	836.01	1.31	0.1	551	11/14	1
jmfag5minigg600mmnacl, 670	- LDHNNARSK.-	1055.13	2	580.28	1.23	0.0	461	5/8	
jmigG150rawphag3007, 1262	- PSPLSEPRRK.-	1167.34	2	503.47	1.02	0.2	140	4/9	1
jmiggactinrawphag3007, 1652	- LLTEKNAVIESLQEQVSNAK -	2215.49	3	648.21	1.69	0.1	307	1/4	1
JMMAGTube1B15E3, 412	-.PVVNFKDDLK -	1175.36	3	451.68	1.62	0.0	274	7/18	
JMMAGTube1B16E3, 426	- PVVNFKDDLK.-	1175.36	3	507.91	1.58	0.1	280	13/36	

control

G protein-coupled receptor 156; GABAB-related G-protein coupled recept					**33.35**	40254201.0		6	
rawextr_300beadigg_Mar4, 2854	-.MEPEINCSEFCDSFPGQELDRRPLHDLCK.-	3410.83	2	33.35	0.83	0.0	28	1/8	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
trescle [Mus musculus] metabotropic 6; G protein-co					**5115.74**	2145149.0	31		
jmraw5minigg500mmnaclsd, 200	-.ANPPPTK.-	724.83	2	373.17	1.03	0.1	190	7/12	4
jmrawigg5min150mmnacl, 322	-.EKPDGELLGIK.-	1199.38	3	998.86	1.45	0.0	690	1/2	3
jmfagfrench20minigg1mnacldtt, 488	-.KEDVSESSSAELDSDGPGSPAK.-	2193.22	3	641.21	1.71	0.1	212	3/14	4
ajrawphagactin20, 598	-.TPPASASGK.-	815.90	2	228.20	0.91	0.0	239	1/2	4
jmfagfrench20minigg1mnacldtt,1142-1144	-.DPPARTAPGPTKLGNVAPTPAK.-	2157.46	3	545.46	1.64	0.1	182	19/84	4
ajrawphag1MNaCl20, 1756	-.QKSKSQHAADTALPK.-	1610.80	2	133.92	0.87	0.1	113	5/14	3
jmraw5minigg600mmnaclsd, 1760	-.EDVSESSSAELDSDGPGSPAK.-	2065.05	3	1146.89	1.88	0.2	284	3/10	4
ajrawphagactin20, 1844	-.ATPRPTPVNSATAALPSKVK.-	2007.32	3	183.52	0.90	0.0	198	7/38	4
jmrawigg5min350mmnaclsyringednase,2527-2529	-.GAHPGTPGKTGSSATQAQPGK.-	1936.08	3	260.05	1.29	0.0	199	1/5	4
jmrawrminigg200mmnaclsyringdnas, 2786	-.GKPPVPNSTVSAR.-	1310.49	2	353.80	1.37	0.1	176	1/3	4
jmrawrminigg200mmnaclsyringdnas, 2790	-.GKPPVPNSTVSAR.-	1310.49	2	250.65	1.34	0.1	161	1/3	4

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to MrgA4 RF-amide G protein-coupled receptor [Mus musculus]					**7951.84**	38086685.0	14		
jmfag5minigg400mmnacl, 570	- ESDVDTASSPSSR.-	1338.32	3	997.45	2.28	0.0	435	5/12	
jmfag5minigg400mmnacl, 1482	-.TVLYITGLSMLSAISTER.-	1956.29	2	36.48	0.73	0.0	48	3/17	
JMMAGNEGB16D3, 1590	-.QLALENTNSACRPALRGK -	1943.22	2	666.65	1.32	0.2	184	9/34	
JMFAGNACL5B21E3, 2514	- LAFPVLTQAQAHQAATGHDDPPTGSSEK.-	2876.09	3	490.67	1.34	0.1	276	5/27	
jmfag1mnacl7,5minigg, 2516	-.TVLYITGLSMLSAISTERCLSVLCPIWYR.-	3290.95	2	106.75	0.78	0.0	134	9/56	
jmrawigg5min350mmnaclsyringednase, 1901	-.FLLPFFFPLATLLACIDSSAKPLLYYMKGR.-	3438.19	2	51.11	0.86	0.0	59	7/58	
ajrawphagjun20actinDPI, 292	- TKGLDINGMIK.-	1190.44	3	900.02	1.66	0.0	530	2/5	
jmfag5minigg400mmnacl, 570	-.ESDVDTASSPSSR.-	1338.32	3	997.45	2.28	0.0	435	5/12	
jmrawigg5minbeadsfreezethaw, 826	- KRATAQPPVR.-	1124.32	2	490.07	1.28	0.0	380	11/18	
jmiggactinrawphag3007, 892	-.ESDVDTASSPSSR.-	1338.32	3	1103.20	1.59	0.1	649	3/8	
jmIgG400rawphag3007, 1196	- VEMSRSSFR -	1099.25	2	1495.84	1.36	0.3	225	1/2	
jmfag5mincont150mmnacl, 157	- ESDVDTASSPSSR -	1338.32	3	616.15	1.77	0.1	295	5/16	

control

similar to MrgG G protein-coupled receptor [Mus musculus]					**1549.78**	38088301.0	1		
rawextr_400bead_Mar04, 721	-.FCKLAQCSGILLFFCR.-	1850.31	3	986.44	1.69	0.0	576	11/30	
rawextr_250bead_Mar04, 864	-.FCKLAQCSGILLFFCR.-	1850.31	3	563.34	1.59	0.0	329	19/60	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor kinase 5 [Mus musculus]					**6053.52**	3005012.0	12		
jmfag1mnacl7,5minigg, 378	-.GKEIMTKYLTPK.-	1409.72	3	1131.62	1.64	0.1	525	19/44	2
AJRAWActinIgG_june13, 1316	-.GKEIMTKYLTPK.-	1409.72	2	185.96	1.22	0.1	104	3/11	2
jmrawigg5minbeadsyringdnase,1481-1483	-.QRLGCQEEGAAEVK.-	1518.68	2	303.02	1.36	0.0	215	9/26	2
jmfag5minigg600mmnacl, 1636	-.RLEAGMLDPPFVPDPRAVYCK.-	2375.80	3	861.73	1.47	0.2	275	17/80	2
jmfag5minigg400mmnacl, 1638	-.SQPPEPPKKGLFHR.-	1618.87	3	773.66	1.33	0.0	562	9/26	2
jmldl1000naclrawphag3007, 1352	-.ALFYAAEILCGLEDLHRENTVYR.-	2698.05	3	500.07	1.37	0.1	167	7/44	2
phagrawF500_dec20, 1620	-.GESMALNEKQILEKVNSQFVVNLAYAYETK.-	3418.86	3	946.31	1.57	0.2	286	11/58	2
rawsucrfp_250phagigg_Mar04,1818-1820	-.GESMALNEKQILEKVNSQFVVNLAYAYETK.-	3418.86	3	942.56	2.19	0.1	405	21/116	2
phagrawFsuc400_dec20, 2654	-.GDPFHEYLDSMYFDRFLQWK.-	2595.87	3	408.58	1.82	0.1	186	15/76	1

control

G protein-coupled receptor kinase 5 [Mus musculus]					**1597.12**	3005012.0	7		
FPbeads1000_Dec19, 2074	-.QRLGCQEEGAAEVK.-	1518.68	2	129.33	1.23	0.0	105	7/26	2
rawextr_900beadigg_Mar04,2162-2164	-.LLQSPCK.-	788.98	1	61.72	0.64	0.0	88	1/3	2
rawextr_250beadigg_Mar04, 2086	-.DLKPENILLDDYGHIR.-	1912.14	2	188.44	1.36	0.1	84	7/30	1
jmbsaactinrawphag3007, 740	-.LGCQEEGAAEVK.-	1234.36	3	202.89	1.17	0.0	153	15/44	2
jmraw5minbsabeads,2514-2516	-.GESMALNEKQILEKVNSQFVVNLAYAYETK.-	3418.86	3	578.27	2.15	0.0	260	19/116	2
jmbsa300naclrawphag3007, 1164	-.ENTVYRDLKPENILLDDYGHIR.-	2674.95	3	436.46	1.73	0.1	204	3/14	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor kinase 2, groucho gene related; G protein-co					**2869.31**	9506749.0	8		
jmfag5minigg400mmnacl, 332	-.QFCDTKPDLK.-	1195.37	3	398.30	1.19	0.0	331	7/18	
jmag5mincon500mmnacl, 2176	-.EFGLAIFSRFFK.-	1462.72	2	829.29	1.19	0.2	427	1/2	
jmfag5minigg350mmnacl, 2247	- YLSETPFEEYQESTYFNRFLQWK.-	3007.26	2	90.03	0.92	0.0	93	7/44	
jmldl250naclrawphag3007, 1338	-.QNSPSQNVFEECAGIVCK.-	1954.18	3	754.08	1.50	0.1	350	19/68	
phagrawFsuc400_dec20, 2014	-.NETEEYSERFSEDAK.-	1834.83	2	797.62	1.14	0.2	181	9/28	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
G protein-coupled receptor kinase-interactor 2; ARF GTPase activating					**5381.83**	34447227.0	26		
ajrawphagjun20actinDPI, 304	-.DTASHSSLKRR.-	1258.37	3	367.89	1.19	0.0	308	13/40	2
JMFAGNACL5B21E3,662-664	-.LQPFPTHASR.-	1154.30	2	425.12	1.80	0.0	232	1/2	1
jm5miniggrawlowionic, 926	-.EDDSVTAKDLSK.-	1308.38	3	381.00	1.14	0.1	266	7/22	2
jmIgG500rawphag3007,1251-1253	-.LQPFPTHASR.-	1154.30	2	392.63	1.44	0.0	271	5/9	1
jmIgG350naclrawphag3007, 2533	-.SDTVRTSLRLLTSSAYR.-	1927.15	2	287.39	1.08	0.0	255	5/16	2
AJRAWSoluteContr_june13,396-398	-.LQPFPTHASR.-	1154.30	2	450.20	1.77	0.0	254	5/9	1
AJRAWpelletl_contr_jun13, 455	-.TRLQPFPTHASRLEK.-	1782.04	3	417.67	1.01	0.0	410	17/56	1
jmfagcont5minbead,1168-1170	-.LQPFPTHASR.-	1154.30	2	579.15	1.48	0.1	366	5/9	1
rawphag2007chlfsol2,1274-1276	-.LQPFPTHASR.-	1154.30	2	669.33	1.56	0.1	356	11/18	1
jmkdlbeadschlfrawphag3007,1290-1292	-.LQPFPTHASR.-	1154.30	2	490.84	1.60	0.0	286	1/2	1
ajrawmediapbsnocells, 590	-.LQPFPTHASR.-	1154.30	2	546.73	1.58	0.0	342	5/9	1
phagrawFsuc200_dec22,885-887	-.LQPFPTHASR.-	1154.30	2	373.88	1.46	0.0	256	1/2	1

control

G protein-coupled receptor kinase-interactor 2; ARF GTPase activating					**654.58**	34447227.0	9		
rawextr_700bead_Mar04,651-653	-.LQPFPTHASR.-	1154.30	2	551.11	1.56	0.1	276	1/2	1
FPbeads350_Dec19, 2647	-.AKYQMLAFVHRLPCR.-	1834.25	2	103.47	0.73	0.0	141	2/7	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RGSE_MOUSE Regulator of G-protein signaling 14 (RGS14) (RAP1/RAP2 interacting					2510.75	3914638.0	17		
jmrawgg5minbeadsfreezethaw, 538	- HLGVPNGR -	849.96	2	418.19	1.27	0.1	250	1/2	1
jmlag1mnacl5minigg, 574	- VVRISAKPTK.-	1099.35	3	99.99	1.14	0.0	76	5/18	2
jmlag5minigg350mmnacl, 1257	- KSLGSGESESESR -	1353.38	2	580.78	1.37	0.1	274	11/24	2
JMFAGNACL15B21E3, 1692	- ACERFQQIPASDTK -	1594.78	2	150.21	0.81	0.1	151	7/28	1
jmlag5minigg350mmnacl, 1733	- REMTGGAMNSALRR.-	1550.79	2	447.27	1.02	0.1	365	6/13	2
jm5minggrawlowionic, 3418	- QTCDIEGLVELLNRVQSSGAHDQRGLLR.-	3109.47	2	198.00	0.98	0.1	93	5/27	2
jmbeads300rawphag3007, 1502	- PGEKQPMDLETPVSSVASQTLVLDTPPDAK.-	3152.52	2	42.81	0.83	0.0	49	7/58	
jmag5minconi500mmnacl, 2986	- PGKYDCVYLPDGTASLALARPGLTIR.-	2737.24	2	188.86	1.04	0.0	174	11/50	2
phagrawFsuc150_dec22, 1564	- SPLYQECLLAEAEGR -	1679.88	2	384.64	1.35	0.1	165	9/28	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
RGSE_MOUSE Regulator of G-protein signaling 14 (RGS14) (RAP1/RAP2 interacting					1127.97	3914638.0	18		
FPbeads250_Dec19, 136	-.PKHLGVPNGRMVLAVSDGELTSTAGSQAQGEGR.-	3321.67	2	171.05	0.95	0.1	116	9/64	1
rawexfr_actnbeadigg_Mar04, 1091	- KSLGSGESESESRPGK -	1635.72	2	249.55	1.67	0.0	136	1/3	2
rawexfr_150bead_Mar04, 1239	- DSHLPPSSSSLLVEDASSSTGNR -	2344.44	3	547.46	1.66	0.1	230	17/88	2
FPbeads500_dec19, 2722	-.LKPGKSLPLGVEELGQLPLAEGPCGR -	2660.13	2	159.91	1.28	0.0	112	1/5	2

APPENDIX G – TYROSINE PHOSPHATASE SUMMATION OF IONS

The summation of peptides from Tyrosine Phosphatases found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 3 [Mus musculus]					4736.82	38078421.0	14		
JMMAGTube1B16E3, 270	- IVAVRSSDPVAISAESR -	1757.97	3	453.13	1.50	0.1	212	19/64	1
jmfag5minggbead, 1773	- SSSSVSPSSNAPGSCSPDGVDQRFLEDYHK.-	3142.27	2	173.93	1.03	0.1	99	5/29	1
jmrawgg5minggfreebead, 3052	- EYFGLQHGDDPVDSPGKPNLFLK.-	2574.83	3	377.23	1.27	0.0	283	17/88	
jmfag5minigg600mmnacl, 840	- LPQNLDKNR.-	1098.24	2	365.69	1.21	0.0	301	9/16	1
jmfag5minigg250mmnacl, 1112	-.INNTRTSELPK.-	1273.42	2	651.62	1.87	0.1	301	1/2	2
jmfgG150rawphag3007, 1162	-.ESHSRELALVIRR.-	1566.79	3	1027.05	1.45	0.1	667	3/8	1
jmraw5minggiowionc, 1283	- PNLFLKNVVGGFPCTLHFR.-	2160.57	3	617.81	1.35	0.2	157	5/24	1
RawPhg2007MeEthmeth3digest,1022-1024	- KQLKGEYALASLGR.-	1534.79	3	439.13	1.60	0.0	252	4/13	
phagrawFsucchlfbead_dec23, 1424	EHIVAFNMLNYRSCKNLWK.-	2367.78	3	284.15	1.40	0.1	145	7/36	1
jmidl1000nacirawphag3007, 1386	EHIVAFNMLNYR.-	1507.74	2	51.79	0.86	0.0	59	5/22	1
jmfag1mecon7.5min.1104.1104.2	- GEYALASLGR -	1037.15	0	173.17	1.09	0.0	148	1/2	
jmfag5mnconf150mmnacl, 1571	-.FGFNLKGGVDQK.-	1310.48	2	121.93	1.05	0.0	99	3/11	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 3 [Mus musculus]					1567.93	38078421.0	19		
rawextr_actinbead_Mar04,1112-1114	- KPGLAVSFAKLPQNLQK.-	1827.16	3	464.71	1.35	0.1	278	19/64	1
rawextr_actinbeadigg_Mar04, 1177	-.EKTRSEVICSIR.-	1421.65	2	160.57	1.04	0.1	114	7/22	2
rawextr_500bead_Mar04,1336-1338	-.EKTRSEVICSIR.-	1421.65	2	177.74	1.43	0.0	123	4/11	2
rawextr_800beadigg_Mar04, 1970	-.DQRAMMVQTSSQYKFVCEAILR.-	2606.04	3	764.91	1.63	0.1	379	19/84	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 4; testis-enriched prot					5006.98	9910518.0	25		
ajrawphagactin20, 874	-.FVCEAILK.-	923.16	3	692.31	1.76	0.1	347	3/7	
jmfag5minigg150mmnacl, 1124	-.PNAVYDVVEEK.-	1263.38	2	1161.26	1.39	0.2	258	11/20	
jmfag5minigg350mmnacl, 1479	-.STPNGGIPHDNLVLIK.-	1675.91	2	350.51	1.05	0.1	217	1/3	1
jmfagfrench20minigg1mnacldtt, 1848	-.DRQHTEVVCNILLLDNTVQAFRVNK -	2927.33	3	538.07	2.28	0.1	234	17/96	1
jmigG400rawphag3007,1982-1984	- HLDLTER.-	883.97	1	364.77	0.97	0.2	121	7/12	1
jmfag5minigg600mmnacl, 2828	-.DRQHTEVVCNILLLDNTVQAFRVNK -	2927.33	2	119.12	0.85	0.1	103	3/15	1
jmfag1mnacl5minigg, 3056	-.TGVLITMETAMCLIECNQPVYPLDIVR.-	3024.63	2	181.70	1.00	0.0	180	3/13	
jmidlactinrawphag3007, 1934	-.LNEGDQVVLINGR.-	1427.59	2	381.02	1.38	0.0	274	5/12	
jmraw5minbsabeads,1954-1956	-.SPPGTPNHR.-	963.03	1	364.48	1.27	0.0	275	5/8	1
jmrawbas5min1mnacl, 2002	-.SPPGTPNHR.-	963.03	1	72.25	0.98	0.0	72	3/8	1
jmbeads400rawphag3007,1303-1305	-.HLDLTER.-	883.97	1	529.06	0.96	0.2	75	1/2	1
phagrawF150_dec22, 1098	-.MKPDENGR.-	947.05	2	152.43	0.99	0.0	136	3/7	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 4; testis-enriched prot					680.58	9910518.0	10		
rawextr_800bead_Mar04, 1344	-.DYFGLQLADDSTDNPRWLDPNK.-	2581.74	3	680.58	1.86	0.0	349	1/4	1
rawextr_200beadigg_Mar04, 1495	-.DFWQMIWEQGSSMVVMLTTQVER.-	2803.23	3	453.08	1.94	0.1	193	17/88	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 8; PEST domain-enriched					11231.00	6679555.0	1		
jmraw5minbsafreebeads, 2004	-.NPPSAWNM.-	917.03	2	388.03	0.79	0.1	319	4/7	1
jmfag5miniggbead, 1297	-.NPPSAWNM.-	917.03	2	1209.02	1.16	0.3	214	4/7	1
jmfag5miniggbead, 1301	-.NPPSAWNM.-	917.03	2	686.97	0.96	0.2	258	4/7	1
jmfag5miniggbead_030528200105, 1509	- NPPSAWNM.-	917.03	2	210.31	0.87	0.0	240	1/2	1
jmfag1mnacl7.5minigg, 1854	-.EIQAQCSIPEQSLTVEADSCPLDLPK.-	2818.16	3	686.28	1.88	0.1	407	11/50	1
jmfag1mnacl2.5minigg, 3282	- RTDDEIPPPLPERTPESFIVVEEAGEPSPR.-	3361.66	2	59.35	0.63	0.1	20	3/29	1
jmrawgg5min150mmnacl, 554	- ADKIYPTTVAQRPK.-	1588.83	3	1159.59	1.62	0.1	628	19/52	1
jmfag5minfrench1mnackdttdpl, 1356	-.RTDDEIPPPLPER.-	1535.68	2	125.34	0.97	0.0	106	1/4	1
jmfag_20_minfrench1mnackdttdpl, 1356	-.RTDDEIPPPLPER.-	1535.68	2	125.34	0.97	0.0	106	1/4	1
jmrawgg5min1mnacl,1497-1499	-.NPPSAWNM.-	917.03	2	272.46	0.92	0.0	296	4/7	1
jmrawgg5min1mnacl, 1501	-.NPPSAWNM.-	917.03	1	95.41	0.71	0.1	53	3/7	1
ajrawphagjun20dpi1MNaCl,1682-1684	-.NPPSAWNM.-	917.03	2	837.08	0.92	0.2	294	4/7	1
jmfag1mnacl7.5minigg, 1854	-.EIQAQCSIPEQSLTVEADSCPLDLPK.-	2818.16	3	886.28	1.88	0.1	407	11/50	1
ajrawphagactin20, 2278	-.NPPSAWNM.-	917.03	2	218.60	0.91	0.1	187	1/2	1
ajrawphag1MNaCl20, 2492	- NPPSAWNM.-	917.03	2	454.31	0.94	0.2	239	4/7	1
ajrawphag1MNaCl20, 2496	-.NPPSAWNM.-	917.03	2	251.84	0.87	0.0	275	4/7	1
jmfag1mnacl2.5minigg, 3282	-.RTDDEIPPPLPERTPESFIVVEEAGEPSPR.-	3361.66	2	59.35	0.63	0.1	20	3/29	1
jmraw5minbsafreezthaw, 2150	-.NPPSAWNM.-	917.03	2	1090.59	1.11	0.3	152	3/7	1
jmrawbas5min1mnacl, 2204	-.NPPSAWNM.-	917.03	2	121.38	0.91	0.1	103	3/7	1
jmrawbas5min1mnacl, 2208	-.NPPSAWNM.-	917.03	2	1111.70	0.81	0.4	113	3/7	1
jmraw5minbsabeads, 2244	-.NPPSAWNM.-	917.03	2	496.78	1.09	0.1	267	4/7	1
jmfagcont5minbead, 756	-.QTLRTPGKSFTR.-	1392.59	3	687.01	1.33	0.1	467	4/11	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 8; PEST domain-enriched					2496.47	6679555.0	11		
rawextr_chlfbeadIgG_Mar04, 1408	-.TSTMNAEEELVLHSAK.-	1760.95	2	364.38	1.07	0.1	222	3/10	1
FPbeads450_Dec19, 2086	-.TQRPSLVQTQEQYELVYSAVLELFK.-	2971.35	3	1248.38	1.54	0.2	206	17/96	1
rawextr_400beadigg_Mar04, 2480	-.PSLVQTQEQYELVYSAVLELFKR.-	2742.12	2	82.58	0.65	0.0	75	2/11	1
jmrawbsaSminlowionic, 1970	-.NPPSAWNM.-	917.03	2	801.15	0.64	0.3	73	5/14	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 9; protein-tyrosine pho					**3560.06**	9790181.0	14		
jmfagfrench5minigg1mnackdtt, 829	-.FGFLTVTNLGVENMNHYKK -	2213.54	3	971.03	1.84	0.2	119	13/72	1
jmrawbas5min1mnacl, 1200	- VLIVRAPIWFR -	1370.71	2	259.01	0.99	0.0	243	2/5	
AJRAWpellet1_contr_jun13, 2170	- NGLVFIYDMCGSNYANFELDLGKKVLNLLK -	3393.97	2	294.42	0.93	0.2	53	7/58	1
rawsucrfp_60MeOHphagigg_MAr04, 1062	- NQQSMAVGNMGARSK.-	1579.79	2	1027.67	1.51	0.2	362	3/7	
rawsucrfp_450phagigg_Mar04, 1892	- MEPATAPRPDMAPELTPEEEQATK.-	2640.93	3	1007.92	1.80	0.1	418	5/23	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 9; protein-tyrosine pho					**563.51**	9790181.0	7		
FPbeads300_Dec19, 2518	-.DFWLMVWEQKVLVIVMTTRFEEGGR -	3071.61	2	96.90	1.15	0.0	84	5/24	1
jmbsaactinrawphag3007, 587	- NLGGYVK.-	750.87	1	444.03	1.00	0.1	273	2/3	
jmbsa400naclrawphag3007_030802135631, 2715	- DFWLMVWEQKVLVIVMTTRFEEGGR -	3071.61	2	22.58	0.72	0.0	31	5/48	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 18 [Mus musculus]					**9770.03**	6755236.0	14		
jmrawigg5min1mnacl, 579	-.EQEPLK.-	743.83	2	1225.75	1.75	0.0	700	9/10	2
jmlgG150rawphag3007,904-906	- DPPAEWTRV -	1071.17	2	167.03	1.07	0.1	121	3/8	2
jmfag1mnacl7.5minigg, 996	- SLLEQLEAR.-	1059.20	2	564.85	1.30	0.0	428	5/8	
jmrawigg5min1mnacl,1673-1675	-.EAFSLRTSSALPATSR.-	1694.87	3	1805.78	1.89	0.0	932	2/5	2
jmraw5minigg250mmnaclsyringdnase, 2944	- SISVPAPPTLPMADTYAVVQKRGLR.-	2669.14	3	415.92	1.45	0.1	262	19/96	
jmfreebeadsrawphag3007, 510	- ARSVAWKSEGVCSTK.-	1609.83	3	519.77	1.39	0.2	70	2/7	2
rawphag2007chlfsol2, 3268	- RVPADQNSSGPDAYEEVTDGAQTGGLGFNLR.-	3223.37	2	42.14	0.70	0.1	31	7/60	2
jmldl400firstnaclrawphag3007, 3068	- CLQGLGPGPLGVHCSAGCGR.-	1929.31	2	164.49	1.00	0.0	151	9/38	2
jmbsa1000naclrawphag3007, 1895	-.AGSRLGNTNKNR.-	1288.40	2	197.62	1.00	0.0	188	4/11	1
jmrawbas5min1mnacl,2440-2442	-.EAFSLRTSSALPATSR.-	1694.87	3	3786.88	2.16	0.3	863	23/60	2
jmfagtmecon5min, 525	- PPGGVLRSISVPAPPTLPMADTYAVVQKR.-	3019.55	2	172.08	0.82	0.1	90	9/56	2
jmfagtmecont10min_030601202502, 2352	-.APTSTDTPIYSQVAPR -	1704.86	2	166.54	1.22	0.0	117	1/3	1
rawsucrfp_actinphagigg_Mar04, 1208	-.APTSTDTPIYSQVAPR.-	1704.86	2	134.88	1.20	0.0	110	4/15	1
phagrawFsuc150_dec22, 1258	-.APTSTDTPIYSQVAPR -	1704.86	2	153.44	1.09	0.0	140	1/3	1
phagrawFsuc150_dec22, 1328	-.APTSTDTPIYSQVAPR -	1704.86	2	64.86	1.11	0.0	49	4/15	1
phagrawFsuc450_dec20, 2246	-.GIDGSQAYIATQGPLPHTLLDFWR.-	2657.97	2	186.00	0.95	0.1	32	7/46	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 18 [Mus musculus]					**276.40**	6755236.0	7		
rawextr_350beadigg2_Mar04, 2534	- AGPFCITLTKETTLNADITLRTLQVTFQK -	3225.75	2	86.27	0.95	0.0	78	9/56	2
FPbeads300_Dec19, 3152	-.TLQDTSPHYQNLKENCAPICKEAFSLR.-	3108.50	2	190.12	1.27	0.1	102	5/26	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 21 [Mus musculus]					**3987.77**	6755240.0	23		
JMFAGNACL10_2B21E3, 266	- RDSVKK.-	732.85	2	248.45	1.04	0.0	239	7/10	1
jmfag1mnacl2.5minigg, 604	-.VLIQFLKSSRLI.-	1417.77	3	783.04	1.84	0.1	353	17/44	2
jmfag5minigg400mmnacl, 734	-.ITTRFRTDSGCYATTGLK.-	1992.25	3	913.28	1.79	0.1	412	9/34	2
jmfag5minigg1000mmnacl, 2092	- HSALIPPSYRPTPDYETVMK.-	2303.62	3	278.45	0.94	0.1	159	1/4	1
jmfag1mnacl0minigg, 2100	-.ERTVSASAADVAPRTFSAGSQSSVFSDK.-	2860.04	3	1053.52	1.78	0.2	358	23/108	
rawphag2007chfbead3,785-787	-.PTPDYETVMK.-	1181.34	2	120.76	0.95	0.0	125	4/9	1
rawphag2007chfbead2, 1520	- LEQGMVFTEYERILKK.-	1985.34	1	68.25	0.85	0.1	46	1/5	2
jmbeads500rawphag3007,1881-1883	- RHTNSTSEPKSHNPPLLVHCSAGVGR.-	2783.08	3	244.38	1.57	0.0	149	7/50	2
phagrawF250_dec22, 625	-.NGRPPVVFR.-	1042.22	2	68.09	0.71	0.0	97	5/16	
phagrawF600_dec20, 966	- LAALNGLSLSR -	1115.31	2	169.56	1.15	0.1	110	2/5	2
phagrawFsuc400_dec20, 2702	- RPVVGAVSVPELTNVQLQAQDYPAPNIMR.-	3164.63	2	39.97	0.92	0.0	35	3/28	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, non-receptor type 21 [Mus musculus]					**546.88**	6755240.0	10		
rawextr_1000_beadigg_Mar04, 782	- AKDISPVHLVVETHR.-	1701.95	3	449.61	1.73	0.0	260	2/7	1
rawextr_actinbeadigg_Mar04, 2181	-.PTPDYETVMKQLNR.-	1692.92	2	97.27	0.88	0.0	109	4/13	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase DPZPTP [Mus musculus]					**5616.72**	517125.0	31		
jmfag5minigg200mmnacl, 908	-.VPLGDEGGYINASFIR.-	1708.90	3	2704.62	1.99	0.3	359	19/60	1
jmrawigg5minbeadsyringdnase, 1343	-.LVLGRILELPR.-	1279.60	2	237.32	1.06	0.1	115	3/10	3
JMFAGNACL15B21E3, 1408	-.QTPHVKDYSFVTEDNTFEVK.-	2385.57	3	692.14	1.78	0.2	154	7/38	2
jmfagfrench5minigg1mnackdtt, 2221	-.ESYSDHSESGEDDSVRAPAKMPNVTR.-	2865.99	3	447.31	1.26	0.1	328	1/5	3
RawPhg2007Etsolutiondigest, 1827	-.GQVPTSRERDPAGPQSPPPDQDAQR.-	2687.82	3	446.31	1.65	0.0	256	11/48	1
phagrawFchlf_dec23, 2172	-.ANGLTSMEPSGQPALMPK.-	1830.12	2	148.77	1.07	0.0	135	5/17	3
phagrawF1000_Dec23, 1932	-.IKCQRYWPSILGTTTMANER.-	2369.75	3	465.80	1.28	0.0	357	17/76	4
phagrawF800_Dec23, 2114	-.IKCQRYWPSILGTTTMANER.-	2369.75	3	325.67	1.55	0.1	184	4/19	4
phagrawFchlf_dec23, 2172	-.ANGLTSMEPSGQPALMPK.-	1830.12	2	148.77	1.07	0.0	135	5/17	3

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase DPZPTP [Mus musculus]					**1508.72**	517125.0	22		
rawextr_700beadigg_Mar04, 566	-.EGTLSSQDSR.-	1080.09	3	390.36	1.25	0.0	290	1/3	
FPbeads150_Dec19, 691	-.IDVGDVILK.-	972.16	2	422.45	1.20	0.0	342	9/16	3
rawextr_chlfbead_Mar04,904-906	-.ALDLSLPSVVLKVTR.-	1611.95	3	393.50	1.79	0.0	205	17/56	3
rawextr_500bead_Mar04, 1318	-.HATRRACSPDPLR.-	1480.68	2	302.40	0.87	0.1	176	1/3	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, receptor-type, F interacting protein, bin					8600.19	6679435.0	26		
jmrawgg5min150mmnacl, 418	-.KLVLAVK.-	771.03	2	350.87	1.18	0.0	294	3/4	3
jmrawmmigg200mmnaclsyringdnas, 738	-.KLVLAVKAINAK.-	1268.62	3	766.69	1.45	0.1	481	17/44	3
jmfag5minigg500mmnacl, 756	-.ATAGPRLSR.-	929.06	2	717.24	1.03	0.0	693	3/4	3
JMFAGNACL10_1B21E3, 1510	-.MGMETLLVANEDKDR.-	1722.97	2	1299.45	1.75	0.1	626	1/2	1
JMFAGNACL10_1B21E3, 1580	-.KKFDESTDYICPMEPGDAVSDSHR.-	2728.95	3	1131.46	1.79	0.0	613	1/4	3
jmfreebeadsrawphag3007, 564	-.KWNTTNK.-	892.00	2	489.04	1.23	0.0	389	2/3	2
RawPhg2007Etsolutiondigest, 1069	-.CAIHVLHVNKFNPNCLHR.-	2116.50	3	653.53	1.19	0.1	522	19/68	2
jmidl600naclrawphag3007,1198-1200	-.KKFDESTDYICPMEPGDAVSDSHR.-	2728.95	3	753.83	1.66	0.1	388	5/23	3
jmidl300naclrawphag3007, 1710	-.KFDESTDYICPMEPGDAVSDSHR.-	2600.78	3	951.20	1.34	0.0	693	23/88	3
jmidl400naclrawphag3007_03080215331 3, 1720	-.FDESTDYICPMEPGDAVSDSHR.-	2472.61	3	548.44	1.38	0.1	267	3/14	3
jmfagcon5minn600mmnacl,538-541	-.RHLTTK.-	755.89	2	112.71	0.80	0.1	103	3/5	3
jmbeads350rawphag30072nd, 898	-.KLSCSLEDLR.-	1164.36	3	451.18	1.47	0.0	299	13/36	2
jmbeads250rawphag3007, 1662	-.LSCSLEDLRRESGDK.-	1708.88	2	155.45	1.46	0.0	104	5/14	2
phagrawF200_dec22, 2343	-.MGMETLLVANEDKDR.-	1722.97	2	219.10	0.80	0.0	255	11/28	1

control

protein tyrosine phosphatase, receptor-type, F interacting protein, bin					2696.09	6679435.0	19		
rawextr_800beadigg_Mar04, 1038	-.DLEVCLEGHQVK.-	1370.58	2	527.08	1.36	0.1	356	5/11	1
FPbeads150_Dec19, 1639	-.GSGVHGGLIILEPR.-	1405.63	1	197.23	1.00	0.1	121	4/13	3
FPbeads500_dec19, 2044	-.FDESTDYICPMEPGDAVSDSHR.-	2472.61	3	473.45	1.29	0.1	331	17/84	3
jmbsa300naclrawphag3007, 1298	-.KWNTTNKSPEEVPK.-	1658.84	2	337.00	1.00	0.0	323	5/13	2
jmbsaactinrawphag3007, 1897	-.CAIHVLHVNKFNPNCLHR.-	2116.50	3	509.84	1.45	0.1	288	19/68	2
jmbsa250naclrawphag3007, 2231	-.LNAAEEMLQQELLSR.-	1745.98	3	386.39	1.08	0.1	277	1/4	1
jmrawbsa5minlowionic, 954	-.GSGVHGGLIILEPR.-	1405.63	3	265.10	1.53	0.1	97	7/26	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, receptor type, F; leukocyte antigen-rela					9883.14	18702313.0	47		
jmrawgg5min300mmnaclsyringednase, 100	-.VTCVSTGSTTVR.-	1211.37	3	569.69	1.49	0.0	383	17/44	1
jmfag5minigg300mmnacl, 272	-.MAPEPAPGR.-	926.08	3	323.78	1.36	0.1	209	5/16	
jmrawgg5min300mmnaclsyringednase,471-473	-.TLRTQR.-	774.89	2	292.60	1.35	0.1	151	7/10	2
jmfag5minigg400mmnacl, 552	-.WMMGAEELTK.-	1196.42	3	520.99	1.80	0.1	232	13/38	
jmrawgg5min1mnacl, 677	-.VLAVNSIGR.-	929.10	2	249.72	1.18	0.0	203	9/18	1
jmfag5minggbead_03052820010 5, 719	-.PKNRYADVIAYDHSR.-	1805.98	3	549.08	1.53	0.1	247	15/56	
jmrawgg5min1mnacl, 1015	-.FEVIEFDDGAGSVLRIQPLR.-	2262.55	3	279.54	1.15	0.1	214	15/76	
jmrawgg5min400mmnactsd, 1397	-.EITTPEDVPSGFPQNLR.-	1901.07	2	847.16	1.63	0.1	205	5/16	1
jmrawgg5min450mmnactsd,1440-1442	-.PLPASAFIEDGR.-	1273.42	2	433.92	1.21	0.1	235	4/11	1
jmrawgg5minbeadsfreezethaw, 1560	-.LGQVPPGESVTAMELEFK.-	1933.22	2	331.34	1.41	0.1	170	4/17	2
jmigG400rawphag3007, 1592	-.MRYEGVVDMFQTVK.-	1704.01	3	389.87	1.50	0.0	252	15/52	2
JMFAGNACL5B21E3, 1624	-.LAAKNRAGPGEEFEK.-	1617.79	2	445.62	1.15	0.1	250	5/14	1
jmigG500rawphag3007, 1647	-.AHTSRFVSANLPCNKFK.-	1921.22	2	132.47	0.99	0.0	129	1/4	2
ajrawphagactin20, 2328	-.EHSSWDLLGLEK.-	1414.55	3	298.97	1.06	0.0	281	7/22	1
rawphag2007chltfsol2, 1252	-.LPVPNKQHGQIR.-	1387.62	2	317.02	1.30	0.1	180	7/22	1
phagrawFsucchltbead_dec23, 1786	-.GRTATMLCAAGGNPDPEISWFK.-	2323.64	2	525.74	1.03	0.2	122	4/21	
phagrawFchlf_dec23, 2508	-.QLRSGALQIESSEESDQGKYECVATNSAGTR.-	3316.52	2	96.62	0.82	0.1	63	3/20	
jmidl450naclrawphag3007, 2174	-.MLSASTMLVQWEPPEEPNGLVRGYR.-	2862.28	3	276.55	1.19	0.1	180	3/16	1
jmrawbas5min1mnacl, 1612	-.FEVIEFDDGAGSVLR.-	1654.80	2	274.07	1.00	0.1	92	1/4	
rawsucrfp_900phagigg_Mar04,142-149	-.ELPGELLGYR.-	1147.31	3	125.98	1.54	0.0	78	11/36	1
rawsucrfp_500phagigg_Mar04, 620	-.PRITWMKK.-	1060.34	2	113.65	1.12	0.0	97	5/14	
rawsucrfp_800phagigg_Mar04, 676	-.PRITWMKK.-	1060.34	2	254.06	1.17	0.1	102	3/7	
rawsucrfp_250phagigg_Mar04, 684	-.ELPGELLGYR.-	1147.31	3	192.40	1.32	0.0	129	1/3	1
phagrawFsuc150_dec22, 888	-.MRYEGVVDMFQTVK.-	1704.01	2	165.34	1.28	0.1	104	4/13	2
rawsucrfp_1000phagigg_Mar04, 1349	-.IVKYELVYWAAEDEGQQHK.-	2307.55	3	547.60	1.60	0.0	334	17/72	1
phagrawFsucchltbead_dec23, 1786	-.GRTATMLCAAGGNPDPEISWFK.-	2323.64	2	525.74	1.03	0.2	122	4/21	
phagrawF250_dec22, 1917	-.AHTDVGPGPESSPVLVRTDEDVPSGPPR.-	2870.08	3	282.26	1.33	0.0	212	19/108	1
rawsucrfp_250phagigg_Mar04, 2470	-.VSWVPPPADSRNGIITQVSVAYEAVDGEDRK.-	3421.72	2	291.65	0.91	0.2	74	2/15	1
phagrawFchlf_dec23, 2508	-.QLRSGALQIESSEESDQGKYECVATNSAGTR.-	3316.52	2	96.62	0.82	0.1	63	3/20	
phagrawFsuc400_dec20, 3600	-.VPEDQTGLSEGVASFVCQATGEPKPRITWMK.-	3363.81	2	33.79	0.67	0.0	50	7/60	
jmfagtimecon2.5min.782.782.2	-.GPPSEAVR.-	812.90	0	152.42	0.97	0.0	168	4/7	1
jmfag5mincontl150mmnacl, 2767	-.TDEQVPSGPPRKVEVEPLNSTAVHVSWK.-	3075.39	2	138.86	1.03	0.1	86	4/27	1

control

protein tyrosine phosphatase, receptor type, F; leukocyte antigen-rela					1906.53	18702313.0	34		
FPbeads200_Dec19, 901	-.AHTDVGPGPESSPVLVRTDEDVPSGPPR.-	2870.08	3	351.00	1.38	0.1	217	17/108	1
FPbeads400_Dec19, 1300	-.GYQVTYVR.-	986.11	1	363.06	1.20	0.1	177	1/2	1
FPbeads250_Dec19, 2354	-.SARYQYFVVDPMAEYNMPQYILREFK.-	3260.73	2	165.57	1.07	0.1	58	7/50	11
FPbeads450_Dec19, 3114	-.FSQEYESIDPGQQFTWENSNSEVNKPK.-	3190.34	2	48.43	0.80	0.0	41	3/26	2
FPbeads800_Dec19, 3816	-.LGQVPPGESVTAMELEFKLLANSK.-	2559.98	3	161.38	1.24	0.0	118	3/23	2
jmraw5minbsafreezthaw, 2206	-.EHSSWDLLGLEK.-	1414.55	3	817.08	1.18	0.2	300	15/44	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase receptor type N [Mus musculus]					3719.71	14193733.0	10		
JMMAGTube1B16E3, 1126	-.NLEGAVNVGGADVK.-	1343.47	2	173.03	1.07	0.0	142	5/13	4
jmigG250rawphag3007, 854	-.EEAAEVLPRQAHGISPMR.-	1992.25	3	820.98	1.60	0.2	215	19/68	3
jmigG350naclrawphag3007, 2041	-.LLEILAEHVHMSSGSFINISVVGPAVTFR.-	3125.63	2	36.82	0.90	0.0	27	9/56	4
jmrawgg5min300mmnaclsyringednase, 2247	-.SVLLTLVALAGVAGLLVALAVALCMRHHSRQR.-	3341.09	2	180.82	0.84	0.1	83	4/31	3
JMFAGNACL10_1B21E3, 2334	-.SELEAQTGLQILQTGVGQR.-	2029.24	3	628.86	1.27	0.1	332	1/4	3
jmigG400rawphag3007, 2340	-.GTGRNLEGAVNVGGADVKK.-	1843.04	2	681.19	1.23	0.2	293	11/36	4
jmfag5minigg250mmnacl, 3438	-.SPLGQSQPTVVGRPSARPSAEEYGYIVTDQK.-	3319.63	2	31.47	0.68	0.0	42	7/60	4
jmrawbas5min1mnacl, 1368	-.TGTYILIDMVLNRMAK.-	1840.25	3	467.15	1.48	0.1	295	4/15	4
phagrawFsuc600_dec20,1272-1274	-.QHMATKSLFNR.-	1333.55	2	490.26	1.22	0.1	373	11/20	4
phagrawFsuc450_dec20, 2458	-.SKDQFEFALTAVAEEVNAILKALPQ.-	2734.10	3	209.12	1.17	0.1	152	3/16	4

control

protein tyrosine phosphatase receptor type N [Mus musculus]					1275.99	14193733.0	11		
rawextr_900bead_Mar04,656-658	-.SPLGQSQPTVVGR.-	1326.49	3	156.43	1.40	0.1	65	1/4	4
rawextr_300beadigg_Mar4,798-800	-.HHSRQRDK.-	1064.14	2	542.44	1.24	0.0	430	9/14	3
FPbeads250_Dec19, 1068	-.PSARPSAEEYGYIVTDQKPLSLVAGVR.-	2905.25	3	250.73	1.13	0.1	122	15/104	4
rawextr_60MeOHbeadigg_Mar04, 2166	-.SDYINASPIEHDPR.-	1727.86	2	213.66	1.09	0.0	194	9/28	4
rawextr_350bead_Mar04, 2426	-.KSPLGQSQPTVVGRPSAR.-	1866.12	1	112.72	0.70	0.1	63	3/17	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, receptor type, N polypeptide 2; protein					**4514.07**	33859598.0	6		
rawextr_700beadigg_Mar04 1554	- TVTQFHFLSWYDQGVPSSTRSLLDFRR.-	3245.60	3	384.28	1.46	0.1	195	5/26	1
jmrawigg5minigglreebead, 1590	- EIDIAATLEHLRDQRPGMVQTK -	2522.87	3	468.31	1.63	0.0	288	3/14	1
jmfagtmecon7.5min 2400 2400 2	- YLPYLELLSQTPTANAHSRIDHETRPAK.-	3223.59	0	23.87	0.66	0.0	36	5/54	
jmfagcont5minbead, 2694	- ADSVAGAIQSDPAEGSQESHGR.-	2170.20	3	330.47	1.29	0.0	253	11/42	1
jmfag5mincont400_030531151834, 3239	- ADSVAGAIQSDPAEGSQESHGRGAEGQPR.-	2865.93	3	145.95	1.10	0.0	126	9/56	1
jmraw5minigglowionic, 239	- WFSLEREVALAKTLR.-	1820.13	3	408.25	1.20	0.1	247	13/56	
ajrawphag1MNaCl20, 1248	- LQPDELSPKVDGDIDK.-	1769.93	3	648.68	1.40	0.1	410	3/10	
jmrawigg5min450mmnaclad, 1296	- TVTQFHFLSWYDQGVPSSTRSLLDFRR -	3245.60	3	412.81	2.22	0.1	122	2/13	1
jmraw5minigg500mmnaclad, 2848	- LSFQLGDLLKDYGSHLLPEGPLLEK -	2784.20	3	454.93	1.30	0.1	322	5/24	
jmfag5minigg400mmnacl, 292	- DSPSMDDDTLLQSLLK.-	1778.96	3	241.76	1.17	0.0	207	7/30	1
jmfag5minigg150mmnacl, 1436	- DLQQNSEVDRLGPLKEEK.-	2099.29	3	593.36	2.06	0.1	195	19/68	1
rawphag2007chfbead3, 1405	- TVTQFHFLSWYDQGVPSSTRSLLDFRR.-	3245.60	3	191.67	1.67	0.0	111	2/13	1
jmldl600naclrawphag3007, 2244	- TVTQFHFLSWYDQGVPSSTRSLLDFRR -	3245.60	3	209.71	1.65	0.0	126	9/52	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
protein tyrosine phosphatase, receptor type, N polypeptide 2; protein					**1139.84**	33859598.0	8		
rawextr_250bead_Mar04, 644	- EVALAKTLR.-	1001.21	2	390.68	1.54	0.0	247	1/2	
rawextr_700beadigg_Mar04, 1554	- TVTQFHFLSWYDQGVPSSTRSLLDFRR.-	3245.60	3	384.28	1.46	0.1	195	5/26	1
FPbeads150_Dec19, 2091	- TVTQFHFLSWYDQGVPSSTRSLLDFRR -	3245.60	3	173.53	1.05	0.1	102	15/104	1
rawextr_450bead_Mar04, 2254	- TVTQFHFLSWYDQGVPSSTRSLLDFRR -	3245.60	3	191.15	1.58	0.0	121	17/104	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to protein tyrosine phosphatase, non-receptor type 13 isoform					**9049.74**	38075912.0	17		
jmrawigg5minbeadsynngdnase, 761	- LLQVDGVSLCGLTHK.-	1583.88	2	80.00	0.87	0.0	90	9/28	
jmfag5minigg1000mmnacl, 1836	- NSTASSGMFCTDILSNR -	1804.99	2	522.28	1.37	0.1	228	9/32	
jmfag1mnacl7.5minigg, 2332	-.DTRLCKVAPEGWR -	1531.77	2	135.57	0.92	0.1	106	3/8	
jmraw5minigg250mmnaclsynngdnase, 2412	-.NRSCSLR.-	835.96	2	232.84	0.91	0.1	139	1/2	
jmfag1mnacl7.5minigg, 2784	- IKRLFPGQPAEEHGAIAAGDILAVNGK.-	2887.33	3	298.72	1.24	0.0	235	1/6	
jmldl300naclrawphag3007, 1304	- MALGVCTKGIIVYEVR.-	1753.17	3	1131.66	1.88	0.2	373	11/30	
jmfagcont5minbead, 232	- EPGKER -	715.78	2	345.39	1.05	0.1	302	7/10	
jmbeads250rawphag3007, 492	- LVGLVLGTISEVER.-	1485.75	3	989.04	1.51	0.0	633	19/52	
jmfag5mincon450mmnacl, 556	-.LCKVAPEGWR -	1159.39	3	715.69	1.59	0.1	251	11/36	
jmfag5mincon450mmnacl, 1158	-.LTITSSTTGK.-	1009.14	2	210.33	1.50	0.0	140	4/9	
jmbeadsactinrawphag3007, 1737	-.NSTASSGMFCTDILSNR.-	1804.99	2	93.51	1.24	0.0	74	3/16	
jmfagcont5minbead, 2170	-.VVEENACEQR -	1177.27	1	164.51	0.95	0.1	116	7/18	
AJRAWpellet_contr_jun13, 2372	- EGQILQGDRLLQVDGVSLCGLTHKQAVQCLK.-	3351.89	2	216.51	0.83	0.1	46	7/60	
phagrawF300_dec20, 1239	- YTFVTNSSK -	1047.14	2	441.91	1.13	0.0	380	9/16	
phagrawFsuc60MeOH_dec23, 2056	- LQDATGGQLGTSMENKQGFKEPGK.-	2522.78	3	511.24	1.33	0.1	339	21/92	
phagrawFsuc700_dec23, 2215	- SIIPGGPAAKEGQILQGDR.-	1908.15	2	303.12	0.82	0.1	152	1/4	
phagrawFsuc400_dec20, 3334	- GPRAAPQCPSADDRMGDVHMAVSLVTAR.-	2910.31	2	2657.42	1.28	0.4	105	5/27	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to protein tyrosine phosphatase, non-receptor type 13 isoform					**1505.19**	38075912.0	21		
rawextr_150beadigg2_Mar04, 1136	-.MIQNSPDDMELIISQPKGVCGTIHSEEK.-	3101.52	2	180.26	0.98	0.1	114	1/6	
rawextr_chfbeadigG_Mar04, 1166	- LIERMTAIRVQVEVSEMHR -	2298.72	3	480.48	1.45	0.0	329	19/72	
rawextr_800beadigg_Mar04, 1436	- KYTFVTNSSKTCK.-	1507.74	2	118.79	0.89	0.0	129	7/24	
FPbeads600_Dec19, 1470	- EPGKERIGSSPYTGGEQLHSIGLNQK.-	2784.03	3	211.32	1.40	0.1	73	7/50	
rawextr_200bead_Mar04, 2488	-.RQPLQAVLEACRIHQEEVAVYPAPASLHISR.-	3483.99	3	514.34	1.38	0.1	339	7/40	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to protein tyrosine phosphatase, receptor type, Q [Mus musculu					**8028.87**	38090755.0	6		
jmfreebeadsrawphag3007, 1026	- SFLQHVEELCTNNNLK.-	1890.11	3	1586.84	1.77	0.2	652	1/3	
jmldl400naclrawphag3007_030802153313, 1286	- YTDYIFKITPSTEK.-	1706.92	2	154.69	1.12	0.1	87	3/13	
jmfagtmecon2.5min.318.318.3	-.TLVMLTQCFEKGR -	1526.85	0	988.32	1.40	0.2	247	17/48	
jmfagtmecon2.5min.1994 1994.3	-.ARPYFTNEGFPNPPCIEGKTK.-	2367.67	0	680.78	1.78	0.1	266	19/80	
jmfagtmecon10min, 3082	-.LTRSSVSHPPNQSFSDLTTHSATSGSMK.-	2962.20	2	631.98	1.04	0.2	55	4/27	
phagrawFsuc500_dec20,1026-1028	-.GFSETYTAQLHIK.-	1495.66	2	665.99	1.87	0.1	265	3/8	
phagrawFsuc200_dec22, 1791	- FKLDQLITVADLELK.-	1747.07	2	357.41	0.98	0.1	328	11/28	
phagrawFsuc500_dec20, 1886	- SERMCMVQNLAQYIFLHQCILDLLSNK.-	3212.82	3	495.68	1.01	0.2	151	2/13	
phagrawFsuc200_dec22, 1927	-.GGHQPVCFVNYSTLQK.-	1779.01	2	182.39	0.90	0.0	195	1/3	
phagrawF500_dec20, 1950	- SSAEVIITTLESVPKDPPNNMTFQK.-	2748.10	2	1252.80	1.15	0.3	100	3/16	
rawsucfp_chfphagigg_Mar04, 2026	-.CHQYWPEDNKPVTVFGDILITK -	2604.97	2	615.21	1.08	0.2	193	11/42	
phagrawFsuc300_dec20, 3168	- EWEPEECVEHQEVQYLYEANQTEDTVR.-	3355.50	2	35.53	0.84	0.0	42	3/26	
jmIgG400rawphag3007, 1436	-.FQEEFSELPK.-	1254.37	2	381.28	1.23	0.1	235	4/9	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to protein tyrosine phosphatase, receptor type, Q [Mus musculu					**840.79**	38090755.0	14		
FPbeads450_Dec19, 178	-.QCNFTGWPEHGVPENTTPLIHFVK.-	2753.09	2	248.81	1.07	0.1	157	6/23	
rawextr_350beadigg2_Mar04, 1162	- WYDAYFNK -	1107.20	2	390.70	1.45	0.0	267	4/7	
rawextr_actinbeadigg_Mar04, 1855	-.AKTLVMLTQCFEK.-	1512.86	2	201.28	1.06	0.0	165	7/24	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
JC5981 prenylated protein tyrosine phosphatase (EC 3.1.3.-) 2 - mouse					**5419.20**	7513774 0	1		
JMFAGNACL15B21E3, 756	- QLLYLEKYR -	1228 45	2	1146 88	1 54	0 1	558	5/8	3
jmtag5mnigg250mmnacl, 1190	- RRGAINSK -	902 04	2	243 19	0 97	0 0	241	4/7	2
rawsucrfp_actinphagigg_Mar04, 1454	- PAPVEISYENMRFLITHNPTNATLNK -	2972 37	3	1182.81	1 50	0 2	245	19/100	1
rawphag2007chifbead3,150-152	- QLTYLEK -	895 04	2	374 77	1 51	0 0	245	2/3	2
jmtag5mincont350, 282	- FKDPHTHK -	1010 13	2	1363 53	1 48	0 2	882	5/7	2
jmbeads250rawphag3007, 656	- FKDPHTHK -	1010 13	2	318.18	1 10	0 0	278	4/7	2
jmtagcont5minbead, 2596	- APVLVALALIECGMK -	1528 95	1	789 85	1 15	0 2	157	9/28	2

control

JC5982 prenylated protein tyrosine phosphatase (EC 3.1.3.-) 3 - mouse					**197.60**	7513775 0	1		
FPbeads250_Dec19, 2032	- HMRFLITHNPSNATLSTFIEDLKK -	2815 24	3	197 60	1 30	0 1	103	9/48	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
LPA2_MOUSE Liprin-alpha 2 (Protein tyrosine phosphatase receptor type f polyp					**7480.17**	42558981 0	15		
jmtag5mnigg0ead, 523	- HELLEEAR -	997 09	2	127 55	0 95	0 0	130	1/2	2
jmtag5mnigg0bead, 1385	- KAETLPEVEAELAQR.-	1884 87	2	225 53	1 31	0 0	158	5/14	2
jmrawgg5mnibeadsfreezethaw, 998	- ERLTALSSRVGEVEQEAETAR.-	2332 51	3	188 15	1 39	0 1	100	9/40	1
jmigG150rawphag3007, 1354	-.VGEVEQEAETAR.-	1318 37	2	181 87	0 90	0 0	172	4/11	1
jjrawphag1MNaCl20, 1404	- LTPRSPAREMDR.-	1429 63	3	1339 52	1 41	0 2	399	7/22	1
jmtag5mnigg300mmnacl, 1522	-.LELAEQKLQQTMRK.-	1717 03	2	507 04	1 73	0 1	211	9/28	1
jmigG400rawphag3007, 1692	- VSLAEEIEKLASELDQMK -	2119 43	3	869 12	1.43	0 1	443	9/34	
jmrawgg5mnigg0freebead, 92	- SELDQMKMRTGSLIEPTSR -	2293 65	3	389 42	1 15	0 1	313	17/78	1
rawphag2007chifsol3,779-781	-.LELAEQKLQQTMRK.-	1717 03	2	444 68	1 79	0 0	248	11/28	1
phagrawF500_dec20,392-394	- LELAEQKLQQTMRK.-	1717 03	2	573 41	1 79	0 0	319	5/13	1
rawsucrfp_500phagigg_Mar04, 970	- LELAEQKLQQTMRK -	1717 03	2	264 18	1 57	0 0	148	4/13	1
rawsucrfp_250phagigg_Mar04,1142-1144	-.LELAEQKLQQTMRK.-	1717 03	2	608 12	2 07	0 0	276	5/13	1
phagrawFsuc350_dec20, 1520	- LELAEQKLQQTMRK -	1717 03	2	613.10	1 78	0 1	309	11/28	1
phagrawFsuc250_dec22, 1697	- VHPGTSITASVTASSLASSSPPSGHSTPK.-	2749 97	3	292 42	1 33	0 0	213	19/112	1
phagrawFsucchif_dec23, 1774	- SSLSASLEPDSLQLGSANSSQDSLHK -	2588 73	3	171 57	1 15	0 0	145	3/20	
phagrawF300_dec20, 2659	- MVSSEGSTESEHLEGMEAGQKVHEKR.-	2874 12	3	494 52	1.35	0 1	289	19/100	1

control

LPA2_MOUSE Liprin-alpha 2 (Protein tyrosine phosphatase receptor type f polyp					**2137.47**	42558981 0	17		
rawextr_700bead_Mar04, 1071	- GADPPEFAALTKELNACR.-	1904 14	2	520 85	1 69	0 1	182	5/17	2
rawextr_500bead_Mar04, 1136	- LELAEQKLQQTMRK -	1717 03	2	533 47	1 62	0 1	228	9/28	1
FPbeads200_Dec19, 1925	- GFMETEAAAQESLQLGKLGTQAEKDR.-	2739 01	3	244 26	1 17	0 1	155	3/20	1
jmbsa150nacirawphag3007, 843	- KHELLEEAR.-	1125 26	2	838 90	1.43	0 1	457	9/18	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to receptor-type tyrosine phosphatase [Mus musculus]					**6475.58**	38074950 0	6		
jmtag5mincont350, 1188	-.GQKLASVMEMPIALLR.-	1758.19	3	381.84	1 44	0 0	240	1/4	1
jmtag5mincon250mmnacl, 1696	- GQKLASVMEMPIALLR.-	1758.19	3	321 47	1 27	0 1	125	7/30	1
rawsucrfp_150phagigg_Mar04, 1669	-.THEEDDNFGNMQVATAQNG.-	2079.11	3	1659.81	1 38	0 3	401	23/72	
phagrawF400_dec20, 2042	-.MDPEESQHEDLSSHGLGNARSTASPSR.-	2897 00	2	68 48	0.90	0.0	73	7/52	
jmfreebeadsrawphag3007, 1510	-.THEEDDNFGNMQVATAQNG.-	2079 11	3	3098.58	2 18	0 3	263	7/24	
jmtag5mnigg450mmnacl_030527025134, 1746	- SLAIHSGTTGSVKR.-	1414 59	2	279.53	1 09	0 1	213	9/28	
jmiggactinrawphag3007,2386-2388	- THEEDDNFGNMQVATAQNG.-	2079 11	3	667.89	1.44	0 1	242	1/4	

control

similar to protein tyrosine phosphatase-like [Mus musculus]					**446.42**	38087160 0	3		
rawextr_150bead_Mar04, 1601	- SLAIHSGTTGSVK.-	1258 41	2	317.85	1.12	0.1	160	3/8	
rawextr_350beadigg2_Mar04, 2710	-.SPLQDVSASLLIEKGSDSLMVWLLVAR.-	2929 43	2	90 88	1 00	0.1	47	3/26	
rawextr_250beadigg_Mar04, 2332	- LTIQMMSPLQIERSLAIHSGTTGSVKR -	2956.48	2	37.69	0.82	0.0	34	3/26	

APPENDIX H – ADAPTOR SUMMATION OF IONS

The summation of peptides from Adaptors found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Delta CN	Accession Sp	Peptides Ions	Count
14-3-3 zeta [Mus musculus] [Mus musculus]					**28403.75**	1841387.0	7		
jmfag5minigg150mmnacl,816-818	-.FLIPNASQPESK.-	1331.50	2	2683.97	2.04	0.3	483	13/22	3
jmIgG300rawphag3007, 880	-.YLAEVAAGDDKK.-	1280.41	2	1737.12	1.87	0.1	719	13/22	3
jmfag5minigg400mmnacl, 920	-.FLIPNASQPESK.-	1331.50	2	574 44	1.78	0.0	320	5/11	3
jmfag5minigg200mmnacl, 960	-.FLIPNASQPESK.-	1331.50	2	1320.53	1.79	0.2	400	7/11	3
jmrawminigg200mmnaclsyringdnas, 1218	-.FLIPNASQPESK.-	1331.50	2	566.18	1.39	0.1	286	1/2	3
jmIgG350naclrawphag3007, 1251	-.FLIPNASQPESK.-	1331.50	2	1082.81	1.43	0.1	606	7/11	3
jm5miniggrawlowionic, 1480	-.FLIPNASQPESK.-	1331.50	2	365.48	1.55	0.1	188	9/22	3
jm5miniggrawlowionic, 1484	-.FLIPNASQPESK.-	1331.50	2	1969.37	2.05	0.3	314	6/11	3
jmfag1mnacl7,5minigg, 2196	-.TAFDEAIAELDTLSEESYK.-	2133.25	3	9141.52	2.95	0.4	1229	13/36	3
jmfag1mnacl7,5minigg, 2200	-.TAFDEAIAELDTLSEESYK.-	2133.25	3	4492.25	2.87	0.3	709	1/3	3
jmfag5mincont200mmnacl, 980	-.FLIPNASQPESK.-	1331.50	2	4470.09	2.47	0.4	584	8/11	3

control

14-3-3 zeta [Mus musculus] [Mus musculus]					**279.58**	1841387.0	2		
jmraw5minbsafreezthaw,1856-1858	-.GIVDQSQQAYQEAFEISKK.-	2170.37	3	279.58	1.55	0.0	155	7/36	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to 14-3-3 PROTEIN TAU (14-3-3 PROTEIN THETA) [Mus musculus]					**4285.41**	38076709.0	1		
jmraw5minbsareebeads, 3076	-.QDASVHELLGASLAIFTLSQCLPNIFIYSPR.-	3405.91	2	82.22	0.92	0.0	86	3/20	
JMMAGNEGB16D3, 420	-.DQGPAQTLPV.-	1026 13	2	1361.51	1.77	0.1	593	13/18	
jmfag5minigg150mmnacl, 384	- ADPEGQAGR.-	900.92	2	322.52	1.08	0.1	211	5/8	
jmraw5minigg1000mmsd,1308-1310	-.HLAEVACGDDRK.-	1314.45	2	411.44	1.32	0.0	307	9/22	
rawsucrfp_chlfphagigg_Mar04,1290-1292	- ADPEGQAGRER.-	1186.22	2	108.65	0.93	0.1	57	2/5	
jmIgG400rawphag3007,1598-1600	- KLQLIKDHR.-	1151.39	2	777.56	1 83	0.0	408	9/16	
phagrawF60MeOH_dec23, 1852	- MKGDYFWYLAEVAYGNDR.-	2199.43	3	234.09	1.15	0.0	202	9/34	
jm5miniggrawlowionic, 2504	- VFYLKMNGDYFQDLAEVACGDDGK.-	2700.00	2	260.82	0.89	0.1	164	5/23	
jmfagcon5min1000mmnacl_030601180404, 1832	- VELELRSICITVLELLGKYLIANAINPESK.-	3343.97	2	108.96	1.02	0.1	64	4/29	
phagrawFsuc200_dec22, 1469	- DCQEKVELELR.-	1362.54	2	151.02	0.91	0.0	158	7/20	
AJRAWActinIgG_june13, 2820	-.QTIENSQGAYQEAFDISKKEMQPTHLIR.-	3264.62	2	56 60	0.81	0.0	55	7/54	
phagrawFsucchlf_dec23, 1596	-.TVRLLLGSSSFYEDV -	1686.89	2	410.21	1.24	0.2	72	9/28	

control

similar to 14-3-3 PROTEIN TAU (14-3-3 PROTEIN THETA) [Mus musculus]					**175.06**	38076709.0	1		
rawextr_350beadigg2_Mar04, 1106	- SAWMVISSIEKKTDTSNK -	2026.30	3	175.06	1.43	0.0	116	15/68	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1; gamma-aminobu					**4411.17**	6679919 0	3		
AJRAWpellet1_contr_jun13, 335	-.INTHAIDK.-	912.03	2	923.78	1.70	0 2	206	4/7	
jmfagcon5minn600mmnacl, 759	-.VPLGITTVLTMSTIITGVNASMPR.-	2473.98	3	348.24	1.25	0.1	206	4/23	
rawsucrfp_500phagigg_Mar04, 730	-.KGNDSLKTDER.-	1263.34	2	130.86	0.91	0.1	104	3/10	
rawsucrfp_actinphagigg_Mar04, 1218	-.LREKISCTCGLPQPR -	1702.04	2	1534.38	1.51	0.3	243	5/14	
rawsucrfp_actinphagigg_Mar04, 1226	-.LREKISCTCGLPQPR -	1702.04	2	407.41	1.22	0.1	296	5/14	
phagrawFsuc200_dec22, 1289	-.SFIHDTTTDNVMLR.-	1650.84	3	1066.53	1.95	0.0	537	19/52	

control

gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1; gamma-aminobu					**1569.95**	6679919.0	7		
rawextr_1000bead_Mar04, 1222	-.QGSPILRRSSDITK.-	1558.77	3	459.38	1.49	0.1	270	4/13	
rawextr_actinbead_Mar04, 1802	-.LSFPSSNNLSMTFDGRLVK.-	2114.41	3	1022.16	1.64	0.1	512	5/18	
jmbsa450naclorawphag3007, 1242	-.GSYVSMRINTHAIDKYSR.-	2099.36	3	88.41	1.10	0.0	77	7/34	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2 [Mus musculu					**3261.65**	6679901.0	8		
jmfag1mnacl7,5minigg, 1138	- ILDRLLDGYDNR.-	1463.62	2	1069.95	1.33	0.2	362	5/11	3
jmIgG350naclrawphag3007, 1543	-.LVLANIQEDEAKNNITIFTR.-	2303.60	3	1014.39	1.53	0.2	253	1/4	
jmrawgg5min1mnacl,1953-1955	-.WKDERLK.-	975.13	2	565.91	1.22	0.1	433	3/4	
jmbeads150rawphag3007, 1912	-.KSVAHNMTMPNK.-	1358.62	1	611.39	1.66	0.1	343	5/11	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon					**4482.26**	38077221.0		4	
phagrawFsuc400_dec20,1076-1078	-.EPQPDPHEGPSTGTPARSPRGSLHGNPNPISK.-	3316.55	3	2960.38	2.67	0.3	191	6/31	
jmrawigg5min300mmnaclsyringednase, 535	- EPQTNPHEGPSMGTPDRSLHGNLR.-	2628.82	3	428.26	1.29	0.0	317	21/92	
phagrawFsuc1000_dec23, 1933	-.VPPREPQPDPREGLSTGTPTR.-	2288.51	3	419.32	1.15	0.1	327	19/80	
phagrawFsucchfbead_dec23, 1950	-.VPPREPQPDPREGLSTGTPTR -	2288.51	3	674.31	1.42	0.1	393	21/80	

control

similar to gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon					**201.85**	38077221.0		3	
rawextr_1000bead_Mar04, 602	- SPRGSLHGNPNPISK.-	1561.73	3	201.85	0.99	0.0	197	13/56	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Mus musculus (Mouse). GABA-A receptor epsilon-like subunit [D					**26339.31**	28850332.0		15	
jmfag1mnacl5minigg, 360	-.KLIQIK.-	742.97	2	1122.89	1.66	0.0	863	9/10	
JMFAGNACL10_2B21E3, 1924	-.KLIQIKGLPINR.-	1393.75	2	99.50	0.82	0.0	121	3/11	
jmrawigg5min150mmnacl, 128	-.KLIQIK.-	742.97	2	439.92	1.08	0.0	385	7/10	
jmrawigg5min150mmnacl, 142	-.KLIQIK.-	742.97	2	967.49	1.32	0.0	730	9/10	
jmfagfrench5minigg1mnacldtt, 208	- KLIQIK.-	742.97	2	604.47	1.33	0.0	451	7/10	
ajrawphagjun20dpi1MNaCl, 280	-.FGDFPNGIVKNLK.-	1449.68	3	876.41	1.57	0.2	317	7/24	
jmfagfrench5minigg1mnacldtt, 341	-.KLIQIK.-	742.97	2	758.38	1.53	0.1	421	7/10	
jmfag1mnacl5minigg, 360	-.KLIQIK.-	742.97	2	1122.89	1.66	0.0	663	9/10	
jmrawigg5min150mmnacl, 438	- KLIQIK.-	742.97	2	674.70	1.38	0.0	469	4/5	
jmrawigg5min150mmnacl,618-620	-.VMNSQQFFK.-	1129.31	3	212.13	1.43	0.0	146	3/8	
jmIgG250rawphag3007, 818	-.KLIQIK.-	742.97	2	1027.49	1.47	0.1	644	4/5	
jmraw5minigg250mmnaclsyringdnase, 900	-.KLIQIK.-	742.97	2	919.89	1.84	0.0	476	4/5	
jmIgG500rawphag3007, 949	-.KLIQIK.-	742.97	2	660.83	1.28	0.1	402	7/10	
ajrawphagactin20, 996	-.KLIQIK.-	742.97	2	1098.01	2.06	0.0	532	9/10	
jmigg450rawphag3007, 998	-.KLIQIK.-	742.97	2	1063.15	1.66	0.1	484	4/5	
jm5minggrawlowionic, 1224	-.KLIQIK.-	742.97	2	630.06	1.17	0.1	408	7/10	
jmIgG350naclrawphag3007,1689-1691	-.LIQNYIFSTSTNQDEFNK.-	2163.33	3	474.69	1.21	0.1	304	9/34	
JMFAGNACL10_2B21E3, 1924	- KLIQIKGLPINR.-	1393.75	2	99.50	0.82	0.0	121	3/11	
jmfagtimecon2.5min.373.373.2	-.KLIQIK.-	742.97	0	537.94	1.45	0.1	342	7/10	
jmfagtimecon2.5min.111.111.2	-.KLIQIK.-	742.97	0	728.76	1.42	0.1	463	4/5	
jmfag5mincont400_030531151834, 148	-.KLIQIK.-	742.97	2	743.27	1.54	0.0	469	4/5	
jmbeads250rawphag3007, 311	-.KLIQIK.-	742.97	2	465.55	1.32	0.0	351	3/5	
jmfagcon5min1000mmnacl_030601180404, 341	- KLIQIK.-	742.97	2	1236.47	1.73	0.1	640	9/10	
jmbeads350rawphag30072nd, 1018	-.KLIQIK.-	742.97	2	536.56	1.27	0.0	413	7/10	
AJRAWActinContr_june13, 1472	-.FGDFPNGIVKNLK.-	1449.68	2	684.84	0.93	0.2	159	7/24	
jmbeads300rawphag3007, 1656	-.QVGFLDFSSLEIINYAKNK.-	2187.48	3	459.02	1.77	0.0	234	2/9	
jmbeads350rawphag30072nd,2288-2290	-.QVGFLDFSSLEIINYAKNK.-	2187.48	3	921.17	1.67	0.2	284	17/72	
jmfagcont5minbead,2474-2476	-.QVGFLDFSSLEIINYAKNK.-	2187.48	3	2368.87	2.01	0.3	400	7/24	
rawphag2007chfbead2, 266	-.KLIQIK.-	742.97	2	539.55	1.61	0.0	311	9/10	
rawphag2007chlfsol1, 950	-.KLIQIK.-	742.97	2	606.97	1.30	0.0	461	4/5	
phagrawFsuc60MeOH_dec23, 1250	- KQSTENLIKLIEILNNCDYK.-	2380.75	3	273.12	1.26	0.0	214	7/38	
jmrawigg5miniggfreebead, 138	-.KLIQIK.-	742.97	2	703.21	1.38	0.1	449	4/5	
jmrawigg5miniggfreebead, 212	- KLIQIK.-	742.97	2	621.73	1.35	0.1	417	7/10	
jmrawbas5min1mnacl, 1132	-.KLIQIK.-	742.97	2	493.93	1.16	0.0	409	7/10	
jmrawbas5min1mnacl, 1264	-.KLIQIK.-	742.97	2	287.86	1.25	0.0	228	7/10	
phagrawFsuc60MeOH_dec23, 1250	- KQSTENLIKLIEILNNCDYK.-	2380.75	3	273.12	1.26	0.0	214	7/38	
phagrawFsuc450_dec20, 1692	-.FKNYLLENKSNMDNIIIK.-	2198.57	3	771.91	1.49	0.1	478	11/34	
phagrawFActin_dec23, 2322	-.NTSVENFSIVLDHSIFHSIYYLAIK.-	2912.29	2	233.02	1.09	0.1	31	1/8	

control

similar to Mus musculus (Mouse). GABA-A receptor epsilon-like subunit [D					**2579.45**	28850332.0		16	
rawextr_250beadigg_Mar04, 1940	-.QVGFLDFSSLEIINYAKNK.-	2187.48	3	581.47	1.31	0.1	377	5/18	
jmrawbsa5minlowionic, 908	- KLIQIK.-	742.97	2	859.05	1.61	0.0	531	4/5	
jmraw5minbsabeads, 930	- KLIQIK.-	742.97	2	514.48	1.41	0.0	343	7/10	
jmraw5minbsabeads, 934	- KLIQIK.-	742.97	2	624.45	1.64	0.0	375	7/10	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to GABA-B receptor 2 [Mus musculus] mal					**7269.71**	38078306.0		16	
jmfag5minigg400mmnacl, 124	-.EYNSKR.-	796.85	2	104.25	0.88	0.0	103	1/2	1
jmfag5minigg400mmnacl,128-130	-.RSGVGPSK.-	787.89	2	515.06	1.52	0.1	156	4/7	1
JMMAGTube1B16E3, 202	-.TLQRAMETLHASSR.-	1601.81	3	828.48	1.93	0.0	421	19/52	1
jmIgG250rawphag3007,740-742	-.ANACIVLVR.-	959.19	2	818.53	1.89	0.1	300	11/16	
jmrawigg5minbeadsfreezethaw, 1770	-.TWILTVGYTTAFGAMFAKTWRVHAIFK.-	3118.69	2	311.14	1.26	0.1	51	7/52	
jmigg600rawphage3007, 1904	-.RTVERYSMESFDHWSVNVGGAR.-	2584.81	3	523.59	1.87	0.0	256	4/21	
jmraw5minigg600mmnaclsd, 3394	-.TGACLWPAVWAPGNRFLLNASFPISSAFK.-	3123.62	2	443.68	1.03	0.2	48	1/8	
jmfag5mincon250mmnacl,750-752	-.ANACIVLVR.-	959.19	2	449.12	1.80	0.1	224	9/16	
jmfag5mincon300mmnacl, 780	-.ANACIVLVR.-	959.19	2	279.13	1.52	0.0	184	9/16	
rawphag2007chlfsol1, 1606	-.HRYDPLGSASCFCPR.-	1709.94	2	266.06	1.23	0.1	147	5/14	
phagrawFsucchlf_dec23, 1816	-.TALWGMEQMWGDAGYR.-	1873.11	2	259.41	1.00	0.1	98	4/15	1
jmldlactinrawphag3007,848-850	-.ANACIVLVR.-	959.19	2	553.26	1.97	0.0	261	5/8	
jmldl450naclrawphag3007, 1362	-.TSTSVTSVNQASTSRLEGLQSENHR.-	2690.82	3	269.40	1.31	0.1	179	19/96	
rawsucrfp_450phagigg_Mar04, 1470	-.AMETLHASSRHQR.-	1524.69	2	243.57	1.11	0.0	220	1/3	1
phagrawF450_dec20, 1492	-.VTMGRPDPAGR.-	1157.33	2	175.25	1.18	0.1	102	9/20	
phagrawFsuc200_dec22, 1637	-.RSLLAAMEGYIGVDFEPLSSK.-	2284.62	3	970.38	1.64	0.2	324	19/80	1
phagrawFsucchlf_dec23, 1816	-.TALWGMEQMWGDAGYR.-	1873.11	2	259.41	1.00	0.1	98	4/15	1

control

similar to GABA-B receptor 2 [Mus musculus] uscu					**1646.67**	38078306.0		14	
rawextr_actinbeadigg_Mar04, 1819	-.TVPSDNAVNPAILK.-	1439.64	2	643.90	1.29	0.2	203	5/13	
FPbeads1000_Dec19, 1838	-.IILNAMNETNFFGVTGQVVFRNGER.-	2828.20	3	174.07	0.97	0.0	179	5/32	
rawextr_600bead_Mar04, 1980	-.SLLAAMEGYIGVDFEPLSSK.-	2128.43	2	184.12	1.11	0.1	116	9/38	1
rawextr_actinbead_Mar04, 2362	-.IILGQFDQNMAAK.-	1449.70	2	323.63	1.11	0.0	291	5/12	
jmraw5minbsabeads,944-946	-.GAKGDLARR.-	944.08	3	320.96	1.69	0.1	155	11/32	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
GAD_MOUSE Gamma-aminobutyric-acid receptor delta subunit precursor (GABA(A) rec					**3659.92**	120792.0	7		
jmraw5minigg500mmnacisd, 1318	- VSLGITTVLTMTTLMVSARSSLPR.-	2536.05	3	785.28	1.82	0.0	407	21/92	2
jmigg600rawphagg3007, 1904	- LSYNHTNETLGLDSR.-	1720.82	2	768.14	1.38	0.2	211	9/28	2
jmfagtimecont10min, 844	- PGGPGGIR.-	710.81	2	140.47	0.93	0.0	147	3/7	2
jmfagtimecont10min_030601202502, 1316	- LSYNHTNETLGLDSR -	1720.82	3	907.88	1.54	0.1	285	17/56	2
rawsucrtp_150phagigg_Mar04, 1367	- QGRVPGNLMGSYRSVEVEAK.-	2178.46	3	687.23	1.61	0.1	387	9/38	1
phagrawF600_dec20, 1506	- AVFPAAFAAVNIIYWAAYTM -	2191.58	3	370.92	1.61	0.0	216	9/38	1

control

GAD_MOUSE Gamma-aminobutyric-acid receptor delta subunit precursor (GABA(A) rec					**1578.20**	120792.0	6		
rawextr_1000bead_Mar04, 942	- PGGPGGIR.-	710.81	2	150.85	0.93	0.0	153	4/7	2
rawextr_actinbead_Mar04, 1136	- SRLKPIDADTIDIYAR.-	1848.09	2	379.59	1.22	0.1	284	11/30	2
rawextr_700bead_Mar04, 1199	- MDVLGWLLLPLLLLCTQPHHGAR -	2598.17	3	466.92	1.55	0.1	275	19/88	2
rawextr_600bead_Mar04, 1838	-.LWLPDTFIVNAKSAWFHDVTVENK.-	2832.21	3	580.85	1.87	0.1	202	17/92	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Grb10 interacting GYF protein 1 [Mus musculus] us					**7213.70**	33943105.0	7		
rawphag2007chlfsol3, 1289	-.VQLGGLGSAPLNQWVSEAGPLWGGPDK.-	2735.05	3	2772.51	1.91	0.3	526	3/13	1
jmfag5minigg600mmnacl, 456	-.EHGERRR.-	940.00	2	360.46	1.18	0.0	304	2/3	1
jmrawigg5min450mmnaclsd,558-560	-.HSTAATALPLSHGAAR.-	1561.73	3	634.82	1.90	0.0	318	19/60	1
ajrawphagjun20dp1MNaCl, 764	-.VGGGNSHLR.-	896.98	1	266.94	1.25	0.0	192	7/16	1
jmrawigg5minbeadsfreazethaw, 970	-.LMGKGAGPPLPATSR.-	1453.74	2	518.88	1.36	0.1	242	3/7	1
jmbeads150rawphag3007, 992	-.GRGDSCFYQRSIEEGDGAFGR.-	2308.43	3	398.92	1.41	0.1	214	3/16	1
jmfagtimecont0min_030601230741, 1178	-.RQEEEELFRR.-	1392.50	3	209.01	1.04	0.1	168	1/4	1
jmbeads150rawphag3007, 1398	-.RGCDEGFQPLGEVIK.-	1648.87	2	515.59	1.26	0.1	236	5/14	1
rawphag2007chlfsol3, 492	-.KTEEEEK.-	892.93	2	692.95	1.43	0.2	171	7/12	1
RawPhag2007EtBeadsdigest_030718152503, 2894	-.QLHKQAAPR.-	1049.21	2	504.41	1.34	0.1	172	5/16	1
jmrawigg5miniggfreebead, 298	-.KTEEEEK.-	892.93	2	213.84	1.07	0.1	150	7/12	1
phagrawF400_dec20, 1098	-.TLLELQMESERQLHK.-	1856.14	2	125.37	1.02	0.0	120	1/4	1

control

Grb10 interacting GYF protein 1 [Mus musculus] 857					**618.28**	33943105.0	13		
rawextr_700bead_Mar04, 695	-.TEEEEKLLKLLQGIPR.-	1897.21	3	510.57	1.36	0.1	349	17/60	
rawextr_actinbeadigg_Mar04, 1877	-.ELPPAEGDELRALSLSPR.-	1951.17	2	107.71	0.78	0.0	135	9/34	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
LCP2_MOUSE Lymphocyte cytosolic protein 2 (SH2 domain-containing leucocyte pr					5760.77	10720066.0	2		
jmfag5minigg300mmnacl, 2140	- NHSPLSPPHPNHEEPSRSGNNKTAK.-	2733.90	3	924.58	2.08	0.1	342	1/4	1
jmfag1mnacl5minigg, 2244	-.GKEDFLSVSDIIDYFR.-	1905.10	2	4401.99	1.95	0.4	515	7/15	1
rawphag2007chlfsol3, 1769	-.TAKLPAPSIDR.-	1169.36	2	434.19	1.02	0.1	366	1/2	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Gprin1 protein [Mus musculus] el SH2-containing pr					**3461.17**	34784265.0	20		
phagrawF350_dec20, 768	-.SIGSLPEREPSASTSQK.-	1774.91	3	1423.75	1.72	0.2	313	17/64	1
phagrawFsuc200_dec22, 1369	-.AEGIPELQASEKGNPVNSTRVDTGATGSTEPK.-	3242.46	3	376.69	1.47	0.1	104	17/124	1
rawsucrtp_1000phagigg_Mar04, 1606	-.TVPTSSGKTALVSPGKVDLMTSER.-	2462.81	3	672.53	1.37	0.2	242	9/46	1
phagrawFsuc400_dec20,2194-2196	-.SLGTWGSLSAAKAEVTEGKGDPQPWK.-	2701.97	3	297.52	1.71	0.0	172	9/50	1
phagrawF350_dec20, 2422	-.GMTWEVYGASMEVEVLGMAIQK -	2430.85	3	529.21	1.36	0.0	376	5/21	1
phagrawF600_dec20, 2744	-.SVATGPMTPQAAAPPAVPPVFPEVRVR.-	2744.21	2	161.47	1.12	0.1	69	9/52	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
JC7278 adaptor protein containing PH and SH2 domains - mouse					**13076.82**	11292017.0		10	
jmfagfrench20miniggl mnacldtt, 600	- KGFWLR.-	806.98	2	220.17	1.12	0.1	169	7/10	1
jmrawgg5min450mmnacisd, 838	- VELVDIQR -	972.12	2	132.08	0.93	0.1	40	3/7	2
jmIgG400rawphag3007, 1686	- VLGSAADTMEPEPAVTSVTSALK.-	2275.56	3	1061.86	1.78	0.1	522	23/88	2
jmfag5miniggbead_030528200105, 1925	- QSETRPGECVLTFNFQGKGK.-	2227.49	2	937.79	1.10	0.3	160	5/19	
jmfagtimecon7 5min 534 534.3	- SSPEPDGGATPK.-	1143.19	0	359.80	1.23	0.0	292	17/44	2
jmbeadsactinrawphag3007, 1689	- PPETTTAVGAVVTAPHGRAR.-	1989.23	3	162.03	1.27	0.1	64	11/76	2
jmbeads400rawphag3007, 1746	- QFCELHAQVAAVDFAHK.-	1915.17	2	151.80	0.98	0.1	95	7/32	2
rawsucrfp_chifphagigg_Mar04, 1150	- RSSPEPDGGATPK.-	1299.37	3	384.03	1.36	0.1	209	5/16	2
rawphag2007chfbead3, 1217	- VLGSAADTMEPEPAVTSVTSALK.-	2275.56	3	705.32	2.46	0.0	281	19/88	2
jmldl300nacirawphag3007, 2110	-.TLAAKVELVDIQR -	1456.71	2	650.97	1.56	0.2	108	3/8	2
jmbsa450nactorawphag3007, 1182	-.VLGSAADTMEPEPAVTSVTSALK.-	2275.56	3	1069.99	2.33	0.1	422	1/4	2
jmraw5minbsabeads, 2220	-.TLAAKVELVDIQR -	1456.71	2	145.23	1.32	0.0	100	1/3	2
rawsucrfp_450phagigg_Mar04,904-906	-.PPETTTAVGAVVTAPHGRAR.-	1989.23	3	363.30	1.90	0.0	189	17/76	2
rawsucrfp_350phagigg_Mar04, 980	-.HFAANFLAVFSEEVR.-	1737.94	3	384.54	1.67	0.1	195	1/4	2
rawsucrfp_1000phagigg_Mar04, 1133	-.HFAANFLAVFSEEVR.-	1737.94	3	1642.02	2.18	0.2	227	5/14	2
rawsucrfp_chifphagigg_Mar04, 1150	-.RSSPEPDGGATPK.-	1299.37	3	384.03	1.36	0.1	209	5/16	2
rawsucrfp_700phagigg_Mar04, 1431	- VLGSAADTMEPEPAVTSVTSALK.-	2275.56	3	916.32	2.44	0.0	376	1/4	2
rawsucrfp_actinphagigg_Mar04, 1510	-.VSIPLSAIIEVRTTMPLEMPEK.-	2455.96	2	181.02	0.99	0.1	86	3/14	2
rawsucrfp_450phagigg_Mar04, 1584	- VLGSAADTMEPEPAVTSVTSALK.-	2275.56	3	1883.74	1.98	0.2	617	13/44	2
phagrawF300_dec20, 1637	-.TLAAKVELVDIQR.-	1456.71	2	94.34	1.11	0.0	83	1/3	2
rawsucrfp_450phagigg_Mar04,1650-1652	-.TLAAKVELVDIQR.-	1456.71	2	1060.74	1.69	0.2	240	11/24	2
phagrawFsuc400_dec20,2234-2236	-.TLAAKVELVDIQR.-	1456.71	2	184.72	1.33	0.0	138	3/8	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
JC7278 adaptor protein containing PH and SH2 domains - mouse					**985.91**	11292017.0		14	
rawextr_60MeOHbeadigg_Mar04, 1022	-.DNPTYDTPDAGTSFSR.-	1744.76	2	99.35	1.19	0.0	83	4/15	2
rawextr_700beadigg_Mar04, 1690	- DNPTYDTPDAGTSFSR.-	1744.76	2	220.37	1.30	0.0	169	4/15	2
FPbeads250_Dec19, 1850	- TATYGHSRSSEDVSAHAATKAR.-	2304.42	3	413.87	1.38	0.0	295	3/14	2
rawextr_450beadigg_Mar04, 2854	-.VELVDIQREGALRFMVADDAASGPGGTAQWQK.-	3417.80	2	117.63	0.84	0.1	59	9/62	2
FPbeads250_Dec19, 3710	-.SSEDVSAHAATKAR.-	1430.51	2	134.69	0.92	0.0	135	7/26	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH2 domain containing 3C; novel SH2-containing protein 3; Cas/HEF1-asso					**5339.27**	7305329.0		27	
jmrawgg5minbeadsfreezethaw, 480	-.HTEGAILYEKK.-	1289.46	2	195.88	0.99	0.1	125	3/10	1
jmfag5miniggl350mmnacl, 541	-.RSITMTDGLTTDK.-	1439.62	3	1783.82	1.64	0.2	780	3/9	1
jmrawgg5min150mmnacl, 1176	-.EKYILDSSPEK.-	1309.45	2	223.94	1.22	0.0	181	2/5	1
jmrawgg5minbeadsyringdnase,1315-1317	-.FDKVLTALSHK.-	1259.48	2	437.49	1.07	0.1	289	9/20	1
jmrawminiggl200mmnaclsyringdnas, 1542	-.TAAELEAAGDYVK.-	1338.45	2	373.43	0.93	0.0	397	5/12	1
jmfag5miniggl250mmnacl, 1892	-.TASPASPSGSKGSHMKR.-	1686.88	2	364.48	1.25	0.0	290	11/32	1
jmfag1mnacl7,5miniggl, 2430	-.EVSETLVQRNGDFLIRDSLTSLGDYVLTCR.-	3401.79	2	90.97	1.05	0.0	63	4/29	1
jmIgG300rawphag3007, 2944	-.FKGLGSLSNLPRSFSLR.-	1880.18	3	299.85	1.15	0.1	212	7/32	
JMFAGNACL10_2B21E3, 3054	- YLEASYGLSQGSSKTASPASPSGSKGSHMK.-	3002.26	2	88.59	0.87	0.1	41	7/58	1
AJRAWpellet1_contr_jun13, 367	- VDCLVAR.-	775.94	2	453.58	1.12	0.2	168	1/2	1
jmfagcont5minbead, 2584	-.VTRSDGCPNSTSLPHPRDSIR.-	2296.51	3	279.37	1.34	0.1	120	3/16	1
RawPhg2007MeEthmeth3digest, 1102	- YHVGSR.-	718.78	2	369.90	1.03	0.0	358	7/10	1
rawphag2007chfbead2, 1410	-.AQKQQAVQKAQEVSR.-	1699.89	2	139.62	1.32	0.1	71	1/4	
phagrawFsuc400_dec20, 2518	-.RSSEPQLCPGNTPK.-	1514.69	2	238.25	0.99	0.0	237	9/26	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PSM/SH2-B delta [Mus musculus]					**3716.12**	15787983.0		7	
JMFAGNACL10_1B21E3, 1438	-.LSIPCSTITDVR.-	1305.53	2	201.68	0.98	0.0	190	9/22	4
jmIgG450rawphag3007_030801205617, 180	-.SWSPWLSWSPWLNWK.-	1961.21	1	33.87	0.72	0.0	47	5/28	
jmrawigg5minbeadsyringdnase, 465	-.LLLRSEGEGGGGSR.-	1388.51	2	219.93	1.11	0.0	187	9/26	5
jmbeads400rawphag3007, 408	-.QPQPQQPK.-	951.06	2	527.71	1.25	0.1	234	4/7	
jmfag5mincont400_030531151834, 612	-.QPQPQQPKRGK.-	1292.47	3	311.62	1.24	0.0	247	13/40	
jmbeadsactinrawphag3007, 1087	-.ALANDGTSPGERWTHR.-	1768.87	3	738.48	1.71	0.0	427	1/3	4
JMFAGNACL10_1B21E3, 1438	-.LSIPCSTITDVR.-	1305.53	2	201.68	0.98	0.0	190	9/22	4
jmbeads300rawphag3007, 1780	-.AAQLVLEGGTGSHGVFLVR.-	1912.18	2	373.33	1.21	0.0	309	1/3	5
phagrawFsuc600_dec20, 1780	-.PMTLPLAPGTSFFTK.-	1608.93	2	235.02	0.99	0.1	202	9/28	4
jmraw5minbsafreezthaw, 1758	-.LSQGAYGGLSDR.-	1224.31	2	224.08	0.83	0.1	50	7/22	4
jmraw5minbsafreezthaw, 1832	-.LSLNEEGQCR.-	1149.26	2	230.66	1.16	0.1	174	7/18	6
phagrawFsuc300_dec20, 2134	-.SEGEGGGGSRLEFFVPPK.-	1851.01	3	218.03	1.62	0.1	105	15/68	5
jmrawbsa5minlowionic, 2312	-.LLLRSEGEGGGGSRLEFFVPPK.-	2346.67	3	200.04	1.00	0.1	170	5/28	5

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PSM/SH2-B delta [Mus musculus]					**1111.86**	15787983.0		6	
rawextr_150bead_Mar04,1023-1025	-.DGAGMIQR.-	847.96	2	461.58	0.96	0.2	222	4/7	4
rawextr_400bead_Mar04, 2326	-.ENTFVVKVEGPSEYILETSDALHVK.-	2806.12	3	650.28	1.57	0.1	337	19/96	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ASH2_MOUSE ASH2-like protein					**2581.56**	32141377.0	6		
jmldlactinrawphag3007,848-850	-.LTVVGEKGYSMVR.-	1439.71	3	171.61	1.66	0.0	87	7/24	1
jmag5mincon500mmnacl, 2128	-.QTPHSEIIFYKNGVNQGVAYR.-	2422.68	2	232.70	1.20	0.1	126	13/40	1
JMFAGNACL5B21E3, 2570	-.MTWPNNIVKTMSK.-	1550.87	2	85.01	0.90	0.0	71	7/24	1
jmIgG150rawphag3007,720-722	-.LTVVGEKGYSMVR.-	1439.71	3	164.65	1.70	0.0	96	5/16	1
jmIgG250rawphag3007,740-742	-.LTVVGEKGYSMVR.-	1439.71	3	144.33	1.32	0.0	88	7/24	1
jmIgG500rawphag3007,1961-1963	-.ARSDPLFSAQR.-	1248.37	2	187.92	1.17	0.1	58	7/20	1
jmfagtimecon2.5min.2086.2086.3	-.QSSAVSASGNLNGGIAAGSSGK.-	1921.02	0	488.89	1.42	0.1	241	19/84	1
jmag5mincon500mmnacl, 2128	-.QTPHSEIIFYKNGVNQGVAYR.-	2422.68	2	232.70	1.20	0.1	126	13/40	1
jmrawigg5miniggfreebead, 2862	-.EMCLSALANLTWQSR.-	1724.00	2	142.04	0.81	0.1	135	1/4	1
rawsucrfp_800phagigg_Mar04, 1068	-.RKQQDGGTTGTTK.-	1378.48	2	209.78	1.02	0.0	204	1/3	1
phagrawF150_dec22, 1192	-.LELDCWAGKPIPGDLYRACLYER.-	2683.10	3	92.71	1.10	0.0	81	13/88	1
phagrawFsuc500_dec20, 1940	-.EMCLSALANLTWQSRTQDEHPK.-	2559.87	3	238.42	1.58	0.1	80	1/6	1
phagrawFsuc300_dec20, 2132	-.SYLYFEEK.-	1079.18	1	190.81	0.78	0.1	214	3/7	1

control

ASH2_MOUSE ASH2-like protein					**165.27**	32141377.0	4		
rawextr_60MeOHbead_Mar04, 492	-.LTVVGEKGYSMVR.-	1439.71	3	165.27	1.63	0.1	45	11/48	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
suppressor of cytokine signaling 1; cytokine inducible SH2-containing p					**3251.05**	6753424.0	6		
jmfag5minigg150mmnacl, 944	- AEPVGTFLVR -	1089 27	2	335.99	1.23	0.0	274	1/2	1
jmrawigg5min400mmnacisd, 130	- RSEPSSSSSSSSPAAPVR -	1776 85	3	248.73	1 23	0.0	200	4/17	1
phagrawFsuc60MeOH_dec23, 1096	- LAKALRELSQTGWYWGSMTVNEAK.-	2741 12	3	224.29	1 07	0.1	183	17/92	
jmbeadst150rawphag3007, 1380	-.NCFFALSVKMASGPTSIR.-	1930 29	2	792.72	1 23	0.2	251	11/34	1
jmfagtimecon10min, 2678	- IQCEGGSFSLQSDPRSTQPVPRFDCVLK.-	3096.49	2	148.93	0.88	0.1	47	7/54	
rawphag2007chfbead2, 126	- IPLNPVLR -	922 15	2	155.15	0.88	0.0	175	4/7	1
ajrawmediapbsnocells, 1884	- PCPAVPAPAPGDTHFRTFRSHSDYR.-	2784 06	3	359.89	1 69	0.1	169	1/6	
phagrawFsucchlfbead_dec23, 1328	-.TSALLDACGFYWGPLSVHGAHERLR.-	2758.11	3	211.46	1.27	0 1	101	5/32	1
phagrawF300_dec20, 1643	- SEPSSSSSSSSPAAPVRPR.-	1873.96	2	94.32	0 90	0.0	103	2/9	1
phagrawF350_dec20, 2738	- ITRTSALLDACGFYWGPLSVHGAHER.-	2859 22	2	455 31	1 09	0.2	111	1/5	1
phagrawFsuc60MeOH_dec23, 1096	-.LAKALRELSQTGWYWGSMTVNEAK.-	2741 12	3	224.29	1.07	0 1	183	17/92	

control

suppressor of cytokine signaling 3; cytokine inducible SH2-containing p					**451.68**	6671758.0	1		
rawextr_1000bead_Mar04, 1990	-.TVNGHLDSYEKVTQLPGPIREFLDQYDAPL.-	3417 77	2	32.58	0.84	0.0	38	7/58	
jmbsa150naclrawphag3007, 595	-.RAYYIYSGGEK.-	1307 44	3	419.10	1.11	0.1	266	13/40	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Shc SH2-domain binding protein 1 [Mus musculus]					**7474.49**	6755508.0	3		
jmrawigg5minbeadsyringdnase, 2669	-.FIQHDSVEGILIIHHGK.-	1944.23	1	70.27	0.82	0.0	77	3/16	
jmfag5minigg150mmnacl,1886-1888	-.QNGQKVIHVVSSTMK.-	1656.93	2	289.07	1.63	0.1	116	9/28	
jmfag5minigg500mmnacl, 1968	-.GDTFVDCTGMDVKISGIK.-	1887.17	2	138.12	1.11	0.0	124	9/34	
jmfag5mincont350, 1624	-.YVFGYQKNSNIQGK.-	1646.83	2	842.47	1.40	0.1	448	6/13	
jmfagtimecont10min_030601202502, 2100	-.NSDVYGAKGAGIEIYPGSK.-	1927.11	3	5733.19	2.25	0.5	409	1/3	
phagrawFchlfbead_dec23, 738	-.EFTVSFLEK.-	1100.25	2	272.76	0.72	0.1	310	9/16	
phagrawFsuc200_dec22, 2617	-.AYQDYILADCKASEVK.-	1818.04	2	128.62	0.99	0.0	124	4/15	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3-binding domain glutamic acid-rich protein like [Mus musculus]					**53456.92**	9910548.0	1		
jmraw5minbsafreezthaw, 2404	-.ENNAVYAFLGLTAPPGSK.-	1850.06	2	8009.31	2.79	0.5	395	13/34	
jmfreebeadsrawphag3007, 1188	-.IQYQLVDISQDNALRDEMR.-	2308.56	3	3660.57	2.33	0.4	345	23/72	
jmfag1mnacl2,5minigg, 1268	-.IQYQLVDISQDNALR.-	1776.97	2	17233.85	3.60	0.5	1765	11/14	
jmfag5minigg150mmnacl, 1298	-.IQYQLVDISQDNALRDEMR.-	2308.56	3	3488.78	2.37	0.4	202	2/9	
JMFAGNACL5B21E3,1334-1336	-.IQYQLVDISQDNALRDEMR.-	2308.56	3	4884.26	2.80	0.4	285	5/18	
jmfag1mnacl7,5minigg, 1338	-.IQYQLVDISQDNALRDEMR.-	2308.56	3	9920.20	3.72	0.5	513	29/72	
jmfag5minigg200mmnacl, 1398	-.VFVATSSGSIAIRKK.-	1564.86	2	753.80	1.35	0.1	347	11/28	2
jmfag5minigg300mmnacl,1536-1538	-.ELDIAGDEDNRKWMR.-	1849.02	2	130.59	1.11	0.0	112	1/4	2
jmrawminigg200mmnaclsyringdnas, 1758	-.IQYQLVDISQDNALRDEMR.-	2308.56	3	2274.35	2.56	0.3	214	5/18	
jmfag5minigg300mmnacl, 2022	-.IQYQLVDISQDNALRDEMR.-	2308.56	3	2135.24	1.97	0.3	187	2/9	
jmrawigg5miniggfreebead, 1232	-.IQYQLVDISQDNALRDEMR.-	2308.56	3	856.79	1.76	0.2	174	2/9	
phagrawF400_dec20, 410	-.EEEGEDGEEGEEGEER.-	1809.65	2	109.18	1.02	0.0	95	4/15	1

control

SH3-binding domain glutamic acid-rich protein [Mus musculus]					**855.61**	20897168.0	2		
rawextr_60MeOHbeadigg_Mar04, 1404	-.NLRMGSLCPLR.-	1260.56	2	395.92	1.09	0.0	361	1/2	
jmbsa500naclrawphag3007, 1078	-.NLRMGSLCPLR.-	1260.56	2	459.69	0.95	0.1	437	9/20	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3 domain protein D19; SH3 domain containing protein D 19 [Mus musculu					7254.12	7657564.0	8		
jmfag1mnacl2.5minigg, 256	-.CRNQTGVFPANYVK.-	1597.82	3	828.79	1.48	0.0	555	19/52	2
jmfag5minigg0bead, 547	-.GELMGRAGMFPK.-	1294.57	3	2089.26	2.21	0.0	934	5/11	2
jmfag1mnacl5mincon, 1184	-.YMLSVPHGIANEDIVSRNPTELSCKR.-	2931.34	3	697.40	1.89	0.2	138	19/100	
jmfag5minigg400mmnacl, 1520	-.PKPGHPLYR.-	1085.25	2	485.45	1.09	0.2	186	7/16	
jmrawigg5minbeadsyringdnase, 451	-.GVASAIPK.-	742.89	2	1315.16	1.73	0.2	401	5/7	2
jmbeadsactinrawphag3007, 202	-.GVASAIPK.-	742.89	2	441.91	1.37	0.0	322	4/7	2
jmfag5mincon250mmnacl, 1382	-.YMLSVPHGIANEDIVSRNPTELSCKR.-	2931.34	3	510.85	1.50	0.1	157	1/5	
jmbeads350rawphag3007znd, 1540	-.VGGAEGTKLDDDFKDMEK.-	1956.12	2	446.94	1.12	0.2	174	9/34	
rawphag2007chfbead3, 170	-.GVASAIPK.-	742.89	2	460.57	1.26	0.1	273	4/7	2

control

SH3 domain protein D19; SH3 domain containing protein D 19 [Mus musculu					939.37	7657564.0	3		
rawextr_200bead_Mar04,1926-1928	-.QSHPVSGLSKAK.-	1289.47	2	209.86	0.92	0.1	102	3/11	
FPbeads350_Dec19, 1339	-.KYMLSVPHGIANEDIVSRNPTELSCK.-	2903.33	3	327.46	1.96	0.0	146	9/50	
jmbsaactinrawphag3007, 1550	-.GRPNDSGHSQK.-	1183.22	1	402.04	0.91	0.2	85	1/4	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3 multiple domains 1; five SH3 domains [Mus musculus]					16536.82	6679801.0	17		
jmrawminigg200mmnaclsyringdnas, 688	-.TGEVSKR.-	776.86	2	73.56	0.86	0.1	51	1/3	
jmIgG150rawphag3007, 796	-.RATPPIPSKPPGGFGK.-	1607.88	3	117.70	1.00	0.0	108	7/30	
jmrawigg5miniggfreebead, 796	-.EGWAPASYLKK.-	1250.43	2	233.00	0.95	0.1	151	7/20	1
jmrawigg5minbeadsfreezathaw, 944	-.GWVPSNYLEK.-	1193.33	2	740.62	1.20	0.2	305	1/2	
jmiggactinrawphag3007, 1518	-.PKVPPPAPPSKPK.-	1340.64	2	123.03	1.03	0.0	117	1/3	
jm5miniggrawlowionic, 1552	-.KGIPVSPVR.-	953.16	2	115.54	0.80	0.1	76	3/8	
jmraw5minigg500mmnaclsd, 1942	-.YLGKEGWAPASYLKK.-	1711.99	2	355.20	1.08	0.1	194	5/14	
JMFAGNACL10_2B21E3, 186	-.KKPNLSR.-	843.01	2	922.64	1.52	0.2	91	2/3	
jmfag5minigg1000mmnacl, 226	-.KPNLSRR.-	871.02	2	403.75	1.28	0.0	315	7/12	
jmfag5minigg200mmnacl, 454	-.TGEVSKR.-	776.86	2	541.55	1.32	0.1	351	3/4	
jmfag1mnacl2.5minigg, 458	-.VPPPAPPSK.-	890.06	2	405.23	1.44	0.1	236	1/2	
JMFAGNACL10_1B21E3, 494	-.RNESLTATDSLR.-	1363.46	3	627.04	1.40	0.1	401	17/44	
jmfag5minigg200mmnacl, 590	-.PEDVNPPK.-	895.98	2	821.56	1.30	0.1	492	9/14	
jmfag5minigg150mmnacl, 632	-.SSSLLKLKAEK.-	1204.44	2	466.70	1.07	0.0	433	11/20	
jmfag1mnacl2.5minigg, 644	-.DDSDINTSKTGEVSK.-	1596.63	3	468.99	1.62	0.0	273	9/28	
jmrawminigg200mmnaclsyringdnas, 688	-.TGEVSKR.-	776.86	2	73.56	0.86	0.1	51	1/3	
jmfag5minigg450mmnacl_030527025134, 992	-.KNLAGPVEIGNIMEISNLLNKK.-	2510.00	3	101.20	0.96	0.0	104	7/44	
jmfag5minigg350mmnacl, 1161	-.RNESLTATDSLR.-	1363.46	2	197.92	0.89	0.0	215	9/22	
jmiggactinrawphag3007, 1518	-.PKVPPPAPPSKPK.-	1340.64	2	123.03	1.03	0.0	117	1/3	
jm5miniggrawlowionic, 1552	-.KGIPVSPVR.-	953.16	2	115.54	0.80	0.1	76	3/8	
JMFAGNACL15B21E3, 1594	-.EGDTGKSSQNEGKSDSLEK.-	1997.02	3	406.97	1.12	0.0	362	19/72	
jmraw5minigg500mmnaclsd, 1942	-.YLGKEGWAPASYLKK.-	1711.99	2	355.20	1.08	0.1	194	5/14	
jmfag5minigg300mmnacl, 2076	-.GWVPSNYLEK.-	1193.33	2	246.49	0.97	0.1	214	4/9	
jmfagtimecon7.5min.984.986.2	-.GIPVSPVR.-	824.99	0	73.22	0.95	0.0	68	3/7	
jmbeads250rawphag3007, 608	-.GSADIIPLTATTPPCVPKK.-	1910.27	3	975.93	1.68	0.1	490	23/72	
jmfagcon5min1000mmnacl_030601180404, 734	-.FFEARPEDVNPPK.-	1546.71	2	374.33	1.10	0.1	312	11/24	
jmfag5mincon250mmnacl, 890	-.PKVPPPAPPSKPK.-	1340.64	3	1713.40	1.88	0.3	258	5/16	
jmbeadsactinrawphag3007, 1005	-.GIPVSPVR.-	824.99	1	900.50	1.22	0.2	279	4/7	
jmfag5mincont150mmnacl, 1467	-.GGQKAEVIDKNSGGWWYVQIGEK.-	2550.81	3	224.03	1.22	0.1	151	15/88	
jmfag5mincon450mmnacl, 1644	-.ALVRLPPHISQCDEVFR.-	1981.31	3	422.38	1.17	0.0	341	1/4	
jmfagtimecont10min_030601202502, 2810	-.DVTGADTNAEPMILEQYVVVSNYK.-	2657.94	3	472.19	1.39	0.1	198	19/92	
rawphag2007chfbead1,1044-1046	-.GIPVSPVR.-	824.99	2	205.77	1.09	0.0	177	4/7	
phagrawFsuc150_dec22, 482	-.EWEGQQATYVTCSAYQK.-	1922.06	2	149.54	0.86	0.0	157	1/4	
phagrawFsuc150_dec22, 770	-.KQENSELSLQAGEVVDVIEK.-	2216.43	3	698.43	1.62	0.1	344	1/4	
phagrawFsuc200_dec22, 1315	-.DPKQRIIPFLPGK.-	1509.82	2	181.31	1.04	0.0	173	1/3	3
phagrawF1000_Dec23, 1624	-.YVTVQPYTSQSK.-	1401.55	2	310.36	0.79	0.2	73	5/22	
phagrawFsuc600_dec20,1874-1876	-.ATPPIPSKPPGGFGK.-	1451.69	2	446.23	1.03	0.0	433	1/2	
phagrawF200_dec22, 1999	-.NLAGPVEIGNIMEISNLLNKKASGDK.-	2840.29	3	990.50	1.67	0.2	355	21/104	
phagrawF1000_Dec23, 2704	-.NLEGWWYIRYLGKEGWAPASYLK.-	2802.18	2	231.75	0.84	0.1	71	7/44	
phagrawFsuc500_dec20, 3666	-.NQSNISFSSSVTISTTCSSSSSSSSLSKNNGDLK.-	3443.61	2	130.94	0.88	0.1	59	4/33	

control

SH3 multiple domains 1; five SH3 domains [Mus musculus]					3726.01	6679801.0	12		
rawextr_450beadigg_Mar04, 648	-.YLGKEGWAPASYLK.-	1583.81	3	518.48	1.56	0.0	325	15/52	
rawextr_400beadigg_Mar04, 966	-.SDSLEKIEK.-	1049.16	2	232.88	1.26	0.0	185	7/16	
FPbeads150_Dec19, 1055	-.NGVRQVAVRPQSVFVSPPPK.-	2163.51	3	449.61	1.31	0.1	216	4/19	
rawextr_1000bead_Mar04, 1716	-.KGIPVSPVR.-	953.16	2	53.20	0.71	0.0	73	5/16	
FPbeads300_Dec19, 1762	-.EAEENPVGACESQGSPLKVK.-	2073.27	3	646.69	1.47	0.0	419	1/4	
rawextr_350beadigg2_Mar04, 1960	-.KQENSELSLQAGEVVDVIEK.-	2216.43	3	540.16	1.34	0.0	400	1/4	
FPbeads350_Dec19, 1999	-.AHFKVGESSEDVALEEETIYENEGFR.-	2987.14	2	181.61	0.87	0.1	112	4/25	
rawextr_900beadigg_Mar04, 2118	-.NQSNISFSSSVTISTTCSSSSSSSSLSKNNGDLK.-	3443.61	2	1103.42	1.18	0.3	85	3/22	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3/ankyrin domain gene 3; Shank3b protein [Mus musculus]					**7273.78**	10946786.0	19		
jmrawigg5min150mmnacl,112-114	- RRAPPPPK -	919.11	2	58.74	0.90	0.0	64	2/7	
JMFAGNACL10_1B21E3, 918	-.AHSPQGEGEIPLHR.-	1528.66	3	702.01	1.82	0.1	307	17/52	
jmraw5minigg600mmnaclsd,938-940	-.RRAPPPPK -	919.11	2	84.40	0.98	0.0	76	5/14	
JMFAGNACL15B21E3, 942	-.AHSPQGEGEIPLHR.-	1528.66	3	829.77	1.95	0.0	426	17/52	
jmrawigg5min350mmnaclsyringednase,1013-1015	-.RAPSTTLTLRSK.-	1331.55	2	179.16	1.04	0.0	167	4/11	
jmraw5minigg500mmnaclsd, 1744	-.LAGPSGLASPRPLQR -	1520.76	2	534.84	1.16	0.2	166	2/7	
AJRAWActinIgG_june13, 1768	-.NGGAHLDFRTRDGLTAVHCATR.-	2369.61	3	309.31	1.27	0.1	218	19/84	
JMFAGNACL5B21E3, 1838	-.GDQPAASPGPTLRSLPHQLLLQR.-	2453.79	3	1360.65	1.72	0.2	270	21/88	
jmbeads600naclrawphage3007, 120	- RRLAGPSGLASPR.-	1338.55	3	176.82	1.22	0.1	119	1/4	
jmbeads350rawphag30072nd, 1572	-.FMDYVQLHSTDKVARLLDK.-	2280.63	3	867.85	1.78	0.0	484	7/24	
phagrawFsuc500_dec20, 1226	-.VAILQKRDHEGFGFVLR.-	1986.31	3	286.23	1.08	0.0	258	1/4	
rawsucrfp_600phagigg_Mar04, 1412	-.NAGALTTLLDLGASPDYKDSR.-	2179.37	2	587.49	1.35	0.2	202	11/40	
phagrawFsuc600_dec20,1594-1596	- RAPSTTLTLRSK.-	1331.55	2	390.80	1.71	0.1	160	4/11	
phagrawF250_dec22, 2565	-.ITPAEISSLFERQGLPGPEKLPGSLR.-	2794.20	3	905.73	1.22	0.2	119	13/100	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3/ankyrin domain gene 3; Shank3b protein [Mus musculus]					**1386.02**	10946786.0	17		
rawextr_actinbead_Mar04, 1092	- GIPRTKSVGSSAASVS.-	1504.67	3	894.27	1.60	0.0	552	1/3	
rawextr_400beadigg_Mar04, 1400	-.GEAVKVLSIGEGGFWEGTVK.-	2064.33	3	274.79	1.18	0.0	230	15/76	
jmbse1000naclrawphag3007,1095-1097	-.LHTKANLK.-	925.11	2	216.96	1.06	0.0	201	1/2	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3 domain-containing adaptor protein METS-I [Mus musculus]					**3280.79**	8131948.0	6		
JMMAGNEGB16D3, 532	-.VGEIIRNVKK.-	1156.40	2	1022.72	1.58	0.1	493	5/9	2
JMMAGNEGB16D3,810-812	-.KIRGIGFGDIFK.-	1351.62	3	1007.49	1.67	0.2	374	4/11	2
jmrawigg5min150mmnacl,1074-1076	-.DDNLPIKR.-	971.09	1	103.28	0.99	0.0	103	5/14	2
jmraw5minigg250mmnaclsyringdnase, 1450	-.LQEEGWLEGELNGRR.-	1786.93	3	458.36	1.51	0.0	290	15/56	2
jmldl1000naclrawphag3007, 1610	-.LRTRTSSSETEEK.-	1524.62	2	165.01	1.01	0.0	161	3/8	2
jmldl150naclrawphag3007, 1770	-.KTEKPLILQPLGSR.-	1580.90	2	377.74	1.04	0.1	325	5/13	1
phagrawF250_dec22, 1323	-.SLLEQKPSKPAAPQVPPK.-	1916.25	2	146.19	0.92	0.1	133	9/34	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3 domain protein 3 [Mus musculus]					**2588.47**	22267440.0	5		
jmfag1mnacl2,5minigg, 234	-.GNLSWLRECLDNR.-	1576.76	3	181.43	1.23	0.0	138	1/4	
jmfag1mnacl5mincon, 1588	-.TGLIPSNYVAEQAESIDNPLHEAAK.-	2668.90	3	125.46	1.51	0.0	78	1/6	
jmldl150naclrawphag3007, 2898	-.MNNSNGNWKSSVRSTNSWNYNGPGDK.-	2916.05	3	365.49	1.32	0.0	272	17/100	
phagrawFsuc150_dec22, 622	-.KQQGTDGARTLSNAEDYLDDEDSD.-	2644.62	3	568.38	1.22	0.2	218	4/23	
rawsucrfp_450phagigg_Mar04, 1394	-.GNLSWLRECLDNR.-	1576.76	2	112.31	1.02	0.1	57	7/24	
phagrawF350_dec20, 2248	-.LGDTALHAAAWKGYADIVQLLLAK.-	2539.96	3	916.51	1.50	0.1	540	1/4	
phagrawFsuc450_dec20, 2976	-.MNNSNGNWKSSVRSTNSWNYNGPGDK.-	2916.05	2	59.70	0.71	0.1	42	7/50	
jmrawigg5min400mmnaclsd, 248	-.LALDMATNAACASLLKK.-	1735.11	3	259.19	1.34	0.1	156	7/32	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3 domain protein 3 [Mus musculus]					**379.53**	22267440.0	2		
rawextr_600bead_Mar04, 1676	-.DIVEVLFTQPNVELNQQNKLGDTALHAAAWK.-	3464.87	3	379.53	1.13	0.1	243	3/20	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3-domain binding protein 5 (BTK-associated) [Mus musculus]					**2587.89**	6755498.0	11		
JMMAGNEGB16D3,1480-1482	-.VLGSTNGGSGR.-	1005.07	1	203.66	0.84	0.1	93	7/20	2
AJRAWActinIgG_june13, 906	- MKQLSLQCSKGR.-	1379.68	3	1129.04	2.12	0.0	518	19/44	2
jmigG500rawphag3007, 2753	-.VLGSTNGGSGRSRSQSSTSLESQALETR.-	2854.00	3	385.30	1.24	0.1	229	7/36	2
jmfag5mincont200mmnacl, 298	-.QLSLQCSK.-	907.07	2	330.48	1.19	0.0	275	4/7	2
jmfag5mincon300mmnacl, 2630	- AINKSKPYFELK.-	1438.70	2	83.01	0.87	0.0	82	5/22	2
rawphag2007chitsol2, 824	- RSNAMGPR.-	889.02	2	114.75	0.85	0.0	111	5/14	2
jmldl300naclrawphag3007, 1028	- DGIIADIKMVQIG.-	1373.65	3	197.07	1.00	0.0	196	13/48	1
phagrawFsuc500_dec20, 2110	- ANNNRVLGSTNGGSGRSR.-	1817.91	2	144.57	1.26	0.1	89	9/34	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH3-domain binding protein 5 (BTK-associated) [Mus musculus]					**163.02**	6755498.0	3		
rawextr_800bead_Mar04, 1412	-.RSNAMGPRGCGVGAEGSIASVENLPVSK -	2745.09	3	163.02	1.41	0.0	95	19/108	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
intersectin (SH3 domain protein 1A); intersection (SH3 domain protein 1					**4571.63**	6754392.0	33		
jmfag5minigg350mmnacl, 515	- SYVKLISGPVRK.-	1347.63	3	345.98	1.18	0.0	300	7/22	1
ajrawphagjun20dpi1MNaCl, 1174	- DSEGSGTAGKTGSLGK.-	1452.51	2	255.57	1.06	0.0	229	3/10	3
jmrawigg5min1mnacl, 1599	- QSRLFHPHQEPAK -	1575.76	3	368.13	1.80	0.0	199	5/16	1
jmfag1mnacl0minigg, 1844	- KRQIGWFPANYVK.-	1607.88	2	106.64	0.79	0.1	97	1/4	3
jmlgG1000naclrawphag3007,1972-1974	- CRLATQRQEIESTNK.-	1777.99	2	320.63	1.38	0.1	76	2/7	2
jmlgG250rawphag3007, 2426	- DGDWWTGTVGDKSGVFPSNYVR -	2444.50	2	113.88	0.87	0.0	121	3/14	2
jmfag5minigg150mmnacl, 2528	- LQKAQSFDVASAPPAAEWAVPQSSRLK.-	2884.24	3	530.09	1.28	0.2	158	17/104	2
jmbeads450naclrawphag3007,1438-1440	-.LATQAPWSTTEKGPLTISAQESVK.-	2544.84	2	136.23	0.94	0.1	41	3/23	2
rawphag2007chfbead2, 362	- CRLATQRQEIESTNK -	1777.99	3	580.33	1.95	0.0	295	2/7	2
rawphag2007chfbead3, 1029	- LQKAQSFDVASAPPAAEWAVPQSSRLK -	2884.24	3	875.59	1.87	0.1	396	11/52	2
RawPhag200780MeBeadsdigest, 1808	- VEGLQAQALYPWRAKK.-	1859.17	2	172.02	0.83	0.1	135	7/30	1
jmldl350naclrawphag3007, 964	- SDVITVLEQQDMWWFGEVQGQK.-	2624.91	3	97.19	1.18	0.0	72	4/21	1
jmldl600naclrawphag3007, 1026	- GQIINVLNKEDPDWWK.-	1956.19	3	237.65	1.29	0.0	176	1/4	3
jmldl300naclrawphag3007, 1926	- YRQLFNSHDKTMSGHLTGPQAR.-	2545.82	2	56.41	0.93	0.0	60	4/21	2
rawsucrfp_450phagigg_Mar04, 1676	- LQKAQSFDVASAPPAAEWAVPQSSR -	2642.91	3	375.28	1.80	0.1	175	3/16	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
intersectin (SH3 domain protein 1A); intersection (SH3 domain protein 1					**1753.84**	6754392.0	16		
rawextr_1000bead_Mar04, 1278	- IAEITHLQQQLQESQQMLGR.-	2352.66	3	495.38	1.63	0.0	296	9/38	2
rawextr_600bead_Mar04, 1564	- HQLEGKLQDIRCR.-	1596.84	2	767.77	1.49	0.2	238	3/5	2
rawextr_1000bead_Mar04, 1764	-.VEGLQAQALYPWR -	1531.74	3	490.70	1.45	0.0	338	17/48	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Mus musculus SrcSH3 binding protein, incomplete sequence					**2564.47**	1928966.0	5		
JMFAGNACL10_1B21E3, 296	-.GAIPWGNDVGPLSSSK.-	1585.74	2	132.47	1.18	0.0	104	1/3	2
jmfagfrench5minigg1mnacldtt, 120	-.RPPPPPPGHK.-	1080.27	3	440.01	1.35	0.0	316	7/18	4
JMFAGNACL10_1B21E3, 296	- GAIPWGNDVGPLSSSK.-	1585.74	2	132.47	1.18	0.0	104	1/3	2
jmlgG500rawphag3007,1113-1115	-.LALPGFSTPR.-	1059.24	2	799.28	1.71	0.2	236	4/9	5
jmraw5minigg250mmnaclsyringdnase,1372-1374	-.GPTGPPSTLPLGTQTSSGSSTLSKKR.-	2543.82	3	802.91	1.95	0.2	168	19/100	4
jmfag1mnacl7,5minigg, 1444	-.KGVFPVSFVHILSD.-	1545.81	2	44.33	0.67	0.0	64	9/26	5
jmfag5mincont350, 2504	-.NAGKGPTGPPSTLPLGTQTSSGSSTLSK.-	2629.86	3	213.01	1.24	0.0	170	17/108	4

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Mus musculus SrcSH3 binding protein, incomplete sequence					**618.36**	1928966.0	6		
rawextr_350beadigg2_Mar04, 1860	-.PVELAPKPQVGELPPK.-	1700.02	2	477.08	1.58	0.1	165	3/10	5
rawextr_350bead_Mar04, 2342	-.ATQCEDLLSQAK.-	1307.46	2	141.29	0.91	0.1	102	3/11	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 [Mus					**5281.06**	6755868.0	6		
jmfag1mnacl7,5minigg, 404	-.KEEEDLAKAIELSLK.-	1716.96	3	505.08	1.63	0.1	235	1/4	
jmfag5minigg300mmnacl, 3746	-.DPHVAMQALTLLGACVSNCGKIFHLEVCSR.-	3214.80	2	72.74	0.67	0.1	21	5/58	
ajrawphagjun20dpi1MNaCl, 618	-.SVIKNKAHPK.-	1122.35	2	451.02	1.42	0.1	149	7/18	
jmfag1mnacl7,5minigg, 404	-.KEEEDLAKAIELSLK.-	1716.96	3	505.08	1.63	0.1	235	1/4	
jmraw5minigg250mmnaclsyringdnase, 622	-.KHSELSELNVK.-	1284.44	3	231.01	1.02	0.0	213	3/10	3
jm5miniggrawlowionic, 2738	-.RVNHKDPHVAMQALTLLGACVSNCGK.-	2764.25	2	198.55	0.89	0.1	144	1/5	
jmfag5minigg300mmnacl, 3746	-.DPHVAMQALTLLGACVSNCGKIFHLEVCSR.-	3214.80	2	72.74	0.67	0.1	21	5/58	
jmfaglimacon7 5min.2818.2918 2	- NLKEQGVTFPAIGSQAAEQAKASPALVAK.-	2926.32	0	244.13	1.09	0.1	99	9/56	1
jmfaglimacon2 5min.324.326.3	- KEEEDLAKAIELSLK.-	1716.96	0	578.23	1.78	0.0	325	2/7	
RawPhag2007EtBeadsdigest_030718152503, 963	-.DFASEVSNVLNKGHPK.-	1742.91	2	283.32	1.19	0.0	218	3/10	1
rawphag2007chfbead1, 1334	-.MPLFATNPFDQDVEK.-	1752.97	3	2139.16	2.06	0.1	839	11/28	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
chromosome X open reading frame 9; likely ortholog of mouse SH3 gene SL					**4538.65**	9506363.0	4		
jmrawigg5min350mmnaclsynngednase, 1185	-.ETHLNELNIMDPQHRAK.-	2047.29	3	390.07	1.10	0.1	266	15/64	2
jmfag1mnacl5mincon, 914	-.GDVIQIIEK.-	1015.19	2	358.74	1.13	0.1	161	1/2	
phagrawF400_dec20, 772	-.ELRETHLNELNIMDPQHR.-	2246.49	3	2236.81	2.08	0.2	791	23/68	2
phagrawF1000_Dec23, 2684	-.EFNLDDNIPEDDSQVPTPEDAGKSGK.-	2747.82	2	1543.04	1.39	0.3	327	7/25	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH32_MOUSE SH3-containing GRB2-like protein 2 (SH3 domain protein 2A) (Endoph					**32216.09**	10720274.0	4		
phagrawFchifbead_dec23, 1161	-.ALYDLEPENEGELAFK.-	1838.99	3	869.57	2.07	0.1	268	17/60	
phagrawF250_dec22,1173-1175	- ALYDLEPENEGELAFK -	1838.99	3	1605.32	1.77	0.1	789	11/30	
phagrawF250_dec22, 1177	-.ALYDLEPENEGELAFK -	1838.99	2	1367.94	2.21	0.1	498	13/30	
phagrawFsuc800_dec23, 1384	- ALYDLEPENEGELAFK -	1838.99	2	1407.77	2.17	0.1	577	13/30	
rawsucrfp_350phagigg_Mar04, 1464	- ALYDLEPENEGELAFK -	1838.99	2	1202.15	2.30	0.1	491	2/5	
phagrawF300_dec20, 1465	- ALYDLEPENEGELAFK -	1838.99	2	1743.76	1.80	0.2	610	13/30	
rawsucrfp_450phagigg_Mar04, 1502	- ALYDLEPENEGELAFK.-	1838.99	2	1286.35	2.68	0.0	475	2/5	
rawsucrfp_450phagigg_Mar04, 1508	- ALYDLEPENEGELAFK -	1838.99	2	1491.32	2.74	0.1	491	2/5	
phagrawFsuc400_dec20, 2004	- ALYDLEPENEGELAFK.-	1838.99	2	2430.52	2.59	0.2	642	13/30	
phagrawFsuc600_dec20, 2006	-.ALYDLEPENEGELAFK.-	1838.99	2	642.01	1.45	0.0	432	11/30	
phagrawFsuc350_dec20, 2026	-.ALYDLEPENEGELAFK.-	1838.99	2	3359.60	2.67	0.3	456	13/30	
phagrawFchif_dec23, 2118	-.ALYDLEPENEGELAFK -	1838.99	2	1452.20	1.78	0.2	366	13/30	
rawsucrfp_450phagigg_Mar04, 2214	- VSEKVGGAEGTK.-	1162.28	2	115.06	0.95	0.0	121	4/11	2
phagrawFsuc450_dec20, 2214	-.ALYDLEPENEGELAFK.-	1838.99	2	1100.94	1.91	0.1	409	2/5	
phagrawFsuc300_dec20, 2224	- ALYDLEPENEGELAFK.-	1838.99	3	1163.94	2.04	0.0	569	1/3	
jmraw5minbsabeads, 2050	- ALYDLEPENEGELAFK.-	1838.99	2	2603.37	2.69	0.2	585	13/30	
jmraw5minbsabeads, 2058	-.ALYDLEPENEGELAFK.-	1838.99	2	2928.65	2.20	0.3	445	2/5	
JMMAGNEGB16D3, 1378	- ALYDLEPENEGELAFK.-	1838.99	2	1241.62	2.14	0.1	357	2/5	
jmfag5minigg450mmnacl_030527025134, 1638	- LDDDFKEMER.-	1298.41	2	250.34	1.19	0.1	140	7/18	2
jmrawgg5minbeadsynngdnase, 1109	-.ALYDLEPENEGELAFK.-	1838.99	2	1103.63	2.35	0.0	469	2/5	
AJRAWActinIgG_june13, 1918	- ALYDLEPENEGELAFK.-	1838.99	2	835.70	2.00	0.0	413	11/30	
AJRAWActinIgG_june13, 3112	- PPGVQMDQPCCRALYDLEPENEGELAFK.-	3151.54	2	67.69	0.85	0.1	40	1/9	
rawphag2007chifsol3, 1215	- ALYDLEPENEGELAFK -	1838.99	2	983.34	1.77	0.1	368	2/5	
jmldl600nacirawphag3007, 1328	-.ATQKVSEKVGGAEGTK.-	1590.76	3	963.30	1.47	0.2	273	3/10	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SH32_MOUSE SH3-containing GRB2-like protein 2 (SH3 domain protein 2A) (Endoph					**1903.27**	10720274.0	6		
rawextr_60MeOHbeadigg_Mar04, 1174	- GPGYPQAEALLAEAMLKFGR.-	2120.46	3	453.19	1.52	0.0	297	17/76	3
FPbeads1000_Dec19, 2158	-.ALYDLEPENEGELAFK.-	1838.99	3	1450.09	1.91	0.0	754	11/30	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PDZ domain containing guanine nucleotide exchange factor (GEF) 1 [Mus					**14181.01**	38076580.0	32		
jmfag5minigg200mmnacl, 258	-.IALHCR.-	712.89	2	292.85	1.09	0.0	260	7/10	2
JMMAGNEGB16D3, 766	-.DCLEKDPIDR.-	1204.34	2	155.55	1.13	0.0	120	1/2	
jmfag1mnacl5mincon, 1424	-.YRNVLSGQNLQPPVIPLFPVIK -	2493.98	3	580.99	1.59	0.1	239	19/84	1
jmfag1mnacl0minigg, 1560	-.ELCAVMVFAVVER.-	1466.80	2	413.39	1.21	0.1	240	5/12	
JMMAGTube1B16E3, 1862	-.LPLVIKLPENQEETEPSCLDEK.-	2525.86	2	106.59	1.09	0.0	90	5/21	
JMFAGNACL5B21E3, 2340	-.KLLEWFNDPSLRDK.-	1762.00	2	1050.40	1.81	0.2	122	5/13	
jmfag5minigg200mmnacl, 258	-.IALHCR.-	712.89	2	292.85	1.09	0.0	260	7/10	2
jmrawgg5minbeadsfreezethaw, 620	-.DITNPNDNR.-	1059.07	2	463.96	1.35	0.1	267	9/16	
jmrawgg5minbeadsyringdnase, 807	-.TTWEKLPNK.-	1117.28	2	1330.57	1.83	0.1	508	3/4	1
jm5miniggrawlowionic, 1310	-.KSKANTVGGR.-	1018.15	2	384.38	1.07	0.0	336	1/2	1
jmfag1mnacl0minigg, 1560	-.ELCAVMVFAVVER.-	1466.80	2	413.39	1.21	0.1	240	5/12	
jmIgG350nacirawphag3007, 2267	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	302.66	1.09	0.1	106	5/19	1
jmfagtimecon2.5min.1440.1440 2	-.DLTFLHEGNDSK.-	1376.45	0	159.99	1.05	0.1	62	4/11	1
jmfagcon5minn600mmnacl, 241	-.EYMKGVMRTK.-	1243.53	3	319.61	1.58	0.1	139	13/36	
AJRAWSoluteContr_june13, 306	-.IALHCRECK.-	1073.32	2	186.71	0.85	0.1	125	7/16	2
jmbeads1000nacirawphag3007,336-338	-.EVVIQAIR.-	928.11	2	910.62	1.64	0.1	519	6/7	1
jmbeads400rawphag3007, 590	-.DIVRDCLEK.-	1091.27	2	340.85	1.30	0.0	258	9/16	
jmfag1mnacl5mincon, 1424	-.YRNVLSGQNLQPPVIPLFPVIK.-	2493.98	3	580.99	1.59	0.1	239	19/84	1
jmfagcont5minbead,2286-2288	- VDGLVNFEKLR.-	1290.49	2	471.81	1.25	0.1	174	7/20	2
rawsucrfp_chifphagigg_Mar04,2616-2618	- SSIVSNSSFDSVPVSLHDER.-	2163.29	2	233.58	1.53	0.0	148	5/19	1
jmldl600nacirawphag3007, 1480	- SSIVSNSSFDSVPVSLHDERRQR.-	2603.79	3	422.00	1.45	0.0	290	9/44	1
jmldl600nacirawphag3007, 2002	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	259.52	1.06	0.1	138	9/38	1
ajrawmediapbsnocells, 1962	-.EAPLPFILLQGSEKGFGIFVDSVDSCSK.-	2914.32	3	590.68	1.79	0.1	212	19/108	1
phagrawF600_dec20, 627	-.ESLEQAQSR.-	1048.09	2	388.01	1.10	0.2	100	5/16	1
phagrawFsuc800_dec23, 1298	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	3	421.10	1.56	0.0	263	1/4	1
phagrawFsuc200_dec22, 1369	- SSIVSNSSFDSVPVSLHDER.-	2163.29	2	267.15	1.21	0.1	171	5/19	1
rawsucrfp_250phagigg_Mar04, 1454	-.PTEAPAPGQTPPAAAASRPGSK.-	2060.26	3	905.15	1.62	0.1	462	1/4	1
phagrawF300_dec20, 1481	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	169.18	1.28	0.0	132	9/38	1
rawsucrfp_150phagigg_Mar04,1639-1641	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	578.88	1.63	0.1	163	5/19	1
phagrawFsuc700_dec23, 2111	-.ESLEQAQSRASWASSTGYWGEDSEGDTGTIK.-	3335.41	2	23.76	0.75	0.0	31	7/60	1
rawsucrfp_700phagigg_Mar04, 2128	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	353.76	1.20	0.1	221	6/19	1
phagrawF800_Dec23,2154-2156	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	298.21	1.47	0.1	127	9/38	1
phagrawF400_dec20, 2668	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	300.04	1.35	0.0	222	6/19	1
phagrawFsuc600_dec20, 2716	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	141.37	1.00	0.0	136	5/19	1
phagrawF1000_Dec23, 3848	-.NMAKYRNVLSGQNLQPPVIPLFPVIK.-	2938.53	2	70.47	0.73	0.0	74	4/25	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PDZ domain containing guanine nucleotide exchange factor (GEF) 1 [Mus					**4380.14**	38076580.0	28		
rawextr_1000_beadigg_Mar04, 729	- QNQSRESLEQAQSR.-	1661.72	3	227.32	1.36	0.0	158	15/52	1
rawextr_700bead_Mar04, 1093	-.DIVRDCLEKDPIDR.-	1687.90	2	588.80	1.61	0.1	215	5/13	
rawextr_300bead_Mar04,1226-1228	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	345.55	1.31	0.0	242	6/19	1
rawextr_700bead_Mar04, 1349	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	811.65	1.43	0.2	263	13/38	1
rawextr_900beadigg_Mar04, 1752	- NFNSMFAIISGLNLAPVARLRTTWEK.-	2951.44	2	203.11	0.83	0.1	171	11/50	1
FPbeads1000_Dec19,1890-1892	-.VSQGLQVPAVSLYPSRKK.-	1958.29	3	279.91	1.51	0.1	152	15/68	1
jmbsa150nacirawphag3007, 1351	-.DLPPFGINSPQALKK.-	1625.89	2	335.05	1.24	0.0	269	5/14	1
jmbsa300nacirawphag3007, 1438	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	312.61	1.35	0.0	225	6/19	1
jmbsaactinrawphag3007, 1693	-.NMQKVEEEGEIVMVKEHR.-	2186.50	3	186.59	1.18	0.0	159	3/17	
rawextr_500bead_Mar04, 2036	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	183.54	1.28	0.0	141	5/19	1
FPbeads150_Dec19, 2181	-.EPPPTPPGYVGIPIADFPEGPCHPARK.-	2841.24	3	492.52	1.58	0.1	279	9/52	1
rawextr_400bead_Mar04, 2808	-.IALHCRECKNFNSMFAIISGLNLAPVAR.-	3090.68	2	87.95	0.86	0.0	97	1/6	2
FPbeads500_dec19, 2924	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	167.65	1.06	0.0	158	11/38	1
FPbeads300_Dec19, 3418	-.SSIVSNSSFDSVPVSLHDER.-	2163.29	2	157.88	1.05	0.0	142	11/38	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PDZ-domain protein scribble; Scribble; scribble homolog 1 (Drosophila)				**8342.85**	**20373163.0**	**37**		
jmIgG1000nacirawphag3007, 84	- GSTPYRAGDGGIFISR.-	1654.81	3	215.13	1.24	0.0	159	7/30	5
JMFAGNACL10_1B21E3, 518	- MLKCIPLWRCNR -	1533.98	3	469.28	1.25	0.1	347	7/22	2
jmrawigg5min1mnacl,713-715	-.SLPFALTHLNLK.-	1354.62	2	279.89	1.46	0.1	136	5/11	3
jmfag5minigg bead_030528200105, 773	-.RVSLVGADDLRK.-	1329.53	2	157.59	1.01	0.0	148	4/11	5
jmfag5minigg bead,777-779	-.AQMVLSKSQEGR -	1334.53	3	239.42	1.45	0.0	150	1/4	5
ajrawphag1MNaCl20, 928	- RLVCLDVSENR -	1304.50	3	1231.93	1.64	0.2	408	3/8	3
ajrawphag1MNaCl20, 946	- RLVCLDVSENR.-	1304.50	3	1040.85	1.44	0.2	437	3/8	3
jmIgG400rawphag3007,1152-1154	- LIRKDTPHYK -	1271.49	2	684.21	1.22	0.2	249	1/2	3
ajrawphagjun20dpi1MNaCl, 1158	- HCSLQVVPEEIYR -	1573.80	2	337.48	1.35	0.1	207	5/12	3
jmrawigg5min350mmnaclayringednase, 1259	- DPPPPGMRELCQK -	1581.89	2	135.30	0.91	0.1	92	7/26	4
ajrawphagjun20dpi1MNaCl, 1280	- NEAFVCKPDPSPPSPSEEEKR -	2344.54	3	226.19	1.48	0.1	110	3/16	3
jmraw5minigg250mmnaclsynngdnase, 1584	- VWREAMVEPENAVTITPLR.-	2297.67	3	537.60	1.62	0.0	318	1/4	5
JMMAGNEGB16D3, 2188	- LAEAPSPAPTPSPTPLEDFGLQTSASPGR -	2893.16	3	358.70	1.88	0.1	157	17/112	5
JMFAGNACL15B21E3, 2998	- AGDGGIFISRIAEGGAAHR -	1856.04	2	60.55	0.91	0.0	86	2/9	5
jmfagcon5minn600mmnacl, 293	- AGVRVGDK.-	801.92	2	492.67	1.23	0.0	392	9/14	5
jmbeads400rawphag3007,917-919	- GSTPYKGDDEGIFISR.-	1742.87	2	176.18	1.17	0.0	135	1/3	5
jmbeads150rawphag3007, 1106	- DTPHYKKHFK.-	1301.49	2	199.13	1.27	0.0	140	7/18	3
jmbeads250rawphag3007, 1202	- DNRLAVLPPELAHTAELHVLDVAGNRLR.-	3091.52	2	185.23	0.93	0.1	62	4/27	3
RawPhg2007Etsolutiondigest,679-681	- SLPFALTHLNLK.-	1354.62	2	280.65	1.80	0.0	136	5/11	3
rawphag2007chfbead1, 1158	- SLPFALTHLNLK.-	1354.62	2	198.52	1.19	0.1	117	9/22	3
jmklactinrawphag3007, 882	- AGVRVGDK.-	801.92	2	207.00	1.43	0.0	138	1/2	5
rawsucrfp_1000phagigg_Mar04, 3240	-.GGGLRLPLLQPETPVSLR.-	1904.25	2	188.40	1.02	0.1	101	4/17	5
phagrawFsuc300_dec20, 3570	-.LEQLDLGGNDLEVLPDTLGALPNLR -	2677.00	3	460.95	1.34	0.0	339	19/96	3

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PDZ-domain protein scribble; Scribble; scribble homolog 1 (Drosophila)				**1797.59**	**20373163.0**	**14**		
jmrawigg5minigg freebead, 848	- QRHAACLVRSEK.-	1398.62	3	420.09	1.28	0.1	302	17/44	5
FPbeads250_Dec19, 3260	-.DNRLAVLPPELAHTAELHVLDVAGNR.-	2822.17	2	159.06	1.13	0.1	103	1/5	3
FPbeads450_Dec19, 3518	-.AFAAVPTVHPPENSATQPPTPGPAASPEQLSFR.-	3371.70	2	81.47	0.80	0.1	64	9/64	5
rawextr_actinbead_Mar04, 684	- ELGIQKAPGEK.-	1216.43	2	366.08	1.29	0.0	273	9/20	5
FPbeads250_Dec19, 1636	-.HCSLQVVPEEIYRYSRSLEELLLDANQLR.-	3475.92	2	116.18	1.00	0.1	91	9/56	3
rawextr_60MeOHbead_Mar04, 1648	- NQLSALPPELGNLR.-	1522.73	2	305.42	1.13	0.0	261	5/13	3
jmbsa150nacirawphag3007, 851	-.LPLSGKKFDYR.-	1324.55	2	191.91	1.28	0.0	144	2/5	1
jmbsa250nacirawphag3007, 1239	- NQLSALPPELGNLRR.-	1878.92	2	157.38	1.14	0.0	136	2/7	3

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PDZ and LIM domain 3; actinin alpha 2 associated LIM protein [Mus muscu				**4331.53**	**7948997.0**	**5**		
jmIgG500rawphag3007, 1713	- MPQNVVLPGPAPWGFR -	1767.09	2	382.34	1.45	0.1	236	11/30	
jmfag5minigg200mmnacl, 480	- MPLCDK.-	706.90	2	277.38	0.85	0.2	80	3/5	
JMFAGNACL5B21E3,1446-1448	- QKGYFFVEGELYCETHARAR.-	2405.68	3	1523.48	2.56	0.2	346	6/19	
jmIgG500rawphag3007, 1713	- MPQNVVLPGPAPWGFR.-	1767.09	2	382.34	1.45	0.1	236	11/30	
JMFAGNACL5B21E3, 1844	-.IKAASYQLCLKIDR.-	1622.96	2	193.20	1.00	0.0	175	9/26	
rawsucrfp_450phagigg_Mar04, 1102	-.SVRAPVTKVHGGAGSAQR -	1779.00	3	471.78	1.49	0.1	232	19/68	
phagrawFsuc200_dec22, 1887	- AETRLWSPQVSEDGK.-	1703.84	2	712.44	1.21	0.2	287	5/14	
phagrawFsuc150_dec22, 1902	- MPLCDKCGSGIVGAVVKAR.-	1905.34	2	358.86	1.14	0.1	272	11/36	
phagrawFsuc800_dec23, 3006	-.RQVVSASYNSPIGLYSTSNIQDALHGQLR.-	3176.49	2	29.71	0.85	0.0	24	3/28	

control

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
PDZ domain protein GIPC2; likely ortholog of mouse semaF cytoplasmic d				**3374.15**	**41393579.0**	**3**		
ajrawphagjun20dpi1MNaCl, 460	-.GIEKEVNVYK.-	1179.35	3	593.72	2.03	0.1	128	13/38	
jmfag5minfrench1mnacldttdpi, 878	-.GIEKEVNVYK.-	1179.35	2	161.29	0.94	0.0	171	1/3	
jmfag_20_minfrench1mnacldttdpi, 878	-.GIEKEVNVYK.-	1179.35	2	161.29	0.94	0.0	171	1/3	
jmfagfrench20minigg1mnacldtt, 1422	-.AIEKIDDVLELYMGIR.-	1879.21	3	763.54	1.93	0.2	167	19/60	
jmraw5minigg250mmnaclsynngdnase, 3038	-.DGGVIDSVKTICVGDHIESINGENIVGWR.-	3084.41	2	364.75	0.76	0.2	72	1/7	
RawPhg2007MeEthmeth3digest, 1066	-.RIKDGGVIDSVK.-	1287.49	3	1299.90	1.81	0.2	310	17/44	
phagrawF450_dec20, 2708	- GIEKEVNVYKSEDSLGLTITDNGVGYAFIK.-	3261.63	2	29.66	0.71	0.0	32	3/29	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
DOK1_MOUSE Docking protein 1 (p62(dok)) (Downstream of tyrosine kinase 1)					2854.98	27805460.0	7		
phagrawFsuc700_dac23, 1583	- LTDSKEDPIYDEPEGLAPAPPR -	2411.61	3	306.97	1.10	0.1	165	5/28	2
phagrawFsuc450_dac20, 2084	- MIRLAECVSVVPVTVESPPEPGAVAFR.-	2855.37	3	669.40	1.76	0.2	128	2/13	
phagrawF350_dac20, 2228	- GFSSDTALYSQVQKSGTSGAWDCGLSK.-	2781.99	3	210.77	1.52	0.0	139	7/52	2
JMMAGTube1B16E3, 252	- TKLTDSK -	792.90	2	1473.86	1.63	0.1	756	5/6	2
jmfag5miniggt50mmnact, 2504	- LDTAQRSHLLAADAVSSTAWVQTLCRTAFPK.-	3359.80	2	193.98	1.05	0.1	159	11/60	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Dock8 protein [Mus musculus] ypeptide 9 [Mus muscu					2747.03	37589935.0	5		
phagrawFsuc300_dac20, 1540	-.ILDLLFICVSCFEYKGKQSSDK.-	2537.98	3	597.41	1.51	0.0	393	19/84	
JMMAGNEGB16D3, 826	-.NADQSLIRK.-	1045.18	2	244.30	1.19	0.0	206	1/2	
jmfag5miniggt400mmnacl, 2720	-.QQHFLTGLLFTELAVALDAEGDGISRVQR.-	3186.57	2	101.48	1.00	0.0	89	5/28	
jmfagtimeconf0min_030601230741, 1238	-.ILDLLFICVSCFEYK.-	1807.21	3	551.58	1.42	0.1	174	2/7	
jmbeads350rawphag30072nd, 1524	-.GFVFNLIKHYCSQLSAK.-	1956.30	3	294.95	1.36	0.0	215	7/32	
jmrawgg5miniggfreebead, 232	-.KPEVKVK.-	828.04	2	720.47	1.61	0.1	311	3/4	
rawphag2007chfbead2, 1434	-.HLMICFLWIMK.-	1435.89	2	236.83	0.88	0.0	254	2/5	

control

Dock8 protein [Mus musculus] ulus]					803.58	37589935.0	2		
rawextr_450bead_Mar04,684-686	-.KAVSAIHSLLCSHDLDPRCR.-	2222.58	3	803.58	1.99	0.2	145	9/38	

APPENDIX I – PHOX PROTEINS SUMMATION OF IONS

The summation of peptides from Phox proteins found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
methionine aminopeptidase 2; eIF-2-associated p67; initiation factor 2-					**3670.38**	9789873.0		3	
rawphag2007chfbead1, 1232	-.TYQVKPIRNLNGHSIGPYR.-	2214.52	3	1342.00	2.16	0.1	438	1/4	
jmrawgg5min150mmnacl, 424	-.DATNTGIK.-	819.88	2	740.58	1.06	0.0	685	6/7	
JMFAGNACL10_2B21E3, 1052	-.TAAWRTTSEEKK.-	1408.54	2	191.19	0.91	0.0	204	4/11	
jmfag5minigg500mmnacl, 2178	-.HLLNVINENFGTLAFCR.-	1962.27	3	375.52	1.24	0.1	222	1/4	
jmfag1mnacl2.5minigg, 2908	-.LGESKYLMALKNLCDLGIVDPYPPLCDIK.-	3223.86	2	327.77	1.02	0.2	91	5/28	
AJRAWpellet2_contr_jun13, 730	-.EVVSRGDDY.-	1040.07	2	255.35	1.01	0.0	246	9/16	
jmfag5mincont400_030531151834, 1708	-.YDILLTAVKDATNTGIKCAGIDVR.-	2551.95	3	438.00	1.52	0.1	244	21/92	

control

methionine aminopeptidase 2; eIF-2-associated p67; initiation factor 2-					**1321.51**	9789873.0		12	
rawextr_actinbeadigg_Mar04, 1085	-.HLLNVINENFGTLAFCR.-	1962.27	3	327.42	1.09	0.0	299	17/64	
rawextr_450beadigg_Mar04, 1244	-.EEGTSSTAEEAAKKK.-	1566.65	2	753.62	1.47	0.2	205	5/14	
jmbsa250nacirawphag3007, 1364	-.DDDDEDGDGDADGATGK.-	1668.48	2	240.46	1.10	0.0	219	13/32	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to rat p47 [Mus musculus]					**4254.55**	13386036.0		11	
JMFAGNACL5B21E3, 442	-.SFTGGGYR.-	844.90	2	194.99	0.88	0.0	218	9/14	2
jmfag5minfrench1mnacldttdpi, 1778	-.PEFATTDFILVTSFPSK.-	1901.15	3	534.90	1.37	0.0	374	5/16	2
jmfag_20_minfrench1mnacldttdpi, 1778	-.PEFATTDFILVTSFPSK.-	1901.15	3	534.90	1.37	0.0	374	5/16	2
jmbeads400rawphag3007, 1724	-.LGSLTPEIVSTPSSPEEEDK.-	2116.27	3	569.41	1.02	0.2	283	9/38	2
jmfag5mincont150mmnacl, 2273	-.SILNAAVLIDDSMPTTK.-	1790.07	2	1078.63	1.35	0.2	445	13/32	2
jmfagtimecont0min_030601230741, 2838	-.TKSFTGGGYRLGNSFYK.-	1884.09	2	273.66	1.24	0.1	139	5/16	2
RawPhag200760MeBeadsdigest, 1394	-.EAREHGAVPLNEATR.-	1650.78	3	583.14	1.64	0.0	338	9/28	2
phagrawFsuc1000_dec23, 1113	-.YDGLHIVQPPTGK.-	1425.62	2	484.92	0.97	0.2	137	7/24	2

control

similar to rat p47 [Mus musculus]					**1337.62**	13386036.0		8	
rawextr_450beadigg_Mar04,2234-2236	-.DLQLALAELYEDEMK.-	1782.01	2	474.83	1.38	0.2	109	2/7	2
rawextr_actinbead_Mar04, 2784	-.NGFSLDDGELRPYSDPTNAQFLESVK.-	2901.09	2	862.79	1.30	0.2	257	7/25	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to AP47 protein - mouse [Rattus norvegicus]					**2462.92**	34877759.0		4	
jmraw5minigglowionic, 351	-.GARRALLNAGSSCR.-	1432.64	3	705.22	1.59	0.0	434	4/13	
jmfagfrench20minigg1mnacldtt, 416	-.APPPGTYFR.-	1006.14	2	489.22	1.32	0.1	294	5/8	
jmlggactinrawphag3007,1508-1510	-.AAMSASAVYVLDLKGK.-	1624.93	3	369.55	1.33	0.0	276	17/60	
rawphag2007chfbead3, 2691	-.PSKAAMSASAVYVLDLKGK.-	1937.29	1	184.43	1.03	0.0	179	1/4	
jmldl1000nacirawphag3007, 1456	-.PPISVKFEIPYFTTSGIQV.-	2124.46	3	714.50	1.34	0.2	152	13/72	

control

similar to AP47 protein - mouse [Rattus norvegicus]					**348.11**	34877759.0		3	
rawextr_300bead_Mar04, 1158	-.APPPGTYFRPDWAVGEK.-	1889.10	2	348.11	1.38	0.1	84	7/32	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
P4770					**2923.61**	30704925.0		9	
jmfag5minigg200mmnacl,130-132	-.GNCTFYEKVR.-	1217.38	3	2248.92	1.98	0.0	1130	19/36	
jmfagtimecon2.5min.1478.1478.2	-.VKLTNNEMDDK.-	1307.46	0	85.52	0.86	0.0	91	3/10	2
jmbeads300rawphag3007, 298	-.RLKAESSK.-	919.06	2	342.21	0.83	0.0	408	9/14	2
jmbsaactinrawphag3007, 864	-.IANFSNPIFLYLK.-	1540.83	2	246.95	1.42	0.1	113	3/8	2

control

APPENDIX J – ACTIN SUMMATION OF IONS

The summation of peptides from Actins found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dJ562N20.1.1 (trabeculin alpha (actin binding protein ABP620) (ortholog					**9452.05**	11137614.0		2	
jmrawf5minbsareebeads, 1368	-.KLLPQAEMFEHLSGKLQQFMENK -	2748.22	3	401.12	2.10	0.0	187	15/88	
jmigg450rawphag3007,1228-1230	-.EEVLKSMDAMSSPTK.-	1653.90	3	137.10	1.40	0.0	92	13/56	
jmraw5minigg500mmnaclsd, 1918	-.AGNELLESSAGDDASSLR.-	1792.84	2	132.22	0.94	0.0	136	4/17	
ajrawphagactin20, 2256	-.ARQEQLELTLGR.-	1414.59	2	456.50	1.08	0.1	355	1/2	
jmIgG150rawphag3007, 2634	-.AENMYAQIKEEVR.-	1581.78	2	166.28	0.92	0.1	101	1/4	
jmrawigg5min450mmnaclsd, 758	- EVTSTVLHGK -	1071.21	2	581.58	1.53	0.0	375	1/2	
jmag5mincon500mmnacl, 1120	- LDNFLGEVRDK -	1306.45	3	425.85	1.58	0.0	254	3/8	
jmfag1mnacl5mincon, 2578	-.SEKELENMHKGGSSPETLPSLLK.-	2512.82	3	323.83	1.57	0.0	205	21/88	
AJRAWpellet2_contr_jun13,2939-2941	- DCMQKAQKYQWHVEDLVPWIEDCK -	2994.42	2	210.73	1.05	0.1	102	4/23	
phagrawFsuc1000_dec23, 941	-.WERATEVTVARQR.-	1602.78	2	218.46	0.83	0.1	154	1/3	
phagrawFchlfbead_dec23,1423-1425	-.QLQEELAEHQVPVEKLQKVAR.-	2473.81	3	1747.54	2.24	0.2	333	23/80	
phagrawF350_dec20, 1524	-.SMDAMSSPTKTETVKAQAESNK.-	2342.59	3	456.91	1.55	0.0	276	3/14	
rawsucrfp_600phagigg_Mar04, 1554	-.QRVNSGCVMMENKLEGIGQFHCR -	2638.07	3	868.08	1.85	0.1	359	9/44	
rawsucrfp_250phagigg_Mar04, 1768	-.VTLDPVQLESSLLR -	1570.81	2	438.68	1.07	0.1	282	9/26	
phagrawFchlf_dec23, 3114	-.VNSGCVMMENKLEGIGQFHCR.-	2353.76	2	595.73	1.78	0.1	175	1/4	
rawsucrfp_chlfphagigg_Mar04, 2296	-.EVTSTVLHGKVPLAATAGLNSDEMFQK -	2845.22	3	775.21	1.68	0.0	412	11/52	
AJRAWSoluteContr_june13, 568	- EVTSTVLHGK.-	1071.21	2	378.90	1.43	0.0	263	4/9	
jmldl400nacirawphag3007_030802153313, 1884	-.SSLEATREMVTRFMETADSTTAAVLQGK.-	3032.40	3	372.33	1.32	0.1	257	5/27	
jmldl400firstnacirawphag3007, 2118	-.QRQLEESASHLACFQAAESQLR.-	2503.74	3	765.02	1.24	0.2	343	5/21	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dJ562N20.1.1 (trabeculin alpha (actin binding protein ABP620) (ortholog					**1059.11**	11137614.0		22	
FPbeads600_Dec19, 1550	-.TRYADITVTSSKALR.-	1682.90	2	320.68	1.17	0.1	212	5/14	
jmrawbsa5minlowionic, 882	-.CCRKAALLDQALSNAR.-	1734.04	3	364.14	1.28	0.0	260	4/15	
jmbsa300nacirawphag3007, 1398	-.DASSCQEQLDEFRK.-	1656.76	2	374.29	1.02	0.2	58	5/26	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ADVL_MOUSE Advillin (p92) (Actin-binding protein DOC6)					**5282.27**	14547906.0		13	
jmrawigg5min450mmnaclsd, 452	-.AVEVDQQFDR.-	1207.28	2	232.60	0.90	0.0	250	4/9	
ajrawphag1MNaCl20, 540	-.MSLSSAFR.-	899.05	3	173.48	1.26	0.0	137	5/14	1
jmraw5minigg1000mmsd, 928	-.LVIYEGGTSR.-	1095.23	2	565.28	1.11	0.2	190	4/9	1
jmraw5minigg250mmnaclsyringdnase,1316-1318	-.LVIYEGGTSR.-	1095.23	2	318.03	1.29	0.0	246	4/9	1
jmrawigg5min300mmnaclsyringednase, 1495	-.YYPVEVLLKGQNQELPEDVDPAKK.-	2774.12	2	508.46	1.08	0.2	156	5/23	1
jmfagtimecon7.5min.1894.1894.3	-.SMIKPAVSDEIMDQQQK.-	1949.24	0	331.17	1.63	0.1	154	17/64	1
jmfagtimecont10min_030601202502, 1852	-.YYPVEVLLK.-	1124.35	2	918.44	1.48	0.0	607	3/4	1
jmfag5minigg200mmnacl, 1234	-.GALSTAQEYLVTHPSGR.-	1787.96	2	648.64	1.50	0.2	191	11/32	1
jmfag1mnacl0minigg, 1438	-.TQAEHYLWYGKGSSGDER.-	2085.18	3	243.41	1.16	0.1	167	3/17	1
JMFAGNACL10_2B21E3, 1782	-.GATKVEKQAAMSK.-	1349.58	2	139.25	0.80	0.0	169	1/3	1
JMFAGNACL10_1B21E3, 2464	-.QGIIYKKGGVASGMK.-	1537.85	2	239.70	0.87	0.1	161	2/7	1
jmfag5minigg250mmnacl, 2694	-.DELAASAYRAVEVDQQFDRAPVQVR.-	2835.08	3	963.82	1.53	0.2	282	19/96	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ADVL_MOUSE Advillin (p92) (Actin-binding protein DOC6)					**29.87**	14547906.0		9	
FPbeads600_Dec19, 598	-.GALSTAQEYLVTHPSGR.-	1787.96	2	29.87	0.73	0.0	40	1/8	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
cytoskeletal actin-modulating protein [Mus musculus]				**42725.17**	**17222137.0**	**2**		
jmkdl350naclrawphag3007, 1108	-.ACSAIHAVNLR.-	1155.36	2	4149.64	2.15	0.4	660	13/20	2
jmfagfrench5minigg1mnacldil, 649	- ACSAIHAVNLR -	1155.36	2	518.10	1.51	0.1	262	1/2	2
jmrawigg5min350mmnaclsyringednase, 711	-.ACSAIHAVNLR -	1155.36	2	1209.36	1.82	0.2	383	3/5	2
jmIgG400rawphag3007,1118-1120	- ACSAIHAVNLR.-	1155.36	2	621.11	1.80	0.0	341	11/20	2
jmigg450rawphag3007,1142-1144	-.ACSAIHAVNLR.-	1155.36	2	924.23	1.64	0.1	424	3/5	2
jmIgG350naclrawphag3007, 1151	-.ACSAIHAVNLR.-	1155.36	2	657.13	1.59	0.1	241	1/2	2
jmraw5minigg600mmnaclsd,1252-1254	-.ACSAIHAVNLR.-	1155.36	2	627.46	1.47	0.0	422	11/20	2
jmraw5minigg250mmnaclsyringdnase, 1260	-.ACSAIHAVNLR.-	1155.36	2	1288.87	1.73	0.2	341	11/20	2
jmIggactinrawphag3007,1268-1270	-.ACSAIHAVNLR.-	1155.36	2	908.90	1.59	0.0	568	13/20	2
jmigg600rawphage3007, 1316	-.ACSAIHAVNLR.-	1155.36	2	1236.81	1.56	0.2	303	1/2	2
jmIgG1000naclrawphag3007, 1480	-.ACSAIHAVNLR.-	1155.36	2	450.64	1.13	0.1	369	11/20	2
jmIgG1000naclrawphag3007,1544-1546	-.ACSAIHAVNLR.-	1155.36	2	1162.54	2.02	0.1	443	3/5	2
jmIgG250rawphag3007, 1562	- NQEESIDARAPGGKVR.-	1727.86	3	2392.87	2.04	0.3	210	19/60	1
jmfagtimecon7.5min.718.718.2	- ACSAIHAVNLR.-	1155.36	0	1262.07	1.77	0.2	343	11/20	2
jmfagtimecon7.5min 3158.3158.2	-.FKNWODVLTVDYTR.-	1772.94	0	1173.53	1.36	0.2	261	9/26	2
jmfagcon5minn600mmnacl, 717	- ACSAIHAVNLR.-	1155.36	2	416.82	1.46	0.1	203	9/20	2
AJRAWActinContr_june13, 732	- NQLTSLPSAICK.-	1275.50	2	180.70	1.08	0.0	167	7/22	1
jmfagcon5min1000mmnacl_030601180404, 792	-.CSNEKGYFAVTEK.-	1476.64	2	259.64	1.27	0.0	203	1/3	2
jmbeads500rawphag3007, 814	- ACSAIHAVNLR.-	1155.36	2	1384.77	1.79	0.2	449	3/5	2
jmbeads500rawphag3007, 828	-.ACSAIHAVNLR.-	1155.36	2	531.03	1.59	0.1	252	9/20	2
jmfag5mincon450mmnacl, 898	-.PYDDDAEYMK.-	1247.31	2	281.41	1.15	0.0	236	4/9	2
jmag5mincon500mmnacl, 908	-.TDQMKADLTALFLPR.-	1721.02	3	275.08	1.34	0.0	195	1/4	2
jmbeads150rawphag3007, 1956	-.QLPAMMALQTLHLR.-	1624.01	2	930.92	1.61	0.2	178	4/13	1
jmfagtimecon10min, 3080	-.NTQRTQSNLPTSLEQLSNLSDVDLSCNDLTR.-	3393.64	2	58.55	0.84	0.0	60	7/60	1
jmfag1mnacl5minigg, 262	-.NQEESIDAR.-	1062.07	2	425.91	1.12	0.0	362	5/8	1
JMFAGNACL10_1B21E3, 774	- ACSAIHAVNLR.-	1155.36	2	763.70	1.57	0.1	269	9/20	2
JMFAGNACL15B21E3,806-808	-.ACSAIHAVNLR.-	1155.36	2	989.86	1.65	0.0	600	13/20	2
JMFAGNACL10_1B21E3, 1638	-.PKVELMPGMRLLQSLLDTR.-	2198.68	3	500.23	1.29	0.1	309	17/72	2
rawphag2007chifbead2, 304	-.QLPAMMALQTLHLR.-	1624.01	2	232.75	1.01	0.0	218	9/26	1
rawphag2007chifbead2, 528	-.ACSAIHAVNLR.-	1155.36	2	752.29	1.86	0.1	322	11/20	2
RawPhg2007Etsolutiondigest, 605	-.ACSAIHAVNLR -	1155.36	2	872.54	1.57	0.0	543	13/20	2
rawphag2007chifsol1, 1138	-.ACSAIHAVNLR -	1155.36	2	662.86	1.66	0.1	279	1/2	2
rawphag2007chifbead1, 1176	-.ACSAIHAVNLR.-	1155.36	2	979.88	1.83	0.1	399	3/5	2
rawphag2007chifsol2,1286-1288	-.ACSAIHAVNLR.-	1155.36	2	1384.49	2.11	0.1	446	13/20	2
jmrawbas5min1mnacl,1344-1346	-.ACSAIHAVNLR.-	1155.36	2	335.89	1.44	0.0	233	9/20	2
jmkdl600naclrawphag3007,1098-1100	- ACSAIHAVNLR.-	1155.36	2	567.37	1.63	0.0	329	11/20	2
jmkdl400firstnaclrawphag3007, 1102	-.ACSAIHAVNLR.-	1155.36	2	2177.88	1.91	0.3	259	11/20	2
jmkdl350naclrawphag3007, 1108	- ACSAIHAVNLR.-	1155.36	2	4149.64	2.15	0.4	660	13/20	2
jmkdlchifsolblarawphag3007, 1142	- ACSAIHAVNLR.-	1155.36	2	663.75	1.48	0.2	169	9/20	2
jmkdl500naclrawphag3007, 1199	- ACSAIHAVNLR.-	1155.36	2	532.04	1.26	0.0	422	3/5	2
jmkdl500naclrawphag3007, 1207	- ACSAIHAVNLR.-	1155.36	2	1211.81	1.83	0.2	313	1/2	2
jmkdl400naclrawphag3007_030802153313,1282-1284	-.ACSAIHAVNLR.-	1155.36	2	498.24	1.41	0.0	353	11/20	2
jmkdl1000naclrawphag3007,1310-1312	-.ACSAIHAVNLR.-	1155.36	2	1256.32	1.65	0.2	327	11/20	2
jmkdl150naclrawphag3007,1344-1348	- ACSAIHAVNLR.-	1155.36	2	885.51	1.48	0.1	543	13/20	2

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
cytoskeletal actin-modulating protein [Mus musculus]				**16323.71**	**17222137.0**	**12**		
rawextr_500beadigg_Mar04,782-784	-.ACSAIHAVNLR.-	1155.36	2	1108.66	1.91	0.2	335	11/20	2
rawextr_1000_beadigg_Mar04, 796	-.ACSAIHAVNLR.-	1155.36	2	1096.15	1.82	0.2	238	9/20	2
rawextr_900beadigg_Mar04,804-806	-.ACSAIHAVNLR.-	1155.36	2	495.78	1.42	0.0	348	11/20	2
rawextr_900beadigg_Mar04, 824	-.ACSAIHAVNLR.-	1155.36	2	746.25	1.45	0.1	434	3/5	2
rawextr_450beadigg_Mar04,874-876	-.ACSAIHAVNLR.-	1155.36	2	612.76	1.53	0.0	398	3/5	2
rawextr_250beadigg_Mar04, 892	-.ACSAIHAVNLR.-	1155.36	2	1380.79	1.74	0.2	390	11/20	2
FPbeads150_Dec19, 975	-.KNIKLEPVPLK.-	1279.60	1	97.37	0.88	0.0	110	7/20	2
rawextr_60MeOHbeadigg_Mar04, 982	-.AFTRCFHAWSTFR.-	1630.86	2	320.61	1.32	0.0	218	3/8	2
jmbsa350naclrawphag3007,522-525	-.ACSAIHAVNLR.-	1155.36	2	711.78	1.63	0.1	315	11/20	2
jmbsa400naclrawphag3007_030802135831,580-582	-.ACSAIHAVNLR.-	1155.36	2	1117.69	1.89	0.1	562	13/20	2
jmbsa250naclrawphag3007, 583	-.ACSAIHAVNLR.-	1155.36	2	640.07	1.72	0.1	314	1/2	2
jmbsa350naclrawphag3007, 589	-.ACSAIHAVNLR.-	1155.36	2	1383.93	2.11	0.2	426	3/5	2
jmbsa500naclrawphag3007, 688	-.ACSAIHAVNLR.-	1155.36	2	1758.04	2.02	0.2	338	11/20	2
jmbsa450naclorawphag3007,792-794	-.ACSAIHAVNLR.-	1155.36	2	687.55	1.64	0.0	419	3/5	2
jmbsa300naclrawphag3007,808-810	- ACSAIHAVNLR.-	1155.36	2	1758.61	2.20	0.1	623	13/20	2
jmbsa450naclorawphag3007,816-818	-.ACSAIHAVNLR.-	1155.36	2	852.87	1.85	0.2	208	9/20	2
jmbsa1000naclrawphag3007, 1279	-.ACSAIHAVNLR.-	1155.36	2	645.61	1.25	0.2	255	1/2	2
jmrawbsa5minlowionic, 1148	-.ACSAIHAVNLR.-	1155.36	2	909.17	1.68	0.1	461	3/5	2

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to KIAA0825 protein [Mus musculus] actin				**11085.52**	**38075392.0**	**13**		
jmfag1mnacl5mincon, 1430	-.VILSIERQK.-	1086.31	2	304.07	1.01	0.1	140	9/16
JMFAGNACL5B21E3, 1490	-.NLHSILSSATYVSQR.-	1676.86	3	737.88	1.73	0.1	363	19/56
jmfag5minigg200mmnacl, 1826	-.WNLLLDTLLHSGGLIPRILLKSSK.-	2689.24	3	8238.55	3.16	0.5	429	25/92
jmfag1mnacl5minigg, 1900	-.WNLLLDTLLHSGGLIPRILLKSSK.-	2689.24	3	1524.88	2.08	0.2	314	11/46
jmfag5minigg500mmnacl, 1994	-.GAVHALVSPECSQKERR.-	1868.11	3	280.14	1.16	0.0	225	15/64

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SWI/SNF related, matrix associated, actin dependent regulator of chroma					8344.55	7106417.0	1		
jmraw5minbsarasbeads, 1942	- VESIQRFQNTEAGSPTISTVLKAGGVGLNLCAR -	3418.87	3	514.44	1.95	0.0	324	5/32	
jmrawgg5minbeadsfreezethaw, 440	-.LSEIVR.-	716.85	2	147.86	0.95	0.1	120	3/5	4
jmIggactinrawphag3007, 1232	- DDIDNIAR.-	931.97	2	291.09	1.02	0.1	248	9/14	2
jmkdl250nacirawphag3007, 1432	- PVTTGDEGGLRR -	1258.37	2	199.28	0.77	0.0	252	4/11	2
jmkdl250nacirawphag3007, 1470	-.PAHVAVQMTTDQLK.-	1539.78	2	458.69	1.49	0.0	306	11/28	2
jmIgG250rawphag3007, 1568	- DDIDNIAREVEGK -	1474.56	2	318.60	1.22	0.0	262	3/8	2
jmIgG150rawphag3007, 1810	- DKLLTQGFTNWTKR.-	1708.94	2	521.22	1.19	0.1	236	5/13	1
AJRAWActintgG_june13,1418-1420	- IEYNESMK.-	1014.14	2	388.94	1.14	0.1	258	1/2	2
jmIgG250rawphag3007, 2138	- NHRLISEILSESVVPDVRSVVTTAR.-	2779.16	3	479.59	1.58	0.1	258	5/24	1
jmrawgg5min350mmnaclsyringednase, 659	- LGPTPKTLGSSLENAWGSGRAGPSYSR.-	2748.00	3	220.73	1.24	0.0	168	17/104	
jmfag5minigg600mmnacl, 682	- SSCTLSQLSSVCPKR -	1596.86	3	313.30	1.66	0.0	178	13/56	2
jmIgG500rawphag3007, 1225	- NPNAQQTK.-	900.96	2	168.48	0.78	0.1	183	3/7	2
jmIggactinrawphag3007, 2242	- PCICQVIHSEQPHAK -	1690.97	2	448.34	1.22	0.1	222	9/28	2
jm5miniggrawlowionic, 858	-.VSYKGSPAAR.-	1036.17	2	136.72	0.85	0.1	85	5/18	1
ajrawphagjun20actinDPI, 1430	-.KEVDYSD.-	855.87	2	135.60	0.72	0.1	152	5/12	
jmfagtmecon7.5min.868 868 2	- VSYKGSPAAR.-	1036.17	0	340.41	1.24	0.1	147	4/9	1
jmfag1mnacl5mincon, 952	-.WAPSVVK.-	786.94	2	52.09	0.87	0.0	54	1/2	3
jmfagtmecont10min_030601202502, 1554	- GACIKTGDR.-	921.06	2	180.30	0.90	0.0	196	1/2	4
jmfag5mincont200mmnacl, 46	-.ELYGPDNHLVEWHRMPTTQETDGFQVK -	3229.53	2	69.97	0.70	0.1	70	7/52	
rawsucrfp_500phagigg_Mar04, 1018	- VKEDSKFALTFFASATQR.-	2047.30	3	820.94	1.78	0.0	461	21/68	2
rawsucrfp_700phagigg_Mar04, 1359	- INALMHALIELR.-	1394.71	2	1487.96	1.50	0.3	316	5/11	1
phagrawF350_dec20, 2528	-.SEVHLNFYVYYGPDRIRDSAWLSK.-	2917.23	2	146.59	0.90	0.1	39	3/23	3
phagrawFsuc450_dec20, 3818	LRQICCHTHLLTNGMSSSGPSRSDTPEELR -	3327.72	2	195.94	1.14	0.1	19	7/58	2
rawphag2007chfbead3, 2369	- LRQICCHTHLLTNGMSSSGPSRSDTPEELR.-	3327.72	2	155.25	0.91	0.1	55	4/29	2
phagrawFchlf_dec23, 1522	- AGGVGLNLCARSRVFLMDPAWNPAAEDQCFDR.-	3481.93	3	150.23	1.11	0.0	123	17/124	

control

SWI/SNF related, matrix associated, actin dependent regulator of chromat					1168.60	34785644.0	14		
rawextr_300beadigg_Mar4, 844	- QEVIITK.-	830.99	1	714.62	1.22	0.2	118	1/2	2
rawextr_150beadigg2_Mar04, 1308	-.DSVEENMLKIQNTK.-	1649.85	2	307.30	1.13	0.0	259	9/26	3
rawextr_900beadigg_Mar04, 1600	- ILSSGSDEECAICLDSLTFPVITHCAHVFCK.-	3454.02	2	24.45	0.72	0.0	34	3/31	2
rawextr_200beadigg_Mar04, 1971	- KGMSMMECSEACDTGER.-	1866.13	2	120.23	1.16	0.0	104	7/32	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to actin, gamma, cytoplasmic [Mus musculus]					32046.32	38089775.0	3		
rawsucrfp_60MeOHphagigg_MAr04,361-363	-.AGFAGDDAPR.-	977.01	2	6702.89	2.97	0.3	1092	8/9	13
jmfag1mnacl2,5minigg, 148	-.AGFAGDDAPR.-	977.01	2	8647.26	2.96	0.4	1432	8/9	13
jmfag1mnacl7,5minigg, 1832	-.HQDVMVGMGQKDSYVGDK.-	1995.23	1	92.08	0.98	0.0	89	7/34	
jmrawigg5minbeadsfreezethaw, 486	-.GYSFTTTAKR.-	1132.25	2	208.39	1.06	0.0	197	4/9	
jmIgG150rawphag3007, 822	-.AGFAGDDAPR.-	977.01	2	1206.46	1.49	0.1	677	2/3	13
jmIgG300rawphag3007, 870	-.AGFAGDDAPR.-	977.01	2	1658.37	1.42	0.3	420	5/9	13
jmraw5minigg250mmnaclsyringdnase, 2072	-.LDLAGRVLTDYLMKILTER.-	2221.65	3	207.01	1.13	0.0	159	13/72	
jmfag5mincont350, 434	-.VLTDYLMKILTER.-	1595.93	3	302.92	1.72	0.0	176	5/16	
jmfagtimecont0min_030601230741, 918	-.AGFAGDDAPR.-	977.01	2	2198.65	1.65	0.2	878	7/9	13
jmfagtimecont0min_030601230741, 924	-.AGFAGDDAPR.-	977.01	2	2945.27	2.17	0.2	968	7/9	13
jmfagtimecon10min, 992	-.AGFAGDDAPR.-	977.01	2	2056.46	1.63	0.3	582	2/3	13
jmfagtimecont10min_030601202502, 1008	-.AGFAGDDAPR.-	977.01	2	1547.29	1.62	0.1	792	2/3	13
jmfagtimecont10min_030601202502, 1012	-.AGFAGDDAPR.-	977.01	2	3211.06	1.84	0.3	939	2/3	13
phagrawFchlf_dec23, 3626	-.MEEXIATLFTDNGSSTYKAGFAGDHAPR.-	3001.28	2	285.75	1.15	0.1	60	4/27	
jmrawbas5min1mnacl, 1110	-.AGFAGDDAPR.-	977.01	2	776.47	1.39	0.0	558	11/18	13

control

similar to actin, gamma, cytoplasmic [Mus musculus]					3344.56	38089775.0	5		
rawextr_300beadigg_Mar4, 924	-.GYSFTTTAKR.-	1132.25	2	2311.12	2.16	0.2	564	2/3	
rawextr_250beadigg_Mar04, 1180	-.MQEITIIAPPERK.-	1526.83	2	580.62	1.61	0.1	326	11/24	
FPbeads150_Dec19, 1219	-.VAPEEHLVLLTKVPLSPK -	1971.37	3	452.81	1.35	0.1	306	19/68	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
microtubule-actin crosslinking factor 1 [Mus musculus]					25710.24	25021548.0	5		
jmfag5minigg350mmnacl, 473	-.LQNVQIALDFLKQR.-	1686.98	3	927.78	1.63	0.1	390	4/13	4
jmfag5minigg350mmnacl, 491	- RWTDLLSK.-	1019.18	2	188.43	0.95	0.0	195	3/7	1
jmfag1mnacl0minigg, 498	-.LETVALPLQGLEDLAADRMNR.-	2326.66	3	1030.50	1.55	0.2	324	9/40	1
jmfag5minigg600mmnacl, 672	-.IHQQIIRHKALNEEIINR.-	2226.57	3	668.27	1.84	0.0	357	9/34	1
JMMAGNEGB16D3, 842	-.EALAGLLK.-	814.99	2	981.34	1.95	0.0	494	11/14	2
jmfag5minigg250mmnacl, 900	-.WDTVCGK.-	808.93	2	233.36	0.95	0.0	236	7/12	3
jmfag5miniggbead, 1021	-.DQDGKITRQEFIDGILASK.-	2135.36	3	455.11	1.25	0.1	276	5/24	4
JMMAGTube1B16E3, 1370	-.PSSRAASPTR.-	1030.12	2	233.62	0.87	0.1	241	1/2	4
jmfag1mnacl0minigg, 1396	-.ALERHQGGASR.-	1182.28	2	509.16	1.20	0.2	169	9/20	
jmfag5miniggbead_030528200105, 1431	-.IAEQEHTQEDLQHLR.-	1847.97	2	197.06	1.19	0.1	137	1/4	4
JMFAGNACL5B21E3,1442-1444	-.ALERHQGGASR.-	1182.28	2	1607.35	1.61	0.3	247	11/20	
JMMAGTube1B16E3, 1464	-.ALERHQGGASR.-	1182.28	2	1074.76	1.72	0.2	335	3/5	
jmfag5minigg1000mmnacl, 2028	-.LAELSQRFQQLQLQQQEKESNLK.-	2788.11	3	617.90	1.68	0.0	350	19/88	2
jmfag5minigg400mmnacl, 2284	-.FQNLSCSLDER.-	1312.44	2	329.04	1.24	0.1	165	3/10	1
jmag5minconl500mmnacl, 2374	-.ELEEAVTSALQQETEK.-	1805.92	2	94.47	1.01	0.0	89	4/15	5
jmfag1mnacl7,5minigg, 2768	-.VDEIDAAIQRSQQYEQAADAELAWVAETKR.-	3406.66	2	488.82	0.89	0.2	70	9/58	2
jmfagfrench5minigg1mnackdtt, 559	-.WDTVCK.-	751.88	2	55.77	0.70	0.1	51	1/2	3
jmfagfrench20minigg1mnackdtt, 722	-.DQIIELDQTGNQLK.-	1615.77	3	611.88	1.62	0.0	375	4/13	3
jmrawgg5min350mmnaclsyringednase, 1115	-.LMLLSRGDSGSGSGSK.-	1408.61	2	138.22	0.91	0.1	122	7/28	2
jmfagfrench5minigg1mnackdtt, 1173	-.VAQRIAQLQEALLHCGK.-	1879.22	2	577.85	1.77	0.1	141	9/32	3
jmrawgg5min1mnacl, 1579	-.ILKIGPQLKELNPEEGK.-	1907.24	2	330.11	1.73	0.0	186	5/16	1
jmigG300rawphag3007, 1586	-.RKSVEPTHAPFMEK.-	1657.92	2	349.09	1.32	0.0	246	5/13	3
ajrawphagjun20actinDP1, 1672	-.LLLEECEQRLLK.-	1487.79	2	186.35	1.18	0.1	116	9/22	4
jmraw5minigg500mmnaclsd, 1776	-.FRGALPDDTEALQSLIDTHK.-	2228.45	3	283.24	1.05	0.0	258	4/19	3
ajrawphagjun20dpi1MNaCl, 1886	-.VVKAQIQEQKLLQR.-	1682.01	3	921.45	1.39	0.1	614	19/52	6
jmigg600rawphage3007, 2038	-.IRECISDNKSATVELEK.-	1936.18	2	222.72	1.00	0.1	184	5/16	3
jmfagfrench20minigg1mnackdtt, 2062	-.GEIFSTCGEEQK.-	1328.43	2	285.24	0.98	0.1	215	4/11	1
jmrawgg5min150mmnacl, 2398	-.EQLDTHMELHSQLRAKEEIYNQLLDK.-	3183.54	2	131.61	0.80	0.1	134	1/5	2
jmrawmminigg200mmnaclsyringdnas, 2566	-.GDSGSGSKTEQSVALLEQKWHAVSSK.-	2717.93	3	1081.77	1.74	0.2	320	1/5	2
jmigG250rawphag3007, 2616	-.IQALRFDIEDSEAECR.-	1896.07	1	173.80	1.07	0.0	160	3/10	1
jmrawgg5minbeadsyringdnase, 2889	-.VISSSGSK.-	764.85	1	50.42	0.66	0.0	71	3/7	3
jmrawgg5min150mmnacl, 2924	-.TFQKWLKETEGNVPPAK.-	1974.25	1	982.35	1.06	0.3	163	1/4	2
AJRAWActinIgG_june13,2924-2926	-.FQNLSCSLDER.-	1312.44	2	448.19	1.28	0.1	294	9/20	1
jmrawmminigg200mmnaclsyringdnas, 3136	-.NLQAHYEDFLQDSHDSALFSVADR.-	2779.92	2	41.44	0.81	0.0	40	7/46	4
jmiggactinrawphag3007, 3232	-.TECLIQQYEAVSLLNSERYARLER.-	2886.23	2	57.94	0.92	0.0	51	3/23	1
RawPhag200760MeBeadsdigest, 1718	-.DEKAGLNQNMDAITEELQAK.-	2219.42	3	528.25	1.32	0.2	98	13/76	2
rawphag2007chfbead1, 3732	-.DTQDIVHDLESPGIDPSIIKQQVEAAETIK.-	3291.61	2	179.59	0.89	0.1	39	3/29	3
jmidl400firstnaclrawphag3007, 938	-.KTTTASPR.-	861.97	2	346.22	0.87	0.0	395	9/14	4
jmidl1000naclrawphag3007, 1742	-.NDVLAHQATVATVNK.-	1581.76	2	285.02	1.13	0.0	243	5/14	2
rawsucrfp_200phagigg_Mar04, 113	-.SKMSELQVTLDPVQLESSLLRSK.-	2589.99	3	259.65	1.35	0.0	192	9/44	1
phagrawF500_dec20, 594	-.FMETADSNSASVLQGK.-	1685.84	2	429.37	1.12	0.1	332	11/30	2
rawsucrfp_actinphagigg_Mar04, 726	-.VAEQLRHPASEPNLDLERYQEK.-	2623.96	3	392.79	1.14	0.1	198	17/84	4
phagrawFActin_dec23, 846	-.AREGLDK.-	788.87	2	78.70	0.65	0.0	116	5/12	2
rawsucrfp_350phagigg_Mar04,932-934	-.RKLMALGPIR.-	1155.49	1	391.11	1.46	0.1	236	1/2	2
rawsucrfp_500phagigg_Mar04, 944	-.QLQEELAEHQVPVEK.-	1777.96	3	397.10	1.32	0.0	293	9/28	2
phagrawF300_dec20, 955	-.SQGADKDLAAK.-	1104.20	2	205.11	1.08	0.0	174	9/20	3
rawsucrfp_150phagigg_Mar04,1077-1079	-.QLQEELAEHQVPVEK.-	1777.96	3	218.92	1.25	0.0	170	17/56	2
phagrawFsuc150_dec22, 1206	-.QIEITICKNDECVLEDNSQRTK.-	2580.88	3	526.00	1.69	0.1	225	19/84	4
rawsucrfp_350phagigg_Mar04,1404-1406	-.QSEVESIQEVLRDYR.-	1852.00	3	548.74	2.12	0.0	250	9/28	4
rawsucrfp_800phagigg_Mar04, 1468	-.VIAQLETRQSEVESIQEVLR.-	2328.61	3	322.81	1.20	0.1	118	3/19	4
phagrawF250_dec22, 1489	-.TTTASPRTPGPKR -	1370.54	2	666.47	1.05	0.2	110	1/4	4
phagrawFsuc250_dec22, 1561	-.GALPDDTEALQSLIDTHK.-	1925.09	1	67.95	0.78	0.1	55	7/34	3
phagrawFsuc150_dec22, 1678	-.VAQKELEEAVTSALQQETEKSK.-	2447.68	3	622.67	1.57	0.1	309	3/14	5
phagrawFsuc250_dec22,1717-1719	-.EKDASTCQEQLDEFRK.-	1928.07	2	260.19	1.38	0.0	187	3/10	2
rawsucrfp_350phagigg_Mar04, 1968	-.SKMSELQVTLDPVQLESSLLRSK.-	2589.99	3	437.77	1.65	0.0	255	19/88	1
phagrawF350_dec20, 2052	-.PMTRTELVSISSSEDEGNLR.-	2222.42	2	84.08	0.90	0.0	80	3/19	4
rawsucrfp_chlfphagigg_Mar04, 2106	-.EQLDTHMELHSQLRAK.-	1937.17	2	117.55	1.28	0.0	88	7/30	2
phagrawFsuc300_dec20, 2114	-.DCMQKAQKYQGHVEDLVPWIDECK.-	2865.28	3	788.77	1.43	0.2	268	11/46	2
phagrawFsuc350_dec20, 2190	-.KSLNQPTPPPMPILSQSEAKNPR.-	2531.92	3	345.18	1.44	0.1	199	9/44	3
rawsucrfp_250phagigg_Mar04, 2520	-.ALALDEAVSQSAQFHDKIEPMLETLENLSSR.-	3444.81	2	42.96	0.77	0.1	26	1/10	1
phagrawFsucchlfbead_dec23, 2710	-.IRECISDNKSATVELEK.-	1936.18	2	178.27	0.96	0.0	185	1/4	3
phagrawFsuc500_dec20, 2950	-.SERSGSLSPCPPGDTLPWNLPLHEQKK.-	2975.33	2	54.24	0.80	0.1	14	1/13	2
phagrawFchlf_dec23, 3010	-.HQGGASRQELPALQQNQSDLK.-	2306.48	2	198.30	1.27	0.1	122	9/40	
phagrawFsuc250_dec22, 3085	-.VTAGYTGVKCTNFSSCWSDGKMFNALIHR.-	3195.65	2	170.05	0.80	0.1	44	1/7	4

control

microtubule-actin crosslinking factor 1 [Mus musculus]					6998.58	25021548.0	65		
FPbeads350_Dec19, 515	-.TDRDARQDITLR.-	1460.58	3	469.30	1.62	0.1	256	13/44	4
rawextr_150beadigg2_Mar04, 664	-.LELLLQIANKIQNGALNCEEKLTLAK.-	2882.41	3	217.98	1.76	0.0	110	9/50	4
rawextr_60MeOHbeadigg_Mar04, 1188	-.NCDVQGLEHDMDEINTR.-	1990.12	3	327.12	1.31	0.0	237	15/64	1
rawextr_actinbeadigg_Mar04, 1199	-.LKDCMQKAQK.-	1193.47	2	369.59	1.13	0.0	326	5/9	3
FPbeads400_Dec19,1306-1308	-.MDHVYGLSTVYLNKLK.-	1882.22	2	75.53	1.03	0.0	63	3/10	4
FPbeads150_Dec19, 1561	-.MPPLIPAEVDK.-	1210.47	2	310.85	0.88	0.0	351	11/20	3
rawextr_450baadigg_Mar04, 1736	-.GTALESLIMDITAPDSQAK.-	1962.21	2	56.39	0.89	0.0	56	1/6	2
FPbeads700_Dec19, 1885	-.DQVDPLQVKLQQVNGLGQGLIQSAGK.-	2735.09	3	380.20	1.40	0.1	183	3/20	1
FPbeads250_Dec19, 2664	-.KTYFSELTMELEGKQDVFR.-	2322.52	3	240.56	1.04	0.1	79	1/6	4
jmbsa150naclrawphag3007, 1623	-.ILKIGPQLKELNPEEGK.-	1907.24	2	744.65	1.79	0.1	224	11/32	1
jmraw5minbsareebeads, 2530	-.KPMTRTELVSISSSEDEGNLR.-	2350.59	3	519.26	1.40	0.0	362	11/40	4
jmbsaactinrawphag3007, 678	-.IHQQIIRHKALNEEIINR.-	2226.57	3	818.21	1.63	0.1	411	9/34	1
jmbsa1000naclrawphag3007,1095-1097	-.LQLSKHKEFQK.-	1386.63	3	844.34	1.54	0.1	504	2/5	3
jmraw5minbsafreezthaw, 1304	-.DGHNLISLLEVLSGIK.-	1708.98	3	1624.61	2.20	0.2	440	11/30	4

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Eno1 protein [Mus musculus] ein 2 (Actin-related p					**89548.39**	34784434.0	11		
jmfreebeadsrawphag3007, 844	-.VNQIGSVTESLQACK.-	1577.79	2	3112.55	2.31	0.3	674	15/28	5
jmfreebeadsrawphag3007, 856	-.VNQIGSVTESLQACK.-	1577.79	2	10625.46	3.09	0.5	742	4/7	5
jmfreebeadsrawphag3007,966-968	-.YGKDATNVGDEGGFAPNILENK.-	2310.46	3	6170.95	3.19	0.4	589	25/84	4
jmfreebeadsrawphag3007, 1230	-.DATNVGDEGGFAPNILENK.-	1962.06	2	16704.49	4.24	0.5	1430	7/12	4
jmfreebeadsrawphag3007, 1242	-.DATNVGDEGGFAPNILENK.-	1962.06	2	15635.97	4.13	0.5	1283	11/18	4
jmfreebeadsrawphag3007,1274-1276	-.YITPDQLADLYK.-	1440.62	2	7001.46	3.26	0.4	654	17/22	4
jmfreebeadsrawphag3007, 1406	-.HIADLAGNPEVILPVPAFNVINGGSHAGNK.-	3023.40	3	11011.53	3.62	0.5	1010	35/116	7
jmfreebeadsrawphag3007, 1612	-.LAMQEFMILPVGASSFR.-	1898.28	2	16180.91	3.86	0.6	847	19/32	6
jmfreebeadsrawphag3007, 1858	-.SFVQNYPVVSIEDPFDQDDWGAWQK.-	2972.17	2	3105.07	2.17	0.3	350	13/48	4

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
nexilin; nF actin binding protein [Mus musculus]					**8572.32**	41054994.0	20		
jmfag5mincont350, 448	-.RSGSIQAKNLK.-	1202.39	3	1309.47	1.66	0.1	714	19/40	
jmfag5mincont200mmnacl, 1154	-.RTEEERR.-	976.03	2	300.48	1.27	0.0	224	2/3	
jmbeads300rawphag3007, 1812	-.FEKIGQLSEKEVQK.-	1663.90	2	487.64	1.33	0.0	344	11/26	
jmfag5mincont200mmnacl, 1940	-.EDEEEEEGSIVNGSTTEDEEQTR.-	2613.51	3	761.99	2.07	0.0	348	19/88	
phagrawF150_dec22, 516	-.KSESPFTHK.-	1061.17	3	202.34	1.09	0.1	100	1/4	
phagrawFsuc600_dec20, 1716	-.EDEEEEEGSIVNGSTTEDEEQTR.-	2613.51	3	671.38	1.84	0.1	263	9/44	
phagrawF800_Dec23, 2240	-.EDEEEEEGSIVNGSTTEDEEQTR.-	2613.51	3	1897.97	2.16	0.2	283	5/22	
phagrawF800_Dec23, 2244	-.EDEEEEEGSIVNGSTTEDEEQTR.-	2613.51	3	1698.11	2.28	0.2	416	1/4	
ajrawphag1MNaCl20, 386	-.QAEEEARR.-	989.03	3	378.93	1.09	0.0	349	11/28	
jmfag5minigg600mmnacl, 1476	-.EIDAALQKKR.-	1172.36	2	314.51	1.20	0.1	152	7/18	
jmfag1mnacl5minigg, 1938	-.MQFEQKEIDAALQKK.-	1808.09	1	280.37	1.01	0.1	167	2/7	
jmrawbsa5minlowionic, 1422	-.LEINFEQLLRQK.-	1531.78	2	269.13	1.20	0.1	133	3/11	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
nexilin; nF actin binding protein [Mus musculus]					**1368.75**	41054994.0	9		
FPbeads150_Dec19, 697	-.KSESPFTHK.-	1061.17	3	501.48	1.55	0.0	319	1/2	
rawextr_400beadigg_Mar04, 1236	-.QKMEEERR.-	1106.24	2	434.45	1.21	0.0	354	9/14	
rawextr_350beadigg2_Mar04, 1818	-.CLSLVMDDETEAK.-	1454.65	2	432.82	1.07	0.1	306	11/24	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
SAC2 (supressor of actin mutations 2, homolog)-like [Mus musculus]					**51100.65**	28499084.0	15		
JMMAGTube1B16E3, 264	- LGGLDTR.-	731.82	2	670.31	1.25	0.0	529	3/4	4
jmfag5minggbead,441-443	- AELINIHHLMVELKKHK.-	2054.49	3	882.20	1.86	0.1	261	9/32	2
JMMAGNEGB16D3, 484	- AELINIHHLMVELKKHK.-	2054.49	3	359.04	1.35	0.0	265	19/64	2
jmfag5minigg350mmnacl,495-497	- AELINIHHLMVELKKHK.-	2054.49	3	980.45	1.63	0.2	351	19/64	2
jmfag5minigg600mmnacl, 502	- LMKVQYEEVAEK -	1467.71	3	717.24	1.26	0.1	427	4/11	4
JMMAGTube1B16E3, 502	-.AELINIHHLMVELKKHK.-	2054.49	3	1898.31	1.55	0.3	403	9/32	2
JMFAGNACL5B21E3,504-506	- AELINIHHLMVELKKHK -	2054.49	3	801.19	1.77	0.1	237	17/64	2
JMMAGTube1B16E3, 506	-.AELINIHHLMVELKKHK.-	2054.49	3	807.19	1.74	0.1	287	19/64	2
jmfag5minigg600mmnacl,506-508	- AELINIHHLMVELKKHK.-	2054.49	3	1116.61	2.35	0.1	361	21/64	2
JMFAGNACL10_2B21E3, 508	-.AELINIHHLMVELKKHK.-	2054.49	3	2227.18	1.86	0.3	250	19/64	2
jmfag5minigg150mmnacl,518-520	- AELINIHHLMVELKKHK.-	2054.49	3	3980.17	2.27	0.4	498	11/32	2
jmfag1mnacl2.5minigg,554-556	-.AELINIHHLMVELKKHK.-	2054.49	3	556.65	1.52	0.1	258	9/32	2
jmfag1mnacl7.5minigg,558-560	- AELINIHHLMVELKKHK.-	2054.49	3	352.41	1.50	0.0	222	15/64	2
jmfag5minigg400mmnacl, 576	-.AELINIHHLMVELKKHK.-	2054.49	3	1195.38	1.82	0.2	396	19/64	2
jmfag5minigg400mmnacl, 580	- AELINIHHLMVELKKHK.-	2054.49	3	2216.74	2.07	0.3	323	19/64	2
jmfag5minigbead_030528200105, 603	-.AELINIHHLMVELKKHK.-	2054.49	3	2024.14	2.05	0.3	257	19/64	2
jmfag5minigg1000mmnacl, 606	- AELINIHHLMVELKKHK.-	2054.49	3	278.21	1.33	0.1	177	7/32	2
jmfag5minigg200mmnacl, 606	- AELINIHHLMVELKKHK.-	2054.49	3	882.32	1.55	0.1	471	11/32	2
jmfag5minigg1000mmnacl, 610	- AELINIHHLMVELKKHK.-	2054.49	3	364.46	1.39	0.0	240	17/64	2
JMFAGNACL15B21E3, 628	-.AELINIHHLMVELKKHK.-	2054.49	3	1387.26	1.74	0.2	313	19/64	2
jmfag1mnacl5mincon,632-634	-.AELINIHHLMVELKKHK.-	2054.49	3	1095.66	1.71	0.2	316	19/64	2
jmfag5minigg600mmnacl, 770	-.VLSQPQLRALPAR.-	1449.73	3	695.11	1.46	0.0	469	17/48	2
jmfag5minigg500mmnacl, 972	- AELINIHHLMVELKKHK.-	2054.49	3	565.15	1.24	0.1	429	21/64	2
jmfag5minigg500mmnacl, 978	- AELINIHHLMVELKKHK.-	2054.49	3	517.04	1.50	0.1	216	17/64	2
jmfag1mnacl5minigg, 1036	-.DEYVETLSK.-	1084.16	2	137.32	1.15	0.0	119	3/8	4
jmfag5minigg300mmnacl,1178-1180	- AELINIHHLMVELKKHK.-	2054.49	3	560.25	1.69	0.1	281	5/16	2
jmfag5minigg150mmnacl, 2698	- GKLGELVDGLVVPSALVTAILEAPVTEPR.-	2945.44	2	132.67	0.91	0.1	88	1/7	3
jmfag5minigg150mmnacl, 2912	-.HLESYLADCYDAIAVFLCIHIVLRFR.-	3082.63	2	187.42	1.03	0.1	91	9/50	4
jmrawigg5minbeadsfreezethaw,512-514	- AELINIHHLMVELKKHK.-	2054.49	3	1682.43	2.22	0.2	321	5/16	2
jmrawigg5min150mmnacl, 514	-.AELINIHHLMVELKKHK.-	2054.49	3	488.89	1.45	0.0	336	5/16	2
jmIgG400rawphag3007, 1040	-.AELINIHHLMVELKKHK.-	2054.49	3	770.32	1.58	0.1	449	5/16	2
jmigG350naclrawphag3007,1041-1043	-.AELINIHHLMVELKKHK.-	2054.49	3	542.46	1.61	0.0	329	19/64	2
jm5miniggrawlowionic,1228-1230	-.AELINIHHLMVELKKHK.-	2054.49	3	385.69	1.53	0.1	185	15/64	2
jmfagfrench20minigg1mnacldtt, 1524	-.YAEFSSALVSINQTIPNER.-	2140.34	3	1282.10	1.70	0.2	276	17/72	4
jmrawigg5min1mnacl, 2015	-.RYAEFSSALVSINQTIPNER.-	2296.53	3	513.68	1.53	0.1	231	17/76	4
jmfagtimecon2.5min.604.606.3	-.AELINIHHLMVELKKHK.-	2054.49	0	348.42	1.83	0.1	155	15/64	2
jmfagtimecon7.5min.436.436.3	-.AELINIHHLMVELKKHK.-	2054.49	0	581.45	1.61	0.0	358	5/16	2
jmfagcon5minn600mmnacl, 425	-.AELINIHHLMVELKKHK.-	2054.49	3	274.14	1.35	0.0	198	15/64	2
jmfag5mincont400_030531151834, 466	-.AELINIHHLMVELKKHK.-	2054.49	3	1525.47	1.55	0.3	173	7/32	2
jmbeads400rawphag3007, 468	- AELINIHHLMVELKKHK.-	2054.49	3	810.08	1.69	0.2	216	17/64	2
jmbeads400rawphag3007, 476	-.AELINIHHLMVELKKHK.-	2054.49	3	367.80	1.26	0.1	148	15/64	2
jmfag5mincont150mmnacl,495-497	-.AELINIHHLMVELKKHK.-	2054.49	3	1626.29	1.96	0.2	352	5/16	2
jmfag5mincont350,538-540	-.AELINIHHLMVELKKHK.-	2054.49	3	587.32	1.71	0.1	250	9/32	2
jmfag5mincont200mmnacl,620-622	-.AELINIHHLMVELKKHK.-	2054.49	3	2804.58	2.05	0.3	258	19/64	2
jmfag1mnacl5mincon,632-634	-.AELINIHHLMVELKKHK.-	2054.49	3	1095.66	1.71	0.2	316	19/64	2
jmfag5mincon450mmnacl, 916	-.AELINIHHLMVELK.-	1661.01	3	604.82	1.53	0.0	395	17/52	2
jmfag5mincon250mmnacl,996-998	-.AELINIHHLMVELKKHK.-	2054.49	3	1001.56	1.59	0.2	382	21/64	2
jmfagtimecont0min_030601230741,1056-1058	-.AELINIHHLMVELKKHK.-	2054.49	3	965.68	2.03	0.1	321	19/64	2
jmbeads350rawphag30072nd,1128-1130	-.AELINIHHLMVELKKHK.-	2054.49	3	579.88	1.62	0.0	357	21/64	2
jmfag5mincon300mmnacl,1164-1166	-.AELINIHHLMVELKKHK.-	2054.49	3	1124.06	2.07	0.1	357	19/64	2
jmag5mincon500mmnacl,1200-1202	-.AELINIHHLMVELKKHK.-	2054.49	3	1045.14	1.68	0.2	256	19/64	2
jmfagtimecont10min_030601202502,1224-1226	-.AELINIHHLMVELKKHK.-	2054.49	3	978.78	1.93	0.2	247	17/64	2
ajrawmediapbsnocells,460-462	- AELINIHHLMVELKKHK.-	2054.49	3	506.32	1.59	0.0	309	19/64	2
jmldl1000naclrawphag3007, 1300	-.DDLMGVEDTAK.-	1194.30	2	104.10	0.93	0.0	112	1/4	4
phagrawF350_dec20, 1018	-.KPMTNYQIPQAALLK.-	1717.07	3	397.26	1.69	0.0	213	13/56	4
phagrawFsuc600_dec20, 1574	-.SFTNFRNGTSIIQGALTQLIQLYHR.-	2880.25	3	303.51	1.44	0.1	160	1/6	2
phagrawFsuc150_dec22, 1610	-.PSLRSRNTIFTLGTR.-	1719.97	2	214.68	1.01	0.1	164	2/7	2

control

SAC2 (supressor of actin mutations 2, homolog)-like [Mus musculus]					**214.30**	28499084.0	2		
rawextr_60MeOHbeadlgg_Mar04, 808	-.AELINIHHLMVELKKHK.-	2054.49	3	214.30	1.17	0.0	183	1/4	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ARP1 actin-related protein 1 homolog B [Mus musculus]					**2781.93**	22122615.0	4		
jmbeads150rawphag3007, 1080	-.LLLRKEGADFHTSAEFEVVR.-	2318.62	3	929.24	1.60	0.1	507	6/19	
jmfag5mincont400_030531151834, 1358	-.DQLQTFSEEHPVLLTEAPLNPSK.-	2594.86	3	385.95	1.60	0.0	241	15/88	
phagrawFsuc60MeOH_dec23, 1348	-.EYEEDGSRAIHR.-	1462.51	2	339.18	1.03	0.1	287	1/2	1
rawsucrfp_350phagigg_Mar04, 1524	-.TLFSNIVLSGGSTLFK.-	1684.96	2	765.82	1.41	0.2	314	11/30	2
phagrawFchlf_dec23, 2092	-.EYEEDGSRAIHR.-	1462.51	2	361.75	1.62	0.1	165	9/22	1

control

ARP1 actin-related protein 1 homolog B [Mus musculus]					**374.43**	22122615.0	6		
rawextr_150beadigg2_Mar04, 30	-.TIKERACYLSINPQK.-	1765.07	3	374.43	1.36	0.0	276	1/4	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog				**26207.20**	5031571.0	9		
jmfag5minigg350mmnacl, 355	-.HLWDYTFGPEK -	1393.53	3	2552.49	2.14	0.2	677	17/40	3
jmfag1mnacl0minigg, 874	- RKHMVFLGGAVLADIMK.-	1887.35	3	4293.32	2.36	0.3	644	11/32	3
jmfag1mnacl7.5minigg, 1158	- HLWDYTFGPEK	1393.53	2	740.95	1.32	0.1	383	3/5	3
jmfag5minigg500mmnacl, 1492	- RLDIAGRDITR -	1286.47	2	97.61	0.91	0.0	107	3/10	4
jmfag5minigg250mmnacl, 1560	- DLMVGDEASELR -	1335.47	2	401.41	1.09	0.1	288	5/11	3
jmIgG150rawphag3007, 750	- RLDIAGR -	800.93	2	2323.63	2.72	0.0	842	11/12	4
jmIgG250rawphag3007, 770	- RLDIAGR -	800.93	2	3231.79	2.73	0.2	731	11/12	4
jmIgG350nacIrawphag3007, 855	- RLDIAGR.-	800.93	2	1379.59	2.04	0.1	609	5/6	4
jmbeads300rawphag3007, 127	- RLDIAGR -	800.93	2	1640.30	2.39	0.1	650	5/6	4
jmbeads250rawphag3007, 594	- RLDIAGRDITR.-	1286.47	2	306.19	1.15	0.0	251	1/2	4
jmbeads350rawphag30072nd,932-934	- RLDIAGR -	800.93	2	3830.16	3.03	0.2	997	11/12	4
jmfag5mincon250mmnacl, 1336	- ILLTEPPMNPTK -	1354.64	2	508.70	1.41	0.1	273	1/2	3
AJRAWpellet2_contr_jun13, 1391	-.STTKVGNIEIKDLMVGDEASELR.-	2506.82	3	563.43	1.58	0.1	224	19/88	3
jmfag5mincon300mmnacl, 1920	- SMLEVNYPMENGIVR -	1753.04	2	2137.31	2.49	0.2	501	1/2	4
phagrawFsuc150_dec22, 850	- RLDIAGRDITR -	1286.47	2	549.59	1.20	0.1	421	1/2	4
phagrawFsuc400_dec20, 1858	-.YLIKLLLLR.-	1145.51	1	454.71	1.37	0.0	331	1/2	3
jmraw5minbsafreezthaw, 1966	-.NCKILLTEPPMNPTK -	1700.06	2	423.34	1.82	0.1	192	9/28	3
jmrawgg5miniggfreebead, 200	- QEYQEKGVR -	1137.23	2	772.70	1.32	0.1	532	5/8	2

control

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub				**19800.19**	5031595.0	5		
jmIgG300rawphag3007, 1676	- PYLSAVRATLQAALCLENFSSQVVERHNK -	3246.69	3	132.22	1.12	0.0	116	15/112	2
jm5miniggrawlowionic, 1904	-.ELLLQPVTISR.-	1269.52	2	2028.27	1.61	0.3	465	3/5	3
jmIgG150rawphag3007, 2178	- PVEGYDISFLITNFHTEQMYK.-	2533.84	3	648.45	1.84	0.1	256	17/80	3
jm5miniggrawlowionic, 3162	-.HNKPEVEVRSSK.-	1410.56	2	344.58	0.94	0.2	135	7/22	3
rawphag2007chfbead2, 622	-.LSVNARARIVAEEFLK.-	1817.13	3	702.40	1.83	0.1	246	4/15	3
AJRAWSoluteContr_june13, 1034	-.LVDFVIHFMEEIDK -	1736.03	3	535.42	1.36	0.1	370	17/52	3
jmbeads250rawphag3007, 1548	-.PVEGYDISFLITNFHTEQMYK.-	2533.84	3	1250.34	2.17	0.2	278	1/5	3
jmfag5mincon250mmnacl, 3160	-.LVDFVIHFMEEIDKEISEMK -	2453.86	3	9483.18	3.55	0.5	532	6/19	3
JMMAGNEGB16D3, 1168	-.ELLLQPVTISR -	1269.52	2	2742.43	2.11	0.3	526	7/10	3
JMMAGTube1B16E3, 1198	-.ELLLQPVTISR.-	1269.52	2	1744.83	1.47	0.2	760	13/20	3
JMMAGNEGB16D3,1738-1740	- EISEMK.-	736.86	1	188.08	1.26	0.0	149	3/5	3

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub				**474.05**	5031595.0	2		
FPbeads150_Dec19, 1767	-.VSIAVKQADEIEKILCHK.-	2025.40	3	333.84	1.02	0.1	300	15/68	2
FPbeads300_Dec19, 3958	- PYLSAVRATLQAALCLENFSSQVVERHNK.-	3246.69	3	140.21	1.15	0.1	93	1/7	2

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ARP8 actin-related protein 8 homolog; actin-related protein 8 homolog				**8899.80**	13937369.0	5		
jmraw5minigg250mmnaclsynngdnase, 396	-.EWQRFGVR.-	1078.21	3	288.33	1.03	0.1	203	5/14	1
jmrawgg5min400mmnaclsd, 741	-.YYRCILLIPDIYNK.-	1788.15	3	604.32	1.50	0.1	326	5/13	1
jmIgG300rawphag3007, 1462	- DLKYYRCILLIPDIYNK.-	2144.57	3	1734.83	2.47	0.1	546	11/32	1
jmbeads250rawphag3007, 876	-.ATDTLPVSVPHVIARR.-	1733.01	3	542.79	1.49	0.1	316	19/60	1
rawsucrfp_300phagigg_Mar04, 1121	-.CILLIPDIYNKQHVK.-	1798.19	2	206.09	1.13	0.0	177	9/28	1
rawsucrfp_1000phagigg_Mar04,1213-1215	-.YYRCILLIPDIYNK.-	1788.15	3	627.80	1.80	0.1	319	9/28	1
rawsucrfp_700phagigg_Mar04, 1429	-.RGQLNIHPGPGGSLTAVLADIEVIWSHAIQK.-	3279.74	3	482.07	1.56	0.1	236	3/20	1
phagrawF600_dec20, 2440	-.LIAWKGGAVLACLDTTQELWIYQR.-	2750.21	2	219.14	0.87	0.1	80	4/23	1
phagrawF150_dec22, 2664	-.CILLIPDIYNKQHVK.-	1798.19	2	833.32	1.59	0.2	285	3/7	1
rawphag2007chfsol1, 1302	-.YYRCILLIPDIYNK.-	1788.15	3	1014.79	1.51	0.1	470	17/52	1
jmidl250nactrawphag3007, 1156	-.PAILDHCSGNK.-	1155.31	2	810.28	1.76	0.1	162	7/20	1
jmfag1mnacl5minigg, 2762	-.HPDSPALLYQFRLGDEK.-	1987.21	1	1736.05	1.21	0.4	165	5/16	1

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
ARP8 actin-related protein 8 homolog; actin-related protein 8 homolog				**455.30**	13937369.0	12		
FPbeads350_Dec19, 1987	-.SQGDPEDPHDEHYLLATQSKQEQSAK.-	2940.04	2	66.46	0.95	0.0	70	4/25	1
jmbsa150nacIrawphag3007,801-803	- PAILDHCSGNK.-	1155.31	2	388.83	1.91	0.1	128	3/10	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to beta actin [Mus musculus] usculus] X&					**87131.81**	38086870.0		6	
jmfagtimecon2.5min.724.724.3	-.IWHHTFYNELR.-	1516.69	0	7198.13	2.84	0.4	995	11/20	18
jmfagtimecon7.5min.947.949.3	-.IWHHTFYNELR.-	1516.69	0	8065.55	3.34	0.4	932	11/20	18
jmfagtimecon7.5min.852.854.3	-.IWHHTFYNELR.-	1516.69	0	4753.65	3.00	0.2	979	21/40	18
jmfagtimecon2.5min.738.738.3	-.IWHHTFYNELR.-	1516.69	0	4403.97	2.43	0.3	728	1/2	18
jmfag5mincont150mmnacl, 611	-.IWHHTFYNELR.-	1516.69	3	1640.96	2.15	0.2	433	7/20	18
jmfagcon5minn600mmnacl, 791	-.IWHHTFYNELR.-	1516.69	3	7961.70	3.10	0.4	1283	3/5	18
jmfagcon5minn600mmnacl, 795	-.IWHHTFYNELR.-	1516.69	3	4822.87	2.17	0.4	840	21/40	18
jmfagtimecont0min_030601230741, 1084	-.IWHHTFYNELR.-	1516.69	3	1704.35	1.67	0.2	633	9/20	18
jmfagcon5minn600mmnacl,1947-1949	-.MXKEIAALAPSTMKIK.-	1746.22	2	394.02	1.74	0.0	212	3/10	1
jmfagcon5minn600mmnacl, 2643	-.ALESDGGCGSDGLLHGDEAQSKRGIPTLK.-	2913.17	2	75.16	1.01	0.0	74	5/28	1
ajrawmediapbsnocells, 564	-.IWHHTFYNELR.-	1516.69	2	1983.16	1.92	0.2	491	1/2	18
jmfag5minigg350mmnacl,569-571	-.IWHHTFYNELR.-	1516.69	3	7343.21	3.48	0.2	1525	5/8	18
jmfag5minigg600mmnacl,586-588	-.IWHHTFYNELR.-	1516.69	3	10871.40	3.53	0.4	1090	23/40	18
JMFAGNACL5B21E3, 624	-.IWHHTFYNELR.-	1516.69	3	7194.25	3.15	0.4	627	19/40	18
jmfag5minigg400mmnacl, 694	-.IWHHTFYNELR.-	1516.69	3	8261.02	3.02	0.4	1048	3/5	18
jmfag5minigg400mmnacl, 704	-.IWHHTFYNELR.-	1516.69	3	10458.41	2.97	0.5	1140	3/5	18

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
put. beta-actin (aa 27-375) [Mus musculus]					**3074987.26**	49858.0		8	
AJRAWActinIgG_june13, 1470	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	1205.00	1.58	0.2	410	5/17	7
AJRAWActinIgG_june13, 1474	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	937.68	1.85	0.1	430	5/17	7
AJRAWActinIgG_june13, 1478	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	4679.38	2.82	0.3	560	9/17	7
AJRAWActinIgG_june13,1288-1290	-.EITALAPSTMK.-	1162.38	2	3457.09	2.13	0.3	454	11/20	17
AJRAWActinIgG_june13,1756-1758	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	10926.63	3.87	0.4	803	13/42	7
AJRAWActinIgG_june13,1924-1926	-.SYELPDGQVITIGNER.-	1791.94	2	15899.61	4.36	0.5	1492	11/15	19
AJRAWActinIgG_june13,1992-1994	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	24002.15	4.61	0.6	1806	19/58	8
AJRAWActinIgG_june13,888-890	-.HQGVMVGMGQK.-	1172.41	2	10826.72	3.30	0.5	970	4/5	17
ajrawmediapbsnocells, 1294	-.SYELPDGQVITIGNER.-	1791.94	2	12111.75	3.68	0.5	627	3/5	19
ajrawmediapbsnocells, 130	-.HQGVMVGMGQK.-	1172.41	3	1792.30	2.46	0.1	619	9/20	17
ajrawmediapbsnocells, 1310	-.SYELPDGQVITIGNER.-	1791.94	2	9751.65	3.54	0.4	1186	7/10	19
ajrawmediapbsnocells, 928	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	2825.45	2.36	0.3	536	5/17	7
ajrawmediapbsnocells, 932	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5577.84	2.79	0.4	695	23/68	7
ajrawphag1MNaCl20, 1182	-.IIAPPER.-	795.95	2	1196.35	1.35	0.3	244	7/12	17
ajrawphag1MNaCl20, 1186	-.IIAPPER.-	795.95	2	818.35	1.35	0.2	199	1/2	17
jm5miniggrawlowionic, 1422	-.EITALAPSTMK.-	1162.38	2	6507.93	2.48	0.4	674	13/20	17
jm5miniggrawlowionic, 1426	-.EITALAPSTMK.-	1162.38	2	1652.45	1.68	0.2	590	13/20	17
jm5miniggrawlowionic, 1638	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	14140.30	4.05	0.5	572	9/17	7
jm5miniggrawlowionic, 1642	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	10639.73	2.96	0.5	689	19/34	7
jm5miniggrawlowionic, 2100	-.SYELPDGQVITIGNER.-	1791.94	3	371.57	1.27	0.1	221	1/4	19
jm5miniggrawlowionic,1626-1628	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	3819.26	2.16	0.4	525	11/34	7
jm5miniggrawlowionic,1918-1920	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	4070.13	2.48	0.3	458	1/4	7
jm5miniggrawlowionic,2086-2088	-.SYELPDGQVITIGNER.-	1791.94	2	12499.20	3.98	0.4	1475	11/15	19
jm5miniggrawlowionic,2174-2176	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	1810.80	2.11	0.2	499	13/58	8
jmag5mincon500mmnacl, 1144	-.QEYDESGPSIVHR.-	1517.58	3	1245.46	1.65	0.1	538	17/48	5
jmag5mincon500mmnacl, 1152	-.QEYDESGPSIVHR.-	1517.58	3	2171.07	2.06	0.2	471	17/48	5
jmag5mincon500mmnacl, 1388	-.EITALAPSTMK.-	1162.38	2	1555.60	2.05	0.2	348	11/20	17
jmag5mincon500mmnacl, 1604	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	12434.89	3.67	0.5	869	10/17	7
jmag5mincon500mmnacl, 1608	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	16755.86	4.19	0.6	748	19/34	7
jmag5mincon500mmnacl, 1886	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	15301.57	4.26	0.5	590	25/84	7
jmag5mincon500mmnacl, 2048	-.SYELPDGQVITIGNER.-	1791.94	2	7927.73	2.46	0.5	778	3/5	19
jmag5mincon500mmnacl, 2052	-.SYELPDGQVITIGNER.-	1791.94	2	11415.55	3.61	0.4	1243	2/3	19
jmag5mincon500mmnacl, 2166	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	21172.58	4.32	0.6	1705	37/116	8
jmag5mincon500mmnacl, 2172	-.DLTDYLMK.-	999.16	1	838.55	1.33	0.1	551	9/14	15
jmag5mincon500mmnacl, 2178	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	9497.38	2.94	0.5	936	31/116	8
jmag5mincon500mmnacl,1184-1186	-.GYSFTTTAER.-	1133.19	2	9243.76	2.60	0.5	1450	8/9	6
jmag5mincon500mmnacl,1380-1382	-.EITALAPSTMK.-	1162.38	2	7683.43	2.70	0.5	471	3/5	17
jmag5mincon500mmnacl,1600-1602	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	4396.72	2.49	0.3	700	23/68	7
jmag5mincon500mmnacl,2160-2162	-.DLTDYLMK.-	999.16	2	881.04	1.58	0.2	272	9/14	15
jmag5mincon500mmnacl,876-878	-.HQGVMVGMGQK.-	1172.41	2	5708.44	2.54	0.4	865	4/5	17
jmfag1mnacl0minigg, 1374	-.DLTDYLMK.-	999.16	2	1291.46	1.80	0.2	429	11/14	15
jmfag1mnacl0minigg, 1412	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	11590.12	3.67	0.5	831	15/58	8
jmfag1mnacl0minigg, 1418	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	19317.74	4.55	0.5	2068	39/116	8
jmfag1mnacl0minigg, 406	-.QEYDESGPSIVHR.-	1517.58	3	5905.12	2.62	0.3	1074	7/16	5
jmfag1mnacl0minigg, 410	- QEYDESGPSIVHR.-	1517.58	3	5427.81	2.46	0.4	883	5/12	5
jmfag1mnacl0minigg, 710	-.EITALAPSTMK.-	1162.38	2	4625.42	2.03	0.4	618	7/10	17
jmfag1mnacl0minigg, 714	-.EITALAPSTMK.-	1162.38	2	5427.38	2.41	0.4	540	13/20	17
jmfag1mnacl0minigg,1298-1300	-.SYELPDGQVITIGNER.-	1791.94	2	9514.51	3.42	0.4	1205	11/15	19
jmfag1mnacl0minigg,926-928	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	9659.67	3.42	0.4	920	27/68	7
jmfag1mnacl0minigg,926-928	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	9659.67	3.42	0.4	920	27/68	7
jmfag1mnacl2,5minigg, 136	-.HQGVMVGMGQK.-	1172.41	2	7814.16	2.89	0.4	1075	9/10	17
jmfag1mnacl2,5minigg, 1420	-.DLTDYLMK.-	999.16	2	2899.40	2.20	0.3	398	11/14	15
jmfag1mnacl2,5minigg, 1428	-.DLTDYLMK.-	999.16	2	2008.86	1.84	0.2	501	6/7	15
jmfag1mnacl2,5minigg, 1454	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	15771.92	4.14	0.5	1015	1/4	8
jmfag1mnacl2,5minigg, 1458	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	6226.96	2.70	0.4	944	31/116	8

jmfag1mnacl2,5minigg, 162	-.HAPPER.-	795.95	2	309.67	1.24	0.1	193	1/2	17
jmfag1mnacl2,5minigg, 500	-.GYSFTTTAER.-	1133.19	2	11370.98	2.84	0.5	1046	5/6	6
jmfag1mnacl2,5minigg,1204-1206	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	6303.52	3.19	0.4	470	2/7	7
jmfag1mnacl2,5minigg,1342-1344	-.SYELPDGQVITIGNER.-	1791.94	2	16697.46	4.29	0.5	1802	23/30	19
jmfag1mnacl2,5minigg,496-498	-.QEYDESGPSIVHR.-	1517.58	3	6531.03	2.65	0.4	866	5/12	5
jmfag1mnacl2,5minigg,782-784	-.EITALAPSTMK.-	1162.38	2	5160.34	2.13	0.4	785	4/5	17
jmfag1mnacl2,5minigg,978-980	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5639.91	2.53	0.4	748	25/68	7
jmfag1mnacl2,5minigg,988-990	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	16791.42	4.10	0.6	951	11/17	7
jmfag1mnacl5mincon, 1184	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	11051.30	3.21	0.5	768	21/34	7
jmfag1mnacl5mincon, 1188	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	16298.52	4.44	0.5	882	21/34	7
jmfag1mnacl5mincon, 1574	-.SYELPDGQVITIGNER.-	1791.94	1	3186.18	1.70	0.4	161	2/5	19
jmfag1mnacl5mincon, 1580	-.SYELPDGQVITIGNER.-	1791.94	2	8322.33	3.07	0.4	698	17/30	19
jmfag1mnacl5mincon, 1646	-.DLTDYLMK.-	999.16	1	1414.10	1.63	0.0	852	11/14	15
jmfag1mnacl5mincon, 1674	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	17537.05	4.78	0.5	1025	17/58	8
jmfag1mnacl5mincon, 1684	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	2	7416.88	2.97	0.5	326	17/58	8
jmfag1mnacl5mincon, 538	-.GYSFTTTAER.-	1133.19	2	10465.70	2.66	0.5	1388	8/9	6
jmfag1mnacl5mincon, 544	-.GYSFTTTAER.-	1133.19	2	10655.90	2.72	0.5	1135	5/6	6
jmfag1mnacl5mincon, 546	-.QEYDESGPSIVHR.-	1517.58	3	6875.02	2.94	0.3	1238	23/48	5
jmfag1mnacl5mincon,1178-1180	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	2498.82	2.36	0.3	422	19/68	7
jmfag1mnacl5mincon,1418-1420	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	4855.45	2.76	0.4	501	23/84	7
jmfag1mnacl5mincon,1558-1560	-.SYELPDGQVITIGNER.-	1791.94	2	13124.34	4.11	0.4	1421	2/3	19
jmfag1mnacl5mincon,1642-1644	-.DLTDYLMK.-	999.16	2	3099.01	2.40	0.3	434	6/7	15
jmfag1mnacl5mincon,1642-1644	-.DLTDYLMK.-	999.16	2	3099.01	2.40	0.3	434	6/7	15
jmfag1mnacl5mincon,2042-2044	-.CPEALFQPSFLGMESCGIHETTFNSIMK.-	3119.61	2	1763.68	1.57	0.3	187	11/54	8
jmfag1mnacl5mincon,940-942	-.EITALAPSTMK.-	1162.38	2	5451.83	2.30	0.4	605	7/10	17
jmfag1mnacl5minigg, 1156	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	15638.21	3.55	0.6	828	10/17	7
jmfag1mnacl5minigg, 1160	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	7627.04	3.97	0.3	713	10/17	7
jmfag1mnacl5minigg, 1596	-.DLTDYLMK.-	999.16	2	1214.55	2.12	0.0	560	6/7	15
jmfag1mnacl5minigg, 1600	-.DLTDYLMK.-	999.16	2	3464.59	2.27	0.3	511	11/14	15
jmfag1mnacl5minigg, 1604	-.DLTDYLMK.-	999.16	1	1630.59	1.68	0.2	595	5/7	15
jmfag1mnacl5minigg, 1640	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	10162.43	2.97	0.5	1374	35/116	8
jmfag1mnacl5minigg, 530	-.QEYDESGPSIVHR.-	1517.58	3	5285.63	2.49	0.4	814	19/48	5
jmfag1mnacl5minigg, 534	-.QEYDESGPSIVHR.-	1517.58	3	4183.99	2.57	0.3	772	19/48	5
jmfag1mnacl5minigg,1148-1150	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	11140.69	3.46	0.5	630	23/68	7
jmfag1mnacl5minigg,1526-1528	-.SYELPDGQVITIGNER.-	1791.94	2	13465.08	3.70	0.5	1540	11/15	19
jmfag1mnacl5minigg,526-528	-.GYSFTTTAER.-	1133.19	2	13680.23	2.90	0.6	1560	8/9	6
jmfag1mnacl5minigg,918-920	-.EITALAPSTMK.-	1162.38	2	6840.34	2.36	0.5	618	7/10	17
jmfag1mnacl7,5minigg, 1004	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	9769.82	3.83	0.4	752	10/17	7
jmfag1mnacl7,5minigg, 1368	-.SYELPDGQVITIGNER.-	1791.94	2	10925.61	4.09	0.4	1389	23/30	19
jmfag1mnacl7,5minigg, 1372	-.SYELPDGQVITIGNER.-	1791.94	2	7637.53	2.89	0.4	812	3/5	19
jmfag1mnacl7,5minigg, 1452	-.DLTDYLMK.-	999.16	2	1815.08	1.81	0.2	461	6/7	15
jmfag1mnacl7,5minigg, 2514	-.CDVDIRKDLYANTVLSGGTTMYPGIADR.-	3046.43	2	225.49	1.03	0.1	96	5/27	7
jmfag1mnacl7,5minigg, 492	-.QEYDESGPSIVHR.-	1517.58	3	7083.98	2.61	0.4	929	11/24	5
jmfag1mnacl7,5minigg, 502	-.QEYDESGPSIVHR.-	1517.58	3	6406.74	2.37	0.4	968	7/16	5
jmfag1mnacl7,5minigg, 798	-.EITALAPSTMK.-	1162.38	2	3100.35	1.75	0.4	349	1/2	17
jmfag1mnacl7,5minigg, 802	-.EITALAPSTMK.-	1162.38	2	6626.41	2.47	0.4	699	7/10	17
jmfag1mnacl7,5minigg,1484-1486	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	6164.07	2.55	0.4	907	1/4	8
jmfag1mnacl7,5minigg,1822-1824	-.CPEALFQPSFLGMESCGIHETTFNSIMK.-	3119.61	3	602.57	1.72	0.1	304	19/108	8
jmfag1mnacl7,5minigg,998-1000	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	8075.36	3.17	0.4	636	25/68	7
jmfag5minigg1000mmnacl, 1100	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	16130.06	4.35	0.5	817	10/17	7
jmfag5minigg1000mmnacl, 1450	-.SYELPDGQVITIGNER.-	1791.94	2	13004.29	4.10	0.4	1388	23/30	19
jmfag5minigg1000mmnacl, 1454	-.SYELPDGQVITIGNER.-	1791.94	2	11992.78	3.86	0.4	1161	2/3	19
jmfag5minigg1000mmnacl, 1460	-.SYELPDGQVITIGNER.-	1791.94	1	1565.08	1.96	0.2	176	2/5	19
jmfag5minigg1000mmnacl, 1526	-.DLTDYLMK.-	999.16	2	1239.25	1.74	0.2	464	6/7	15
jmfag5minigg1000mmnacl, 1530	-.DLTDYLMK.-	999.16	2	667.83	1.74	0.1	209	4/7	15
jmfag5minigg1000mmnacl, 1910	-.CPEALFQPSFLGMESCGIHETTFNSIMK.-	3119.61	2	1598.06	1.74	0.3	146	5/27	8
jmfag5minigg1000mmnacl, 510	-.GYSFTTTAER.-	1133.19	2	7567.19	2.27	0.5	1285	5/6	6
jmfag5minigg1000mmnacl, 528	-.GYSFTTTAER.-	1133.19	2	11511.73	2.74	0.6	1029	5/6	6
jmfag5minigg1000mmnacl,1086-1088	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	2130.00	1.77	0.3	426	5/17	7
jmfag5minigg1000mmnacl,124-126	-.HQGVMVGMGQK.-	1172.41	2	7344.98	2.83	0.4	847	4/5	17
jmfag5minigg1000mmnacl,546-548	-.QEYDESGPSIVHR.-	1517.58	3	6740.84	2.91	0.4	747	5/12	5
jmfag5minigg1000mmnacl,864-866	-.EITALAPSTMK.-	1162.38	2	5069.05	2.24	0.4	733	3/4	17
jmfag5minigg150mmnacl, 1066	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	728.27	1.38	0.0	527	19/68	7
jmfag5minigg150mmnacl, 130	-.HQGVMVGMGQK.-	1172.41	3	9121.27	2.95	0.3	1930	3/5	17
jmfag5minigg150mmnacl, 1410	-.DLTDYLMK.-	999.16	2	2047.29	1.79	0.3	314	11/14	15
jmfag5minigg150mmnacl, 1428	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	24360.79	5.54	0.5	1661	37/116	8
jmfag5minigg150mmnacl, 746	-.EITALAPSTMK.-	1162.38	2	4999.93	2.40	0.4	514	3/5	17
jmfag5minigg150mmnacl, 750	-.EITALAPSTMK.-	1162.38	2	3608.30	2.32	0.3	396	1/2	17
jmfag5minigg150mmnacl, 958	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	14625.46	3.33	0.6	815	19/34	7
jmfag5minigg150mmnacl,1328-1330	-.SYELPDGQVITIGNER.-	1791.94	2	13753.61	3.97	0.5	1205	11/15	19
jmfag5minigg150mmnacl,460-462	-.QEYDESGPSIVHR.-	1517.58	3	1593.95	2.06	0.1	642	17/48	5
jmfag5minigg200mmnacl, 544	-.QEYDESGPSIVHR.-	1517.58	2	1498.44	1.32	0.3	324	11/24	5
jmfag5minigg200mmnacl, 564	-.GYSFTTTAER.-	1133.19	2	8037.01	2.15	0.5	1009	7/9	6
jmfag5minigg200mmnacl, 572	-.GYSFTTTAER.-	1133.19	2	9968.72	2.62	0.5	1019	5/6	6
jmfag5minigg200mmnacl,1092-1094	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	9124.01	3.24	0.4	874	13/34	7
jmfag5minigg200mmnacl,1100-1102	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	19285.36	4.72	0.5	1130	11/17	7
jmfag5minigg200mmnacl,1478-1480	-.SYELPDGQVITIGNER.-	1791.94	2	16111.10	4.17	0.5	1533	11/15	19
jmfag5minigg200mmnacl,1548-1550	-.DLTDYLMK.-	999.16	2	3686.65	2.16	0.4	475	6/7	15
jmfag5minigg200mmnacl,1574-1576	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	8125.64	3.08	0.4	694	7/29	8
jmfag5minigg200mmnacl,1918-1920	-.CPEALFQPSFLGMESCGIHETTFNSIMK.-	3119.61	2	203.49	1.54	0.0	118	1/6	8
jmfag5minigg200mmnacl,548-550	-.QEYDESGPSIVHR.-	1517.58	3	3711.83	2.41	0.3	915	19/48	5
jmfag5minigg200mmnacl,872-874	-.EITALAPSTMK.-	1162.38	2	5448.36	2.43	0.4	352	11/20	17
jmfag5minigg250mmnacl, 1020	-.GYSFTTTAER.-	1133.19	2	14565.62	2.98	0.6	1530	8/9	6
jmfag5minigg250mmnacl, 1970	-.DLTDYLMK.-	999.16	1	2844.74	1.85	0.3	523	9/14	15
jmfag5minigg250mmnacl, 1976	-.DLTDYLMK.-	999.16	1	2423.73	1.75	0.3	749	5/7	15
jmfag5minigg250mmnacl,1160-1162	-.EITALAPSTMK.-	1162.38	2	6354.44	2.49	0.5	488	3/5	17
jmfag5minigg250mmnacl,1374-1376	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	13311.89	4.21	0.5	586	9/17	7
jmfag5minigg250mmnacl,1862-1864	-.SYELPDGQVITIGNER.-	1791.94	2	18015.73	4.59	0.5	1469	23/30	19
jmfag5minigg250mmnacl,1956-1958	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	15275.64	3.69	0.5	1397	17/58	8
jmfag5minigg250mmnacl,1966-1968	-.DLTDYLMK.-	999.16	2	1054.12	1.56	0.2	236	9/14	15
jmfag5minigg250mmnacl,798-800	-.HQGVMVGMGQK.-	1172.41	2	6421.20	2.68	0.4	1043	4/5	17
jmfag5minigg250mmnacl,964-966	-.QEYDESGPSIVHR.-	1517.58	3	6742.33	2.99	0.3	1106	11/24	5

jmfag5minigg300mmnacl, 1176	-.GYSFTTTAER -	1133.19	2	8583.33	2.26	0.5	972	13/18	6
jmfag5minigg300mmnacl, 1182	-.GYSFTTTAER.-	1133.19	2	4806.66	1.74	0.5	703	2/3	6
jmfag5minigg300mmnacl, 1580	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	10930.59	2.83	0.6	503	1/2	7
jmfag5minigg300mmnacl, 1588	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	7927.36	2.72	0.5	844	10/17	7
jmfag5minigg300mmnacl, 2076	-.SYELPDGQVITIGNER.-	1791.94	3	1555.40	1.84	0.0	833	23/60	19
jmfag5minigg300mmnacl, 2174	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	15454.15	3.53	0.5	1820	35/116	8
jmfag5minigg300mmnacl, 2178	- TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	4764.54	2.82	0.3	858	31/116	8
jmfag5minigg300mmnacl,1130-1132	- QEYDESGPSIVHR.-	1517.58	3	7566.14	2.82	0.4	985	7/18	5
jmfag5minigg300mmnacl,1344-1346	- EITALAPSTMK.-	1162.38	2	3912.91	2.20	0.4	491	13/20	17
jmfag5minigg300mmnacl,2060-2062	-.SYELPDGQVITIGNER.-	1791.94	2	20205.50	4.50	0.5	1478	23/30	19
jmfag5minigg300mmnacl,2162-2164	- DLTDYLMK.-	999.16	2	3024.23	2.31	0.3	371	11/14	15
jmfag5minigg300mmnacl,894-896	-.HQGVMVGMGQK.-	1172.41	2	6251.60	2.46	0.4	691	3/4	17
jmfag5minigg350mmnacl, 1103	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	539.76	1.87	0.0	287	3/14	7
jmfag5minigg350mmnacl, 1241	-.SYELPDGQVITIGNER.-	1791.94	2	14014.35	4.52	0.4	1306	11/15	19
jmfag5minigg350mmnacl, 1309	-.DLTDYLMK.-	999.16	2	1103.24	1.46	0.2	239	9/14	15
jmfag5minigg350mmnacl, 1315	- DLTDYLMK.-	999.16	2	1641.77	1.52	0.3	425	6/7	15
jmfag5minigg350mmnacl, 134	-.HQGVMVGMGQK.-	1172.41	2	7463.30	2.71	0.4	844	4/5	17
jmfag5minigg350mmnacl, 449	-.QEYDESGPSIVHR.-	1517.58	3	3120.04	2.00	0.3	914	7/16	5
jmfag5minigg350mmnacl, 461	-.QEYDESGPSIVHR.-	1517.58	3	4819.01	2.16	0.4	921	7/16	5
jmfag5minigg350mmnacl, 463	-.GYSFTTTAER.-	1133.19	2	8172.44	2.06	0.5	978	7/9	6
jmfag5minigg350mmnacl, 893	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	14903.45	3.27	0.6	752	10/17	7
jmfag5minigg350mmnacl,1233-1235	-.SYELPDGQVITIGNER.-	1791.94	2	16522.50	4.05	0.5	1627	11/15	19
jmfag5minigg350mmnacl,1335-1337	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	8234.49	3.32	0.4	831	15/58	8
jmfag5minigg350mmnacl,695-697	-.EITALAPSTMK.-	1162.38	2	4307.93	2.13	0.4	558	13/20	17
jmfag5minigg350mmnacl,881-883	- VAPEEHPVLLTEAPLNPK.-	1955.24	3	6879.65	2.91	0.4	748	6/17	7
jmfag5minigg400mmnacl, 1392	- SYELPDGQVITIGNER.-	1791.94	2	11339.69	3.79	0.4	1213	11/15	19
jmfag5minigg400mmnacl, 1396	-.SYELPDGQVITIGNER.-	1791.94	2	15766.86	3.81	0.5	2023	5/6	19
jmfag5minigg400mmnacl, 1458	-.DLTDYLMK.-	999.16	2	2512.52	1.90	0.3	400	11/14	15
jmfag5minigg400mmnacl, 1462	- DLTDYLMK.-	999.16	2	3376.52	2.25	0.3	406	11/14	15
jmfag5minigg400mmnacl, 510	-.GYSFTTTAER.-	1133.19	2	10686.18	2.37	0.6	1020	7/9	6
jmfag5minigg400mmnacl, 516	-.GYSFTTTAER.-	1133.19	2	11040.95	2.66	0.6	901	5/6	6
jmfag5minigg400mmnacl, 520	-.QEYDESGPSIVHR.-	1517.58	3	7554.47	2.54	0.4	1351	1/2	5
jmfag5minigg400mmnacl, 526	-.QEYDESGPSIVHR.-	1517.58	3	4677.58	2.19	0.4	884	7/16	5
jmfag5minigg400mmnacl,1044-1046	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	15441.35	4.50	0.5	730	19/34	7
jmfag5minigg400mmnacl,1464-1466	-.DLTDYLMK.-	999.16	1	4715.62	2.68	0.3	776	5/7	15
jmfag5minigg400mmnacl,1498-1500	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	3152.29	1.94	0.3	978	31/116	8
jmfag5minigg400mmnacl,828-830	-.EITALAPSTMK.-	1162.38	2	2878.94	2.09	0.3	545	13/20	17
jmfag5minigg450mmnacl_030527025134, 1154	-.GYSFTTTAER.-	1133.19	2	10809.15	2.51	0.6	1170	5/6	6
jmfag5minigg450mmnacl_030527025134, 1158	-.GYSFTTTAER.-	1133.19	2	14403.66	2.59	0.7	1103	5/6	6
jmfag5minigg450mmnacl_030527025134, 1872	- KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	4642.09	2.56	0.3	755	13/42	7
jmfag5minigg450mmnacl_030527025134, 1878	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	6470.44	2.92	0.4	774	9/28	7
jmfag5minigg450mmnacl_030527025134, 2034	-.SYELPDGQVITIGNER.-	1791.94	2	5137.61	2.56	0.4	643	8/15	19
jmfag5minigg450mmnacl_030527025134, 2144	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	8613.59	3.39	0.4	589	7/29	8
jmfag5minigg450mmnacl_030527025134, 2146	-.DLTDYLMK.-	999.16	1	856.42	1.40	0.1	535	5/7	15
jmfag5minigg450mmnacl_030527025134, 2148	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	10263.38	3.09	0.4	1688	19/58	8
jmfag5minigg450mmnacl_030527025134, 982	- IIAPPER.-	795.95	2	818.31	1.36	0.2	221	7/12	17
jmfag5minigg450mmnacl_030527025134,1116-1118	-.QEYDESGPSIVHR.-	1517.58	3	7275.44	2.64	0.4	1157	7/16	5
jmfag5minigg450mmnacl_030527025134,1342-1344	-.EITALAPSTMK.-	1162.38	2	5890.90	2.33	0.5	468	13/20	17
jmfag5minigg450mmnacl_030527025134,2136-2138	-.DLTDYLMK.-	999.16	2	3401.84	2.21	0.4	289	5/7	15
jmfag5minigg450mmnacl_030527025134,878-880	-.HQGVMVGMGQK.-	1172.41	2	10169.85	2.96	0.5	978	17/20	17
jmfag5minigg500mmnacl, 1312	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	17925.21	3.82	0.6	1134	11/17	7
jmfag5minigg500mmnacl, 1318	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	11223.00	3.79	0.5	699	19/34	7
jmfag5minigg500mmnacl, 1850	- DLTDYLMK.-	999.16	2	1973.16	1.66	0.3	400	11/14	15
jmfag5minigg500mmnacl, 1854	-.DLTDYLMK.-	999.16	2	472.48	1.56	0.1	240	9/14	15
jmfag5minigg500mmnacl, 1862	-.DLTDYLMK.-	999.16	1	717.58	1.23	0.0	557	5/7	15
jmfag5minigg500mmnacl, 1874	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	15532.24	3.49	0.6	1261	33/116	8
jmfag5minigg500mmnacl, 1878	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	2226.92	1.69	0.2	955	15/58	8
jmfag5minigg500mmnacl, 762	-.HQGVMVGMGQK.-	1172.41	2	4275.03	2.04	0.4	508	7/10	17
jmfag5minigg500mmnacl, 766	-.HQGVMVGMGQK.-	1172.41	2	4855.74	2.09	0.4	920	4/5	17
jmfag5minigg500mmnacl, 962	-.GYSFTTTAER.-	1133.19	2	8867.17	2.24	0.5	1309	8/9	6
jmfag5minigg500mmnacl,1104-1106	-.EITALAPSTMK.-	1162.38	2	6673.47	2.35	0.5	449	3/5	17
jmfag5minigg500mmnacl,1300-1302	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	6227.85	3.09	0.4	740	25/68	7
jmfag5minigg500mmnacl,1754-1756	-.SYELPDGQVITIGNER.-	1791.94	2	13151.62	3.63	0.5	1018	19/30	19
jmfag5minigg500mmnacl,900-902	-.QEYDESGPSIVHR.-	1517.58	3	1892.10	2.26	0.2	566	3/8	5
jmfag5minigg600mmnacl, 1332	-.DLTDYLMK.-	999.16	2	3595.89	2.54	0.3	368	11/14	15
jmfag5minigg600mmnacl, 1336	-.DLTDYLMK.-	999.16	2	3638.09	2.09	0.4	391	11/14	15
jmfag5minigg600mmnacl, 1358	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	8058.39	3.08	0.4	1172	8/29	8
jmfag5minigg600mmnacl, 470	-.GYSFTTTAER.-	1133.19	2	5867.14	1.92	0.5	868	13/18	6
jmfag5minigg600mmnacl, 480	-.GYSFTTTAER.-	1133.19	2	10922.84	2.78	0.5	1255	8/9	6
jmfag5minigg600mmnacl,1258-1260	- SYELPDGQVITIGNER.-	1791.94	2	14741.63	4.18	0.5	1242	2/3	19
jmfag5minigg600mmnacl,132-134	-.HQGVMVGMGQK.-	1172.41	2	7873.38	3.01	0.4	906	4/5	17
jmfag5minigg600mmnacl,462-464	-.QEYDESGPSIVHR.-	1517.58	3	6520.87	2.79	0.4	745	19/48	5
jmfag5minigg600mmnacl,714-716	-.EITALAPSTMK.-	1162.38	2	4610.04	2.78	0.4	364	3/5	17
jmfag5minigg600mmnacl,904-906	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	584.69	1.68	0.0	329	9/34	7
jmfag5minigg600mmnacl,908-910	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	18926.07	4.41	0.6	1105	11/17	7
jmfag5miniggbead, 1009	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	6610.63	2.77	0.4	445	23/84	7
jmfag5miniggbead, 1137	-.SYELPDGQVITIGNER.-	1791.94	2	8188.61	3.22	0.4	693	19/30	19
jmfag5miniggbead, 1141	-.SYELPDGQVITIGNER.-	1791.94	2	16086.67	4.40	0.5	1423	11/15	19
jmfag5miniggbead, 1229	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	25921.37	5.88	0.5	1454	9/29	8
jmfag5miniggbead, 1233	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	16388.67	4.27	0.5	1279	35/116	8
jmfag5miniggbead, 128	-.HQGVMVGMGQK.-	1172.41	3	4646.39	2.60	0.3	674	1/2	17
jmfag5miniggbead, 803	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5386.28	2.40	0.4	420	11/34	7

jmfag5miniggbead, 803	-.VAPEEHPVLLTEAPLNPK -	1955.24	3	5386.28	2.40	0.4	420	11/34	7
jmfag5miniggbead, 803	- VAPEEHPVLLTEAPLNPK -	1955.24	3	5386.28	2.40	0.4	420	11/34	7
jmfag5miniggbead,410-412	-.QEYDESGPSIVHR.-	1517.58	3	3269.98	2.70	0.2	615	17/48	5
jmfag5miniggbead,623-625	-.EITALAPSTMK -	1162.38	2	4006.95	2.21	0.4	439	11/20	17
jmfag5miniggbead,805-807	-.VAPEEHPVLLTEAPLNPK -	1955.24	2	18121.68	4.80	0.5	927	21/34	7
jmfag5miniggbead_030528200105, 1017	- VAPEEHPVLLTEAPLNPK.-	1955.24	2	9718.16	2.96	0.5	602	9/17	7
jmfag5miniggbead_030528200105, 1337	-.SYELPDGQVITIGNER.-	1791.94	2	13908.87	3.56	0.5	1216	7/10	19
jmfag5miniggbead_030528200105, 1341	- SYELPDGQVITIGNER.-	1791.94	2	9849.26	3.62	0.4	1029	19/30	19
jmfag5miniggbead_030528200105, 997	-.VAPEEHPVLLTEAPLNPK -	1955.24	3	5330.31	2.63	0.4	772	6/17	7
jmfag5miniggbead_030528200105,1209-1211	- KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	5984.02	2.69	0.4	478	5/21	7
jmfag5miniggbead_030528200105,1441-1443	- TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	9446.21	3.19	0.4	1075	8/29	8
jmfag5miniggbead_030528200105,809-811	-.EITALAPSTMK.-	1162.38	2	5006.87	2.53	0.4	442	3/5	17
JMFAGNACL10_1B21E3,1110-1112	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	2869.79	2.88	0.2	634	23/68	7
JMFAGNACL10_2B21E3, 914	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	4839.61	2.55	0.4	437	21/68	7
jmfreebeadsrawphag3007, 1090	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	2	15823.14	4.21	0.5	980	19/42	7
jmfreebeadsrawphag3007, 646	- EITALAPSTMK -	1162.38	2	4116.66	1.81	0.4	507	13/20	17
jmfreebeadsrawphag3007, 866	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	10997.46	3.39	0.5	641	9/17	7
jmfreebeadsrawphag3007, 876	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	13629.77	4.58	0.5	821	21/34	7
jmfreebeadsrawphag3007,1074-1076	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	2542.10	2.38	0.3	312	5/21	7
jmfreebeadsrawphag3007,1206-1208	-.SYELPDGQVITIGNER.-	1791.94	2	13501.38	4.45	0.4	1342	23/30	19
jmfreebeadsrawphag3007,1310-1312	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	15268.16	4.11	0.5	858	33/116	8
jmfreebeadsrawphag3007,860-862	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5578.51	3.13	0.4	489	11/34	7
jmIgG150rawphag3007, 756	-.HQGVMVGMGQK.-	1172.41	2	6368.18	2.49	0.4	927	4/5	17
jmIgG150rawphag3007, 762	- HQGVMVGMGQK.-	1172.41	2	6134.16	2.13	0.4	1204	9/10	17
jmIgG250rawphag3007,1786-1788	-.SYELPDGQVITIGNER.-	1791.94	2	14314.01	3.97	0.4	1654	23/30	19
jmIgG250rawphag3007,772-774	-.HQGVMVGMGQK.-	1172.41	2	6901.41	2.87	0.4	1065	17/20	17
jmIgG300rawphag3007, 1004	-.HQGVMVGMGQKDSYVGDEAQSK.-	2352.59	3	11422.19	3.47	0.5	1047	1/3	16
jmIgG300rawphag3007, 1750	-.SYELPDGQVITIGNER.-	1791.94	2	11078.70	3.50	0.4	1286	7/10	19
jmIgG300rawphag3007, 796	-.HQGVMVGMGQK.-	1172.41	3	1926.95	2.25	0.2	418	2/5	17
jmIgG300rawphag3007,800-802	-.HQGVMVGMGQK.-	1172.41	2	9624.49	3.03	0.5	1086	17/20	17
jmIgG350naclrawphag3007, 1015	- QEYDESGPSIVHR.-	1517.58	3	4672.49	2.70	0.3	785	5/12	5
jmIgG350naclrawphag3007, 1019	-.QEYDESGPSIVHR.-	1517.58	3	1967.03	1.97	0.2	760	19/48	5
jmIgG350naclrawphag3007, 1057	-.HQGVMVGMGQKDSYVGDEAQSK.-	2352.59	3	22994.35	4.33	0.6	1458	17/42	16
jmIgG350naclrawphag3007, 1203	-.EITALAPSTMK.-	1162.38	2	3247.76	1.66	0.4	582	3/5	17
jmIgG350naclrawphag3007, 1207	-.EITALAPSTMK.-	1162.38	2	3381.48	1.99	0.3	487	3/5	17
jmIgG350naclrawphag3007,1763-1765	-.SYELPDGQVITIGNER.-	1791.94	2	14649.15	3.68	0.5	1358	11/15	19
jmIgG350naclrawphag3007,849-851	- HQGVMVGMGQK.-	1172.41	2	9192.44	2.69	0.5	943	4/5	17
jmIgG400rawphag3007, 1752	-.SYELPDGQVITIGNER.-	1791.94	2	8316.90	2.50	0.5	683	3/5	19
jmIgg450rawphag3007, 1740	-.SYELPDGQVITIGNER.-	1791.94	2	8171.38	2.57	0.5	724	8/15	19
jmkdl150naclrawphag3007,950-952	-.HQGVMVGMGQK.-	1172.41	2	8945.32	3.24	0.4	1115	17/20	17
jmkdl250naclrawphag3007, 854	-.HQGVMVGMGQK.-	1172.41	2	5303.91	2.49	0.3	972	3/4	17
JMMAGNEGB16D3, 1348	-.SYELPDGQVITIGNER.-	1791.94	2	8809.57	3.36	0.4	1084	7/10	19
JMMAGNEGB16D3, 1352	-.SYELPDGQVITIGNER.-	1791.94	2	9959.49	3.34	0.5	751	3/5	19
JMMAGNEGB16D3, 1428	-.DLTDYLMK.-	999.16	2	3809.43	2.39	0.3	393	11/14	15
JMMAGNEGB16D3, 450	-.GYSFTTTAER.-	1133.19	2	6308.99	1.94	0.5	709	2/3	6
JMMAGNEGB16D3, 452	-.QEYDESGPSIVHR.-	1517.58	3	3537.31	2.09	0.3	797	19/48	5
JMMAGNEGB16D3, 978	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	15316.70	3.63	0.6	974	10/17	7
JMMAGNEGB16D3, 982	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	14453.15	3.64	0.5	1009	11/17	7
JMMAGNEGB16D3,1420-1422	-.DLTDYLMK.-	999.16	1	1351.67	1.50	0.1	766	5/7	15
JMMAGNEGB16D3,974-976	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	2594.74	2.48	0.3	291	19/68	7
JMMAGTube1B16E3, 1388	-.SYELPDGQVITIGNER.-	1791.94	1	189.74	1.26	0.1	84	3/10	19
JMMAGTube1B16E3, 1486	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	2	657.83	1.36	0.2	158	7/29	8
JMMAGTube1B16E3, 1492	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	2	14028.15	3.48	0.6	387	21/58	8
JMMAGTube1B16E3, 472	-.QEYDESGPSIVHR.-	1517.58	2	5241.18	2.07	0.5	477	13/24	5
JMMAGTube1B16E3, 482	-.QEYDESGPSIVHR.-	1517.58	3	2755.26	2.05	0.3	716	3/8	5
JMMAGTube1B16E3, 488	-.QEYDESGPSIVHR.-	1517.58	2	5184.19	2.35	0.4	364	13/24	5
JMMAGTube1B16E3,1000-1002	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	20048.28	4.46	0.6	998	11/17	7
JMMAGTube1B16E3,1008-1010	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	13987.18	3.99	0.5	945	7/17	7
JMMAGTube1B16E3,1228-1230	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	14322.25	3.86	0.5	910	9/28	7
JMMAGTube1B16E3,1238-1240	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	2	37139.96	5.37	0.7	2347	9/14	7
JMMAGTube1B16E3,1374-1376	-.SYELPDGQVITIGNER.-	1791.94	2	15881.82	4.32	0.5	1402	4/5	19
JMMAGTube1B16E3,1454-1456	-.DLTDYLMK.-	999.16	2	3610.92	2.22	0.3	467	6/7	15
JMMAGTube1B16E3,1480-1482	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	15897.46	4.20	0.6	598	1/4	8
JMMAGTube1B16E3,464-466	-.GYSFTTTAER.-	1133.19	2	12327.80	2.56	0.6	1279	8/9	6
JMMAGTube1B16E3,790-792	-.EITALAPSTMK.-	1162.38	2	3010.50	2.06	0.3	444	3/5	17
jmraw5minbsafreezthaw, 1780	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	2	24507.02	4.65	0.5	2297	9/14	7
jmraw5minbsafreezthaw, 880	-.HQGVMVGMGQK.-	1172.41	3	4091.82	2.83	0.2	923	1/2	17
jmraw5minbsafreezthaw,1490-1492	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	8037.01	2.90	0.5	738	23/68	7
jmraw5minbsafreezthaw,1500-1502	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	18547.05	3.95	0.6	1005	11/17	7

jmraw5minbsafreezthaw,1948-1950	-.SYELPDGQVITIGNER.-	1791.94	2	17544.63	4.22	0.5	1685	11/15	19
jmraw5minbsafreezthaw,1954-1956	-.SYELPDGQVITIGNER.-	1791.94	3	5588.77	2.52	0.3	1041	13/30	19
jmraw5minbsafreezthaw,2030-2032	- TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	17204.14	4.83	0.5	1150	35/116	8
jmraw5minbsafreezthaw,868-870	- HQGVMVGMGQK.-	1172.41	2	6003.56	2.81	0.4	761	3/4	17
jmraw5minigg250mmnaclsyringdnase,1536-1538	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	3729.24	2.61	0.3	760	23/68	7
jmraw5minigg250mmnaclsyringdnase,1820-1822	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	402.93	1.51	0.1	143	5/28	7
jmraw5minigg250mmnaclsyringdnase,1984-1986	-.SYELPDGQVITIGNER.-	1791.94	2	11003.90	3.34	0.5	1013	19/30	19
jmraw5minigg500mmnaclsd, 1624	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	6563.10	2.89	0.4	447	11/42	7
jmraw5minigg500mmnaclsd, 1628	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	9176.67	2.92	0.5	712	25/84	7
jmraw5minigg500mmnaclsd,1360-1362	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	1087.92	1.56	0.1	502	5/17	7
jmraw5minigg500mmnaclsd,1782-1784	-.SYELPDGQVITIGNER.-	1791.94	2	17104.53	4.40	0.5	1485	7/10	19
jmraw5minigg600mmnaclsd, 1534	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	1238.04	1.57	0.2	244	1/4	7
jmraw5miniggiowonic, 1609	-.EIVRDIK.-	873.03	1	388.94	1.08	0.1	288	7/12	19
jmraw5minbsareebeads, 1642	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	387.79	1.74	0.0	220	4/21	7
jmraw5minbsareebeads, 1650	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	3743.87	2.26	0.3	520	11/42	7
jmraw5minbsareebeads, 922	-.IIAPPER.-	795.95	2	297.54	1.02	0.1	197	7/12	17
jmraw5minbsareebeads,1210-1212	-.EITALAPSTMK.-	1162.38	2	5451.72	2.52	0.4	667	7/10	17
jmraw5minbsareebeads,1392-1394	- VAPEEHPVLLTEAPLNPK.-	1955.24	3	2368.13	1.75	0.3	410	1/4	7
jmraw5minbsareebeads,1404-1406	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	22132.18	4.32	0.6	1367	23/34	7
jmraw5minbsareebeads,1816-1818	-.SYELPDGQVITIGNER.-	1791.94	2	18870.83	4.43	0.5	1605	23/30	19
jmraw5minbsareebeads,832-834	-.HQGVMVGMGQK.-	1172.41	2	7575.79	2.66	0.4	997	9/10	17
jmrawigg5min150mmnacl, 1244	- KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	16734.41	4.68	0.5	893	29/84	7
jmrawigg5min150mmnacl, 474	-.QEYDESGPSIVHR.-	1517.58	3	6868.79	2.50	0.4	1154	11/24	5
jmrawigg5min150mmnacl, 818	-.EITALAPSTMK.-	1162.38	2	1719.78	1.69	0.3	245	9/20	17
jmrawigg5min150mmnacl,1026-1028	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	8617.18	3.33	0.4	785	25/68	7
jmrawigg5min150mmnacl,1370-1372	-.SYELPDGQVITIGNER.-	1791.94	2	16401.43	4.22	0.5	1591	23/30	19
jmrawigg5min300mmnaclsyringednase, 1155	-.SYELPDGQVITIGNER.-	1791.94	2	7328.04	3.25	0.3	1086	2/3	19
jmrawigg5min300mmnaclsyringednase,825-827	- VAPEEHPVLLTEAPLNPK.-	1955.24	3	4555.21	3.16	0.3	564	21/68	7
jmrawigg5minbeadsfreezethaw, 1196	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	2	23579.68	4.49	0.6	1662	4/7	7
jmrawigg5minbeadsfreezethaw, 1324	-.SYELPDGQVITIGNER.-	1791.94	2	9928.37	3.75	0.4	1255	7/10	19
jmrawigg5minbeadsfreezethaw, 1328	- SYELPDGQVITIGNER.-	1791.94	2	11482.80	3.69	0.4	1234	7/10	19
jmrawigg5minbeadsfreezethaw, 1426	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	2	9676.99	3.21	0.5	299	9/29	8
jmrawigg5minbeadsfreezethaw, 962	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	12094.23	3.01	0.6	667	21/34	7
jmrawigg5minbeadsfreezethaw, 966	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	10896.33	3.39	0.5	717	10/17	7
jmrawigg5minbeadsfreezethaw,1330-1332	-.SYELPDGQVITIGNER.-	1791.94	1	4079.88	2.13	0.4	276	1/2	19
jmrawigg5minbeadsfreezethaw,1430-1432	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	20093.27	5.22	0.5	951	8/29	8
jmrawigg5minbeadsfreezethaw,954-956	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	6057.56	3.14	0.4	458	5/17	7
jmrawrminigg200mmnaclsyringdnas, 1360	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	10825.02	3.30	0.5	690	9/17	7
jmrawrminigg200mmnaclsyringdnas, 1364	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	10959.90	3.64	0.5	571	9/17	7
jmrawrminigg200mmnaclsyringdnas, 1634	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	7585.69	3.20	0.4	420	1/4	7
jmrawrminigg200mmnaclsyringdnas, 1638	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	4616.92	2.48	0.4	510	23/84	7
jmrawrminigg200mmnaclsyringdnas, 760	-.HQGVMVGMGQK.-	1172.41	2	5806.60	2.54	0.4	739	3/4	17
jmrawrminigg200mmnaclsyringdnas,1350-1352	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	3817.98	2.49	0.2	972	13/34	7
jmrawrminigg200mmnaclsyringdnas,1804-1806	-.SYELPDGQVITIGNER.-	1791.94	2	14868.15	4.45	0.4	1330	23/30	19
jmrawrminigg200mmnaclsyringdnas,1894-1896	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	30885.94	5.89	0.6	1822	41/116	8
phagrawFsuc60MeOH_dec23, 966	-.DSYVGDEAQSK.-	1199.21	2	521.80	1.02	0.2	178	7/20	22
rawsucrfp_1000phagigg_Mar04, 1269	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	8274.72	2.65	0.5	870	25/68	7
rawsucrfp_150phagigg_Mar04, 1126	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	1466.56	2.40	0.1	568	11/34	7
rawsucrfp_150phagigg_Mar04,1450-1452	-.SYELPDGQVITIGNER.-	1791.94	2	7763.89	3.12	0.4	807	3/5	19
rawsucrfp_250phagigg_Mar04, 1500	-.SYELPDGQVITIGNER.-	1791.94	2	11832.00	3.21	0.5	1333	7/10	19
rawsucrfp_250phagigg_Mar04, 1506	-.SYELPDGQVITIGNER.-	1791.94	2	8019.45	3.89	0.3	961	2/3	19
rawsucrfp_300phagigg_Mar04, 1175	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	336.12	1.60	0.1	184	4/21	7
rawsucrfp_300phagigg_Mar04,1301-1303	-.SYELPDGQVITIGNER.-	1791.94	2	10050.99	3.67	0.4	1371	7/10	19
rawsucrfp_300phagigg_Mar04,969-971	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	6978.39	3.35	0.4	652	6/17	7
rawsucrfp_400phagigg_Mar04, 1162	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	4830.28	2.09	0.4	755	13/34	7
rawsucrfp_400phagigg_Mar04, 1168	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5755.60	2.74	0.4	589	6/17	7
rawsucrfp_400phagigg_Mar04,1499-1501	-.SYELPDGQVITIGNER.-	1791.94	2	18196.39	4.56	0.5	1489	4/5	19
rawsucrfp_450phagigg_Mar04, 1152	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	8632.12	3.02	0.5	795	13/34	7
rawsucrfp_450phagigg_Mar04, 1160	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	1727.65	2.01	0.2	461	5/17	7
rawsucrfp_600phagigg_Mar04, 1472	-.SYELPDGQVITIGNER.-	1791.94	2	9251.99	3.66	0.4	767	17/30	19
rawsucrfp_60MeOHphagigg_MAr04, 1282	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.50	3	4950.73	3.25	0.3	650	25/116	8
rawsucrfp_60MeOHphagigg_MAr04, 632	-.HQGVMVGMGQKDSYVGDEAQSKR.-	2508.78	3	17908.46	4.41	0.6	894	31/88	16
rawsucrfp_60MeOHphagigg_MAr04, 678	-.GYSFTTTAER.-	1133.19	2	7086.16	2.07	0.5	1199	5/6	6
rawsucrfp_60MeOHphagigg_MAr04, 830	-.EITALAPSTMKIK.-	1403.71	2	2418.22	2.76	0.2	479	5/8	17
rawsucrfp_60MeOHphagigg_MAr04, 930	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	19018.02	4.55	0.6	765	10/17	7
rawsucrfp_60MeOHphagigg_MAr04,1242-1244	-.SYELPDGQVITIGNER.-	1791.94	2	15411.63	4.17	0.5	1498	4/5	19
rawsucrfp_60MeOHphagigg_MAr04,790-792	-.EITALAPSTMK.-	1162.38	2	2661.52	2.34	0.2	595	13/20	17
rawsucrfp_60MeOHphagigg_MAr04,918-920	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5577.68	3.24	0.3	691	23/68	7
rawsucrfp_700phagigg_Mar04, 1492	-.SYELPDGQVITIGNER.-	1791.94	2	9130.78	3.57	0.4	1223	2/3	19
rawsucrfp_700phagigg_Mar04,1161-1163	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	6276.01	2.94	0.4	686	23/68	7
rawsucrfp_800phagigg_Mar04, 1034	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	7670.52	2.86	0.5	518	21/68	7
rawsucrfp_800phagigg_Mar04, 1040	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	2188.81	1.96	0.2	771	23/68	7
rawsucrfp_800phagigg_Mar04, 1360	-.SYELPDGQVITIGNER.-	1791.94	2	13790.81	3.42	0.5	1199	2/3	19
rawsucrfp_900phagigg_Mar04, 1022	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	6559.72	3.11	0.4	800	13/34	7
rawsucrfp_900phagigg_Mar04, 1026	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	8024.20	3.18	0.4	738	27/68	7
rawsucrfp_900phagigg_Mar04, 1369	-.SYELPDGQVITIGNER.-	1791.94	2	15840.58	3.73	0.6	1040	19/30	19
rawsucrfp_actinphagigg_Mar04, 1340	-.SYELPDGQVITIGNER.-	1791.94	2	11398.93	3.73	0.4	1474	11/15	19
rawsucrfp_actinphagigg_Mar04, 712	-.QEYDESGPSIVHR.-	1517.58	3	1189.58	1.86	0.1	524	17/48	5
rawsucrfp_chlfphagigg_Mar04, 1242	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	8956.42	3.05	0.5	421	1/2	7
rawsucrfp_chlfphagigg_Mar04, 1644	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	2659.61	1.93	0.3	484	25/116	8
rawsucrfp_chlfphagigg_Mar04, 756	-.IIAPPER.-	795.95	2	758.73	1.53	0.2	254	2/3	17
rawsucrfp_chlfphagigg_Mar04, 950	-.GYSFTTTAER.-	1133.19	2	8407.18	2.28	0.5	1319	8/9	6
rawsucrfp_chlfphagigg_Mar04,1072-1074	-.EITALAPSTMK.-	1162.38	2	2526.71	2.30	0.2	508	13/20	17
rawsucrfp_chlfphagigg_Mar04,1238-1240	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	2703.38	2.08	0.3	661	11/34	7
rawsucrfp_chlfphagigg_Mar04,1594-1596	-.SYELPDGQVITIGNER.-	1791.94	2	15130.52	4.32	0.5	1358	11/15	19

control

put. beta-actin (aa 27-375) [Mus musculus]					**850033.95**	**49868.0**	**11**		
FPbeads150_Dec19,1335-1337	- SYELPDGQVITIGNER.-	1791.94	2	18334.32	4.04	0.6	1441	7/10	19
FPbeads200_Dec19, 1299	- SYELPDGQVITIGNER.-	1791.94	2	8475.07	2.83	0.4	1161	2/3	19
FPbeads200_Dec19, 1309	-.SYELPDGQVITIGNER.-	1791.94	2	12155.13	3.25	0.5	1340	2/3	19
FPbeads250_Dec19,1572-1574	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	3064.02	2.43	0.3	526	5/17	7
FPbeads300_Dec19,2264-2266	- SYELPDGQVITIGNER -	1791.94	2	7067.21	2.67	0.4	1209	19/30	19
jmbsa300naclrawphag3007, 1409	- SYELPDGQVITIGNER.-	1791.94	2	6189.75	2.66	0.4	811	3/5	19
jmbsa400naclrawphag3007_030802135631, 1168	- SYELPDGQVITIGNER.-	1791.94	2	10348.29	3.06	0.5	821	19/30	19
rawextr_1000_beadigg_Mar04,967-969	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	3604.76	3.07	0.3	418	5/17	7
rawextr_150bead_Mar04,1385-1387	-.SYELPDGQVITIGNER.-	1791.94	2	19790.11	4.65	0.5	1380	11/15	19
rawextr_150bead_Mar04,1437-1439	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR -	3185.60	3	26866.00	5.03	0.6	1421	9/29	8
rawextr_150beadigg_Mar04, 622	-.HQGVMVGMGQK.-	1172.41	2	8608.51	2.73	0.5	952	4/5	17
rawextr_150beadigg2_Mar04, 18	-.EITALAPSTMK.-	1162.38	2	3419.61	1.76	0.3	765	7/10	17
rawextr_150beadigg2_Mar04, 26	-.EITALAPSTMK.-	1162.38	2	3925.98	2.13	0.4	552	7/10	17
rawextr_150beadigg2_Mar04, 704	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR -	3185.60	3	4130.77	2.42	0.3	938	15/58	8
rawextr_150beadigg2_Mar04,192-194	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5701.13	2.70	0.4	473	21/68	7
rawextr_150beadigg2_Mar04,198-200	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	13577.45	3.58	0.5	792	21/34	7
rawextr_150beadigg2_Mar04,710-712	-.SYELPDGQVITIGNER.-	1791.94	2	18797.72	4.88	0.5	1651	11/15	19
rawextr_200bead_Mar04,1666-1668	-.SYELPDGQVITIGNER.-	1791.94	2	16828.59	4.43	0.5	1524	11/15	19
rawextr_200beadigg_Mar04, 1339	-.SYELPDGQVITIGNER.-	1791.94	2	11910.14	3.61	0.4	1297	23/30	19
rawextr_200beadigg_Mar04, 1343	-.SYELPDGQVITIGNER.-	1791.94	2	14803.93	3.99	0.5	1540	23/30	19
rawextr_200beadigg_Mar04, 1389	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	5390.55	2.23	0.4	772	27/116	8
rawextr_200beadigg_Mar04, 1397	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	11624.70	3.39	0.5	1060	33/116	8
rawextr_200beadigg_Mar04,943-945	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	12096.82	3.89	0.5	810	6/17	7
rawextr_250bead_Mar04, 1514	-.SYELPDGQVITIGNER.-	1791.94	2	4147.85	2.55	0.3	601	8/15	19
rawextr_250bead_Mar04, 1518	- SYELPDGQVITIGNER.-	1791.94	2	9219.89	2.98	0.5	1035	2/3	19
rawextr_250bead_Mar04, 976	-.EITALAPSTMK.-	1162.38	2	3975.86	1.81	0.4	799	3/4	17
rawextr_250beadigg_Mar04, 1098	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5705.82	2.74	0.4	668	6/17	7
rawextr_250beadigg_Mar04, 1102	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	6126.29	3.07	0.3	772	25/68	7
rawextr_250beadigg_Mar04,1502-1504	-.SYELPDGQVITIGNER.-	1791.94	2	15382.22	4.12	0.5	1393	11/15	19
rawextr_250beadigg_Mar04,930-932	-.EITALAPSTMK -	1162.38	2	4307.30	2.43	0.4	459	3/5	17
rawextr_300bead_Mar04, 962	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	2705.56	2.05	0.3	523	21/68	7
rawextr_300bead_Mar04,1318-1320	-.SYELPDGQVITIGNER.-	1791.94	2	14420.65	4.45	0.4	1378	23/30	19
rawextr_300beadigg_Mar4, 1058	-.EITALAPSTMK.-	1162.38	2	2694.86	1.66	0.4	331	1/2	17
rawextr_300beadigg_Mar4, 1062	-.EITALAPSTMK.-	1162.38	2	2718.21	1.97	0.3	492	11/20	17
rawextr_300beadigg_Mar4, 1246	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	3807.68	2.57	0.3	556	23/68	7
rawextr_300beadigg_Mar4, 1252	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	15400.27	4.14	0.5	785	10/17	7
rawextr_300beadigg_Mar4, 1636	-.SYELPDGQVITIGNER.-	1791.94	2	9275.25	3.28	0.4	1016	19/30	19
rawextr_300beadigg_Mar4, 1640	-.SYELPDGQVITIGNER.-	1791.94	2	6734.69	2.86	0.4	543	7/15	19
rawextr_300beadigg_Mar4, 652	-.HQGVMVGMGQK.-	1172.41	2	5844.01	2.30	0.4	750	3/4	17
rawextr_350bead_Mar04, 1058	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5954.79	2.59	0.4	775	13/34	7
rawextr_350bead_Mar04, 896	-.EITALAPSTMK.-	1162.38	2	3977.42	1.83	0.4	735	13/20	17
rawextr_350bead_Mar04,1456-1458	- SYELPDGQVITIGNER.-	1791.94	2	15454.13	4.35	0.5	978	2/3	19
rawextr_350beadigg2_Mar04, 1050	-.EITALAPSTMK.-	1162.38	2	3718.97	2.05	0.4	434	11/20	17
rawextr_350beadigg2_Mar04,1222-1224	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	10031.07	3.70	0.4	849	13/34	7
rawextr_350beadigg2_Mar04,1622-1624	-.SYELPDGQVITIGNER.-	1791.94	2	15216.37	3.60	0.5	1313	11/15	19
rawextr_350beadigg2_Mar04,908-910	-.GYSFTTTAER.-	1133.19	2	7846.29	2.59	0.4	1078	5/6	6
rawextr_400bead_Mar04, 1325	-.SYELPDGQVITIGNER.-	1791.94	2	12166.94	3.63	0.5	1194	7/10	19
rawextr_400beadigg_Mar04, 1182	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	3099.18	1.93	0.3	654	21/68	7
rawextr_400beadigg_Mar04, 1198	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	16809.52	3.86	0.6	785	10/17	7
rawextr_400beadigg_Mar04,1034-1036	-.EITALAPSTMK.-	1162.38	2	2966.24	1.94	0.3	505	3/5	17
rawextr_400beadigg_Mar04,1552-1554	-.SYELPDGQVITIGNER.-	1791.94	2	11989.55	3.37	0.5	1313	11/15	19
rawextr_400beadigg_Mar04,1598-1600	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	17821.41	3.76	0.6	1189	17/58	8
rawextr_400beadigg_Mar04,896-898	-.GYSFTTTAER.-	1133.19	2	5970.13	2.41	0.4	860	7/9	6
rawextr_450bead_Mar04, 1048	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	4234.25	2.54	0.3	484	11/34	7
rawextr_450bead_Mar04, 1416	-.SYELPDGQVITIGNER.-	1791.94	2	12775.88	3.26	0.5	1103	2/3	19
rawextr_450bead_Mar04, 768	-.GYSFTTTAER -	1133.19	2	3871.18	1.89	0.4	523	2/3	6
rawextr_450beadigg_Mar04, 1092	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	13966.84	3.78	0.5	984	25/68	7
rawextr_450beadigg_Mar04, 1096	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	8120.44	3.12	0.4	1018	15/34	7
rawextr_450beadigg_Mar04, 1100	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	10137.31	3.25	0.5	826	10/17	7
rawextr_450beadigg_Mar04, 1348	-.KDLYANTVLSGGTTMYPGIADR.-	2344.63	3	3525.12	2.19	0.3	486	1/4	7
rawextr_450beadigg_Mar04, 1480	-.SYELPDGQVITIGNER.-	1791.94	2	11778.07	3.93	0.4	1230	2/3	19
rawextr_450beadigg_Mar04, 1486	- SYELPDGQVITIGNER.-	1791.94	2	17622.73	4.60	0.5	1123	7/10	19
rawextr_450beadigg_Mar04, 606	-.HQGVMVGMGQK.-	1172.41	2	9645.53	2.97	0.4	1379	9/10	17
rawextr_450beadigg_Mar04, 612	-.HQGVMVGMGQK.-	1172.41	2	4155.99	1.92	0.4	622	7/10	17
rawextr_450beadigg_Mar04,808-810	-.GYSFTTTAER.-	1133.19	2	4057.55	2.35	0.3	751	13/18	6
rawextr_450beadigg_Mar04,926-928	-.EITALAPSTMK.-	1162.38	2	2978.87	1.96	0.3	522	13/20	17
rawextr_500bead_Mar04, 1532	-.SYELPDGQVITIGNER.-	1791.94	2	7786.66	2.78	0.4	824	3/5	19
rawextr_500bead_Mar04, 1536	-.SYELPDGQVITIGNER.-	1791.94	2	11102.18	3.20	0.5	733	17/30	19
rawextr_500beadigg_Mar04, 1306	-.SYELPDGQVITIGNER.-	1791.94	2	11757.92	3.37	0.5	1046	19/30	19
rawextr_500beadigg_Mar04, 1316	-.SYELPDGQVITIGNER.-	1791.94	2	13923.97	3.93	0.5	1309	23/30	19
rawextr_500beadigg_Mar04, 842	-.EITALAPSTMK.-	1162.38	2	3033.27	1.89	0.4	378	11/20	17
rawextr_600bead_Mar04, 1542	-.SYELPDGQVITIGNER.-	1791.94	2	13756.69	4.00	0.5	1268	2/3	19
rawextr_600bead_Mar04, 1558	-.SYELPDGQVITIGNER.-	1791.94	2	12845.91	3.65	0.5	996	2/3	19
rawextr_700bead_Mar04, 1105	-.SYELPDGQVITIGNER.-	1791.94	2	9558.47	3.85	0.4	928	19/30	19
rawextr_700bead_Mar04,777-779	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	9059.12	3.25	0.4	1064	27/68	7
rawextr_700beadigg_Mar04, 1072	-.VAPEEHPVLLTEAPLNPK.-	1955.24	2	4291.92	2.01	0.4	240	6/17	7
rawextr_700beadigg_Mar04,1042-1044	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	8552.32	3.93	0.4	733	13/34	7
rawextr_700beadigg_Mar04,1376-1378	-.SYELPDGQVITIGNER.-	1791.94	2	12927.54	3.91	0.5	1129	19/30	19
rawextr_800bead_Mar04, 1232	-.SYELPDGQVITIGNER.-	1791.94	2	9931.77	3.51	0.4	1032	2/3	19
rawextr_800bead_Mar04,884-886	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	4232.19	2.26	0.4	358	19/68	7
rawextr_800beadigg_Mar04, 1028	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	5019.44	2.42	0.4	773	6/17	7
rawextr_800beadigg_Mar04, 1358	-.SYELPDGQVITIGNER.-	1791.94	2	10114.32	3.58	0.4	1059	2/3	19
rawextr_800beadigg_Mar04, 1366	-.SYELPDGQVITIGNER.-	1791.94	2	9871.63	3.22	0.5	537	1/2	19
rawextr_900beadigg_Mar04, 1332	-.SYELPDGQVITIGNER.-	1791.94	2	4837.06	2.83	0.3	702	17/30	19
rawextr_actinbead_Mar04, 1032	-.EITALAPSTMK.-	1162.38	2	4686.24	2.21	0.4	576	3/5	17
rawextr_actinbead_Mar04,1186-1188	-.VAPEEHPVLLTEAPLNPK.-	1955.24	3	6872.54	2.46	0.5	579	11/34	7
rawextr_actinbead_Mar04,1592-1594	-.SYELPDGQVITIGNER.-	1791.94	2	14201.01	4.02	0.5	1204	11/15	19
rawextr_actinbeadigg_Mar04, 1419	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	11153.20	3.93	0.4	919	31/116	8
rawextr_actinbeadigg_Mar04, 1423	-.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.-	3185.60	3	12109.60	3.29	0.5	1043	31/116	8
rawextr_actinbeadigg_Mar04, 256	-.HQGVMVGMGQK.-	1172.41	2	7902.74	2.82	0.4	878	4/5	17
rawextr_actinbeadigg_Mar04, 279	-.HQGVMVGMGQK.-	1172.41	3	5929.77	2.80	0.3	1003	11/20	17
rawextr_actinbeadigg_Mar04, 805	-.EITALAPSTMK.-	1162.38	2	4745.46	2.41	0.4	569	3/5	17
rawextr_actinbeadigg_Mar04,1367-1369	-.SYELPDGQVITIGNER.-	1791.94	2	15855.05	4.02	0.5	1252	7/10	19
rawextr_chlfbead_Mar04, 1540	-.SYELPDGQVITIGNER.-	1791.94	2	2413.25	1.95	0.3	450	13/30	19
rawextr_chlfbead_Mar04, 658	-.IIAPPERK.-	924.12	2	2493.98	1.77	0.3	487	5/7	16

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
actin-like [Mus musculus]					**401898.34**	8850209.0		1	
jmraw5minbsafreezthaw, 1780	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	2	24507.02	4.65	0.5	2297	9/14	
jmrawgg5minbeadsfreezethaw, 1196	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	2	23579.68	4.49	0.6	1662	4/7	
jmfag1mnacl2,5minigg,1204-1206	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	6303.52	3.19	0.4	470	2/7	
jmrawgg5min150mmnacl, 1244	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	16734.41	4.68	0.5	893	29/84	
jmraw5minigg500mmnaclsd, 1624	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	6563.10	2.89	0.4	447	11/42	
jmraw5minigg500mmnaclsd, 1628	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	9176.67	2.92	0.5	712	25/84	
jmrawrminigg200mmnaclsyringdnas, 1634	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	7585.69	3.20	0.4	420	1/4	
jmrawrminigg200mmnaclsyringdnas, 1638	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	4616.92	2.48	0.4	510	23/84	
jmraw5minigg1000mmsd, 1710	-.HQGVMVGIMVGMGQKDSYVGDEAQSK.-	2753.13	3	852.84	2.02	0.1	356	11/50	
jmraw5minigg250mmnaclsyringdnase,1820-1822	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	402.93	1.51	0.1	143	5/28	
AJRAWActinIgG_june13,1756-1758	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	10926.63	3.87	0.4	803	13/42	
jmfag5minigg450mmnacl_030527025134, 1872	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	4642.09	2.56	0.3	755	13/42	
jmfag5minigg450mmnacl_030527025134, 1878	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	6470.44	2.92	0.4	774	9/28	
jm5miniggrawlowionic,1918-1920	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	4070.13	2.48	0.3	458	1/4	
jmrawigg5miniggfreebead,1124-1126	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	26205.75	5.64	0.6	1244	8/21	
jmrawf5minbsareebeads, 1642	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	387.79	1.74	0.0	220	4/21	
jmrawf5minbsareebeads, 1650	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	3743.87	2.26	0.3	520	11/42	
jmfag5miniggbead, 1009	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	6610.63	2.77	0.4	445	23/84	
jmfag5minigg350mmnacl, 1103	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	539.76	1.87	0.0	287	3/14	
jmfag1mnacl2,5minigg,1204-1206	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	6303.52	3.19	0.4	470	2/7	
jmfag5miniggbead_030528200105,1209-1211	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	5984.02	2.69	0.4	478	5/21	
JMMAGTube1B16E3,1228-1230	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	14322.25	3.86	0.5	910	9/28	
JMMAGTube1B16E3,1238-1240	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	2	37139.96	5.37	0.7	2347	9/14	
jmfag1mnacl5mincon,1418-1420	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	4855.45	2.76	0.4	501	23/84	
jmag5mincon500mmnacl, 1886	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	15301.57	4.26	0.5	590	25/84	
jmfag1mnacl7,5minigg, 2514	-.CDVDIRKDLYANTVLSGGTTMYPGLADR.-	3046.43	2	225.49	1.03	0.1	96	5/27	
jmfagtimecon2.5min.1326.1326.3	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	0	9428.05	3.05	0.5	696	13/42	
jmfagcon5min1000mmnacl_030601180404, 1096	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	3417.93	2.53	0.3	563	1/4	
jmfag5mincont400_030531151834, 1134	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	2	5257.55	2.28	0.4	929	10/21	
jmfag5mincont150mmnacl, 1153	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	1046.06	1.77	0.1	564	23/84	
jmfag5mincont350,1164-1166	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	12087.14	4.30	0.5	595	2/7	
jmfag5mincont200mmnacl,1368-1370	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	14879.01	3.73	0.6	741	1/3	
jmfagcon5minn600mmnacl, 1397	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	20107.05	4.57	0.6	1137	31/84	
jmfagcon5minn600mmnacl, 1401	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	2	10150.04	2.80	0.5	751	19/42	
jmfag1mnacl5mincon,1418-1420	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	4855.45	2.76	0.4	501	23/84	
jmfag5mincon250mmnacl, 1644	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	675.61	1.56	0.1	363	3/14	
jmfag5mincon450mmnacl,1652-1654	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	4729.93	3.04	0.3	538	2/7	
jmfag5mincon450mmnacl, 1660	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	2	8541.70	2.58	0.5	1186	1/2	
jmfag5mincon250mmnacl,1664-1666	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	2	20081.17	3.79	0.6	1485	23/42	
jmbeads350rawphag30072nd, 1684	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	3080.29	2.81	0.2	589	2/7	
jmfagtimecont0min_030601230741, 1716	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	4941.73	2.20	0.4	291	5/21	
jmag5mincon500mmnacl, 1886	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	15301.57	4.26	0.5	590	25/84	
jmfagtimecont10min_030601202502,1958-1960	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	15265.94	4.63	0.5	1220	29/84	

control

actin-like [Mus musculus]					**29730.87**	8850209.0		1	
jmrawigg5miniggfreebead,1124-1126	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	26205.75	5.64	0.6	1244	8/21	
rawextr_450beadigg_Mar04, 1348	-.KDLYANTVLSGGTTMYPGLADR.-	2344.63	3	3525.12	2.19	0.3	486	1/4	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
FLNB_MOUSE Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP					32979.13	38257404.0	31		
jmfag5minigg200mmnacl, 432	- ASGRGLQPK.-	914.05	2	640.01	1.19	0.1	450	5/8	3
jmfag1mnacl5mincon,432-434	- ASGRGLQPK -	914.05	2	503.63	1.42	0.1	302	5/8	3
jmfag5minigg1000mmnacl, 436	- ASGRGLQPK -	914.05	2	1473.04	1.79	0.2	534	11/16	3
jmfag5minigg600mmnacl, 598	FNGSHVVGSPFKVR -	1531.74	3	672.57	1.72	0.0	373	15/52	3
JMFAGNACL10_2B21E3, 696	- VIVLFAGQHISKSPFEVNVDK -	2328.70	3	278.17	1.46	0.0	168	17/80	1
jmfag5minigg250mmnacl, 702	- VHAGGPGLK.-	907.05	2	369.51	0.85	0.1	229	7/16	1
jmfag5minigg350mmnacl, 909	-.CLATGPGIAPTVKTGEEVGFVVDAKTAGK -	2818.24	2	164.41	0.96	0.1	43	1/8	1
jmfag5minigg250mmnacl, 960	- ASGRGLQPK -	914.05	2	1150.10	1.76	0.1	627	3/4	3
jmfag1mnacl2.5minigg,1250-1252	- ETADFKVDTKAAGSGELGVTVK.-	2224.45	3	1789.23	2.61	0.1	657	25/84	1
jmfag5minigg bead, 1369	-.FADEHVPGSPFTVKISGEGR.-	2131.33	3	477.69	1.07	0.0	448	5/19	3
jmfag1mnacl0minigg, 1726	- YSVAVTWGGHHIPKSPFEVQVGPEAGMQK.-	3138.55	2	328.67	1.05	0.2	78	1/7	1
jmfag1mnacl7.5minigg, 1732	- VKVFGPGVERSGLK -	1473.75	3	215.65	1.08	0.0	196	1/4	1
jmfag5minigg300mmnacl,2040-2042	- ANEPTHFTVDCTEAGEGDVSVGIKCDAR -	2923.14	3	351.21	1.79	0.0	191	19/108	1
jmfag5minigg150mmnacl, 2108	- EAFTNKSNVFTVVTRGAGIGGLGITVEGPSESK.-	3324.69	2	97.88	0.95	0.1	77	9/64	1
jmfag5minigg400mmnacl, 2744	- VMYTPMAPGNYLIGVKYGGPNHISRSPFK.-	3198.74	2	42.70	0.79	0.0	34	3/28	3
jmfag5minigg400mmnacl, 3064	- RCSQVKLGSAADFLLDISETDLSTLTASIK.-	3184.61	2	104.10	0.75	0.0	138	11/58	2
ajrawphagjun20actinDPI,600-602	-.VDIQTEDLEDGTCK.-	1566.67	3	117.30	1.36	0.0	76	1/4	3
jmrawgg5min300mmnacisyringednase,743-745	- VKAEGPGLSK -	986.15	2	651.14	0.98	0.2	241	1/2	1
jmIgG150rawphag3007, 1306	- PFDLVIPFAVRK -	1402.71	2	887.84	1.76	0.0	491	1/2	1
jmIgG250rawphag3007, 1332	- PFDLVIPFAVRK -	1402.71	2	1349.08	1.85	0.2	477	1/2	1
jmfagtimecon2.5min,458,458.2	- ASGRGLQPK -	914.05	0	510.57	1.38	0.0	368	9/16	3
jmfagtimecon2.5min,452,452.2	- ASGRGLQPK.-	914.05	0	836.08	1.47	0.1	485	11/16	3
jmfagtimecon2.5min,2000,2000.3	-.AEGPGLSKAGVENGKPTHFTVHTK.-	2453.74	0	1117.78	2.07	0.2	311	5/23	1
jmfag5mincont150mmnacl, 321	- INGLENRVEVGK -	1328.50	3	772.58	1.55	0.0	487	17/44	1
jmfag5mincont400_030531151834, 358	- VDPSHDASK.-	955.99	2	609.04	1.23	0.1	381	9/16	3
jmfagtimecont10min_030601202502, 364	- QQYNVTYVVK -	1242.41	3	706.41	1.44	0.1	432	7/18	3
jmfag1mnacl5mincon,432-434	- ASGRGLQPK -	914.05	2	503.63	1.42	0.1	302	5/8	3
AJRAWpellet_contr_jun13, 698	- VDPSHDASKVKAEGPGLSK -	1923.12	3	979.48	1.38	0.0	687	7/24	1
jmbeads400rawphag3007, 953	- KGEITGTVHMPSGKK -	1570.84	3	772.38	1.75	0.1	308	2/7	1
jmbeads600nacirawphage3007, 1176	-.QQYNVTYVVKER.-	1527.71	2	141.77	0.98	0.1	84	7/22	3
jmbeads600nacirawphage3007, 1248	-.DAGYGGISLAVEGPSK -	1521.65	2	338.94	1.12	0.1	235	1/3	2
jmfag5mincont150mmnacl, 1589	-.VEPAIDTSGIK.-	1130.27	2	166.28	1.22	0.0	123	9/20	1
jmbeads300rawphag3007, 1840	- IRATQTGDASKCLATGPGIAPTVK.-	2357.72	3	809.89	1.65	0.1	394	11/46	1
jmfagtimecon10min, 1930	-.TATFTIVTEDAGEGGLDLAIEGPSKAEISCIDNK.-	3467.80	3	220.23	1.24	0.0	178	3/22	1
AJRAWSoluteContr_june13, 2512	- GFHVVEVTYDDVPIPNSPFKVAVTEGCQPSR.-	3389.78	2	81.95	0.70	0.0	105	3/20	1
phagrawF400_dec20, 980	-.NGNHVANSPVSIMVVQSEIGDARR -	2551.83	3	478.55	1.62	0.0	285	19/92	2
phagrawFsuc700_dec23, 1369	- PFDLVIPFAVRK.-	1402.71	2	505.88	1.01	0.1	288	9/22	1
phagrawF350_dec20, 1668	-.LDVTILSPSR.-	1101.28	1	911.10	1.29	0.0	692	11/18	1
phagrawFchlfbead_dec23, 1681	- ANEPTHFTVDCTEAGEGDVSVGIKCDAR.-	2923.14	3	1925.02	2.33	0.3	146	1/6	1
phagrawFsuc350_dec20, 2090	-.NGNHVANSPVSIMVVQSEIGDARR.-	2551.83	2	28.73	0.73	0.0	35	4/23	2
rawsucrfp_600phagrgg_Mar04, 2210	- DSPYMAFIHPATGDYNPDLVQAYGPGLEK.-	3158.48	2	183.67	0.94	0.1	41	3/28	1
phagrawF200_dec22, 2277	- AKVTGQRLVSPGSANETSSILVESVTR.-	2788.11	3	500.51	1.28	0.1	233	19/104	3
phagrawFsuc600_dec20, 3274	-.ERGDYVLAVKWGEEHIPGSPFHVTVP.-	2921.26	2	95.21	0.84	0.1	62	9/50	3
RawPhg2007MeEthmeth3digest, 1028	-.VNQPASFAIR.-	1103.26	2	337.51	0.91	0.0	367	1/2	3
rawphag2007chlfsol3, 1053	- YNDKHIPGSPFTAKITDDNR.-	2290.48	3	498.83	1.64	0.0	304	1/4	2
phagrawFchlfbead_dec23, 1681	-.ANEPTHFTVDCTEAGEGDVSVGIKCDAR.-	2923.14	3	1925.02	2.33	0.3	146	1/6	1
rawphag2007chlfbead3,2023-2025	-.VMYTPMAPGNYLIGVKYGGPNHISR.-	2737.20	3	312.69	1.53	0.0	192	1/4	3
ajrawphagjun20actinDPI,600-602	-.VDIQTEDLEDGTCK.-	1566.67	3	117.30	1.36	0.0	76	1/4	3
jmfag5minigg250mmnacl, 702	-.VHAGGPGLK.-	907.05	2	369.51	0.85	0.1	229	7/16	1
jmrawgg5min300mmnacisyringednase,743-745	-.VKAEGPGLSK.-	986.15	2	651.14	0.98	0.2	241	1/2	1
jmIgG150rawphag3007, 1306	- PFDLVIPFAVRK.-	1402.71	2	887.84	1.76	0.0	491	1/2	1
jmIgG250rawphag3007, 1332	-.PFDLVIPFAVRK.-	1402.71	2	1349.08	1.85	0.2	477	1/2	1
jmbsa600nacirawphag3007, 1276	-.PVQPGPHVVKVSFAGDAIPK.-	2044.39	3	373.84	1.81	0.0	206	7/38	1
jmbsa300nacirawphag3007,1344-1346	-.EAGAGGLSIAVEGPSK.-	1443.59	2	161.20	1.13	0.0	122	3/10	7
jmkdactinrawphag3007, 1002	- NSHCVRFVPQEMGVHTVSVK.-	2255.61	3	597.71	1.59	0.1	324	1/4	3
jmkdl1000nacirawphag3007, 1562	-.TSRAPAVATVGSICDLNLK.-	1917.22	2	237.21	1.02	0.1	112	1/4	3
jmkdl250nacirawphag3007, 1882	-.ATVHDNKDGTYAVTYIPDKTGR.-	2423.62	3	302.62	1.39	0.1	126	17/84	1

control

FLNB_MOUSE Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP					4924.09	38257404.0	22		
FPbeads500_dec19, 146	-.CSQVKLGSAADFLLDISETDLSTLTASIK.-	3028.42	2	175.37	0.97	0.0	162	5/28	2
rawextr_chlfbeadIgG_Mar04, 318	- LNGAKGKIDAK.-	1115.31	3	234.13	1.64	0.0	126	3/8	3
rawextr_450beadigg_Mar04, 570	-.YHQRPTFR -	1105.23	2	460.52	1.22	0.0	374	9/14	3
jmrawgg5miniggfreebead, 788	-.ARAYGRGIEPTGNMVK.-	1720.98	3	981.37	1.81	0.2	267	1/3	2
rawextr_chlfbeadIgG_Mar04, 1232	-.PVQPGPHVVKVSFAGDAIPK.-	2044.39	3	1330.61	1.74	0.1	707	21/76	1
rawextr_chlfbeadIgG_Mar04, 1928	- CVYKPVQPGPHVVKVSFAGDAIPK.-	2538.01	3	598.62	1.53	0.1	359	21/92	1
FPbeads500_dec19, 1966	-.AQGDASKVTAKGPGLETTGNIANK.-	2329.55	3	1143.48	1.73	0.1	582	8/23	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
profilin 1; actin binding protein [Mus musculus]					**466850.53**	6755040.0	10		
jm5miniggrawlowionic,2132-2134	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	1469.58	2.09	0.2	209	9/34	1
jmbeads250rawphag3007, 2062	-.DSLLQDGEFTMDLR.-	1640.80	2	1886.13	1.73	0.3	205	9/26	1
jmbeads500rawphag3007, 1246	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	709.51	1.43	0.0	474	5/17	1
jmbeads600naclrawphage3007,1273-1275	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	610.66	1.40	0.1	406	1/4	1
jmfag1mnacl0minigg, 1496	-.TFVSITPAEVGVLVGK.-	1617.91	2	10209.61	2.81	0.5	941	11/15	1
jmfag1mnacl2,5minigg, 1534	-.TFVSITPAEVGVLVGK.-	1617.91	2	3288.48	2.15	0.3	616	17/30	1
jmfag1mnacl2,5minigg, 1546	-.TFVSITPAEVGVLVGK.-	1617.91	2	9619.83	2.59	0.5	828	2/3	1
jmfag1mnacl2,5minigg, 1956	-.DSLLQDGEFTMDLR.-	1640.80	2	4824.18	2.61	0.3	891	8/13	1
jmfag1mnacl5mincon,1770-1772	-.TFVSITPAEVGVLVGK.-	1617.91	1	2102.14	2.04	0.3	323	11/30	1
jmfag1mnacl5minigg, 1328	-.STGGAPTFNVTVTMTAK.-	1683.91	2	211.48	1.52	0.0	139	9/32	1
jmfag1mnacl5minigg, 1724	-.TFVSITPAEVGVLVGK.-	1617.91	2	9597.63	3.50	0.4	806	2/3	1
jmfag1mnacl5minigg, 1730	-.TFVSITPAEVGVLVGK.-	1617.91	2	8766.98	2.99	0.5	812	2/3	1
jmfag1mnacl7,5minigg, 1900	-.DSLLQDGEFTMDLR.-	1640.80	2	3105.36	2.35	0.3	664	1/2	1
jmfag1mnacl7,5minigg,1562-1564	-.TFVSITPAEVGVLVGK.-	1617.91	2	12911.06	3.57	0.5	941	11/15	1
jmfag5mincon300mmnacl,1640-1642	-.DSPSVWAAVPGK.-	1214.35	2	2657.93	1.83	0.2	882	13/22	1
jmfag5mincon450mmnacl, 1470	-.DSPSVWAAVPGK.-	1214.35	2	612.42	1.36	0.1	327	9/22	1
jmfag5mincon450mmnacl,2042-2044	-.TFVSITPAEVGVLVGK.-	1617.91	2	9531.98	3.15	0.5	679	3/5	1
jmfag5mincont150mmnacl, 1473	-.TFVSITPAEVGVLVGK.-	1617.91	2	4007.35	2.43	0.4	366	7/15	1
jmfag5mincont200mmnacl, 1704	-.TFVSITPAEVGVLVGK.-	1617.91	2	10262.00	3.22	0.5	762	19/30	1
jmfag5mincont200mmnacl, 1714	-.TFVSITPAEVGVLVGK.-	1617.91	1	218.35	1.29	0.0	169	4/15	1
jmfag5mincont350, 122	-.EGVHGGLINK.-	1024.16	2	753.98	1.59	0.1	420	11/18	1
jmfag5mincont350, 1494	-.TFVSITPAEVGVLVGK.-	1617.91	1	487.66	1.30	0.1	302	1/3	1
jmfag5mincont400_030531151834,1456-1458	-.TFVSITPAEVGVLVGK.-	1617.91	2	14117.92	3.33	0.6	970	2/3	1
jmfag5minigg1000mmnacl, 2154	-.DSLLQDGEFTMDLR.-	1640.80	2	725.29	1.71	0.1	283	11/26	1
jmfag5minigg150mmnacl, 1014	-.DSPSVWAAVPGK.-	1214.35	2	3869.69	1.68	0.3	1209	15/22	1
jmfag5minigg200mmnacl, 1516	-.SSFFVNGLTLGGQK.-	1455.64	2	4722.71	2.12	0.4	425	6/13	1
jmfag5minigg200mmnacl,1662-1664	-.TFVSITPAEVGVLVGK.-	1617.91	2	11119.36	4.10	0.4	872	7/10	1
jmfag5minigg250mmnacl,1482-1484	-.DSPSVWAAVPGK.-	1214.35	2	3567.48	1.89	0.3	1037	8/11	1
jmfag5minigg250mmnacl,2094-2096	-.TFVSITPAEVGVLVGK.-	1617.91	2	11698.00	3.33	0.5	660	3/5	1
jmfag5minigg300mmnacl, 1976	-.SSFFVNGLTLGGQK.-	1455.64	2	6674.16	2.41	0.4	824	8/13	1
jmfag5minigg300mmnacl, 1980	-.SSFFVNGLTLGGQK.-	1455.64	2	7349.71	2.52	0.5	523	1/2	1
jmfag5minigg300mmnacl,1676-1678	-.DSPSVWAAVPGK.-	1214.35	2	1146.51	1.51	0.2	413	1/2	1
jmfag5minigg300mmnacl,2300-2302	-.TFVSITPAEVGVLVGK.-	1617.91	2	12270.37	3.18	0.6	811	19/30	1
jmfag5minigg350mmnacl, 1413	-.TFVSITPAEVGVLVGK.-	1617.91	2	7830.80	2.63	0.5	753	3/5	1
jmfag5minigg350mmnacl, 1417	-.TFVSITPAEVGVLVGK.-	1617.91	2	7103.51	2.35	0.5	642	3/5	1
jmfag5minigg350mmnacl, 3187	-.DSLLQDGEFTMDLR.-	1640.80	2	2124.78	1.47	0.3	489	11/26	1
jmfag5minigg400mmnacl, 1570	-.TFVSITPAEVGVLVGK.-	1617.91	2	9031.11	2.65	0.5	635	17/30	1
jmfag5minigg400mmnacl, 1576	-.TFVSITPAEVGVLVGK.-	1617.91	2	11329.97	2.98	0.6	672	3/5	1
jmfag5minigg450mmnacl_030527025134, 1632	-.TLVLLMGK.-	875.16	2	1771.10	1.92	0.2	449	11/14	2
jmfag5minigg450mmnacl_030527025134, 1958	-.SSFFVNGLTLGGQK.-	1455.64	2	6152.95	2.49	0.4	618	15/26	1
jmfag5minigg450mmnacl_030527025134, 1964	-.SSFFVNGLTLGGQK.-	1455.64	2	12370.37	2.70	0.6	1320	9/13	1
jmfag5minigg450mmnacl_030527025134,2262-2264	-.TFVSITPAEVGVLVGK.-	1617.91	2	9510.52	3.14	0.5	606	17/30	1
jmfag5minigg500mmnacl, 1830	-.SSFFVNGLTLGGQK.-	1455.64	2	4433.10	2.22	0.4	433	7/13	1
jmfag5minigg500mmnacl,1996-1998	-.TFVSITPAEVGVLVGK.-	1617.91	2	7971.87	2.90	0.5	603	3/5	1
jmfag5minigg600mmnacl, 1172	-.SSFFVNGLTLGGQK.-	1455.64	2	10560.62	3.11	0.5	1005	9/13	1
jmfag5minigg600mmnacl, 1322	-.SSFFVNGLTLGGQK.-	1455.64	2	1545.95	1.50	0.3	362	11/26	1
jmfag5miniggbead_030528200105, 1513	-.TFVSITPAEVGVLVGK.-	1617.91	2	13513.86	3.59	0.5	944	2/3	1
jmfag5miniggbead_030528200105, 1517	-.TFVSITPAEVGVLVGK.-	1617.91	2	5960.04	2.85	0.4	456	1/2	1
jmfagcon5minn600mmnacl, 1713	-.TFVSITPAEVGVLVGK.-	1617.91	2	3941.40	1.86	0.4	507	1/2	1
JMFAGNACL5B21E3, 1424	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	283.92	1.57	0.0	178	9/34	1
JMFAGNACL5B21E3, 994	-.TLVLLMGK.-	875.16	2	257.29	1.07	0.0	232	1/2	2
JMFAGNACL5B21E3,1262-1264	-.SSFFVNGLTLGGQK.-	1455.64	2	11861.86	3.01	0.5	1173	9/13	1
jmfagtimecon2.5min.1364.1364.2	-.SSFFVNGLTLGGQK.-	1455.64	0	12248.09	3.28	0.5	1344	9/13	1
jmfagtimecon2.5min.1368.1368.2	-.SSFFVNGLTLGGQK.-	1455.64	0	10259.25	3.21	0.5	662	15/26	1
jmfagtimecon2.5min.1658.1658.2	-.TFVSITPAEVGVLVGK.-	1617.91	0	8100.41	2.50	0.5	658	17/30	1
jmfagtimecon2.5min.1664.1664.2	-.TFVSITPAEVGVLVGK.-	1617.91	0	9892.53	3.31	0.5	653	19/30	1
jmfagtimecon2.5min.2000.2000.2	-.DSLLQDGEFTMDLR.-	1640.80	0	1002.09	1.65	0.0	594	1/2	1
jmfagtimecon5min, 1593	-.STGGAPTFNVTVTMTAK.-	1683.91	2	1970.97	2.12	0.2	370	1/2	1
jmfagtimecon5min, 1860	-.STGGAPTFNVTVTMTAK.-	1683.91	2	417.82	1.33	0.1	143	11/32	1
jmfagtimecon7.5min.1506.1506.2	-.TLVLLMGK.-	875.16	0	3611.23	2.06	0.3	545	6/7	2
jmfagtimecon7.5min.1824.1826.2	-.SSFFVNGLTLGGQK.-	1455.64	0	13415.62	3.54	0.5	792	8/13	1
jmfagtimecont0min_030601230741, 1802	-.SSFFVNGLTLGGQK.-	1455.64	1	857.33	1.49	0.2	166	9/26	1
jmfagtimecont0min_030601230741, 1946	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	304.71	1.23	0.0	237	1/4	1
jmfagtimecont0min_030601230741, 2106	-.TFVSITPAEVGVLVGK.-	1617.91	2	12432.22	3.44	0.6	574	3/5	1
jmfagtimecont0min_030601230741, 2114	-.TFVSITPAEVGVLVGK.-	1617.91	2	1445.42	1.74	0.2	265	2/5	1
jmfagtimecont0min_030601230741,1798-1800	-.SSFFVNGLTLGGQK.-	1455.64	2	4945.55	2.11	0.4	885	8/13	1
jmfagtimecont10min_030601202502, 2026	-.SSFFVNGLTLGGQK.-	1455.64	2	12075.82	3.19	0.5	1182	19/26	1
jmfagtimecont10min_030601202502, 2030	-.SSFFVNGLTLGGQK.-	1455.64	2	8053.42	2.17	0.5	969	17/26	1
jmfagtimecont10min_030601202502,1692-1694	-.TLVLLMGK.-	875.16	2	2435.40	2.06	0.3	308	5/7	2
jmfreebeadsrawphag3007, 1122	-.SSFFVNGLTLGGQK.-	1455.64	2	10519.74	3.24	0.5	814	8/13	1
JMMAGNEGB16D3, 1032	-.DSPSVWAAVPGK.-	1214.35	2	988.98	1.32	0.0	740	13/22	1
JMMAGNEGB16D3, 1538	-.TFVSITPAEVGVLVGK.-	1617.91	2	1022.52	1.77	0.2	285	2/5	1
JMMAGTube1B16E3, 1818	-.DSLLQDGEFTMDLR.-	1640.80	2	3159.92	2.24	0.3	326	5/13	1
JMMAGTube1B16E3,1578-1580	-.TFVSITPAEVGVLVGK.-	1617.91	2	15005.53	4.25	0.5	738	2/3	1
jmrawigg5minbeadsfreezethaw, 1388	-.TFVSITPAEVGVLVGKDR.-	1889.19	2	2509.09	2.16	0.3	237	13/34	1
jmrawigg5minbeadsfreezethaw, 1396	-.TFVSITPAEVGVLVGKDR.-	1889.19	2	4356.67	2.12	0.4	188	6/17	1
jmrawigg5minbeadsfreezethaw, 1516	-.TFVSITPAEVGVLVGK.-	1617.91	2	14304.61	3.46	0.6	604	3/5	1
jmrawigg5minbeadsfreezethaw,1390-1392	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	603.95	1.80	0.1	254	1/4	1
jmrawrminigg200mmnaclsyringdnas, 1850	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	3626.37	2.72	0.3	506	23/68	1
jmrawrminigg200mmnaclsyringdnas, 1854	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	1841.82	1.99	0.3	175	15/68	1
jmrawrminigg200mmnaclsyringdnas, 2002	-.TFVSITPAEVGVLVGK.-	1617.91	2	1814.70	2.10	0.2	336	13/30	1
phagrawFsuc60MeOH_dec23,1168-1170	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	647.05	1.81	0.1	307	9/34	1
rawphag2007chfbead3, 2239	-.DSLLQDGEFTMDLR.-	1640.80	2	321.22	1.10	0.1	206	4/13	1

control

profilin 1; actin binding protein [Mus musculus]					**13772.56**	6755040.0			
jmraw5minbsafreezthaw, 1838	-.SSFFVNGLTLGGQK.-	1455.64	2	2250.81	1.79	0.3	392	11/26	1
jmraw5minbsafreezthaw, 1984	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	1772.23	1.86	0.3	204	1/4	1
jmraw5minbsafreezthaw, 1992	-.TFVSITPAEVGVLVGKDR.-	1889.19	3	1246.99	2.06	0.2	288	5/17	1
jmraw5minbsafreezthaw, 1994	-.TFVSITPAEVGVLVGKDR.-	1889.19	2	4251.27	2.18	0.4	223	13/34	1
jmraw5minbsafreezthaw, 1994	-.TFVSITPAEVGVLVGKDR.-	1889.19	2	4251.27	2.18	0.4	223	13/34	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
CAPB_MOUSE F-actin capping protein beta subunit (CapZ beta)					**15537.88**	1345668.0	5		
jmfag5mincont400_030531151834, 592	-.SGSGTMNLGGSLTR.-	1338.47	2	4958.43	2.48	0.3	805	17/26	1
jmbeads450naclrawphag3007, 800	-.MSDQQLDCALDLMRR.-	1796.09	3	322.46	1.27	0.1	160	2/7	1
rawphag2007chlfsol3.827-829	-.FKQLQRELSQVLTQR.-	1875.17	3	461.78	1.58	0.0	278	17/56	
jmfagtimecont10min_030601202502, 1308	-.MSDQQLDCALDLMR.-	1639.90	3	336.07	1.39	0.1	191	15/52	1
jmfagtimecont10min_030601202502, 1326	-.SGSGTMNLGGSLTR.-	1338.47	2	2731.50	1.77	0.2	1034	8/13	1
JMFAGNACL5B21E3, 666	-.MSDQQLDCALDLMR.-	1639.90	3	289.06	1.28	0.0	213	1/4	1
jmfag1mnacl2.5minigg, 670	-.MSDQQLDCALDLMR.-	1639.90	3	430.93	1.56	0.0	271	4/13	1
JMFAGNACL5B21E3, 1014	-.SPWSNKYDPPLEDGAMPSAR.-	2219.42	3	6007.66	2.76	0.4	829	13/38	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
CAPB_MOUSE F-actin capping protein beta subunit (CapZ beta)					**578.75**	1345668.0	2		
rawextr_chlfbeadIgG_Mar04, 768	-.MSDQQLDCALDLMR.-	1639.90	3	578.75	1.62	0.0	350	4/13	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
capping protein (actin filament), gelsolin-like [Mus musculus]					**277641.04**	6680842.0	14		
jmfag1mnacl5minigg, 326	- VSDATGQMNLTK.-	1265.42	2	3397.37	1.91	0.2	1483	9/11	3
jmfag5minigg600mmnacl, 398	-.VSDATGQMNLTK.-	1265.42	2	5050.06	2.48	0.3	1080	15/22	3
jmfag1mnacl2.5minigg, 406	-.VSDATGQMNLTK.-	1265.42	2	4891.13	2.05	0.4	984	8/11	3
jmfag1mnacl2.5minigg, 410	-.VSDATGQMNLTK.-	1265.42	2	4174.01	2.34	0.3	996	8/11	3
jmfag1mnacl7.5minigg, 414	-.VSDATGQMNLTK.-	1265.42	2	4861.48	2.38	0.3	1395	9/11	3
jmfag5minigg350mmnacl, 1003	-.QAALQVADGFISR.-	1376.54	2	7861.09	2.42	0.5	765	5/8	2
jmfag1mnacl5minigg, 1276	-.QAALQVADGFISR.-	1376.54	2	6901.22	2.28	0.5	773	2/3	2
jmfag5minigg500mmnacl, 1494	-.QAALQVADGFISR.-	1376.54	2	7143.35	2.31	0.5	653	5/8	2
jmrawigg5minbeadsfreezethaw, 1566	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	3	9647.80	3.14	0.5	695	29/100	3
jmrawminigg200mmnaclsyringdnas, 2064	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	3	3329.96	2.31	0.3	661	7/25	3
jmrawigg5miniggfreebead, 1496	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	3	3730.86	2.77	0.3	460	6/25	3
jmfag1mnacl0minigg, 266	-.VSDATGQMNLTK.-	1265.42	2	1325.09	1.49	0.1	679	13/22	3
jmfag1mnacl5mincon, 302	-.VSDATGQMNLTK.-	1265.42	2	5754.67	2.68	0.4	925	8/11	3
jmfag1mnacl5mincon, 316	-.VSDATGQMNLTK.-	1265.42	2	6448.84	2.90	0.4	999	17/22	3
JMMAGNEGB16D3, 352	-.VSDATGQMNLTK.-	1265.42	2	3238.32	2.01	0.3	978	15/22	3
JMMAGTube1B16E3, 362	-.VSDATGQMNLTK.-	1265.42	2	3535.89	2.42	0.2	1210	9/11	3
jmfag1mnacl7.5minigg, 1142	-.EGNPEEDITADQTNAQAAALYK.-	2350.44	3	934.34	1.62	0.1	549	11/42	2
jmfag5minigg400mmnacl, 1320	-.ELQGNESDLFMSYFPRGLK.-	2232.50	3	288.83	1.24	0.1	201	5/24	1
jmfag1mnacl5mincon, 1326	-.EGNPEEDITADQTNAQAAALYK.-	2350.44	2	12680.59	3.43	0.6	607	17/42	2
jmfag5minigg300mmnacl,1776-1778	-.QAALQVADGFISR.-	1376.54	2	1695.43	1.94	0.2	457	7/12	2
JMFAGNACL5B21E3, 2938	-.DEQGACAVLAVHLNTLLGERPVQHR.-	2728.09	3	295.35	1.32	0.0	223	17/96	3
jmraw5minigg250mmnaclsyringdnase, 822	-.KNIRATER.-	988.13	2	208.43	0.81	0.1	222	1/2	3
ajrawphagactin20, 924	-.VGISQDNLR.-	1002.11	2	732.87	1.65	0.1	383	5/8	1
jmrawigg5minbeadsfreezethaw, 2108	-.VADSSPFASELLIPDDCFVLDNGLCGK.-	2827.18	3	634.20	2.28	0.0	277	5/26	2
jmfagtimecon7.5min.2154 2154.3	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	0	6231.73	2.81	0.4	496	1/4	3
jmfagtimecon2.5min.1212.1214.2	-.QAALQVADGFISR.-	1376.54	0	15307.35	4.11	0.5	1197	19/24	2
jmfag5mincont200mmnacl, 296	-.VSDATGQMNLTK.-	1265.42	2	10577.45	3.05	0.5	1250	9/11	3
jmfag1mnacl5mincon, 302	-.VSDATGQMNLTK.-	1265.42	2	5754.67	2.66	0.4	925	8/11	3
jmfag1mnacl5mincon, 316	-.VSDATGQMNLTK.-	1265.42	2	6448.84	2.90	0.4	999	17/22	3
jmfag5mincont150mmnacl, 331	-.VSDATGQMNLTK.-	1265.42	2	5661.74	2.78	0.3	1031	9/11	3
jmfagtimecont0min_030601230741, 1002	-.VSDATGQMNLTK.-	1265.42	2	3184.75	2.36	0.1	1171	17/22	3
jmfagtimecont0min_030601230741, 1006	-.VSDATGQMNLTK.-	1265.42	2	6376.70	2.38	0.4	833	15/22	3
jmfag5mincont150mmnacl,1051-1053	-.QAALQVADGFISR.-	1376.54	2	12693.22	3.53	0.5	1222	19/24	2
jmfagtimecont10min_030601202502, 1154	-.VSDATGQMNLTK.-	1265.42	2	4656.67	2.54	0.3	1001	17/22	3
jmfag5mincont200mmnacl, 1258	-.QAALQVADGFISR.-	1376.54	2	5910.83	2.24	0.4	831	17/24	2
jmfag1mnacl5mincon, 1326	-.EGNPEEDITADQTNAQAAALYK.-	2350.44	2	12680.59	3.43	0.6	607	17/42	2
jmfag5mincont400_030531151834, 1512	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	3	13097.76	4.38	0.5	616	7/25	3
jmfag5mincon250mmnacl, 1534	-.QAALQVADGFISR.-	1376.54	2	10052.64	2.75	0.5	1094	3/4	2
jmfagtimecont0min_030601230741, 1610	-.QAALQVADGFISR.-	1376.54	2	9196.62	3.03	0.5	931	17/24	2
jmfag5mincon300mmnacl, 1706	-.EGNPEEDITADQTNAQAAALYK.-	2350.44	3	4165.73	3.12	0.3	697	25/84	2
jmfag5mincont200mmnacl, 1754	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	3	4483.05	2.57	0.4	441	23/100	3
jmfag5mincont200mmnacl, 1786	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	2	7553.41	2.73	0.5	489	9/25	3
jmfag5mincon250mmnacl, 2100	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	3	4534.25	2.54	0.4	464	23/100	3
jmfagtimecont10min_030601202502,2416-2418	-.AQVEIITDGEEPAEMIQVLGPKPALK.-	2778.22	3	13614.75	3.87	0.5	844	3/10	3
ajrawmediapbsnocells, 1042	-.QAALQVADGFISR.-	1376.54	2	10832.94	3.13	0.5	995	3/4	2
phagrawF200_dec22, 2263	-.YSPNTQVEILRQGR.-	1661.85	2	69.88	0.92	0.0	71	3/13	1
phagrawFsuc400_dec20, 2436	-.VGISQDNLRATPAAIRK.-	1811.08	1	87.10	0.62	0.1	75	5/32	1
jmfag1mnacl5minigg, 326	-.VSDATGQMNLTK.-	1265.42	2	3397.37	1.91	0.2	1483	9/11	3
jmraw5minigg250mmnaclsyringdnase, 822	-.KNIRATER.-	988.13	2	208.43	0.81	0.1	222	1/2	3
ajrawphagactin20, 924	-.VGISQDNLR.-	1002.11	2	732.87	1.65	0.1	383	5/8	1
jmrawigg5minbeadsfreezethaw, 2108	-.VADSSPFASELLIPDDCFVLDNGLCGK.-	2827.18	3	634.20	2.28	0.0	277	5/26	2
jmkdl400naclrawphag3007_030802153313, 1686	-.EGNPEEDITADQTNAQAAALYK.-	2350.44	3	734.34	1.62	0.1	307	5/21	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
capping protein (actin filament), gelsolin-like [Mus musculus]					**250.79**				
jmbsa1000naclrawphag3007, 1679	-.EGNPEEDITADQTNAQAAALYK.-	2350.44	3	250.79	1.43	0.1	130	3/14	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Coronin, actin binding protein 1A [Mus musculus] g					**10780.84**	31418362.0	14		
JMFAGNACL5B21E3, 164	-.NLNAIVQK.-	900.06	2	3115.91	2.24	0.3	494	11/14	2
jmfag1mnacl2.5minigg, 186	-.NLNAIVQK.-	900.06	2	3090.69	2.21	0.3	414	5/7	2
JMFAGNACL5B21E3, 422	-.LDRLEETVQAK.-	1302.46	3	2674.63	2.79	0.2	617	19/40	2
jmfagfrench20minigg1mnackdit, 1620	-.MSRQVVRSSK.-	1178.39	2	298.45	1.30	0.1	204	4/9	2
jmrawigg5min450mmnaclsd, 1944	-.YFEITFEAPFLHYLSMFSSKESQR.-	2959.32	2	272.28	0.74	0.2	66	7/46	
jmfagtimecont10min_030601202502, 1078	-.NLNAIVQK.-	900.06	2	1328.90	2.06	0.1	525	11/14	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
Shroom-related protein; F-actin-binding protein; likely ortholog of mo					**8144.07**	18699722.0	40		
ajrawphag1MNaCl20, 288	- DLELGAPVASR.-	1128.26	3	405.31	1.37	0.1	147	1/4	
jmfag5minfrench1mnacldttdpi, 1872	-.GDLLSGANGGTRGTQR.-	1560.66	2	213.58	1.39	0.0	154	1/3	
jmfag_20_minfrench1mnacldttdpi, 1872	-.GDLLSGANGGTRGTQR.-	1560.66	2	213.58	1.39	0.0	154	1/3	
jmIgG1000nacirawphag3007, 1970	- STHSNKPSSHPHSLK.-	1644.77	2	220.82	0.83	0.1	238	9/28	
jmfag5minfrench1mnacldttdpi, 2040	- GCEGDGPEHGVEEGTRKR.-	1914.01	2	339.32	0.99	0.1	314	11/34	
jmfag_20_minfrench1mnacldttdpi, 2040	- GCEGDGPEHGVEEGTRKR.-	1914.01	2	339.32	0.99	0.1	314	11/34	
jmrawigg5minbeadsyringdnase, 2057	- MNEVGIVEEAEPAPLGPQRNGMR.-	2495.82	3	220.22	1.26	0.0	174	7/44	
jmfagtimecon2.5min 820.820.2	-.GPQRPDARLLR.-	1279.48	0	82.32	0.79	0.0	104	7/20	
jmfagcon5minn600mmnacl, 265	- LTPEQK -	715.82	2	366.28	1.06	0.1	299	7/10	
jmfagtimecont0min_030601230741, 950	-.KEAVSLVKGSYK.-	1309.54	3	1726.91	1.87	0.3	227	7/22	
jmbeads250rawphag3007, 2400	- QPCGQQLSGGASDSGR.-	1548.62	2	81.02	1.02	0.0	68	1/5	
jmfagtimecont0min_030601230741, 3398	- NEDKEAVSMLVNCPAYYSVSAPKAELLNK.-	3185.62	2	53.84	0.67	0.1	27	5/56	
ajrawmediapbsnocells, 284	- GDLLSGANGGTRGTQR.-	1560.66	3	358.26	1.27	0.0	258	1/3	
rawphag2007chifbead1,1222-1224	- CLLESLPSDFIPK -	1462.74	3	359.61	1.68	0.0	190	7/24	
rawphag2007chifbead1,1390-1392	-.RGPGPGSASALQGFQYGK.-	1778.95	3	248.21	1.14	0.0	198	19/68	
jmfag1mnacl2,5minigg, 68	- LARVENVLSGLGEDASNEERSSLYEK.-	2867.08	3	295.20	1.29	0.0	207	3/20	
jmbsa350nacirawphag3007, 55	- PKHNYTQK.-	1016.14	3	484.73	1.15	0.2	133	9/28	
jmbsa400nacirawphag3007_030602135631, 1430	-.GVPPPSWSQQCPSSLETATDNLPPK.-	2637.91	3	298.67	1.52	0.0	179	3/16	
jmraw5minbsafreezthaw, 2350	-.PSSWSSLDQKRLCR.-	1663.88	3	769.13	1.67	0.1	424	19/52	
jmbsa1000nacirawphag3007, 3429	-.PVPPAAR.-	707.85	2	274.60	0.88	0.1	167	5/12	
jmidl300nacirawphag3007, 2002	-.LEREGLGQSLSGNFGK.-	1692.86	2	433.64	1.07	0.0	405	11/30	
jmidl300nacirawphag3007, 3184	-.EMPAEVNEEEEQADVNEK.-	2091.15	3	359.49	1.43	0.1	219	7/34	

control

Shroom-related protein; F-actin-binding protein; likely ortholog of mo					**2434.42**	18699722.0	28		
FPbeads150_Dec19, 363	-.TKSAFSSLQNIPESLRR.-	1935.18	2	168.80	0.94	0.1	125	7/32	
rawextr_450beadigg_Mar04, 720	- REATLLPATVAETQQAPRDR.-	2224.48	3	885.16	2.10	0.2	177	5/19	
FPbeads600_Dec19, 790	- EARASANGQGYDK.-	1367.41	2	199.88	1.13	0.1	122	1/3	
rawextr_300beadigg_Mar4,884-886	-.DPCYLAGPGSRSLSCSER.-	1899.10	3	555.98	1.41	0.1	185	5/17	
rawextr_250beadigg_Mar04, 1362	-.GDLLSGANGGTRGTQR.-	1560.66	2	387.62	1.62	0.1	176	11/30	
rawextr_chifbeadIgG_Mar04, 1810	-.AGKSMSAEDLLERSDVLAGPVHVR -	2538.87	3	236.98	1.49	0.0	159	4/23	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
actin binding protein ShroomS [Mus musculus] attus					**13715.15**	6467992.0	39		
ajrawphagactin20, 322	-.RPEPTAK.-	798.91	2	277.86	1.03	0.0	259	7/12	2
jmrawigg5min450mmnaclsd, 347	-.MKSTLLIEQRK.-	1347.65	3	234.01	1.26	0.0	167	11/40	5
jmrawigg5min300mmnaclsyringednase, 459	-.GQDVLLREGSNFGFVK.-	1766.98	3	1968.76	1.64	0.3	469	3/10	2
ajrawphagjun20actinDPI, 528	-.DAHASADSQGCAK.-	1261.31	2	138.20	0.91	0.0	152	1/3	2
jmrawrminigg200mmnaclsyringdnas, 1066	-.RDLEPGTPATSR.-	1300.40	3	237.26	1.11	0.0	210	3/11	2
ajrawphagactin20, 1132	-.PRPASAHVGMR.-	1179.38	2	180.69	0.87	0.0	209	2/5	2
jmrawigg5min350mmnaclsyringednase, 1329	-.HITPPHGHSPYPSERK.-	1841.02	2	158.24	0.91	0.1	138	3/10	2
jmIgG150rawphag3007, 1342	-.MDGAPGGPPSWGMVAGK.-	1615.86	3	1439.22	2.10	0.1	499	23/64	2
jmIgG300rawphag3007,1372-1374	-.MDGAPGGPPSWGMVAGK.-	1615.86	3	846.52	2.11	0.1	351	11/32	2
jmrawigg5min150mmnacl, 1522	-.HSVTPAAPQAARRGPR.-	1672.88	3	3931.79	2.23	0.4	236	3/10	2
jmraw5minigg500mmnaclsd, 2052	-.AGCEAKASDHKEAVSVLVNCPAYYSVSAAK.-	3070.45	2	40.85	0.78	0.0	44	7/58	3
jmIgG300rawphag3007, 2848	-.ATVASSAPPESSGAADHLK.-	1796.92	2	929.84	1.25	0.2	392	11/36	1
jmbeadsactinrawphag3007, 146	-.EPEALPRK.-	940.08	3	751.06	1.68	0.0	447	13/28	2
jmfagtimecon5min, 241	-.PLSVGSSAYGPGNRPGRTGPTPSTSSSDLDDPK.-	3259.44	2	89.27	0.69	0.1	52	7/64	1
jmfagcon5minn600mmnacl, 1329	-.MDGAPGGPPSWGMVAGK.-	1615.86	2	213.61	1.18	0.0	180	9/32	2
jmfagtimecont10min_030601202502,1358-1358	-.VLGATSFR.-	850.99	2	191.69	0.87	0.1	181	1/2	3
jmbeads1000nacirawphag3007, 1516	-.QEEASRPQCSHLIR.-	1654.83	2	246.51	1.24	0.0	197	9/26	2
jmbeads300rawphag3007, 1862	-.TSLPQRPPPPWVK.-	1503.77	2	162.42	0.81	0.1	154	7/24	1
jmraw5minbsareebeads, 1286	-.VLAGQHEDAR.-	1096.18	2	403.17	1.27	0.1	273	4/9	4
jmfag1mnacl7,5minigg,484-486	-.RGVSSEYEVNPSALLLQGR.-	2076.30	3	319.55	1.35	0.1	166	17/72	2
jmfag1mnacl5minigg, 510	-.RGVSSEYEVNPSALLLQGR.-	2076.30	3	257.54	1.38	0.0	179	1/4	2
jmfag5minigg250mmnacl, 706	-.EGQGQGLSGNSGR.-	1247.26	3	114.39	0.87	0.0	128	11/48	2
jmfag5minigg500mmnacl, 842	-.PTGAASHTGGR.-	1012.06	2	582.69	1.13	0.1	486	13/20	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
A50965 vinculin - mouse (fragment) culus]					**5894.72**	482647.0	16		
jmrawigg5min150mmnacl, 534	-.MAKMIDER.-	994.22	3	311.66	1.11	0.1	97	2/7	3
ajrawphagjun20actinDPI, 628	-.GALAEARKIAELCDDPK.-	1801.06	3	900.19	1.46	0.0	595	9/32	3
jmfag5minigg600mmnacl, 736	-.RALASIDSK.-	961.10	2	380.26	1.12	0.1	296	1/2	3
JMFAGNACL10_2B21E3,1128-1130	-.LSGTSDLLLTFDEAEVR.-	1867.05	3	253.03	1.43	0.1	133	7/32	
jmfag5minigg200mmnacl, 2330	-.KIDAAQNWLADPNGGPEGEEQIRGALAEAR.-	3178.42	2	44.09	0.91	0.0	42	7/58	3
jmfagcon5minn600mmnacl, 1847	-.NLGPGMTK.-	817.98	1	250.52	0.86	0.1	117	5/14	3
rawsucrfp_chlfphagigg_Mar04,150-152	-.ERDDILR.-	917.00	3	342.99	1.24	0.0	272	11/24	3
rawsucrfp_chlfphagigg_Mar04, 236	-.KAEAMTNSK.-	980.12	3	325.77	1.26	0.0	240	3/8	
jmidl1000nacirawphag3007, 1676	-.GILEYLTVAEVVETMEDLVTYTK.-	2617.99	3	441.69	1.46	0.0	297	19/88	3
jmidl250nacirawphag3007, 2074	-.GDEAITEILDEAGKVGELCAGK.-	2219.46	3	278.25	1.34	0.0	202	4/21	
rawsucrfp_chlfphagigg_Mar04,150-152	-.ERDDILR.-	917.00	3	342.99	1.24	0.0	272	11/24	3
rawsucrfp_chlfphagigg_Mar04, 236	-.KAEAMTNSK.-	980.12	3	325.77	1.26	0.0	240	3/8	
rawsucrfp_250phagigg_Mar04, 892	-.NQGIEEALKNRNFTVEK.-	1991.19	3	612.12	1.68	0.1	335	9/32	3
rawsucrfp_350phagigg_Mar04, 1110	-.GQGASPVAMQKAQQVSQGLDVLTAK.-	2513.86	3	470.41	1.87	0.0	235	19/96	2
phagrawFsuc450_dec20, 1442	-.ERREILGTCK.-	1205.41	2	615.01	1.03	0.2	306	1/2	3

control

A50965 vinculin - mouse (fragment) culus]					**1211.60**	482647.0	8		
rawextr_chifbeadIgG_Mar04, 684	-.NQGIEEALKNRNFTVEK.-	1991.19	3	535.39	1.60	0.0	329	17/64	3
rawextr_60MeOHbeadIgg_Mar04,2088-2090	-.ARGQGASPVAMQKAQQVSQGLDVLTAK.-	2741.12	3	676.21	1.94	0.1	170	3/13	2

APPENDIX K – MYOSIN SUMMATION OF IONS

The summation of peptides from Myosins found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
erythrocyte protein band 4.1-like 4b; expressed in high-metastatic cell					2436.21	9508567.0	7		
jmiggactinrawphag3007, 904	- GAAGLGDERDGGPR.-	1328.37	3	1530.85	1.57	0.1	831	21/52	
jmrawgg5minbeadsyringdnase, 1429	- EYRGKSPAQAELSYLNK.-	1955.16	3	142.44	1.09	0.0	130	11/64	
jmraw5minigg500mmnaclsd, 1560	- ASNPIIAAQLCSK -	1316.55	2	174.72	1.23	0.0	141	7/24	
jmraw5minigg600mmnaclsd, 1720	- ASNPIIAAQLCSK.-	1316.55	2	515.53	1.32	0.1	188	3/8	
jmrawgg5minbeadsfreezethaw, 2768	- TSASGDGSHFDYVQDQNQRNLGGAYSVTYR -	3295.40	2	72.67	0.85	0.0	65	9/58	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
erythrocyte protein band 4.1-like 1 [Mus musculus]					2792.94	7305029.0	7		
jmIgG350naclrawphag3007, 1269	-.IITGDEDVDQDQALALAIK.-	2142.39	3	434.27	1.24	0.0	346	1/4	2
jmfag1mnacl2,5minigg, 646	-.APESDTGDEDQDQER.-	1692.59	3	829.61	1.74	0.1	380	9/28	
AJRAWSoluteContr_june13, 746	-.APESDTGDEDQDQER.-	1692.59	3	581.87	1.43	0.0	408	9/28	
jmbeads600naclrawphage3007, 1579	-.SLDGAEFSRPASVSENHDAGPDGDK.-	2559.60	3	445.68	1.32	0.1	257	3/16	
phagrawF250_dec22, 1295	-.GACSTPEMPQFESVK.-	1611.82	3	501.50	1.29	0.0	387	2/7	2

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
erythrocyte protein band 4.1-like 3; DAL1P [Mus musculus]					4191.97	7305031.0	13		
jmrawgg5min350mmnaclsyringednase, 1043	-.AEEATPVTALRHEGKTDSER.-	2198.34	3	872.58	1.81	0.1	307	21/76	2
ajrawphag1MNaCl20, 1272	-.LMDGSEILSLLESAR.-	1634.88	3	465.14	1.33	0.1	271	2/7	
jmfagfrench5minigg1mnacldlt, 1571	-.DSVSAAEVGTGQYATTKGISQTNLITTVTPEK.-	3269.56	2	29.95	0.64	0.0	47	7/62	1
jmrawminigg200mmnaclsyringdnas, 2974	-.QQPALEQFPEAAAHSTPVKREIGDK.-	2749.03	2	1184.75	1.18	0.3	145	3/16	1
jmfag5minigg350mmnacl, 435	-.LLLPEAPPKKFLTLGSK.-	1853.28	3	220.29	1.18	0.0	187	15/64	2
jmbeads400rawphag3007, 1249	-.RIVITGDADIDHDQALAQAIK.-	2264.52	3	363.26	1.48	0.0	231	17/80	
phagrawF450_dec20, 1202	-.SGAWHFSFNVKFYPPDPAQLSEDITR.-	3011.29	2	1056.00	1.00	0.3	146	11/50	2

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
erythrocyte protein band 4.1-like 3; DAL1P [Mus musculus]					1750.46	7305031.0	16		
FPbeads150_Dec19, 751	-.PKSMQCK.-	822.03	1	219.75	1.14	0.1	159	5/12	1
rawextr_60MeOHbead_Mar04, 854	-.KAEEATPVTALR.-	1286.46	3	1061.19	1.85	0.0	573	17/44	2
rawextr_1000bead_Mar04, 1628	-.VIELHKSHRGMTPAEAEMHFLENAK.-	2877.29	3	469.55	1.45	0.1	266	11/48	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
erythrocyte protein band 4.1 [Mus musculus]					3334.41	38570129.0	14		
ajrawphagjun20actinDPI,648-650	-.PKSQVSEEEGR.-	1246.31	2	252.30	1.03	0.1	89	9/20	1
jmraw5minigg600mmnaclsd, 1330	-.LDGENIYIR.-	1093.22	2	290.14	1.13	0.0	254	1/2	1
ajrawphag1MNaCl20, 1732	-.TLNINGQVPTGDGPPLVK.-	1821.07	3	649.93	1.57	0.1	205	4/17	
JMFAGNACL15B21E3, 124	-.LRINRFPWPK.-	1327.61	2	233.95	1.20	0.1	129	1/3	1
jmfag5minigg350mmnacl,283-285	-.ISSKRSSFFIK.-	1300.53	3	637.71	1.42	0.0	448	3/8	
JMFAGNACL5B21E3, 1636	-.RVCEHLNLLEEDYFGLALWDSATSK.-	2911.24	3	442.77	1.93	0.0	229	17/96	
jmbeads250rawphag3007, 662	-.DVPIVHTETK.-	1139.28	2	137.59	0.80	0.1	136	1/3	1
jmfagconSminn600mmnacl, 3147	-.QVRGVPWNFTFNVKFYPPDPAQLTEDITR.-	3437.85	2	118.43	0.88	0.0	113	9/56	1
phagrawFsucchlfbead_dec23, 678	-.ASNGDTPTHEDLTK.-	1486.52	3	571.59	1.17	0.1	414	15/52	1

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
erythrocyte protein band 4.1 [Mus musculus]					1664.78	38570129.0	13		
FPbeads250_Dec19, 1580	-.THTEVTVPTSNGDQTQK.-	1843.93	3	247.17	1.15	0.0	209	7/32	
FPbeads700_Dec19, 1619	-.SPRPTSAPAIAQSQVTEGPGRPIK.-	2446.75	2	57.60	0.72	0.0	62	7/46	
rawextr_60MeOHbeadigg_Mar04, 1832	-.AKDLEGVDILGVCSSGLLVYKDK.-	2538.97	3	1134.57	1.53	0.2	303	17/92	1
rawextr_700beadigg_Mar04, 2402	-.TQTVTISDTANAVKSEIPTKDVPIVHTETK.-	3225.59	2	60.78	0.81	0.0	63	4/29	1
FPbeads1000_Dec19, 3218	-.LDGENIYIRHSNLMLEDLDKSQEEIK.-	3104.44	2	164.66	1.00	0.1	67	4/25	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
cofilin 1, non-muscle [Mus musculus]					**34424.95**	6680924.0		3	
jmfag1mnacl5mincon,482-484	-.HELQANCYEEVK.-	1463.60	2	19696.62	4.43	0.5	1476	19/22	
jmfag1mnacl2,5minigg, 1102	-.LGGSAVISLEGKPL.-	1341.58	2	1593.75	1.63	0.2	548	15/26	
JMFAGNACL5B21E3, 1106	-.LGGSAVISLEGKPL.-	1341.58	2	349.78	1.10	0.1	240	11/26	
jmfag1mnacl2,5minigg, 1108	-.LGGSAVISLEGKPL.-	1341.58	2	572.02	1.39	0.1	196	9/26	
jmfag5minigg400mmnacl, 1152	-.LGGSAVISLEGKPL.-	1341.58	2	3039.24	2.05	0.3	478	7/13	
jmfag5minigg1000mmnacl, 1198	-.LGGSAVISLEGKPL.-	1341.58	2	784.81	1.57	0.1	406	6/13	
jmfag1mnacl5minigg,1264-1266	-.LGGSAVISLEGKPL.-	1341.58	2	5166.49	2.80	0.3	728	8/13	
jmfagtimecont0min_030601230741, 1612	-.LGGSAVISLEGKPL.-	1341.58	2	1717.76	1.64	0.2	504	15/26	
jmfagtimecon5min, 1682	-.LGGSAVISLEGKPL.-	1341.58	2	1362.41	1.49	0.2	485	15/26	
jmldl500naclrawphag3007, 1133	-.HELQANCYEEVK.-	1463.60	2	142.07	0.87	0.1	112	7/22	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
myosin, heavy polypeptide 3, skeletal muscle, embryonic [Mus muscul					**22636.88**	38091410.0		36	
phagrawF600_dec20,1052-1054	- KLEGDLKLAQESILDLENDK.-	2272.54	2	245.57	1.33	0.0	176	11/38	
rawsucrfp_500phagigg_Mar04,1102-1104	- KLEGDLKLAQESILDLENDK.-	2272.54	3	1183.88	2.22	0.1	431	21/76	
phagrawFsuc200_dec22, 1131	- KLEGDLKLAQESILDLENDK.-	2272.54	2	191.52	1.24	0.0	137	11/38	
phagrawF200_dec22, 1215	-.GQTVDQVHHAVNALSKSVYEK.-	2311.54	3	2901.86	1.90	0.3	421	1/4	
rawsucrfp_chlfphagigg_Mar04, 1636	- LEEAGGVTSTQIELNK.-	1689.85	2	386.95	1.31	0.1	214	1/3	
phagrawF60MsOH_dec23, 1724	- NKLYDQHLGKSNNFQK.-	1935.13	3	655.95	1.83	0.1	279	3/10	
phagrawFsuc450_dec20, 2596	- KLEGDLKLAQESILDLENDK.-	2272.54	3	764.78	1.67	0.0	439	1/4	
phagrawFsuc350_dec20, 3194	-.QREEQAEPDGTEVADKTAYLMGLNSSDLLK.-	3310.59	2	58.59	0.77	0.1	37	7/58	
jmfag5minigg350mmnacl, 403	- LAKLITRTQAVCR.-	1473.81	3	1026.78	1.49	0.1	589	17/48	
jmfag1mnacl5mincon, 594	-.AQHELEEAEER.-	1341.37	3	391.35	1.36	0.1	262	3/8	
JMFAGNACL5B21E3, 696	-.LAEQELLDSNER.-	1417.51	3	453.73	1.34	0.1	209	13/44	
jmfag5miniggbead_030528200105, 953	-.SKLEGQVDDLESSLEQEKK.-	2234.41	3	396.94	1.28	0.0	296	17/72	
JMFAGNACL10_2B21E3, 1042	- KLEGDLKLAQESILDLENDK.-	2272.54	2	411.40	1.93	0.1	115	11/38	
jmfag5minigg250mmnacl, 1836	- SEFKLEIDDLSSSVESVSK.-	2100.27	3	1890.16	1.94	0.2	371	5/18	
jmfag5minigg150mmnacl, 2182	- NLEQEIADLTEQIAENGKSIHELEK.-	2853.09	3	971.33	1.81	0.2	207	17/96	
jmfag5minigg250mmnacl, 2422	-.VIQYFATIAATGDLAK.-	1682.94	2	625.63	0.96	0.2	189	3/10	
jmrawgg5min300mmnaclsyringednase, 1037	- DPLNETVVGLYQKSSNR.-	1921.10	2	163.84	0.96	0.1	104	9/32	
jmfagfrench20minigg1mnacldtt, 1040	-.RANLLQAEVEELR.-	1541.74	3	710.22	1.61	0.1	368	1/3	
jmrawgg5minbeadsyringdnase, 1663	-.IRELEFELEGEQK.-	1620.79	2	549.96	1.16	0.2	148	1/3	1
jmIgG350naclrawphag3007, 1997	-.TLVVKPEDVYAMNPPK.-	1802.13	2	103.47	0.94	0.0	97	7/30	
jmfag5minfrench1mnacldttdpi, 3248	-.QRLQGEVEDLMVDVER.-	1917.14	3	436.34	1.19	0.1	248	1/4	
jmfagtimecon7.5min.452.452.2	-.LTREKK.-	774.93	0	480.71	1.27	0.1	263	7/10	
AJRAWSoluteContr_june13,930-932	-.KLEGDLKLAQESILDLENDK.-	2272.54	2	948.78	1.62	0.2	253	7/19	
jmfagcon5min1000mmnacl_030601180404, 938	-.VTVETEDSR.-	1036.08	2	112.39	1.22	0.0	88	1/2	
jmfag5mincon450mmnacl, 1542	-.YRVLNASAIPEGQFIDSKK.-	2137.43	3	481.89	1.32	0.0	362	17/72	
jmfagtimecon10min, 1544	-.RANLLQAEVEELR.-	1541.74	3	361.88	1.45	0.0	248	5/16	
jmbeads300rawphag3007, 2328	- EQLAIVERRANLLQAEVEELR.-	2480.81	2	133.65	1.04	0.0	129	9/40	
rawphag2007chlfsol3,1013-1015	-.VKVGNEYVTKGQTVDQVHHAVNALSK.-	2823.16	3	386.57	1.69	0.1	160	1/5	
rawphag2007chlfbead3, 1225	- TVETMQGALDAEVRSRNEAIR.-	2347.60	3	1704.74	2.48	0.2	299	17/80	
RawPhag2007EtBeadsdigest_030718152503, 1402	-.KLRVDLER.-	1029.22	2	227.79	1.10	0.1	156	1/2	
jmrawf5minbsareebeads, 1472	- CIIPNETKTPGAMEHSLVLHQLR.-	2589.03	3	835.32	1.66	0.1	470	5/22	
rawphag2007chlfsol1, 1774	- HADSAAELAEQIDNLQRVKQK.-	2365.59	3	489.56	1.31	0.1	202	17/80	
jmldlactinrawphag3007, 1212	-.TLEDQLSEARGKNEEMQR.-	2135.30	3	284.34	1.38	0.1	163	13/68	
jmldlactinrawphag3007, 1212	- QIQKLETR.-	1016.18	2	1246.42	1.79	0.0	691	5/7	1
jmldlactinrawphag3007, 1212	-.TYCFVVDSKEEYVK.-	1710.93	2	93.96	1.07	0.0	84	3/13	
jmldlactinrawphag3007, 1212	- RANLLQAEVEELRATLEQTER.-	2470.73	3	328.63	1.24	0.1	236	1/5	

control

myosin, heavy polypeptide 3, skeletal muscle, embryonic [Mus muscul					**3193.45**	38091410.0		12	
jmbsaactinrawphag3007, 947	-.NEEMQRSLSELTTQK.-	1794.97	3	827.81	1.53	0.2	312	2/7	
jmbsa300naclrawphag3007, 1928	-.AERSYHIFYQILSNK.-	1870.10	2	70.45	1.03	0.0	66	5/28	
rawextr_400bead_Mar04, 591	-.HADSAAELAEQIDNLQR.-	1881.98	3	973.14	1.81	0.1	408	9/32	
FPbeads200_Dec19, 695	- RQLEEENKAK.-	1245.37	3	341.83	1.58	0.1	170	1/3	
FPbeads150_Dec19, 1089	-.KLEGDLKLAQESILDLENDK.-	2272.54	2	106.44	1.03	0.0	103	5/19	
rawextr_250beadigg_Mar04, 1260	-.KLEGDLKLAQESILDLENDK.-	2272.54	2	605.08	2.13	0.0	261	7/19	
rawextr_350bead_Mar04,2410-2412	- QRYRVLNASAIPEGQFIDSK.-	2293.57	2	268.70	0.91	0.1	131	11/38	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
myosin, heavy polypeptide 6, cardiac muscle, alpha; myosin heavy chain,					17391.32	6754774.0	8		
jmrawbas5min1mnacl, 936	- NALAHALQSSR -	1168 29	3	606 24	1 29	0 1	325	13/40	2
jmrawbsa5minlowionic, 2302	-.QLQKLEARVR -	1241 47	2	219.66	1 02	0 1	134	1/3	1
rawsucrfp_actinphagigg_Mar04, 644	- TEELEEAKKK -	1205 34	3	857.36	1 63	0.1	485	4/9	6
rawsucrfp_60MeOHphagigg_MAr04, 974	- NALAHALQSSRHDCDLLR -	2021 25	3	218.50	1 41	0 1	120	13/68	2
phagrawFsucchfbead_dec23, 1106	- GAEKLLGSLDIDHNQYK.-	1902 10	3	399.88	1 46	0 0	273	17/64	2
phagrawFsuc250_dec22, 1177	- RVIQYFASIAAIGDRSK -	1896 18	3	443.98	1 44	0 1	257	17/64	1
phagrawFsuc60MeOH_dec23, 1224	- NMEQTIKDLQHR -	1513.71	2	235 28	1 14	0 0	194	4/11	1
rawsucrfp_350phagigg_Mar04, 1506	- ALQEAHQQALDDLQAEEDKVNTLTKSK -	3025 27	3	157 27	0 99	0 0	134	15/104	
phagrawFsuc350_dec20, 1692	- KLEGDLKLTQESIMDLENDK -	2320 60	3	1197.85	1 83	0 1	576	5/19	1
rawsucrfp_150phagigg_Mar04, 1795	- LELDDVTSNMEQIIKAKANLEK.-	2503 86	3	757.01	1 76	0 1	362	17/84	1
phagrawFsuc150_dec22, 2178	- DPLNETVVGLYQKSSLK -	1892.14	2	225.59	0.95	0 0	238	5/16	2
phagrawFchlf_dec23, 2588	- ELEEISERLEEAGGATSVQIEMNK.-	2663 90	2	143.93	1 18	0 1	36	3/23	1
JMMAGTube1B16E3, 2054	-.VLSKANSEVAQWRTK -	1717 95	1	255.52	0.91	0 0	268	5/14	1
jmfag5minigg450mmnacl_030527025134, 790	- SNNFQKPR -	991.09	2	227 76	1 13	0 0	202	3/7	2
jmraw5minigg250mmnaclsyringdnase, 792	- NALAHALQSSR.-	1168.29	3	827 26	1 34	0.0	614	1/2	2
jmrawminigg200mmnaclsyringdnas, 826	- ADIAESQVNK -	1075 16	3	1003 28	1 60	0.0	620	4/9	10
jmfag5minigg600mmnacl, 916	- TVRNDNSSR.-	1049 08	2	788.13	1 47	0 1	477	9/16	18
jmigg450rawphag3007, 1118	-.AKVVSREGGK -	1031 19	2	378.81	1 19	0.1	94	4/9	1
jmfag5minigg200mmnacl, 1166	- SKKENPNANK -	1130 24	2	812.27	1 58	0 1	477	11/18	1
jmrawgg5minbeadsyringdnase, 1437	- VQLLHSQNTSLINQK.-	1723.96	2	224 07	0.95	0 0	229	9/28	1
jmfag5minigg500mmnacl, 1892	- LELQSALEEAEASLEHEEGK.-	2213.34	3	1188 64	1 62	0.1	577	11/38	1
ajrawphagjun20dpi1MNaCl, 1940	-.KALQEAHQQALDDLQAEEDKVNTLTK.-	2938.20	2	107 96	0.94	0.0	115	1/5	1
jm5minigrawlowionic, 2558	-.VKEMTERLEDEEEMNAELTAK -	2496.76	3	873.61	1.83	0 1	402	19/80	2
jmfagcont5minbead, 160	- KLEDECSELK -	1194 34	3	67 54	0 84	0.0	80	1/4	8
jmfag1mnacl5mincon, 352	-.LQLEEKLK.-	1001 20	2	372 03	1 40	0 0	264	5/7	
jmfagtimecont0min_030601230741, 460	-.KLEDECSELK.-	1194.34	3	209 47	1 38	0 0	134	1/3	8
jmfagtimecont0min_030601230741, 1214	- VIQYFASIAAIGDRSK -	1740.00	3	127 69	0.85	0 0	137	7/30	1
jmbeads400rawphag3007, 1413	-.ELEEISERLEEAGGATSVQIEMNKK -	2792.07	3	545.20	1 57	0.1	251	3/16	1
jmbeadsactinrawphag3007, 1713	- NWPWMKLYFKIK -	1655.05	2	140.02	1 02	0.0	129	7/22	2
jmbeadsactinrawphag3007, 1717	- RVIQYFASIAAIGDRSK.-	1896 18	2	318.66	1 32	0.1	123	7/32	1
rawphag2007chfbead2, 502	- NKDPLNETVVGLYQK.-	1718 93	3	1347 66	2.14	0.2	373	9/28	7
rawphag2007chfbead3,961-963	- MKKNMEQTIK -	1251 55	2	718.74	1 83	0.0	388	5/9	1
rawsucrfp_60MeOHphagigg_MAr04, 974	-.NALAHALQSSRHDCDLLR -	2021.25	3	218.50	1 41	0.1	120	13/68	2
jmidlactinrawphag3007, 1042	- KAPGVMDNPLVMHQLR -	1807 18	3	1175 96	1 49	0 1	701	11/30	

control

myosin, heavy polypeptide 6, cardiac muscle, alpha; myosin heavy chain,					2809.33	6754774.0	57		
rawextr_600bead_Mar04, 822	-.LASADIETYLLEKSR -	1709 92	3	258.94	1.60	0 1	126	15/56	8
rawextr_300beadigg_Mar4, 906	- KLEGDLKLTQESIMDLENDK -	2320 60	3	436 24	1 79	0.0	244	15/76	1
rawextr_300beadigg_Mar4, 1062	- VIQYFASIAAIGDRSK -	1740 00	3	146 51	1.21	0 0	118	13/60	1
rawextr_200beadigg_Mar04, 1093	-.LEEAQRSLNDFTTQRAK.-	2008 18	3	386.33	1 39	0.0	277	15/64	
rawextr_actinbeadigg_Mar04, 1645	-.APGVMDNPLVMHQLR -	1679.01	2	81 67	1.21	0 1	42	3/14	1
rawextr_400bead_Mar04, 1931	- LQNEIEDLMVDVERSNAAAAALDKK -	2745.06	2	54 35	0 70	0.0	68	7/48	1
rawextr_450beadigg_Mar04, 1976	-.DPLNETVVGLYQKSSLK -	1892 14	2	262.54	1 30	0 0	194	5/16	2
FPbeads500_dec19, 2008	- VRELENELEAEQK.-	1587.71	2	98 92	0 85	0 1	91	7/24	1
rawextr_300bead_Mar04, 2138	-.IEDEQALALQLQKKLK.-	1869.20	2	308.86	1 44	0 1	167	4/15	
FPbeads400_Dec19, 2598	- MEGDLNEMEIQLSQANRIASEAQK.-	2706.99	3	242.34	1.11	0 0	216	9/46	1
rawextr_450beadigg_Mar04, 2660	-.FDKIEDMAMLTFLHEPAVLYNLK.-	2740.23	2	193 60	0.88	0.1	69	7/44	2
jmbsa250nacirawphag3007, 549	-.ANSEVAQWR -	1061.13	2	339.04	1.47	0.0	226	1/2	5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
tropomyosin 1, alpha; alpha tropomyosin [Mus musculus]					58288.56	31560030.0	2		
phagrawFsuc700_dec23,945-947	-.MQMLKLDKENALDR.-	1706.03	3	593.48	1.80	0.0	329	15/52	3
phagrawF450_dec20, 1100	-.MQMLKLDKENALDR.-	1706.03	3	1753.27	2.12	0.2	490	9/26	3
phagrawF300_dec20,1213-1215	-.MQMLKLDKENALDR.-	1706.03	3	412.47	1.70	0.0	242	15/52	3
phagrawF300_dec20, 1407	-.MQMLKLDKENALDR.-	1706.03	3	1056.74	1.89	0.1	422	17/52	3
jmfag1mnacl0minigg, 954	-.MEIQEIQLK.-	1132.36	2	8139.92	3.26	0.3	1802	7/8	3
jmfag1mnacl0minigg, 958	-.MEIQEIQLK.-	1132.36	2	4282.11	2.96	0.1	1227	7/8	3
jmfag1mnacl2,5minigg, 1010	-.MEIQEIQLK.-	1132.36	2	5614.48	2.63	0.2	1550	7/8	3
jmfag1mnacl2,5minigg, 1014	-.MEIQEIQLK.-	1132.36	2	5279.02	3.19	0.2	1310	7/8	3
jmfag1mnacl5minigg, 1180	-.MEIQEIQLK.-	1132.36	2	4571.83	2.86	0.2	1313	7/8	3
jmfag1mnacl5mincon,1204-1206	-.MEIQEIQLK.-	1132.36	2	5431.36	3.11	0.2	1448	7/8	3
jmfag5minigg450mmnacl_030527025134, 1622	-.MEIQEIQLK.-	1132.36	2	3217.42	2.24	0.0	1419	7/8	3
jmrawigg5min450mmnaclsd, 636	-.LVIIESDLERAEER.-	1672.86	3	225.61	1.51	0.1	118	7/26	3
jmraw5minigg600mmnaclsd, 1676	-.MQMLKLDKENALDR.-	1706.03	3	1206.02	1.79	0.2	384	17/52	3
jmfagtimecon2.5min.1316.1320.2	-.ENALDRAEQAEADK.-	1560.61	0	307.17	1.35	0.1	202	5/13	3
jmfag5mincont350, 976	-.MEIQEIQLK.-	1132.36	2	4582.99	2.58	0.2	1285	13/16	3
AJRAWpellet2_contr_jun13, 1103	-.MQMLKLDKENALDR.-	1706.03	3	844.62	1.93	0.1	246	15/52	3
jmfag5mincont200mmnacl, 1162	-.MEIQEIQLK.-	1132.36	2	5338.72	2.72	0.2	1494	7/8	3
jmfag1mnacl5mincon,1204-1206	-.MEIQEIQLK.-	1132.36	2	5431.36	3.11	0.2	1448	7/8	3

control

tropomyosin 1, alpha; alpha tropomyosin [Mus musculus]					2617.01	31560030.0	6		
rawextr_150beadigg2_Mar04, 136	-.SLEAQAEKYSQKEDK.-	1754.88	2	1052.25	1.79	0.1	458	3/7	3
rawextr_500beadigg_Mar04, 1090	-.MQMLKLDKENALDR.-	1706.03	3	375.81	1.58	0.0	218	7/26	3
FPbeads400_Dec19, 1338	-.MQMLKLDKENALDR.-	1706.03	3	729.44	1.59	0.1	325	17/52	3
rawextr_200bead_Mar04, 2710	-.LVIIESDLERAEERAELSEGK.-	2387.63	3	459.51	1.57	0.0	275	9/40	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
A44131 tropomyosin beta 2 - mouse					**120061.38**	346655.0		7	
phagrawFsuc700_dec23,945-947	-.MQMLKLDKENAIDR.-	1706.03	3	593.48	1.80	0.0	329	15/52	5
phagrawF450_dec20, 1100	-.MQMLKLDKENAIDR.-	1706.03	3	1753.27	2.12	0.2	490	9/26	5
phagrawF300_dec20,1213-1215	-.MQMLKLDKENAIDR.-	1706.03	3	412.47	1.70	0.0	242	15/52	5
phagrawF300_dec20, 1407	-.MQMLKLDKENAIDR.-	1706.03	3	1056.74	1.89	0.1	422	17/52	5
phagrawFchlf_dec23, 1960	-.SLEAQADKYSTKEDK.-	1713.83	2	107.68	0.92	0.0	114	3/14	2
JMFAGNACL10_2B21E3, 828	-.RIQLVEEELDRAQER.-	1885.07	3	14332.01	4.05	0.5	1350	25/56	13
JMFAGNACL5B21E3, 900	-.RIQLVEEELDRAQER.-	1885.07	3	9002.06	3.16	0.4	1178	23/56	13
jmfag5minigg600mmnacl, 918	-.IQLVEEELDR.-	1244.38	2	1601.27	1.67	0.2	648	2/3	13
jmfag1mnacl0minigg,934-936	-.IQLVEEELDR.-	1244.38	2	5304.85	3.25	0.3	957	8/9	13
JMFAGNACL10_1B21E3,1010-1012	-.RIQLVEEELDRAQER.-	1885.07	3	8470.26	3.62	0.4	950	11/28	13
JMFAGNACL15B21E3, 1028	-.RIQLVEEELDRAQER.-	1885.07	3	11074.76	3.48	0.5	1038	3/8	13
JMFAGNACL15B21E3, 1036	-.RIQLVEEELDRAQER.-	1885.07	3	9854.72	3.47	0.5	739	3/8	13
JMFAGNACL10_1B21E3,1118-1120	-.IQLVEEELDRAQER.-	1728.89	3	593.38	1.83	0.1	197	17/52	13
jmfag1mnacl5mincon, 1190	-.IQLVEEELDR.-	1244.38	2	3075.98	2.15	0.3	783	5/6	13
jmfag5minigg450mmnacl_030527025134, 1606	-.IQLVEEELDR.-	1244.38	2	1101.20	1.57	0.1	604	11/18	13
jmfagfrench5minigg1mnacldtt, 469	-.GMKVIENRAMK.-	1277.59	3	283.27	1.41	0.0	196	13/40	6
jmrawigg5minbeadsfreezethaw, 1032	-.LATALQKLEEAEKAADESER.-	2203.39	3	1915.43	1.87	0.1	856	23/76	13
jmIgG250rawphag3007, 1244	-.RIQLVEEELDRAQER.-	1885.07	3	2594.38	3.14	0.1	714	5/14	13
jmrawrminigg200mmnaclsyringdnas, 1246	-.RIQLVEEELDRAQER.-	1885.07	3	5856.19	2.74	0.4	787	3/8	13
jmIgG250rawphag3007, 1430	-.LATALQKLEEAEKAADESER.-	2203.39	3	7798.86	3.03	0.4	661	25/76	13
ajrawphagactin20,1544-1546	-.LEQAEKKATDAEADVASLNR.-	2160.33	3	225.71	1.67	0.0	132	5/19	5
jmraw5minigg600mmnaclsd, 1676	-.MQMLKLDKENAIDR.-	1706.03	3	1206.02	1.79	0.2	384	17/52	5
jmfagtimecon7.5min.1410.1410.3	-.LATALQKLEEAEK.-	1444.66	0	286.69	1.48	0.0	186	7/24	14
jmfagtimecon2.5min.1316.1320.2	-.ENAIDRAEQAEADK.-	1560.61	0	307.17	1.35	0.1	202	5/13	3
jmbeads300rawphag3007, 804	-.RIQLVEEELDRAQER.-	1885.07	3	7558.56	3.22	0.3	1167	11/28	13
jmbeads600naclrawphage3007,890-898	-.EDKYEEEIK.-	1183.25	3	1401.67	2.19	0.0	632	9/16	15
jmfag5mincont200mmnacl, 910	-.YEEVARK.-	895.00	2	308.58	1.00	0.2	45	5/12	14
AJRAWpellet2_contr_jun13, 1103	-.MQMLKLDKENAIDR.-	1706.03	3	844.62	1.93	0.1	246	15/52	5
jmfag1mnacl5mincon, 1190	-.IQLVEEELDR.-	1244.38	2	3075.98	2.15	0.3	783	5/6	13
jmbeads250rawphag3007, 2478	-.AQERLATALQKLEEAEK.-	1929.17	2	389.48	1.25	0.0	300	3/8	13
jmldl400naclrawphag3007_030802153313, 127	-.VIENRAMKDEEK.-	1462.66	3	1232.12	1.85	0.0	658	19/44	6
ajrawmediapbsnocells, 836	-.RIQLVEEELDRAQER.-	1885.07	3	16442.56	4.34	0.5	1605	13/28	13

control

A44131 tropomyosin beta 2 - mouse					**1105.25**	346655.0		9	
rawextr_500beadigg_Mar04, 1090	-.MQMLKLDKENAIDR.-	1706.03	3	375.81	1.58	0.0	218	7/26	5
FPbeads400_Dec19, 1338	-.MQMLKLDKENAIDR.-	1706.03	3	729.44	1.59	0.1	325	17/52	5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
S11390 tropomyosin 5 - mouse					737865.99	111212.0		5	
rawsucrfp_250phagigg_Mar04, 646	-.KLVIIEGDLER.-	1285.52	3	221.55	1.25	0.1	121	11/40	3
phagrawFsuc450_dec20,1750-1752	-.EEHLCTQRMLDQTLLDLNEM.-	2433.77	3	147.44	1.39	0.0	91	15/76	2
JMFAGNACL5B21E3, 140	- YSQKEDKYEEEIK.-	1689.80	3	5211.41	3.21	0.3	996	7/16	9
JMFAGNACL5B21E3, 306	-.AREQAEAEVASLNRR.-	1700.84	3	2364.92	2.37	0.1	799	3/8	1
JMFAGNACL10_2B21E3, 402	-.AREQAEAEVASLNR.-	1544.65	3	6014.74	3.32	0.2	1440	1/2	1
JMFAGNACL10_2B21E3, 412	-.AREQAEAEVASLNR.-	1544.65	3	4413.70	2.62	0.3	858	21/52	1
JMFAGNACL5B21E3, 428	- AREQAEAEVASLNR.-	1544.65	3	6266.13	2.84	0.2	1596	27/52	1
jmfag1mnacl0minigg,428-430	-.KIQVLQQQADDAEER.-	1771.91	3	12655.79	3.45	0.5	1604	27/56	1
JMFAGNACL5B21E3, 432	- AREQAEAEVASLNR -	1544.65	3	8184.91	3.26	0.4	1180	6/13	1
JMFAGNACL15B21E3, 436	- AREQAEAEVASLNR.-	1544.65	3	3230.02	2.15	0.3	799	5/13	1
jmfag1mnacl5minigg, 448	-.AREQAEAEVASLNR.-	1544.65	3	2349.53	2.40	0.1	857	21/52	1
JMFAGNACL15B21E3, 452	-.AREQAEAEVASLNR.-	1544.65	3	3312.62	2.40	0.2	1035	11/26	1
jmfag1mnacl5minigg, 456	-.AREQAEAEVASLNR.-	1544.65	3	585.81	1.36	0.0	427	4/13	1
JMFAGNACL10_1B21E3, 470	-.AREQAEAEVASLNR.-	1544.65	3	13089.97	3.50	0.4	2061	7/13	1
jmfag1mnacl5mincon, 476	-.AREQAEAEVASLNR.-	1544.65	3	1269.53	1.80	0.0	706	19/52	1
JMFAGNACL10_1B21E3, 476	-.AREQAEAEVASLNR.-	1544.65	3	4531.60	2.42	0.2	1281	23/52	1
jmfag5minigg350mmnacl,477-479	-.KIQVLQQQADDAEER.-	1771.91	3	18244.25	4.11	0.5	1846	15/28	1
JMFAGNACL10_2B21E3, 482	-.KIQVLQQQADDAEER.-	1771.91	3	11741.33	3.47	0.4	1717	1/2	1
jmfag5minigg600mmnacl, 490	-.KIQVLQQQADDAEER.-	1771.91	3	13225.09	3.15	0.5	1803	1/2	1
JMFAGNACL5B21E3,490-492	-.KIQVLQQQADDAEER.-	1771.91	3	19649.62	4.26	0.5	2124	1/2	1
JMMAGTube1B16E3, 492	-.KIQVLQQQADDAEER.-	1771.91	3	15733.94	3.84	0.5	1707	1/2	1
jmfag5minigg150mmnacl,496-498	-.KIQVLQQQADDAEER.-	1771.91	3	16995.07	3.84	0.5	1603	1/2	1
JMMAGTube1B16E3, 498	-.KIQVLQQQADDAEER.-	1771.91	3	15217.47	3.57	0.5	2061	31/56	1
jmfag1mnacl2,5minigg, 516	-.KIQVLQQQADDAEER.-	1771.91	3	9474.72	2.97	0.4	1455	25/56	1
jmfag1mnacl2,5minigg, 520	-.KIQVLQQQADDAEER.-	1771.91	3	20105.19	4.32	0.5	1883	29/56	1
jmfag1mnacl7,5minigg,520-522	-.KIQVLQQQADDAEER.-	1771.91	3	19926.57	4.17	0.5	2263	29/56	1
jmfag5minigg400mmnacl, 558	-.KIQVLQQQADDAEER.-	1771.91	3	13424.23	3.66	0.4	1689	15/28	1
jmfag1mnacl0minigg, 576	-.EQAEAEVASLNR.-	1317.39	2	376.40	1.60	0.0	235	4/11	1
jmfag1mnacl0minigg, 580	-.EQAEAEVASLNR.-	1317.39	2	1343.54	2.44	0.0	550	6/11	1
jmfag1mnacl5minigg,588-590	-.KIQVLQQQADDAEER.-	1771.91	3	10936.70	3.34	0.4	1437	25/56	1
jmfag1mnacl5mincon, 592	-.KIQVLQQQADDAEER.-	1771.91	3	9690.65	3.15	0.4	1529	13/28	1
jmfag5minigg1000mmnacl,592-594	-.KIQVLQQQADDAEER.-	1771.91	3	15744.73	3.64	0.5	2075	1/2	1
jmfag5minigg200mmnacl, 600	-.KIQVLQQQADDAEER.-	1771.91	3	12297.90	3.60	0.5	1280	25/56	1
jmfag1mnacl5minigg, 606	-.KIQVLQQQADDAEER.-	1771.91	2	35058.87	5.40	0.6	3233	25/28	1
jmfag5minigg200mmnacl, 608	-.KIQVLQQQADDAEER.-	1771.91	3	3227.37	2.37	0.2	915	11/28	1
jmfag5minigg600mmnacl, 610	-.EQAEAEVASLNR.-	1317.39	2	1034.48	2.02	0.0	511	6/11	1
jmfag1mnacl5mincon,614-616	-.KIQVLQQQADDAEER.-	1771.91	2	33614.86	5.18	0.6	2884	23/28	1
JMFAGNACL10_2B21E3, 620	-.KIQVLQQQADDAEERAER.-	2128.29	2	1389.80	1.57	0.3	201	11/34	1
jmfag5minigg150mmnacl, 706	-.IQVLQQQADDAEER.-	1643.74	2	17745.23	3.67	0.5	2182	21/26	1
jmfag1mnacl5minigg, 784	-.EQAEAEVASLNR.-	1317.39	2	1406.67	1.94	0.0	724	7/11	1
jmfag1mnacl5minigg, 792	-.EQAEAEVASLNR.-	1317.39	2	721.32	1.76	0.0	410	1/2	1
jmfag1mnacl5mincon, 798	-.EQAEAEVASLNR.-	1317.39	2	525.20	1.50	0.0	350	6/11	1
jmfag1mnacl0minigg, 806	-.KLVIIEGDLER.-	1285.52	3	5256.40	2.53	0.3	1043	11/20	3
jmfag1mnacl7,5minigg, 890	-.KLVIIEGDLER.-	1285.52	3	8145.01	3.06	0.3	1530	3/5	3
jmfag5minigg500mmnacl, 920	-.KIQVLQQQADDAEER.-	1771.91	3	11045.09	3.07	0.5	1221	3/7	1
jmfag5minigg500mmnacl, 926	-.KIQVLQQQADDAEER.-	1771.91	3	12542.72	3.32	0.4	2098	31/56	1
jmfag5minigg400mmnacl, 946	-.KLVIIEGDLER.-	1285.52	2	2475.85	2.28	0.2	798	13/20	3
jmfag1mnacl0minigg, 954	-.MELQEIQLK.-	1132.36	2	8139.92	3.26	0.3	1802	7/8	3
jmfag1mnacl0minigg, 958	-.MELQEIQLK.-	1132.36	2	4282.11	2.96	0.1	1227	7/8	3
jmfag5minigg250mmnacl, 976	-.KIQVLQQQADDAEER.-	1771.91	3	6867.95	2.79	0.4	943	23/56	1
jmfag5minigg250mmnacl, 982	-.KIQVLQQQADDAEER.-	1771.91	3	18206.92	3.74	0.5	2136	31/56	1
jmfag1mnacl2,5minigg, 1010	-.MELQEIQLK.-	1132.36	2	5614.48	2.63	0.2	1550	7/8	3
jmfag1mnacl2,5minigg, 1014	-.MELQEIQLK.-	1132.36	2	5279.02	3.19	0.2	1310	7/8	3
jmfag1mnacl5mincon, 1058	-.KLVIIEGDLER.-	1285.52	3	5911.00	2.76	0.3	953	21/40	3
jmfag1mnacl5minigg, 1180	-.MELQEIQLK.-	1132.36	2	4571.83	2.86	0.2	1313	7/8	3
jmfag1mnacl5mincon,1204-1206	-.MELQEIQLK.-	1132.36	2	5431.36	3.11	0.2	1448	7/8	3
jmfag5minigg450mmnacl_030527025134, 1622	-.MELQEIQLK.-	1132.36	2	3217.42	2.24	0.0	1419	7/8	3
JMFAGNACL10_1B21E3, 2038	-.MLDQTLLDLNEM.-	1436.68	1	1187.12	1.94	0.2	288	1/2	2
jmrawgg5minbeadsfreezethaw,504-506	-.KIQVLQQQADDAEER.-	1771.91	3	14454.57	3.67	0.5	1677	1/2	1
jmrawgg5minbeadsfreezethaw,752-754	-.IQVLQQQADDAEERAER.-	2000.12	3	1026.20	1.60	0.1	537	19/64	1
jmrawgg5min150mmnacl, 882	-.KLVIIEGDLERTEER.-	1801.04	3	8417.16	2.92	0.4	702	11/28	3
jmIgG250rawphag3007, 1330	-.ALKDEEKMELQEIQLK.-	1946.26	3	8101.58	2.88	0.3	1019	2/5	3
jmIgG300rawphag3007, 1336	-.ALKDEEKMELQEIQLK.-	1946.26	3	3699.08	2.77	0.2	774	7/20	3
jmfagtimecon2.5min.588.588.3	-.KIQVLQQQADDAEER.-	1771.91	0	4351.38	2.29	0.4	605	9/28	1
jmfagtimecon7.5min.468.468.3	-.KIQVLQQQADDAEER.-	1771.91	0	17390.24	3.27	0.5	2462	15/28	1
jmfagtimecon7.5min.460.460.3	-.KIQVLQQQADDAEER.-	1771.91	0	1955.72	2.12	0.1	699	5/14	1
jmfagtimecon7.5min.370.370.3	-.AREQAEAEVASLNR.-	1544.65	0	9716.37	3.59	0.4	1395	6/13	1
jmfagtimecon7.5min.366.366.3	-.AREQAEAEVASLNR.-	1544.65	0	9224.93	3.30	0.4	1394	25/52	1
jmfagtimecon2.5min.596.596.3	-.KIQVLQQQADDAEER.-	1771.91	0	8999.40	3.47	0.4	1063	25/56	1
jmfagtimecon2.5min.486.486.3	-.AREQAEAEVASLNR.-	1544.65	0	2617.57	2.28	0.2	883	5/13	1
jmfagtimecon2.5min.482.482.3	-.AREQAEAEVASLNR.-	1544.65	0	1856.55	2.25	0.1	612	19/52	1
jmfag5mincont400_030531151834, 398	-.AREQAEAEVASLNR.-	1544.65	3	2748.46	2.21	0.3	595	19/52	1
jmfag5mincont400_030531151834, 402	-.AREQAEAEVASLNR.-	1544.65	3	1322.71	1.87	0.1	632	9/26	1
jmfag5mincont150mmnacl, 435	-.AREQAEAEVASLNR.-	1544.65	3	3685.62	2.42	0.2	1168	23/52	1
jmfag5mincont400_030531151834,444-446	-.KIQVLQQQADDAEER.-	1771.91	3	19514.50	3.93	0.5	2036	29/56	1
jmfag5mincont150mmnacl, 481	-.KIQVLQQQADDAEER.-	1771.91	3	15625.45	3.40	0.5	2061	1/2	1
jmfag5mincont150mmnacl, 485	-.KIQVLQQQADDAEER.-	1771.91	3	13042.59	3.31	0.5	1744	29/56	1
jmfag5mincont350, 518	-.KIQVLQQQADDAEER.-	1771.91	3	8778.70	3.06	0.3	1895	29/56	1
jmfag5mincont200mmnacl, 522	-.AREQAEAEVASLNR.-	1544.65	3	1691.54	2.19	0.1	896	9/26	1
jmfag1mnacl5mincon, 592	-.KIQVLQQQADDAEER.-	1771.91	3	9690.65	3.15	0.4	1529	13/28	1
jmfag5mincont200mmnacl, 612	-.KIQVLQQQADDAEER.-	1771.91	3	11650.41	3.00	0.5	1141	3/7	1
jmfag5mincont200mmnacl, 782	-.EQAEAEVASLNR.-	1317.39	2	984.73	1.92	0.0	514	1/2	1
jmfag5mincont400_030531151834, 802	-.KLVIIEGDLER.-	1285.52	2	1473.41	1.59	0.0	924	7/10	3
jmbeadsactinrawphag3007, 961	-.TIDDLEDKLK.-	1190.33	2	2910.87	2.45	0.2	653	7/9	3
jmfag5mincon250mmnacl, 970	-.KIQVLQQQADDAEER.-	1771.91	3	8364.13	3.02	0.3	1684	25/56	1
jmfag5mincont350, 976	-.MELQEIQLK.-	1132.36	2	4582.99	2.58	0.2	1285	13/16	3
jmfag5mincon250mmnacl, 1052	-.EQAEAEVASLNR.-	1317.39	2	318.02	1.30	0.0	244	9/22	1
jmfag5mincon300mmnacl,1118-1120	-.KIQVLQQQADDAEER.-	1771.91	3	15508.18	4.02	0.4	2347	15/28	1
jmfagtimecont10min_030601202502, 1132	-.AREQAEAEVASLNR.-	1544.65	3	2116.12	2.09	0.2	786	11/26	1
jmfagtimecont10min_030601202502, 1144	-.AREQAEAEVASLNR.-	1544.65	3	1819.00	1.98	0.1	821	5/13	1
jmfag5mincont200mmnacl, 1162	-.MELQEIQLK.-	1132.36	2	5338.72	2.72	0.2	1494	7/8	3
jmfagtimecont10min_030601202502, 1184	-.KIQVLQQQADDAEER.-	1771.91	3	9383.56	3.12	0.4	1157	13/28	1
jmfag5mincon300mmnacl, 1222	-.EQAEAEVASLNR.-	1317.39	2	1334.45	2.31	0.0	577	6/11	1
jmfag5mincon300mmnacl, 1228	-.EQAEAEVASLNR.-	1317.39	2	1124.47	1.96	0.0	575	13/22	1
jmfagtimecont10min_030601202502, 1616	-.ALKDEEKMELQEIQLK.-	1946.26	3	3604.94	2.13	0.2	1240	2/5	3
jmfagtimecont0min_030601230741,2552-2554	-.MLDQTLLDLNEM.-	1436.68	2	667.87	1.39	0.1	379	1/2	2
ajrawmediapbsnocells, 388	-.AREQAEAEVASLNR.-	1544.65	3	1898.32	2.04	0.1	813	5/13	1

control

S11390 tropomyosin 5 - mouse					17609.92	111212.0		3	
jmraw5minbsafreezthaw, 1310	-.KLVIIEGDLERTEER.-	1801.04	3	4675.34	2.60	0.3	699	3/8	3
jmraw5minbsafreezthaw, 1472	-.ALKDEEKMELQEIQLK.-	1946.26	3	12934.58	3.74	0.4	1876	1/2	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
nonmuscle myosin II-C heavy chain [Mus musculus] g					3126.81	33638127.0	23		
phagrawFsuc600_dec20,1200-1202	-.LAEFSSQAAEEEEKVKSLNK.-	2238.44	3	864.53	2.12	0.1	210	4/19	1
phagrawFsuc150_dec22, 1224	-.LFIKVKPLLQVTR -	1555.98	2	542.44	1.13	0.1	271	11/24	1
phagrawFsuc60MeOH_dec23, 1370	-.RHEVPPHVYAVTEGAYRSMLQDR.-	2713.03	3	30.91	0.95	0.0	27	1/11	1
phagrawFsuc250_dec22, 1833	-.LAEFSSQAAEEEEKVKSLNK.-	2238.44	3	927.81	1.72	0.1	347	5/19	1
phagrawFsuc500_dec20, 1990	-.KERNTDQATMPDNTAAQK.-	2020.17	2	95.35	0.91	0.0	83	7/34	1
phagrawF350_dec20, 2138	-.QDEVLQARAQELQKVQELQQQSAR.-	2825.09	3	665.77	1.67	0.1	232	19/92	1

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
MYH8_MOUSE Myosin heavy chain, smooth muscle isoform (SMMHC)					17793.41	13431676.0	31		
rawsucrfp_600phagigg_Mar04,962-964	-.VRKATLQAEQLSNELATER -	2158.40	3	541.52	1.83	0.1	241	1/4	3
rawsucrfp_60MeOHphagigg_MAr04, 1134	-.LQDFASTIEVMEEGKKR.-	1982.25	3	291.62	1.27	0.0	227	15/64	3
rawsucrfp_350phagigg_Mar04, 1264	-.DEIFATSKENEKK.-	1539.67	3	419.20	1.30	0.1	116	5/24	3
phagrawF150_dec22, 1336	-.YEILAANAIPKGFMDGKQACILMIK.-	2740.35	2	349.95	1.00	0.2	108	3/15	3
phagrawF200_dec22, 1377	-.VCHLVGINVTDFTR.-	1574.83	2	490.27	1.09	0.1	373	11/26	2
phagrawF150_dec22,1556-1558	- SGKLDAFLVLEQLRCNGVLEGIR.-	2531.96	3	636.30	1.98	0.1	281	19/88	3
rawsucrfp_actinphagigg_Mar04, 1622	- EQLGKLMATLRNTTANFVR.-	2164.52	3	517.59	1.58	0.1	288	1/4	1
phagrawF150_dec22, 2554	- AKSLEADLMQLQEDLAAAERAR -	2430.73	3	1106.15	1.43	0.1	662	11/42	3
phagrawFsucchlf_dec23, 2732	- RHEMPPHIYAIADTAYRSMLQDR.-	2773.15	3	486.08	1.24	0.1	365	21/88	4
jmfagtimecon7 5min.1538,1538.3	- KLQDFASTIEVMEEGKK.-	1954.24	0	502.57	1.24	0.0	391	17/64	3
jmfag5minccon250mmnacl, 374	- QRALAAAAKK -	1028.24	3	286.22	1.28	0.0	210	11/36	3
jmbeads400rawphag3007, 536	- QLHEYETELEDERKQR.-	2104.22	3	151.98	1.30	0.0	107	7/30	3
jmbeads250rawphag3007, 568	- GNEASFVPSRR.-	1220.32	2	230.03	1.11	0.0	202	7/20	1
jmbeads150rawphag3007, 786	- MLKAEMEDLVSSK.-	1481.76	2	2916.17	1.77	0.3	547	1/2	3
jmbeads450nacrawphag3007, 987	-.LDEEIAQKNNALKK.-	1614.83	2	310.10	1.24	0.0	251	5/13	2
jmfag5mincont200mmnacl, 1074	- ARAELSDKVHK.-	1254.42	2	121.70	1.19	0.0	97	7/20	3
AJRAWpellet1_contr_jun13, 1166	- IKKLEDDILVMDDQNSK.-	2005.28	3	222.24	1.34	0.1	134	3/16	3
jmfag5mincon450mmnacl, 1638	-.TENTQKVIQYLAVVASSHKGK.-	2302.62	3	568.01	1.98	0.0	281	9/40	1
JMFAGNACL10_2B21E3, 920	-.STVAALEAK.-	890.02	2	151.65	0.91	0.0	166	7/18	3
jm5minggrawlowionic, 1036	-.GYLARKAFTK.-	1155.38	2	241.14	1.32	0.0	167	1/2	3
jmfag5minigg150mmnacl, 1258	-.LLEERVSDLTTNLAEEEEK.-	2219.39	3	397.55	1.76	0.1	159	2/9	3
jmfag5minigg450mmnacl_030527025134, 1546	- QLEEAEEESQCINANRR.-	2020.13	3	205.45	1.07	0.0	187	3/16	1
jmfag5minigg600mmnacl, 2032	- NSLQDQLDEEMEAKQNLER.-	2291.44	3	904.67	1.60	0.1	450	17/72	3
JMFAGNACL15B21E3, 2302	- AEMEDLVSSKDDVGKNVHELEK.-	2473.70	3	597.68	1.75	0.0	318	17/84	3
ajrawphagjun20dpi1MNaCl, 2414	-.IAQLEEELEEEQGNMEAMSDRVRK.-	2836.11	3	928.67	1.71	0.2	283	19/92	3
rawphag2007chfbead2, 662	-.ERNTDQASMPDNTAAQK.-	1877.97	3	354.46	1.37	0.1	154	15/64	3
rawsucrfp_60MeOHphagigg_MAr04, 1134	-.LQDFASTIEVMEEGKKR.-	1982.25	3	291.62	1.27	0.0	227	15/64	3
RawPhg2007MeEthmeth3digest, 1508	-.EEKSRQELEK.-	1276.38	2	599.74	1.51	0.1	370	1/2	3
rawphag2007chfbead3, 2671	-.HESMISELEVRLKK.-	1700.00	2	348.06	1.25	0.0	269	5/13	3
phagrawFsucchlf_dec23, 2732	-.RHEMPPHIYAIADTAYRSMLQDR.-	2773.15	3	486.08	1.24	0.1	365	21/88	4
jmldl250nacrawphag3007, 1696	-.EQEVTVLKKALDEETR.-	1889.10	2	691.58	1.51	0.1	333	11/30	3
jmldl600nacrawphag3007, 1776	-.LMATLRNTTANFVRCIIPNHEK.-	2544.00	3	1159.50	1.65	0.2	307	3/14	1
ajrawmediapbsnocells, 828	-.MQLAKKEEELQAALAR.-	1830.14	3	297.67	1.01	0.0	284	7/30	5

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
MYH8_MOUSE Myosin heavy chain, smooth muscle isoform (SMMHC)					2987.77	13431676.0	33		
rawextr_150bead_Mar04, 633	-.QLHEYETELEDERKQR.-	2104.22	3	116.41	1.38	0.0	84	1/4	3
rawextr_300bead_Mar04, 672	-.KQADLEKEELAEELASSLSGR -	2304.50	3	552.44	2.04	0.1	167	7/40	3
rawextr_900bead_Mar04,1018-1020	-.EELAEELASSLSGRNTLQDEK.-	2320.45	3	736.82	2.19	0.1	279	17/80	3
rawextr_actinbeadigg_Mar04, 1339	- MLKAEMEDLVSSKDDVGK.-	1996.29	3	709.49	1.40	0.2	259	1/4	3
FPbeads1000_Dec19, 1996	- ENADLAGELRVLGQAKQEVEHK.-	2435.68	2	424.82	1.03	0.2	111	5/21	3
rawextr_250beadigg_Mar04, 2514	-.TLLQEQLQAETELYAESEEMRVRLAAK.-	3151.54	2	49.67	0.99	0.0	46	7/52	1
jmraw5minbsafreezthaw, 750	-.STVAALEAK.-	890.02	2	226.14	1.32	0.1	121	3/8	3
jmrawbsa5minlowionic, 2078	- AEMEDLVSSKDDVGKNVHELEK.-	2473.70	3	171.96	1.18	0.0	139	4/21	3

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
MY1A_MOUSE Myosin Ia (Brush border myosin I) (BBM-I) (BBMI) (Myosin I heavy c					8468.17	13431683.0	20		
rawsucrfp_350phagigg_Mar04, 826	-.QVQTLR.-	744.86	2	414.51	1.41	0.1	97	1/2	
phagrawF400_dec20,1174-1176	-.YMDIEFDFK.-	1208.37	1	263.73	1.39	0.0	178	9/16	5
phagrawFsuc60MeOH_dec23, 1316	-.NFHIFYQLLAGADAQLLKALK.-	2375.80	3	618.55	1.49	0.1	277	19/80	
rawsucrfp_300phagigg_Mar04,1401-1403	-.LKGREEGPVLVADTVK.-	1711.99	2	164.27	1.21	0.0	135	3/10	
phagrawFsuc450_dec20, 2110	-.YMDIEFDFK.-	1208.37	1	348.89	1.30	0.0	269	9/16	5
rawsucrfp_chlfphagigg_Mar04, 2394	- SQILISAWFRGNKQK.-	1777.06	2	166.91	1.22	0.0	136	2/7	
phagrawFsuc250_dec22, 2579	-.LNQLFSKHSHYESK.-	1718.90	2	380.65	1.15	0.1	276	9/26	
phagrawFsucchlfbead_dec23, 2928	-.YMDIEFDFKGSPLGGVITNYLLEK.-	2751.15	3	295.25	1.29	0.1	164	17/92	
jmfag5minigg400mmnacl, 826	-.GREEGPVLVADTVKK -	1598.83	2	1072.27	1.29	0.3	175	9/28	
JMMAGTube1B16E3, 904	-.ISHYAGKVTYNVTGFIDK.-	2014.27	3	246.38	1.41	0.0	165	4/17	
jmfag1mnacl7.5minigg, 1306	-.PHIYALANVAYQSLKDRDR.-	2231.50	3	331.96	1.27	0.0	262	2/9	
jmfag5minigg400mmnacl, 1328	-.PHIYALANVAYQSLKDR.-	1960.23	3	337.16	1.11	0.0	298	1/4	
ajrawphagjun20actinDPI, 430	-.NIYSRLFDWIVK.-	1554.82	3	1265.81	1.87	0.2	380	17/44	
AJRAWActinIgG_june13, 994	-.TIRNNNSSRFGK.-	1394.52	3	358.29	1.24	0.0	288	15/44	
jmIgG500rawphag3007, 1477	-.VEYFDNGIICNLIEHSQR.-	2151.39	3	258.12	1.29	0.0	194	4/17	
jmrawminigg200mmnaclsyringdnas, 2794	- PGVVSDSTFLAKLNQLFSKHSHYESK.-	2921.26	3	297.84	1.59	0.0	186	21/100	
ajrawmediapbsnocells, 756	-.EASLKRPPTAGTQFK.-	1631.86	2	322.11	1.15	0.1	171	2/7	
jmfagtimecon7 5min.3230,3230.3	-.GEQVNSVKEQLLQSNPVLEAFGNAK.-	2700.99	0	469.38	1.40	0.1	252	19/96	
jmbeadsactinrawphag3007, 122	-.LQRLKGR.-	871.07	2	193.25	1.10	0.0	174	7/12	
jmbeads350rawphag3007nd, 2366	-.LQQVFIELTLKEEQEEYK.-	2258.55	3	609.98	1.21	0.2	207	15/68	
jmbeads350rawphag3007nd, 2462	-.THYQQMRK.-	1092.26	2	54.88	0.89	0.0	48	3/7	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
MY1A_MOUSE Myosin Ia (Brush border myosin I) (BBM-I) (BBMI) (Myosin I heavy c					1405.04	13431683.0	26		
rawextr_150beadigg2_Mar04, 556	-.IRSSVLLIQAFVRGWR.-	1902.28	3	712.13	1.37	0.1	493	17/80	
rawextr_60MeOHbead_Mar04, 860	-.GSPLGGVITNYLLEK.-	1561.81	3	355.68	1.35	0.0	244	15/58	
FPbeads600_Dec19, 984	-.PGVVSDSTFLAK.-	1221.39	2	87.72	0.92	0.0	86	7/22	
rawextr_800bead_Mar04, 1756	-.GREEGPVLVADTVKK.-	1598.83	2	67.58	0.76	0.0	89	3/14	
jmraw5minbsareebeads, 1550	-.GIQEIGEMMGLNSTELER.-	2008.26	3	181.95	1.18	0.0	154	13/68	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
myosin 1H [Mus musculus]					3857.57	29725639.0	5		
jmbeads450nacirawphag3007, 103	-.YCRGISAERK.-	1183.37	3	741.03	1.44	0.0	508	7/18	1
jmfagtimecont10min_030601202502,1402-1404	-.VLQLLGSEK.-	987.18	2	2327.96	1.78	0.3	395	11/16	1
jmidl400firstnacirawphag3007,2950-2952	-.QLLLTQRSAYLVELSKVK.-	2090.50	3	788.57	2.46	0.0	321	9/34	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Myosin light chain kinase 2, skeletal/cardiac muscle (MLCK2					13585.55	38075322.0	##		
jmraw5miniggiowionc, 365	-.DPGAPDPKNNPDPPSLK -	1759.90	3	352.52	1.31	0.0	269	17/64	
AJRAWActiniIgG_june13,818-820	-.AGGTNALAEKKK.-	1188.36	3	319.00	1.24	0.1	182	7/22	
ajrawphagjun20actinDPI, 1644	- NNPDPPSLKK.-	1110.25	2	232.65	1.03	0.1	172	7/18	
jmrawigg5min1mnacl, 1719	- EPSAPATEKDLSPPNAK.-	1752.90	2	100.43	1.02	0.1	60	3/16	
jmrawigg5min150mmnacl, 1720	- NNPDPPSLKK -	1110.25	2	881.12	1.29	0.2	262	4/9	
ajrawphagjun20dpi1MNaCl, 1850	- NNPDPPSLKK -	1110.25	2	211.06	0.94	0.1	147	7/18	
jmraw5minigg250mmnaclsyringdnase, 2044	-.KGDPVPASASSQGPSGEGDGGFR.-	2161.23	3	296.32	1.53	0.1	119	17/88	
jmraw5minigg500mmnaclsd,2130-2132	- NNPDPPSLKK -	1110.25	2	288.28	1.27	0.0	225	4/9	
jmrawmmigg200mmnaclsyringdnas,2188-2190	- NNPDPPSLKK.-	1110.25	2	531.86	1.22	0.1	229	4/9	
jm5miniggrawiowionic, 2258	-.DPGAPDPKNNPDPPSLKK -	1888.07	2	318.45	1.14	0.1	84	3/17	
ajrawphagactin20, 2456	- NNPDPPSLKK.-	1110.25	2	232.58	1.05	0.1	158	7/18	
ajrawphagactin20, 2460	-.NNPDPPSLKK.-	1110.25	2	163.39	0.94	0.1	143	7/18	
ajrawphagactin20, 3118	-.NNPDPPSLKK.-	1110.25	2	408.32	1.13	0.1	316	4/9	
rawsucrfp_250phagigg_Mar04, 654	- APSFSSPEK.-	950.03	2	189.89	0.78	0.1	201	7/18	
rawsucrfp_150phagigg_Mar04, 1223	-.KEEAEKASGQAGQAK.-	1532.64	2	638.04	1.25	0.1	473	3/7	
phagrawF600_dec20, 1282	- EPSAPATEK	930.00	2	208.25	0.89	0.1	144	3/8	
rawsucrfp_150phagigg_Mar04, 1349	- AAAGDGPSASEKEPSAPATEK.-	1972.06	3	413.88	1.40	0.1	255	9/40	
phagrawFsuc500_dec20, 1836	- DKEMVLLEIEVMNQLNHR -	2212.58	3	697.40	1.69	0.1	310	1/4	
phagrawFsucchlfbead_dec23, 1886	-.DPGAPDPKNNPDPPSLKK.-	1888.07	2	809.95	1.40	0.2	226	11/34	
phagrawFsuc800_dec23, 2078	- MFVSQVVSGVSVTPDPQDPGPVKAGGTNALAEKK.-	3412.86	2	25.79	0.79	0.0	25	1/11	
phagrawFsuc400_dec20, 2820	- PSQPVVLSYLQSTCIPSVGDRCPRPFWVYK.-	3424.98	2	49.89	0.85	0.0	51	4/29	
jmfag5miniggi500mmnacl, 1252	- DPGAPDPKNNPDPPSLKK.-	1888.07	3	660.12	1.50	0.0	416	5/17	
jmfag5miniggi350mmnacl, 1295	- KGDPVPASASSQGPSGEGDGGFR.-	2161.23	3	332.26	1.51	0.1	155	5/22	
jmfag5miniggi1000mmnacl,1510-1512	- KGDPVPASASSQGPSGEGDGGFR -	2161.23	3	645.55	1.98	0.1	119	19/88	
jmfag5miniggi200mmnacl, 1530	-.KGDPVPASASSQGPSGEGDGGFR.-	2161.23	3	793.83	1.80	0.1	240	1/4	
jmfag1mnacl5miniggi, 1584	- KGDPVPASASSQGPSGEGDGGFR -	2161.23	3	892.40	1.60	0.2	204	21/88	
jmfag5miniggi300mmnacl, 2130	- KGDPVPASASSQGPSGEGDGGFR.-	2161.23	3	393.82	1.30	0.1	206	5/22	
jmfag5miniggi300mmnacl, 2138	- KGDPVPASASSQGPSGEGDGGFR.-	2161.23	3	755.71	1.74	0.1	243	21/88	
jmfag5miniggi1000mmnacl, 2738	- PSQPVVLSYLQSTCIPSVGDRCPRPFWVYK.-	3424.98	2	169.94	0.87	0.1	72	4/29	
jmraw5minbsaraabeads, 2184	- NNPDPPSLKK.-	1110.25	2	263.33	0.87	0.0	303	11/18	
jmlolbeadschlfrawphag3007, 2220	- NNPDPPSLKK.-	1110.25	2	107.94	0.89	0.0	116	7/18	
jmrawbas5min1mnacl,2424-2426	- NNPDPPSLKK.-	1110.25	2	1012.21	1.39	0.2	258	1/2	
jmrawigg5miniggfreebead, 1602	- KDPGAPDPKNNPDPPSLK.-	1888.07	1	191.38	0.77	0.1	76	7/34	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Myosin light chain kinase 2, skeletal/cardiac muscle (MLCK2					598.45	38075322.0	5		
FPbeads250_Dec19, 1940	-.AAAGDGPSASEKEPSAPATEKDLSPPNAK.-	2794.97	3	598.45	1.83	0.1	299	5/28	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
keratin intermediate filament 16a [Mus musculus] &					**155966.04**	11559579.0	20		
phagrawF350_dec20, 303	-.ILNEMR.-	775.94	2	623.62	1.61	0.1	287	7/10	7
phagrawF350_dec20, 463	-.IRDWYQR.-	1037.16	3	2864.70	2.51	0.3	486	13/24	4
phagrawF350_dec20, 479	-.IRDWYQR.-	1037.16	3	1852.54	2.17	0.2	577	5/8	4
phagrawF350_dec20, 506	-.VTMQNLNDR.-	1091.23	2	2420.40	1.87	0.2	781	3/4	14
phagrawF350_dec20,574-576	-.KNHEEEMLALR.-	1370.56	3	7803.07	3.62	0.2	1597	3/5	2
phagrawF350_dec20,604-606	-.ASLENSLEETKGR.-	1434.54	3	4050.28	1.96	0.4	680	11/24	2
rawsucrfp_actinphagigg_Mar04, 608	-.KTEELNK.-	861.96	2	530.11	1.43	0.1	342	2/3	2
phagrawF350_dec20,660-662	-.LAADDFR.-	807.88	2	3246.16	2.23	0.3	482	11/12	34
phagrawF350_dec20, 668	-.LAADDFR.-	807.88	1	196.14	1.05	0.1	129	1/2	34
phagrawF350_dec20,682-684	-.ASLENSLEETK.-	1221.30	2	2546.56	2.34	0.0	1086	3/4	2
phagrawF300_dec20, 711	-.KNHEEEMLALR.-	1370.56	3	4394.43	2.61	0.3	951	21/40	2
phagrawF350_dec20, 746	-.TRLEQEIATYR.-	1380.53	3	4642.46	2.69	0.3	1019	21/40	17
rawsucrfp_350phagigg_Mar04,788-790	-.VTMQNLNDR.-	1091.23	2	4587.87	2.77	0.3	884	13/16	14
rawsucrfp_250phagigg_Mar04, 794	-.VTMQNLNDR.-	1091.23	2	4648.53	2.64	0.3	939	13/16	14
rawsucrfp_250phagigg_Mar04, 798	-.VTMQNLNDR.-	1091.23	2	3415.83	2.39	0.1	1260	15/16	14
rawsucrfp_450phagigg_Mar04,798-800	-.VTMQNLNDR.-	1091.23	2	5186.40	3.09	0.2	1059	7/8	14
phagrawF300_dec20, 903	-.TRLEQEIATYR.-	1380.53	2	2290.08	1.54	0.3	382	1/2	17
phagrawFsuc200_dec22, 1015	-.ALEEANRDLEVKIR.-	1656.87	2	551.34	1.49	0.1	299	9/26	2
phagrawF350_dec20, 1112	-.GQTGGDVNVEMDAAPGVDLSR.-	2089.23	2	5160.76	2.09	0.4	458	7/20	2
phagrawFsuc700_dec23, 1157	-.MATCSRQFTSSSSMK.-	1652.90	2	190.51	1.06	0.1	133	2/7	3
phagrawFsuc400_dec20,1206-1208	-.ASLENSLEETK.-	1221.30	2	7948.14	3.44	0.4	933	3/4	2
phagrawFsuc500_dec20, 1214	-.ASLENSLEETK.-	1221.30	2	6945.20	2.37	0.5	759	13/20	2
phagrawFsuc350_dec20, 1290	-.ASLENSLEETK.-	1221.30	2	1701.44	1.51	0.3	478	11/20	2
phagrawFsuc600_dec20, 1294	-.ASLENSLEETK.-	1221.30	2	2384.68	1.84	0.3	441	1/2	2
phagrawFsuc350_dec20, 1296	-.ASLENSLEETK.-	1221.30	2	1167.69	1.70	0.1	474	3/5	2
phagrawFsuc450_dec20, 1390	-.ASLENSLEETK.-	1221.30	2	865.13	1.45	0.1	412	11/20	2
phagrawFsuc450_dec20,1464-1466	-.TRLEQEIATYR.-	1380.53	2	12347.25	3.22	0.5	942	7/10	17
AJRAWActinIgG_june13, 1034	-.VTMQNLNDR.-	1091.23	2	3458.15	2.43	0.3	677	3/4	14
AJRAWActinIgG_june13, 1038	-.VTMQNLNDR.-	1091.23	2	2500.77	2.44	0.1	799	13/16	14
AJRAWActinIgG_june13, 1126	-.TRLEQEIATYRR.-	1538.72	3	4578.68	2.57	0.3	832	19/44	13
jmfag5minigg600mmnacl, 2840	-.KNHEEEMLALRGQTGGDVNVEMDAAPGVDLSR.-	3440.77	2	75.43	0.76	0.1	71	5/31	2
jmbeads1000naclrawphag3007, 398	-.KTEELNK.-	861.96	1	138.47	0.77	0.0	173	7/12	2
jmbeads400rawphag3007, 1353	-.FDGFGGGFGAGLGGGLGGGIGDGLLVGSEK.-	2626.86	3	650.66	1.57	0.0	396	25/116	2
rawphag2007chlfsol3, 205	-.VTMQNLNDR.-	1091.23	2	3722.98	2.48	0.2	887	7/8	14
rawphag2007chlfsol3, 226	-.VTMQNLNDR.-	1091.23	2	3689.95	2.65	0.2	1072	15/16	14
rawphag2007chlfbead2, 370	-.DVEAWFLRK.-	1164.34	3	839.84	0.94	0.0	890	1/2	2
rawphag2007chlfsol3, 617	-.TRLEQEIATYR.-	1380.53	3	3463.35	2.59	0.3	531	2/5	17
rawphag2007chlfsol3, 619	-.TRLEQEIATYR.-	1380.53	2	16866.82	3.79	0.5	1443	4/5	17
rawphag2007chlfsol3, 621	-.TRLEQEIATYR.-	1380.53	3	1173.57	1.68	0.1	580	9/20	17
rawphag2007chlfbead3, 629	-.ASLENSLEETK.-	1221.30	2	4441.30	2.10	0.3	1060	7/10	2
rawphag2007chlfbead1,968-970	-.VTMQNLNDR.-	1091.23	2	2575.72	2.19	0.2	801	13/16	14
rawphag2007chlfsol1,980-982	-.VTMQNLNDR.-	1091.23	2	3824.89	2.12	0.3	1067	7/8	14
rawphag2007chlfsol2,1068-1070	-.VTMQNLNDR.-	1091.23	2	4314.20	2.82	0.3	739	3/4	14
rawphag2007chlfbead1, 1102	-.LAADDFR.-	807.88	2	5089.97	2.12	0.4	527	5/6	34

control

keratin intermediate filament 16a [Mus musculus] &					**25853.00**	11559579.0	8		
rawextr_300beadigg_Mar4,820-822	-.VTMQNLNDR.-	1091.23	2	5177.60	3.04	0.3	955	7/8	14
rawextr_900beadigg_Mar04, 892	-.EQGSTSFSQSQSQSSRD.-	1846.81	3	321.67	1.46	0.1	158	9/32	2
FPbeads350_Dec19, 1075	-.QSVEGDINQLRK.-	1316.45	2	548.79	1.43	0.1	218	5/11	2
FPbeads250_Dec19, 1238	-.ASLENSLEETK.-	1221.30	2	1585.19	1.83	0.2	576	11/20	2
FPbeads250_Dec19, 1242	-.ASLENSLEETK.-	1221.30	2	1566.50	1.64	0.3	270	1/2	2
FPbeads250_Dec19, 1304	-.TRLEQEIATYR.-	1380.53	2	7768.68	2.66	0.4	1375	4/5	17
FPbeads250_Dec19, 1312	-.TRLEQEIATYR.-	1380.53	2	7096.43	2.40	0.4	1231	3/4	17
jmbsa150naclrawphag3007,562-564	-.ASLENSLEETKGR.-	1434.54	3	291.12	1.41	0.0	196	3/8	2
jmraw5minbsabeads, 1258	-.ASLENSLEETK.-	1221.30	2	1497.02	1.70	0.2	578	3/5	2

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
keratin complex 1, acidic, gene 23; type I intermediate filament cytok					**3880.44**	15431281.0	9		
jmfag5minigg600mmnacl, 386	-.GRQGSCHR.-	900.99	2	451.56	1.33	0.0	340	4/7	1
JMFAGNACL15B21E3, 2086	-.LLEGDTEGTMDGSESR.-	1697.76	2	573.15	0.98	0.0	563	13/30	1
jmfag5minigg500mmnacl, 2440	-.LQEQIVDGKMANAHIVVLIDNAR.-	2548.95	3	1171.71	1.39	0.2	366	19/85	1
jmbeads400rawphag3007, 449	-.WHQEREPSHRK.-	1490.61	2	383.76	1.26	0.1	214	2/5	1
rawphag2007chlfbead2, 628	-.EPSHRKDYSQYEENISR.-	2139.23	3	856.51	1.91	0.1	268	17/64	1
phagrawFchlfbead_dec23, 827	-.WHQEREPSHR.-	1362.44	3	354.70	1.23	0.1	253	7/18	1
phagrawFchlf_dec23, 3672	-.MNSSHSFNQTYSASVHSLGSTRGR.-	2612.78	2	89.05	0.74	0.1	69	4/23	1

control

keratin complex 1, acidic, gene 23; type I intermediate filament cytok					**736.81**	15431281	8		
rawextr_700bead_Mar04, 1081	-.MNSSHSFNQTYSASVHSLGSTR.-	2399.54	3	736.81	1.8	0	407	1/4	1

APPENDIX L – DYNEIN SUMMATION OF IONS

The summation of peptides from Dyneins found to be associated with Fc receptor-mediated phagocytosis in macrophage cells.

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal dynein heavy chain 7 [Mus musculus]					28113.09	38075883.0	46		
rawsucrfp_450phagigg_Mar04,1052-1054	-.WIKNSEKDNQLSVIK.-	1803.05	3	835.42	1.92	0.1	234	19/56	
phagrawFsuc1000_dec23,1197-1199	-.NYPVRYEESMNTVLVQEMER.-	2488.78	3	160.30	1.26	0.0	114	7/38	
rawsucrfp_900phagigg_Mar04, 1243	-.AEQTTGLTTALGRTR.-	1576.74	2	315.52	1.37	0.1	187	11/28	
rawsucrfp_800phagigg_Mar04, 1410	-.LGLPWAWAMNVSHKGQRAER.-	2308.65	3	1062.51	1.70	0.2	327	5/19	
rawsucrfp_250phagigg_Mar04, 1518	-.GAVEKWLIQVEDLMLRSIR.-	2257.69	3	381.57	1.37	0.1	219	1/4	
rawsucrfp_800phagigg_Mar04, 1594	-.MLCCLLIQPADITIVK.-	1775.28	2	329.36	1.44	0.0	227	1/3	
rawsucrfp_150phagigg_Mar04, 1714	-.KWVVFDGPIDTLWIESMNTVLDDNK.-	2937.32	3	206.51	1.24	0.0	155	17/96	
phagrawFsuc350_dec20, 2254	-.RSYPSLKPLGSYITDFLAR.-	2185.51	3	429.47	1.47	0.0	275	19/72	
phagrawFsuc150_dec22, 2474	-.VKLGGTGGKDAIPAVLSR.-	1740.04	2	282.71	1.03	0.1	123	9/34	
phagrawFsuc400_dec20, 3752	-.ESIGFATWGFIKNRMLCCLLIQPADITIVK.-	3383.10	2	36.17	0.66	0.0	55	4/29	
rawsucrfp_700phagigg_Mar04, 1983	-.FFNFVLKWQRTEK.-	1744.03	2	326.53	1.06	0.1	225	1/3	1
rawsucrfp_450phagigg_Mar04, 2038	-.PEEEPKENPTITMCTTVMEQIKSFK.-	2912.35	2	394.85	1.32	0.1	100	1/6	
phagrawFsuc600_dec20, 3086	-.TEKLDSFYNCVSILMSNQLKDLLWR.-	3018.50	2	307.37	0.98	0.2	72	7/48	1
JMFAGNACL15B21E3, 184	-.EGYRPIAK.-	934.08	3	1239.47	1.85	0.0	668	15/28	
JMFAGNACL10_2B21E3, 197	-.EGYRPIAK.-	934.08	3	1055.38	1.89	0.0	540	1/2	
JMMAGTube1B16E3, 220	-.GGGSTTVSKK.-	922.02	2	442.49	1.42	0.1	283	4/9	
JMFAGNACL5B21E3, 754	-.LLGDMNFLRDLR.-	1463.73	2	345.04	1.23	0.1	134	4/11	
jmfag5minigg300mmnacl, 834	-.YDLKDTSK.-	970.06	3	168.23	1.53	0.0	95	9/28	
JMFAGNACL10_1B21E3,858-860	-.LLGDMNFLRDLR.-	1463.73	2	243.33	1.48	0.1	134	4/11	
JMMAGTube1B16E3, 1164	-.EPTLELQPGVCTQSQK.-	1758.98	3	219.73	1.29	0.0	159	1/5	
jmfag5minigg1000mmnacl, 1176	-.QTRITLGALVTIDVHAR.-	1865.17	3	344.91	1.16	0.1	199	7/32	
JMFAGNACL15B21E3, 2338	-.GPERAQTQATSLLSQTGR.-	1902.06	2	544.37	1.26	0.1	304	11/34	
JMFAGNACL5B21E3, 2514	-.ELQYQLNDIVELVRGK.-	1918.18	2	145.50	0.91	0.1	133	4/15	
jmfag1mnacl5mincon, 2632	-.HIRVWTMASFIFSLIWSIGASCDTDGR.-	3071.52	2	95.01	0.71	0.1	94	2/13	
JMFAGNACL10_1B21E3, 1618	-.VPETTEEMMELIAFVER.-	2025.33	3	218.68	1.27	0.1	141	1/4	1
JMMAGNEGB16D3, 1774	-.VINLFTK.-	835.03	1	315.01	1.15	0.1	222	1/2	1
jmfag5miniggbead, 2187	-.QMSYFLDALLMSQEDLNLNATVLLWPTK.-	3256.78	2	140.88	0.82	0.1	83	1/6	1
jmfagfrench5minigg1mnackdtt, 463	-.ESFDTVFHHLR.-	1388.51	3	358.84	1.53	0.0	229	3/8	
jmrawigg5min300mmnaclsyringednase, 749	-.RGPERAQTQATSLLSQTGR.-	2058.25	3	3266.98	1.81	0.4	470	5/18	
jmfgG500rawphag3007, 963	-.VLAATSLTGLLEKLQNCNDLLEK.-	2487.90	2	168.88	1.09	0.0	148	5/22	
jmraw5miniggiowonic, 1323	-.VLAATSLTGLLEKLQNCNDLLEKIMK.-	2860.43	3	254.44	1.50	0.1	122	4/25	
jmigg450rawphag3007, 1654	-.PLLIAVTGEGHSPWETASQSLKR.-	2478.79	3	327.29	1.48	0.0	221	2/11	
jmfgG250rawphag3007, 2252	-.WIKNSEKDNQLSVIK.-	1803.05	2	205.99	0.97	0.1	185	5/14	
jmrawigg5min150mmnacl, 2712	-.HGPLELDSNSDDSVDQQDFEEAIQEYLK.-	3095.19	2	99.97	0.92	0.1	54	7/52	
ajrawphagjun20dpi1MNaCl, 2778	-.MKQIIEVESAQVEAKR.-	1863.19	2	120.59	1.04	0.0	93	4/15	
ajrawphagjun20actinDPI, 1232	-.GPIDCEALRNDLSIQARK.-	2000.27	3	183.97	0.98	0.1	158	13/68	1
ajrawphagactin20, 2662	-.SLFPFL.-	723.88	1	77.96	0.83	0.0	71	2/5	
ajrawphagactin20, 2668	-.SLFPFL.-	723.88	1	67.86	0.81	0.0	83	2/5	
JMFAGNACL15B21E3, 184	-.EGYRPIAK.-	934.08	3	1239.47	1.85	0.0	668	15/28	
JMFAGNACL10_2B21E3, 197	-.EGYRPIAK.-	934.08	3	1055.38	1.89	0.0	540	1/2	
JMFAGNACL5B21E3, 754	-.LLGDMNFLRDLR.-	1463.73	2	345.04	1.23	0.1	134	4/11	
jmfag5minigg300mmnacl, 834	-.YDLKDTSK.-	970.06	3	168.23	1.53	0.0	95	9/28	
JMFAGNACL10_1B21E3,858-860	-.LLGDMNFLRDLR.-	1463.73	2	243.33	1.48	0.1	134	4/11	
jmfag5minigg1000mmnacl, 1176	-.QTRITLGALVTIDVHAR.-	1865.17	3	344.91	1.16	0.1	199	7/32	
JMFAGNACL15B21E3, 2338	-.GPERAQTQATSLLSQTGR.-	1902.06	2	544.37	1.26	0.1	304	11/34	
JMFAGNACL5B21E3, 2514	-.ELQYQLNDIVELVRGK.-	1918.18	2	145.50	0.91	0.1	133	4/15	
jmfag5mincont400_030531151834, 68	-.AQTQATSLLSQTGRGTFR.-	1924.11	2	350.05	1.12	0.1	121	4/17	
jmbeads1000naclrawphag3007, 94	-.QAVMEAK.-	776.93	2	204.59	1.02	0.0	198	7/12	
jmfagcont5minbead, 934	-.VRLGTAETRCVEK.-	1462.70	3	845.44	1.65	0.2	239	1/3	
jmbeads500rawphag3007, 1067	-.NVGVKGQK.-	829.97	2	107.75	0.71	0.0	148	5/14	
jmfagcon5min1000mmnacl_030601180404,1400-1402	-.ICEDFSPETCNPTFR.-	1759.94	2	815.94	2.06	0.1	358	3/7	
jmbeads250rawphag3007, 2466	-.LGLPWAWAMNVSHK.-	1610.91	1	96.70	0.79	0.1	83	3/13	
jmfag1mnacl5mincon, 2632	-.HIRVWTMASFIFSLIWSIGASCDTDGR.-	3071.52	2	95.01	0.71	0.1	94	2/13	
jmbeads300rawphag3007, 287	-.FCAKDPKVK.-	1036.27	2	138.66	0.95	0.0	142	3/8	
jmbeads250rawphag3007, 1840	-.ARAFANILLNDIASKHR.-	1911.20	2	222.57	1.35	0.0	157	9/32	1
jmfag5mincon450mmnacl, 2386	-.QLQKRIQESEEAVQFINK.-	2189.46	3	376.67	1.47	0.1	188	7/34	1
jmfagcon5min1000mmnacl_030601180404, 2534	-.DTGIGILSSVDEIQAILDDQIIKTQTMR.-	3075.48	2	39.56	0.72	0.1	27	1/9	
jmfag5mincont150mmnacl, 3106	-.SMKRYLVQSVLVK.-	1551.92	2	264.71	1.04	0.1	223	1/3	1
rawphag2007chfbead3,905-907	-.WIKNSEKDNQLSVIK.-	1803.05	3	623.39	1.56	0.1	206	17/56	
rawphag2007chfbead2, 1050	-.DAIPAVLSRR.-	1098.28	2	135.76	0.87	0.0	153	1/3	
RawPhag200760MeBeadsdigest, 1938	-.WVVFDGPIDTLWIESMNTVLDDNK.-	2809.14	3	283.17	1.52	0.1	159	1/4	
RawPhg2007MeEthmeth3digest,2076-2078	-.YVNGLDQLAFAESQVGEMK.-	2100.34	3	1260.26	2.04	0.2	221	1/4	
jmkdt350naclrawphag3007, 1104	-.PDKITPAITNYVTDKLGK.-	1975.28	3	1010.91	1.39	0.1	555	5/17	
jmkdtactinrawphag3007, 2604	-.GDNKDGPGSAFSSVAERVK.-	1922.05	3	1436.66	1.68	0.1	818	1/3	

control

similar to axonemal dynein heavy chain 7 [Mus musculus]					3453.46	38075738.0	19		
rawextr_500beadigg_Mar04, 1158	-.DLLWRTVEEFIK.-	1549.80	2	562.81	1.42	0.1	356	5/11	1
rawextr_60MeOHbead_Mar04, 1450	-.MIQRFQAENHTFDEYTEFIEK.-	2677.93	3	585.20	1.87	0.0	310	17/80	1
FPbeads300_Dec19, 1578	-.IILLDLTGIRAR.-	1354.67	2	1389.61	1.56	0.2	410	1/2	1
FPbeads150_Dec19, 1907	-.QLQKRIQESEEAVQFINK.-	2189.46	3	280.22	1.30	0.0	208	7/34	1
jmraw5minbsabeads, 1220	-.TAIAAEKEALNLK.-	1372.59	3	635.62	1.34	0.2	144	1/3	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal dynein heavy chain 7 [Mus musculus]					5911.22	38049489.0	2		
jmrawbas5min1mnacl, 1466	- QGPIAMKMLEKAVK.-	1544.95	2	784.38	1.30	0.2	229	9/26	
rawsucrfp_chfphagigg_Mar04, 120	- ILSSSKSLANEISQK.-	1605.82	2	124.47	0.90	0.0	138	2/7	1
rawsucrfp_60MeOHphagigg_MAr04, 922	-.SYLMDPISDPEFFGSCK.-	1937.18	3	116.76	1.09	0.0	107	3/16	1
phagrawF150_dec22, 1168	-.RGTLSTTGHSTNFVIAMILPSVHPK.-	2666.10	3	184.74	1.34	0.0	134	7/48	
phagrawFsuc500_dec20, 2300	-.VIPMLQEFIIKK.-	1459.87	1	655.44	1.77	0.0	360	1/2	1
phagrawFsuc500_dec20, 2308	-.VIPMLQEFIIKK.-	1459.87	1	471.93	1.14	0.1	372	5/11	1
rawsucrfp_300phagigg_Mar04, 2614	-.GTLSTTGHSTNFVIAMILPSVHPK.-	2509.91	3	265.00	1.13	0.1	126	13/92	
JMMAGNEGB16D3, 34	-.RPSYVAPLYK.-	1194.41	3	343.06	1.11	0.0	292	7/18	1
jmrawigg5min450mmnaclsd,860-862	-.QGPIAMKMLEKAVK.-	1544.95	2	200.40	1.50	0.0	132	7/26	
jmrawigg5min350mmnaclsynngednase, 867	-.QGPIAMKMLEKAVK.-	1544.95	2	218.81	1.21	0.0	179	5/13	
jmIgG150rawphag3007, 1070	-.SYLMDPISDPEFFGSCK.-	1937.18	3	686.26	1.49	0.2	212	17/64	1
jmraw5minigg600mmnaclsd,1512-1514	-.LLFSFCLTVNLLIHDNAINKTEWR.-	2862.34	3	434.34	1.74	0.1	58	15/92	
jmIgG1000naclrawphag3007, 1944	-.AVKGLVVMSTELEEVVSSILNVK.-	2445.90	3	386.70	1.29	0.1	224	17/88	
jmfagcont5minbead, 80	-.LQILRDHFTYSLYVNICRSLFEK.-	2860.33	3	200.26	1.19	0.0	169	15/88	1
jmbeads350rawphag30072nd, 1282	- KAPEDGVYIHGLFLDGASWDR.-	2347.57	3	838.67	1.79	0.1	429	21/80	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal dynein heavy chain 7 [Mus musculus]					3088.81	38049489.0	12		
jmrawigg5minigglreebead, 1624	-.FLLTGGIGLDNPYTNPCTWLPQKSWDEICR.-	3439.91	3	492.29	1.78	0.1	194	15/116	
rawextr_300bead_Mar04, 946	-.SYLMDPISDPEFFGSCKK.-	2065.36	3	727.61	1.52	0.0	474	19/68	1
rawextr_600bead_Mar04, 1048	- APEDGVYIHGLFLDGASWDRK.-	2347.57	3	829.08	1.77	0.1	363	19/80	
rawextr_400beadigg_Mar04, 2534	- SDIPRRPSYVAPLYK.-	1763.03	2	134.23	1.13	0.0	119	1/4	
FPbeads250_Dec19, 2554	-.MITPEGMQDQLLGIVVARER.-	2257.66	3	831.53	1.51	0.2	228	17/76	
FPbeads500_dec19, 3080	-.ESCINIQKAVKGLVVMSTELEEVVSSILNVK.-	3361.96	2	74.07	0.80	0.0	92	3/20	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal dynein heavy chain 7 [Mus musculus]					13137.79	38049491.0	17		
phagrawF1000_Dec23, 1566	-.DKSKQTDGSPIALFNMFIDCCR.-	2490.87	3	172.99	1.16	0.0	130	1/8	
phagrawF600_dec20, 2652	-.MQEDFHDLFKNLDFNHDGTVEEDDLR.-	3181.35	2	57.84	0.93	0.1	29	3/25	
rawsucrfp_200phagigg_Mar04, 2899	-.EIANVDALRMIVEGHLDEYNNMSKK.-	2891.27	3	138.17	1.28	0.0	103	5/32	1
phagrawFsuc300_dec20, 3666	-.LAAHMADYSLFQVEISKGYGSHEWHEDLK.-	3363.70	2	43.32	0.80	0.0	35	1/8	2
jmfag1mnacl7,5minigg, 256	- EGCIDMCK.-	899.09	2	318.38	1.22	0.1	234	9/14	
jmfag5minigg350mmnacl, 489	-.AEQLIGGLGGEKTR.-	1429.61	3	1817.77	2.11	0.1	792	21/52	2
jmfag5minigg250mmnacl, 1352	-.LAAAEGKLKVAMEGLR.-	1658.00	3	786.94	1.55	0.1	424	19/60	
jmfag5minigg600mmnacl, 2756	-.RYEVGLDKLDSASSQVATMQSELEALHPQLK.-	3445.85	2	418.54	1.03	0.2	71	2/15	2
jmrawigg5min450mmnaclsd,800-802	-.IVKADETVANDQAMAAK.-	1776.01	3	179.83	1.30	0.0	136	1/4	2
jmIgG300rawphag3007, 1080	-.RNEVMKMK.-	1036.30	2	271.13	0.87	0.1	264	9/14	2
jmfag5minfrench1mnacldttdpi, 2708	-.RYEVGLDKLDSASSQVATMQSELEALHPQLK.-	3445.85	2	29.58	0.70	0.0	36	1/10	2
jmfag_20_minfrench1mnacldttdpi, 2708	-.RYEVGLDKLDSASSQVATMQSELEALHPQLK.-	3445.85	2	29.58	0.70	0.0	36	1/10	2
ajrawphag1MNaCl20, 2732	-.EGCIDMCKRFHTSTINLSTSFHNELQR.-	3169.57	3	264.41	1.47	0.0	170	17/104	
jmfag1mnacl7,5minigg, 256	- EGCIDMCK.-	899.09	2	318.38	1.22	0.1	234	9/14	
jmfag5minigg350mmnacl, 489	-.AEQLIGGLGGEKTR.-	1429.61	3	1817.77	2.11	0.1	792	21/52	2
ajrawphag1MNaCl20, 2732	-.EGCIDMCKRFHTSTINLSTSFHNELQR.-	3169.57	3	264.41	1.47	0.0	170	17/104	
jmfag5minigg600mmnacl, 2756	-.RYEVGLDKLDSASSQVATMQSELEALHPQLK.-	3445.85	2	418.54	1.03	0.2	71	2/15	2
jmfagcon5minn600mmnacl, 479	-.AEQLIGGLGGEK.-	1172.31	3	490.75	1.26	0.1	297	4/11	2
jmbeads150rawphag3007,1968-1970	- LAKLQDTLELNK.-	1386.62	1	744.21	1.44	0.2	203	4/11	2
RawPhag2007EtBeadsdigest_030718152503, 1190	-.SHALLVGVGGSGRQSVTR.-	1782.00	2	1093.10	1.28	0.2	322	11/34	2
jmldl150naclrawphag3007, 2002	-.VILRKCAESDMQGVFLFTDTQIK.-	2644.11	3	376.92	1.60	0.0	235	17/88	
jmldlactinrawphag3007, 2196	- VAKIVAPK.-	826.06	1	549.42	1.33	0.0	414	4/7	2
rawsucrfp_350phagigg_Mar04, 1688	-.PIPLSRACSSSR.-	1274.48	2	223.93	0.90	0.0	232	4/11	
rawsucrfp_350phagigg_Mar04, 1704	-.QLGQKSRHPTDFK.-	1542.73	2	150.31	1.15	0.0	120	5/12	
rawsucrfp_450phagigg_Mar04,1782-1784	-.QLGQKSRHPTDFK.-	1542.73	2	174.76	1.16	0.0	128	3/8	
phagrawFsuc500_dec20, 3478	-.HPTDFKTEITDGFPARYWLSAFFSPQG.-	3117.42	2	171.42	0.96	0.1	65	7/52	
jmfag1mnacl5mincon, 1110	- IAVEPPQGLK.-	1052.25	2	176.95	0.84	0.0	209	5/9	
JMFAGNACL10_1B21E3,1266-1268	-.AQKYIENLIYMQPK.-	1740.06	2	943.23	1.83	0.0	516	1/2	
jmigg450rawphag3007, 1974	-.EVNYLISEVTFGGR.-	1584.76	2	45.52	0.84	0.0	54	5/26	
rawphag2007chfbead3,1815-1817	-.EVNYLISEVTFGGR.-	1584.76	2	378.13	1.37	0.1	234	9/26	
ajrawmediapbsnocells, 440	-.IAVEPPQGLK.-	1052.25	2	261.55	0.97	0.1	200	4/9	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal dynein heavy chain 7 [Mus musculus]					2783.05	38049491.0	12		
FPbeads500_Dec19, 810	-.TEDFWGPAK.-	1051.13	2	220.82	1.08	0.1	102	7/16	
FPbeads800_Dec19, 1964	-.ADLEHQVDLCSKKLER.-	1885.14	2	176.28	1.12	0.1	115	7/30	1
rawextr_450beadigg_Mar04, 2844	-.WIKNMEKTNSLQLIK.-	1847.22	3	327.13	1.20	0.0	256	1/4	
rawextr_700beadigg_Mar04, 680	-.ILFSICLFSAVLIER.-	1725.13	3	120.96	1.20	0.0	101	15/56	
FPbeads200_Dec19, 1341	-.EVNYLISEVTFGGRVVDEWDMR.-	2815.90	3	229.18	1.19	0.0	188	4/21	
rawextr_600beadigg_Mar04, 3015	-.FGNGQWRLHAEGTPQK.-	1827.00	2	52.05	0.90	0.0	57	1/6	
jmbsa250naclrawphag3007,1440-1442	-.EVNYLISEVTFGGR.-	1584.76	2	1656.64	1.73	0.2	458	11/26	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Dynein intermediate chain 2, axonemal (Axonemal dynein inte					3758.10	38091940.0	4		
jmIgG150rawphag3007,1042-1044	-.ISEPIEVVIMDISR.-	1601.89	3	714.92	1.90	0.1	249	17/52	
jmIgG300rawphag3007, 1706	-.DSHVLLGGCYNGQIACWDTRK.-	2337.63	2	106.69	1.09	0.0	98	9/40	
jmrawigg5minbeadsfreezethaw, 2456	-.KGSLVAELSTIEFSHRDPVYGTIWLQSK.-	3163.57	2	683.01	1.08	0.2	84	1/8	
phagrawFsuc150_dec22, 910	-.NPVDTGIQCSASMSEHEANTER.-	2377.51	3	213.00	1.25	0.0	157	4/21	
phagrawFsuc400_dec20, 2892	-.KGSLVAELSTIEFSHRDPVYGTIWLQSK.-	3163.57	2	60.07	0.96	0.0	62	1/6	
jmbeads300rawphag3007, 610	-.ISEPIEVVIMDISR.-	1601.89	3	414.25	1.81	0.1	174	7/26	
RawPhag2007EtBeadsdigest_030718152503, 1196	-.DSHVLLGGCYNGQIACWDTRK.-	2337.63	3	1346.21	1.83	0.2	318	17/80	
jmldl300naclrawphag3007, 1944	-.VEGKEDDQKEEEAALDLDELVGK.-	2560.71	3	219.95	1.34	0.0	157	2/11	

control

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Dynein intermediate chain 2, axonemal (Axonemal dynein inte					1251.30	38091940.0	6		
rawextr_150bead_Mar04, 389	- KAKTQAEK.-	904.05	2	358.36	1.06	0.1	281	4/7	
rawextr_600bead_Mar04, 1698	- EQLENALGAISLEFESTLPTK.-	2291.54	2	103.38	0.92	0.0	95	1/5	
jmrawbsa5minlowionic, 1276	.EEEAALDLDELVGK.-	1531.64	3	789.56	1.74	0.1	338	9/26	

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
axonemal dynein heavy chain [Mus musculus] 959370				**4253.69**	11991525.0		19	
phagrawFsuc150_dec22, 988	-.LIDENVVSVHOFEWISQLR.-	2300.56	3	339.99	1.33	0.0	256	1/4
rawsucrfp_800phagigg_Mar04, 1072	-.MQRMVLSALIVIEVHAKDVVSK.-	2468.02	3	254.13	1.28	0.0	199	4/21
rawsucrfp_800phagigg_Mar04, 2030	-.TETTKDLGKALAIQTVVFNCSDQLDFMAMGK.-	3377.90	2	103.91	0.86	0.1	67	3/20
jmfag5minigg150mmnacl,872-874	-.IQLMDQNNFQEK.-	1508.68	3	486.40	1.84	0.1	218	3/11
jmrawigg5minbeadsyringdnase, 1235	-.LLDSLRDCNKLLDLVQK.-	1987.35	3	294.67	1.25	0.1	197	15/64
jmrawigg5min350mmnaclsyringednase, 1341	-.PYIPLIQGLRNPGMR.-	1726.08	2	941.26	1.47	0.2	378	11/28
jmIgG250rawphag3007, 2390	-.LVFLEERIVK.-	1246.52	2	175.32	0.97	0.0	180	1/2
jmfagtimecon2.5min.910.910.3	-.LLDLVQKGLSESLETK.-	1774.05	0	408.75	1.40	0.1	238	4/15
rawphag2007chlfsol3, 843	-.KIQLMDQNNFQEK.-	1636.86	2	441.06	1.04	0.2	185	5/12
rawphag2007chlbead3, 1913	-.IMKASVHDIIEMAIKAYLTMLR.-	2549.16	3	808.20	1.41	0.0	558	11/42

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
axonemal dynein heavy chain [Mus musculus] 278205				**1645.43**	11991525.0		24	
rawextr_actinbeadigg_Mar04, 549	-.PKGNLTFAR.-	1004.17	2	195.95	1.25	0.0	141	3/8
rawextr_150bead_Mar04, 2697	-.LVITPLTDRCYLTLTGALHLKFGGAPAGPAGTGP	3412.01	2	152.27	1.06	0.1	107	5/33
jmbsa400nactrawphag3007_030802153340,915-917	-.DIPACQEVALDIR.-	1443.65	3	875.35	2.04	0.0	426	3/8
jmraw5minbsafreezthaw, 2204	-.DIPACQEVALDIR.-	1443.65	3	421.87	1.33	0.1	241	7/24

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal heavy chain dynein type 3 [Mus musculus]				**2915.94**	38348574.0		9	
jmfag5mincon450mmnacl,1234-1236	-.FADDVSMGGTK.-	1128.24	2	883.86	1.42	0.2	296	11/20
JMFAGNACL15B21E3, 1772	-.PDKIVPAIQNFICETMGK.-	2005.39	3	105.85	0.86	0.0	123	5/34
rawsucrfp_60MeOHphagigg_MAr04, 1048	-.SLFEKDKLLFSLLLTVGLLK.-	2278.80	3	313.15	1.43	0.0	217	17/76
phagrawFsuc450_dec20, 2558	-.SLIDLGRAIKGQVLMSSELEEVFNSMLVGK.-	3265.84	3	217.89	1.09	0.1	73	3/29
phagrawFsucchlf_dec23, 2682	-.IEYIIEHFTLSIYNNVCRSLFEK.-	2833.25	3	445.28	1.82	0.1	184	2/11
rawsucrfp_60MeOHphagigg_MAr04, 1048	-.SLFEKDKLLFSLLLTVGLLK.-	2278.80	3	313.15	1.43	0.0	217	17/76
phagrawFsucchlf_dec23, 2682	-.IEYIIEHFTLSIYNNVCRSLFEK.-	2833.25	3	445.28	1.82	0.1	184	2/11
jmidl400firstnactrawphag3007, 1450	-.IEYIIEHFTLSIYNNVCRSLFEK.-	2833.25	3	191.48	1.14	0.1	136	13/88

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal heavy chain dynein type 3 [Mus musculus]				**590.13**	38348574.0		16	
rawextr_150bead_Mar04,359-361	-.VLSEEISEK.-	1034.14	3	590.13	1.70	0.1	315	15/32

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal heavy chain dynein type 3 [Mus musculus]				**10813.28**	38087391.0		29	
phagrawFsuc200_dec22, 1109	-.QLRDASERLEFLMDYADLPNEDIK.-	2883.18	3	946.60	1.71	0.2	173	17/92	1
rawsucrfp_800phagigg_Mar04, 1374	-.HGYMIVGDPMGGKTSAYK.-	1913.21	2	420.82	1.12	0.1	222	6/17
phagrawF200_dec22, 2013	-.APVPWHNIYQSTKK.-	1669.91	3	387.60	1.32	0.1	184	7/26
phagrawFsuc300_dec20, 2682	-.ITDDNIRSLFFGDYLKPESDQK.-	2602.84	2	56.01	0.87	0.0	60	1/7
rawsucrfp_900phagigg_Mar04, 2756	-.NVYQPNFINFSARTSANQTQDIIMSK.-	2989.31	2	66.75	0.76	0.1	61	3/25	1
phagrawF200_dec22, 2909	-.FNLKAKDDVTGMPFVCK.-	1914.28	2	259.66	1.05	0.1	150	9/32
phagrawFchlf_dec23, 3388	-.TLLTTPALEPLQVSLRSEKESDYYYSLMK.-	3377.85	2	106.87	0.93	0.1	61	9/56
jmfag5minigbead_030528200105, 1315	-.AAVENFLPTPSKSHYVFNLR.-	2291.59	3	327.94	1.39	0.1	198	4/19
jmfag1mnacl2.5minigg, 1836	-.GLAQAGAWACFDEFNR.-	1756.92	2	285.06	1.18	0.0	238	1/3	1
jmfag5minigg1000mmnacl, 1974	-.RKGLFGPPIGK.-	1170.43	2	451.94	1.16	0.1	185	2/5
jmfag5minigg400mmnacl, 2026	-.DPIIVFNPTFDDCWQLIK.-	2165.50	3	504.11	1.53	0.1	127	15/68
jmfag1mnacl2.5minigg, 2046	-.EVSEALVEDTLTDFLK.-	1809.99	2	310.18	1.32	0.1	138	4/15
JMFAGNACL5B21E3, 2064	-.DPIIVFNPTFDDCWQLIK.-	2165.50	3	164.57	1.46	0.0	113	3/17
jmfag1mnacl7.5minigg, 2622	-.DTNRLDIVDVLLVTAMGPPGGGRNDITGR.-	3024.40	2	541.64	1.11	0.2	112	9/56
jmfag5minigg1000mmnacl, 2938	-.DFSRVIQGVLLCPHTHLQDLEKFIR.-	2966.45	2	119.45	1.09	0.0	109	5/24
jmfag1mnacl7.5minigg, 3092	-.NVYQPNFINFSARTSANQTQDIIMSKLDR.-	3373.75	2	135.04	0.91	0.1	37	3/28
jmIgG150rawphag3007, 1288	-.IEVEVLSVVAQQILSIQQAIIRKLK.-	2820.41	3	505.64	1.84	0.1	248	19/96	1
ajrawphagjun20actinDPI, 1396	-.TLIDVPAPKR.-	1110.33	2	133.34	0.89	0.0	150	1/3
jmfagfrench5minigg1mnacldtt,1429-1431	-.CFEGIAKLEFTDNLEIKGMISSEK.-	2704.11	3	906.14	2.27	0.1	349	21/92
ajrawphagactin20, 1468	-.VYQPVTISIPRDK.-	1516.77	2	291.33	1.08	0.1	169	1/3
jmrawminigg200mmnaclsyringdnas, 1712	-.VSEIPANTAELVALIEYLKK.-	2202.58	3	104.88	1.18	0.0	90	4/19
jmfagtimecon2.5min.1110.1110.3	-.NVHVQMITTEALYGYEYLGNSPR.-	2656.96	0	450.60	1.81	0.1	209	17/88
jmfagcon5minn600mmnacl, 1293	-.LCSEQLSSQHHYDYGMRAVK.-	2353.62	3	247.56	1.92	0.0	115	15/76	1
jmbeadsactinrawphag3007, 1857	-.DNLILYQVDVNRETNTSICNQYSTIADK.-	3232.53	2	69.34	0.75	0.0	91	4/27
jmfag5mincont350, 1930	-.DPIIVFNPTFDDCWQLIK.-	2165.50	3	452.38	1.40	0.1	179	4/17
jmbeads150rawphag3007, 2566	-.PTETTCLANMLEYGFGK.-	1876.14	2	325.27	1.25	0.1	168	9/32
jmfagtimecont0min_030601230741, 3052	-.MSDTNCSAQKLDKSDSVHHMSHSQAR.-	2902.16	3	205.34	1.33	0.0	154	4/25
rawphag2007chfbead3, 1675	-.SIVDYILMDPMEKKR.-	1839.21	2	461.74	1.09	0.1	339	11/28
RawPhg2007MeEthmeth3digest, 2466	-.SVLTAAGNLK.-	974.14	2	849.44	1.66	0.2	186	1/2	2
phagrawFchlf_dec23, 3388	-.TLLTTPALEPLQVSLRSEKESDYYYSLMK.-	3377.85	2	106.87	0.93	0.1	61	9/56
jmldlbeadschlfrawphag3007, 2096	-.EQDHHRGPSDSIGNNYSLTARDMK.-	2729.89	3	619.16	1.66	0.1	207	19/92

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to axonemal heavy chain dynein type 3 [Mus musculus]				**1766.08**	38087391.0		38	
rawextr_450beadigg_Mar04,912-914	-.VIQGVLLCPHTHLQDLEK.-	2044.41	3	467.71	1.40	0.1	124	7/34
rawextr_150beadigg2_Mar04, 996	-.NDYDSSRNIEEYFASVASFMSLQLR.-	2944.18	2	109.44	0.95	0.0	106	3/16
rawextr_450beadigg_Mar04, 1316	-.SVLTAAGNLKLK.-	1215.47	2	270.28	1.04	0.0	250	4/11
rawextr_500bead_Mar04, 1342	-.DGNDFKEPYQEMDFFIPQLIMIK.-	2820.23	3	352.79	1.64	0.1	51	15/88
FPbeads600_Dec19, 1516	-.ETVPFIQTIYPVKAKGMVEK.-	2279.73	2	84.09	0.90	0.0	85	4/19
FPbeads500_dec19, 3450	-.LEGYSKELEMFRK.-	1630.89	2	341.26	0.98	0.0	334	5/12
jmrawbsa5minlowionic, 2172	-.VIRAPVPWHNIYQSTK.-	1910.21	2	140.50	1.56	0.0	73	1/5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, cytoplasmic, intermediate chain 2 [Mus musculus]					**4345.54**	6753658.0	8		
jmbeads400rawphag3007, 380	-.KEAAVSVQEESDLEKK.-	1790.95	3	229.03	1.39	0.0	148	1/5	
jmfagtimecont10min_030601202502,864-866	-.ADAEEEAATR.-	1063.06	3	352.29	1.10	0.0	317	7/18	
jmbeadsactinrawphag3007, 1355	-.KTTPEYVFHCQSAVMSATFAK.-	2347.70	3	1143.29	1.53	0.2	399	23/80	
jmbeads350rawphag30072nd, 2464	-.EIVTYTKETQTPVTAQPK.-	2035.28	3	651.39	1.11	0.1	409	19/68	
rawsucrfp_800phagigg_Mar04, 1512	-.SVSTPSEAGSQDSGDGAVGSRRGPIK.-	2503.63	3	591.96	1.52	0.1	299	1/5	
phagrawFsuc400_dec20, 1916	-.EIVTYTK.-	853.98	1	117.64	1.04	0.0	99	1/2	
JMFAGNACL10_1B21E3, 1292	-.PPVEPEEEKTLKK.-	1524.74	2	173.05	0.90	0.1	154	7/24	
ajrawphagjun20dpi1MNaCl, 1870	-.ITQVDFPPREIVTYTK.-	1908.19	2	429.49	1.67	0.1	171	1/3	
jmfag5minigg500mmnacl, 1954	-.SVSTPSEAGSQDSGDGAVGSRRGPIK.-	2503.63	3	452.53	1.43	0.0	305	19/100	
jmkdl150naclrawphag3007, 1548	-.DEENDSKAPPHELTEEEK.-	2098.13	2	204.87	1.18	0.0	169	5/17	

control

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
1-beta dynein [Mus musculus]					**9154.41**	29243996.0	8		
jmrawbas5min1mnacl, 1100	-.LREVAEKLEMLK.-	1459.78	3	605.79	1.49	0.1	321	4/11	
rawsucrfp_500phagigg_Mar04, 660	-.QLGEQNFIK.-	1077.22	2	440.44	1.32	0.1	212	7/16	
phagrawFsuc200_dec22, 1111	-.FAIDNFLTNPTKVR.-	1636.88	3	334.33	1.29	0.0	252	4/13	
phagrawFsuc200_dec22, 1155	-.LLGEKRQELLDQANK.-	1756.00	3	295.96	1.27	0.1	163	13/56	
rawsucrfp_600phagigg_Mar04, 1516	-.MLIRIGDKEVEYNPNFR.-	2095.41	3	231.48	1.22	0.1	154	13/64	
phagrawF450_dec20, 2116	-.AGSTDRASFVIGIDLRSGSMTSDHWIK.-	2909.23	2	594.86	0.88	0.2	60	7/52	
JMMAGNEGB16D3, 416	-.WALMIDPQGQALKWIK.-	1899.29	3	342.72	1.61	0.1	126	1/4	
jmrawigg5minbeadsfreezethaw, 476	-.VEQFETWASR.-	1253.35	2	524.02	1.35	0.0	374	1/2	
JMFAGNACL15B21E3, 508	-.WALMIDPQGQALKWIK.-	1899.29	3	208.82	1.41	0.0	142	4/15	
jmfag1mnacl7,5minigg, 932	-.EQGLEAQLLGIVVRK.-	1653.95	2	341.54	1.33	0.0	241	5/14	
jmfag5minigg300mmnacl, 942	-.EEKVLELAADVK.-	1344.54	3	111.42	1.25	0.0	89	1/4	
jmIgG250rawphag3007, 1080	-.KIGAYCAQPDFQPDIIGRVSLAAK.-	2562.97	3	448.41	1.61	0.1	168	9/46	
jmIgG1000naclrawphag3007, 1244	-.ASFVIGIDLR.-	1091.29	2	236.79	1.06	0.0	222	1/2	
jmfag5minigg300mmnacl, 2188	-.KSEEMELKLER.-	1392.61	2	310.26	1.30	0.0	239	1/2	
jmfagtimecon7.5min.390.390.2	-.PELEEQK.-	872.94	0	632.25	1.79	0.1	295	2/3	
jmfagtimecon2.5min.1024.1024.2	-.EQGLEAQLLGIVVRK.-	1653.95	0	606.40	1.69	0.1	219	11/28	
jmfagtimecon7.5min.1512.1512.2	-.DSLVINIAAGKR.-	1257.47	0	174.39	1.27	0.0	137	4/11	
jmfagtimecon7.5min.1780.1780.3	-.DGVWVRGLYLEGAGWDRK.-	2078.32	0	305.28	1.38	0.1	176	13/68	
jmfag5mincont200mmnacl, 1068	-.EQGLEAQLLGIVVRK.-	1653.95	2	411.59	1.14	0.1	298	5/14	
jmfag5mincon450mmnacl, 1202	-.EAYRPCAQR.-	1094.23	3	177.64	0.93	0.1	160	9/32	
jmbeads150rawphag3007, 1766	-.SYGRPPAQVEIVMQAVMILRGNEPTWAEAK.-	3343.87	2	146.73	0.99	0.1	110	5/29	
jmbeads350rawphag30072nd, 2462	-.FAIDNFLTNPTKVR.-	1636.88	3	173.92	1.14	0.1	58	1/4	
rawphag2007chlfsol3, 1727	-.IAIEEVKCQALADNAQK.-	1845.11	2	1338.10	1.29	0.3	118	9/32	
RawPhg2007Etsolutiondigest, 2197	-.DEIINQIWIRKIR.-	1698.01	2	161.26	0.87	0.0	171	1/3	

control

1-beta dynein [Mus musculus]					**3024.99**	29243996.0	23		
rawextr_450beadigg_Mar04,552-554	-.KDIGEIKSYGR.-	1266.43	3	204.36	1.72	0.1	39	1/4	
rawextr_200beadigg_Mar04,609-611	-.WALMIDPQGQALKWIK.-	1899.29	3	786.32	1.80	0.1	234	1/3	
rawextr_900bead_Mar04, 690	-.WALMIDPQGQALKWIK.-	1899.29	3	237.11	1.61	0.0	138	4/15	
FPbeads600_Dec19, 1708	-.SNKLEDRIEYLNDYHTYAVYR.-	2663.88	3	450.72	1.38	0.0	305	9/40	
rawextr_500bead_Mar04, 2416	-.LLALDPSPLNVVLLQEIQRYNK.-	2537.98	3	792.61	1.73	0.1	398	5/21	
jmbsa450naclorawphag3007, 80	-.QLGEQNFIK.-	1077.22	2	23.55	0.82	0.0	21	1/4	
jmrawbsa5minlowionic, 2460	-.VEVMSLELEDAKK.-	1491.73	3	530.32	1.06	0.0	497	1/3	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Dynein heavy chain at 89D CG1842-PA [Mus musculus]					23833.99	38080759 0		13	
jmrawbas5min1mnacl, 1224	- KMTVLYK -	883 13	2	198 97	1 13	0 1	111	1/2	
jmrawbas5min1mnacl, 2624	- GWGWAISPGATEEKK -	1617 79	3	510 65	1 42	0.1	373	17/56	
rawsucrfp_600phagigg_Mar04 824-826	-.LERNFFLTKR -	1324.56	3	2210 83	2 55	0 1	807	7/12	
rawsucrfp_450phagigg_Mar04, 1250	- LVPEYVHSHEKK.-	1466.67	2	277 17	1.14	0.0	242	4/11	
phagrawF150_dec22, 1338	- NIVQQLPPTPSKFHYIFNLR -	2400 76	3	486 92	1 77	0 0	261	17/78	
rawsucrfp_900phagigg_Mar04, 1492	- KHLGLSITPTSVVLLQELGRFNK -	2552 01	2	130 37	1 14	0.0	112	1/4	
rawsucrfp_60MeOHphagigg_MAr04, 2042	- SVLVMAGELKRGSADLQEDVVLMR -	2618 07	3	309 27	1 43	0 1	184	4/23	
phagrawF60MeOH_dec23, 2436	- KHLGLSITPTSVVLLQELGRFNK -	2552.01	3	135 65	1 45	0 0	70	3/22	
rawsucrfp_300phagigg_Mar04, 2755	- ELVQNHIGNLVTEHFNDDFEMVMR -	2889 22	3	130 67	1 19	0 0	109	7/46	
jmfag5miniggbead_030528200105, 1079	-.NLEANVEKR -	1073 19	2	537 20	1 27	0 1	396	9/16	
jmfag1mnacl5minigg,466-468	- ALKSVLVMAGELK -	1359.70	3	682 78	1 49	0 1	318	7/24	
jmfagfrench20minigg1mnacldtt, 840	- ALRDMNLPK -	1058 28	2	447 85	1 25	0 1	330	9/16	
jmfgG400rawphag3007, 1042	- LDKSDVTEIR -	1176 30	2	831 56	1 20	0 2	97	1/3	
jmfgG400rawphag3007,1216-1218	- LAEKTALDIDR -	1245 41	2	378 99	1 29	0 0	283	1/2	
jmfag5minigg350mmnacl, 1247	- HLGLSITPTSVVLLQELGRFNK.-	2423 84	3	222.43	1 44	0 1	91	1/6	
jmfgG250rawphag3007, 1330	- WLQQIQNKLK -	1299 55	2	631.80	1 61	0 1	360	5/9	
jm5miniggrawlowomc, 1470	- GWGWAISPGATEEKK -	1617 79	3	686 91	1 47	0 0	457	9/28	
ajrawphagactin20, 1530	- WLNDLDELMHRR -	1598 81	2	1071 75	1 13	0 3	81	3/11	
ajrawphagjun20dpi1MNaCl, 1760	- GYSENNFR -	987 01	2	348 32	0 88	0 1	259	1/2	
jmrawgg5min1mnacl,1767-1769	- GWGWAISPGATEEKK.-	1617 79	3	685 22	1 65	0 1	380	9/28	
ajrawphagjun20dpi1MNaCl, 1768	- GYSENNFR -	987 01	2	286 97	0 99	0 0	290	1/2	
jmfgG150rawphag3007, 2146	-.TPVYTTSMRRNAMGIGLVFEADLFTAK.-	2991 48	2	110 94	1 02	0 0	108	9/52	
jmfgG250rawphag3007, 2154	- VPQEELDFFLKGNISLEKSK -	2322 64	3	340 93	1 23	0 1	235	4/19	
jmfagtimecon7 5min.122.122 3	- MDRGHALLVGVGGSGK.-	1554 80	0	802 51	1 50	0 1	396	19/60	
jmfagtimecon2.5min.940 940.3	-.GWGWAISPGATEEKK -	1617 79	0	916 54	1 97	0 1	425	5/14	
jmfagcon5minn600mmnacl, 121	- LLILRCFR -	1034 35	2	858.31	1.02	0 3	84	1/2	
jmfagtimecon10min, 508	- DGYRPAARR.-	1062.17	3	190 43	1.01	0 0	181	9/32	
jmbeads300rawphag3007, 576	-.KHLGLSITPTSVVLLQELGR -	2162.56	3	604.42	1.89	0 1	290	1/4	
jmbeads250rawphag3007,740-742	- GWGWAISPGATEEKK -	1617 79	3	1173.59	2.17	0 0	531	3/8	
jmbeads350rawphag30072nd, 994	- VARLERNFFLTK.-	1494 77	3	929 20	1 82	0 1	482	4/11	
jmfagcon5minn600mmnacl, 2703	- KYILFDGDVDALWVENMNSVMDDNK -	2933.26	2	696 47	1 01	0 2	92	1/6	
rawphag2007chlfsolt, 1000	- LERNFFLTKR -	1324.56	3	1946.88	1 86	0 1	1018	19/36	
RawPhag200760MeBeadsdigest, 1344	- LDKSDVTEIRSFAK -	1609.81	2	1052.01	1 48	0 2	295	11/26	
rawphag2007chfbead1, 1904	- NLLKDLEDSLLR -	1429 65	2	225 17	0 89	0 1	217	4/11	
rawphag2007chfbead3, 2397	- QVQTVCECILIMKGYK -	1857 30	2	907 03	1 53	0 2	188	11/30	
jmkdl1000naclrawphag3007, 1718	- SIRDLGFIAAMGKAGGGR -	1778.07	2	665 43	1 24	0 2	179	9/34	
jmkdl350naclrawphag3007, 1924	- TAKGMMSDPNFLR.-	1468 73	2	856 92	1 27	0 2	367	11/24	
jmkdl1000naclrawphag3007, 2066	- KHLGLSITPTSVVLLQELGRFNK.-	2552 01	2	264 93	1 15	0 1	139	1/4	

control

similar to Dynein heavy chain at 89D CG1842-PA [Mus musculus]					4904.75				
jmrawgg5miniggfreebead, 2192	- ALAGEVGMSNELDDVARSLFLGHIPHIWR -	3205 64	2	93 44	0 86	0 1	62	1/7	
rawextr_350beadigg2_Mar04, 1286	- YLIGEVMYGGRAIDSFDR -	2063 32	3	365 38	1 13	0 0	318	1/4	
rawextr_500beadigg_Mar04, 1448	- SNYVTPKNYLDRINTYSKLLDEK.-	2767 08	3	745.64	1 68	0 1	306	19/88	
rawextr_actnbead_Mar04, 1682	- DLSRVFNGLVLTNPDR.-	1817 04	2	368 51	1 45	0 1	199	1/3	
rawextr_700beadigg_Mar04, 1794	- MVVPQTDLNMVTQLTR -	1847 19	2	179 89	1 02	0 1	143	3/10	
rawextr_250beadigg_Mar04, 1812	- NIKGLLKTLNTTIEEMEAVSK.-	2333 73	3	835.88	1 61	0 1	340	17/80	
rawextr_400beadigg_Mar04, 1862	- GHALLVGVGGSGKQSLAR.-	1707 96	2	441 44	1 32	0 1	236	11/34	
FPbeads450_Dec19, 3026	- ILTTYMDEYLGDFIFDTFQPRHFFR -	3165 56	2	41 86	0.67	0 0	41	5/48	
jmraw5minbsafreezthaw, 1028	- GNISLEKSK -	976 11	2	427 21	1 22	0 1	218	1/2	
jmraw5minbsafreezthaw, 1242	- LDKSDVTEIR.-	1176 30	2	441 91	1 34	0 1	291	4/9	
jmbsa400naclrawphag3007_030802135631, 1302	- KHLGLSITPTSVVLLQELGRFNK -	2552 01	3	963 60	1 69	0.2	145	9/44	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, axonemal, heavy chain 5; dynein, axon, heavy chain 5; axonemal					30565.33	20373161 0	28		
AJRAWpellet2_contr_jun13, 1179	- GGASLDLKACPPKPSK -	1569 85	2	264 86	1.07	0 1	206	3/10	
AJRAWpellet2_contr_jun13, 2341	- NGMVFMSSSVLDWSPILEGFLKRR -	2771 25	3	83 79	0 95	0 0	88	3/23	
AJRAWpellet1_contr_jun13, 630	- ANLIVQENR -	1057 19	2	270 54	1 40	0 0	187	9/16	1
ajrawphag1MNaCl20.2298-2300	- TIAKQGKAVLLIGEQGTAK.-	1927 28	2	225 91	1 77	0 0	114	1/4	1
AJRAWSoluteContr_june13, 1492	- LASFIAGYTSFQTLTR -	1890 17	1	86 25	0 90	0 0	102	1/4	1
jmbeads150rawphag3007 2202	- HKMQTASTLISGLAGEKER -	2058 35	3	429 27	1 21	0.1	306	2/9	1
jmbeads150rawphag3007 2602	- FFTLYQLCEEQLSKQVHYDFGLR -	2866 24	2	233 22	1 28	0 1	104	5/22	
jmbeads250rawphag3007, 442	- ELAGKEK.-	774 89	2	113 08	0 97	0 0	99	1/2	1
jmbeads400rawphag3007, 586	- SVAMMVPDR -	1008 23	2	502 79	1 03	0 1	341	9/16	
jmbeadsactinrawphag3007, 2045	- EGHSEALASSFNAGASSLPLTATARKK -	2702 96	2	131 87	0 97	0 0	119	9/52	
jmfag_20_minfrench1mnacldttdpx.2076-2078	- IAKVLLEFEVLYHR -	1731 08	2	375 88	1 11	0.1	238	5/13	
jmfag1mnacl0mngg 870-872	- SPTDFEWLK.-	1123 24	2	537 57	1 22	0.1	256	1/2	
jmfag1mnacl5mngg, 328	- FMDITFEK -	1031 21	2	1498 25	1 52	0 1	886	8/7	
jmfag1mnacl7.5mngg, 1188	- ITALTGHSLDVGNETFK -	1804 00	3	2101 81	1 85	0 1	1048	13/32	
jmfag5mncont350, 70	- RPPTNDNLYEYFMSR.-	1904 10	2	129 03	0 89	0 0	132	9/28	1
jmfag5mncont400, 030531151834, 2384	- FFTLYQLCEEQLSKQVHYDFGLR.-	2866 24	2	247 91	1 01	0 1	151	9/44	
jmfag5mncont400_030531151834 484	- TPRGNALLVGVGGSGK -	1483 70	3	745 35	1 72	0.1	383	1/3	1
jmfag5minfrench1mnacldttdpi 2076-2078	- IAKVLLEFEVLYHR -	1731 08	2	375 88	1 11	0 1	238	5/13	
jmfag5mngg150mmnacl, 1468	- GVSWTTVRYMIGEIQYGGRVTDDYDK.-	3011 31	3	93 75	1.07	0.0	83	11/100	
jmfag5mngg200mmnacl, 268	- VNAVKIDVDK.-	1101 28	3	248 28	1 41	0 0	176	13/36	1
jmfag5mngg350mmnacl, 343	- SYNTSNLMEDLK -	1415 55	3	249 50	1 50	0 1	117	3/11	1
jmfag5mngg400mmnacl, 664	- ILWARQLFHR -	1340 80	3	507 53	1 48	0.1	318	7/18	
jmfag5mnggbead_030528200105 2995	- DTINEEVIEFLNPYFEMSDYNIETAKR -	3282 58	2	58 14	0.71	0 1	39	3/26	1
jmfagcon5min1000mmnacl_030601180404, 1564	- ELEDNLLYR.-	1165 28	2	274 06	1 21	0 0	226	7/16	
jmfagfrench20mngg1mnacldtt, 752	- THLLEDVTANKRR -	1553 75	3	436 11	1 54	0 0	281	17/48	
jmfagfrench5mngg1mnacldtt, 234	- LLKVWRDTDIR -	1415 67	3	198 08	1 45	0 0	129	3/8	
JMFAGNACL10_2B21E3, 1172	- VILTEKQELEK -	1330 55	2	249 82	1 08	0.1	125	7/20	1
JMFAGNACL10_2B21E3, 916	- IETRYYSMGGGQEVHAR.-	1982 18	3	852 29	1 10	0 0	775	21/64	
JMFAGNACL5B21E3 1376	- YRAEMENILTVVEESQK.-	2040 29	3	518 40	1 34	0.1	328	17/64	
jmfagtrmecon10min,1214-1216	- EVITSMDRFK -	1228 43	2	524 90	1 43	0 0	353	11/18	
jmfagtrmecon5min, 1784	- GVRQWSSELLSK -	1390 57	2	348 05	1 06	0 1	183	7/22	
jmIgG1000nacirawphag3007, 1872	- ESQNELQITSLNHK -	1841 77	3	3132 01	2.59	0 1	1094	25/52	1
jmIgG1000nacirawphag3007, 2050	- PALEEAEAALQTIKPSDIATVR -	2324 82	3	204 30	1 13	0 1	107	1/8	1
jmIgG250rawphag3007, 1668	- LLLIRSWCPDRTIAQAR -	2013 40	3	394 51	1 37	0 0	278	17/64	
jmigg600rawphage3007, 1318	- AVLLKGEQGTAK -	1200 41	3	881 03	1 45	0 2	146	15/44	1
jmIdl500nacirawphag3007, 2075	- MQTASTLISGLAGEKERWTEQSK -	2552 85	2	209 26	1 03	0 1	61	7/44	1
JMMAGTube1B16E3, 2646	- KYMDSMGENYAEGVILDLEKTWEESQPR.-	3420 77	2	112 52	0 82	0 1	61	1/8	
jmraw5mnbsabeads,1524-1526	- EFAAQTK -	794 88	1	342 91	1 16	0 1	143	2/3	1
jmraw5mnbsafreezthaw, 896	- HEEFLTLIKGGASLDLK -	1872 18	3	618 57	1.13	0 1	450	17/64	
jmraw5mngg600mmnacled, 930	- LSLTAETK.-	882 99	2	309 59	1 42	0 0	210	1/2	
jmrawgg5min150mmnacl, 2484	- DVLDTILGIQPKDSSGGGDETREAVVAR -	2900 15	2	71 27	0 73	0 1	40	1/9	
jmrawgg5min150mmnacl,1380-1382	- FANEPPGGLRAGLRR -	1682 91	3	141 33	1 19	0 1	88	1/4	
jmrawgg5mnggfreebead, 2754	- WILDMTWLNLVELSKLKQFSDILDQISR -	3406 98	2	115 92	1 11	0 0	85	1/8	
jmrawgg5mnggfreebead, 352	- LAVDGTIHMSENLR.-	1532 79	3	1857 25	2.11	0 0	859	11/26	
phagrawF300_dec20, 2075	- RSTHVTPK -	926 08	2	307 58	0 92	0 0	324	4/7	1
phagrawF350_dec20, 1860	- GNLHIVLCFSPVGEKFR -	1917 27	2	347 81	1 28	0.1	203	9/32	1
phagrawF350_dec20, 560	- EQAGEVDPEHLGR -	1437 50	3	868 98	1 88	0 0	516	19/48	
phagrawFchll_dec23, 3174	- HGMMTLGPSGSGKTTCIHTLMK -	2289 75	3	1675 35	1 85	0 2	577	11/42	
phagrawFsuc1000_dec23, 2493	- NGMVFMSSSVLDWSPILEGFLKRR -	2771 25	3	145 49	1 09	0 1	86	5/46	
phagrawFsuc300_dec20, 1996	- SYNRIAKVLLEFEVLYHR -	2251 62	3	2174 81	1 75	0 3	565	21/68	
phagrawFsuc300_dec20, 2172	- LVGDVLLATAFLSYSGPFNQEFR -	2545 87	2	930 98	1 22	0 3	52	7/44	1
phagrawFsuc400_dec20, 1648	- DEIDEINSDLTPIMKKEHPR -	2381 65	3	545 38	1 52	0 0	358	21/78	1
phagrawFsuc600_dec20, 2320	- QFSIFNCTLPSDASMQK.-	1905 14	2	186 02	1 08	0 0	149	9/32	1
rawphag2007chfbead1, 1148	- ANLIVQENR.-	1057 19	2	281 78	1 13	0.1	110	3/8	1
rawphag2007chfbead2, 290	- ANLIVQENR -	1057 19	2	395 83	1 36	0 1	159	7/16	1
rawphag2007chfbead3, 517	- QTLLEDADR -	1061 13	2	475 51	1 38	0 0	344	9/16	1
RawPhg2007Etsolutionbdgest, 2675	- HMEVQSLANRMNTGLEK.-	1959 24	1	55 11	0 70	0 0	79	7/32	1
rawsucrfp_150cphagcg_Mar04, 1349	- PVIRSYNRIAK -	1317 57	2	136 77	0 92	0 1	119	7/20	
rawsucrfp_150cphagcg_Mar04, 1801	- DDISAPPTEGVYVYGLYLEGAGWDKR -	2873 12	2	68 30	0 86	0 0	80	7/50	
rawsucrfp_350phagcg_Mar04, 1794	- NQPPIAGKILWARQLFHR.-	2148 53	3	132 63	1 37	0 0	93	15/68	
rawsucrfp_350phagcg_Mar04, 606	- DSNDASKAK.-	935 96	2	63 70	0 70	0 0	89	3/9	
rawsucrfp_600phagcg_Mar04, 2132	- CYITLAQALGMSMGGAPAGPAGTGKTETTKDMGR.-	3344 85	2	126 83	0 97	0 1	43	5/33	
rawsucrfp_800phagcg_Mar04, 1176	- DDISAPPTEGVYVYGLYLEGAGWDKR -	2873 12	3	222 63	1 23	0 1	137	7/50	
rawsucrfp_800phagcg_Mar04, 2026	-.TWEESQPRTPLKCLLSMGSDPTDSIIALGK.-	3247 69	3	362 02	1.38	0 1	152	17/116	

control

dynein, axonemal, heavy chain 5; dynein, axon, heavy chain 5; axonemal					10664.41	20373161 0	49		
FPbeads150_Dec19, 581	- QIIIRVK -	870 12	2	379 01	1 50	0 1	216	2/3	
rawestr_250beadcgg_Mar04,628-630	- PSDIATVRTLGR -	1286 46	3	483 22	1 53	0 1	259	7/22	1
rawestr_250beadcgg_Mar04, 998	- MPPAIEQLMFPHLAR -	1752 14	3	508 93	1 48	0.1	301	15/58	
rawestr_500beadcgg_Mar04, 1122	- VIQLFETQRVRHGMMTLGPSGSGK.-	2631 08	3	344 45	1 79	0 1	180	7/48	
rawestr_500beadcgg_Mar04, 1174	- GGASLDLKACPPKPSK.-	1569 85	2	212 93	0 98	0 1	115	4/15	
rawestr_900beadcgg_Mar04, 1330	- ETQCMSQLGLPVSPFAAALFQK -	2367 77	3	2192 88	2 07	0 3	341	3/14	
FPbeads400_Dec19, 1570	- MQTASTLISGLAGEKERWTEQSK.-	2552 85	2	1159 09	1.27	0 3	182	13/44	1
FPbeads350_Dec19, 1533	- ELEDNLLYR.-	1165 28	2	189 67	1 00	0 0	171	7/16	
FPbeads400_Dec19, 1784	- DALVAVSEHFLSSYTIDCTAEIKK -	2641 98	3	551 00	1 68	0 1	228	17/92	1
rawestr_chfbeadcgG_Mar04,1882-1884	- ASDVQNELGALQPSFR -	1732 88	2	806 01	1 67	0 2	98	4/15	
rawestr_800bead_Mar04, 1198	- TIAKQGKAVLLIGEQGTAK.-	1927 28	3	472 49	1.49	0.1	289	17/72	1
rawestr_actinbead_Mar04, 2146	- DALVAVSEHFLSSYTIDCTAEIKK -	2641 98	3	1942 35	2 10	0 2	425	21/92	1
jmbeadactinrawphag3007, 383	- GLEDQLLGRVILTEK.-	1684 98	3	936 30	1 67	0 1	368	9/28	1
jmbea400nacirawphag3007_030802153340,1356-1358	- TWEESQPRTPLKCLLSMGSDPTDSIIALGK.-	3247 69	3	246 61	1 77	0 1	88	9/58	
jmbea300nacirawphag3007, 1550	MQTASTLISGLAGEKERWTEQSK.-	2552 85	3	318 48	1 80	0.1	92	15/88	1
jmbea1000nacirawphag3007, 2473	- DEIDEINSDLTPIMK.-	1733 92	2	119 02	0 99	0 0	119	2/7	1

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, axonemal, heavy chain 8; dynein, axon, heavy chain 8 [Mus musc				**14879.19**	34328061.0	18		
JMMAGTube1B16E3, 404	- AVINVLNVAHSK.-	1265.49	3	586.76	1.30	0.1	410	17/44	3
jmrawgg5min350mmnaclsyringednase, 811	- AWFKEVSQLQYALQATLFVR.-	2399.77	3	663.31	1.40	0.1	312	9/38	1
jmrawgg5min1mnacl, 903	- LSATKGSLVDDESLIGVLRVTK -	2302.66	3	405.66	1.72	0.0	220	3/14	1
jmlgG400rawphag3007,948-950	-.NDVAINSK.-	860.94	2	449.26	1.22	0.1	326	4/7	3
jmraw5minggl600mmnaclsd, 1142	- LSEDMLSK -	923.07	2	669.19	1.88	0.0	355	9/14	1
jmraw5minggl600mmnaclsd, 1150	- LSEDMLSK.-	923.07	2	542.14	1.42	0.0	358	9/14	1
jmraw5minggl500mmnaclsd,1182-1184	-.SLIPSDEEVTLPEDEESGQARVR -	2557.71	3	1544.88	2.04	0.2	337	5/22	3
jmlgG400rawphag3007, 2012	- INEPINYFFKNSDILSSTEGKAVIR -	2857.21	3	109.22	1.38	0.0	75	7/48	3
phagrawF700_Dec23, 106	- GGCKTLK.-	706.88	1	103.18	0.79	0.1	95	1/3	3
rawsucrp_500phagigg_Mar04, 956	-.NSDILSSTEGKAVIRQYNR -	2152.36	3	571.70	1.15	0.1	455	19/72	3
phagrawFsuc500_dec20, 1068	-.KNQYDILDPR -	1262.40	2	208.52	0.90	0.0	228	7/18	3
phagrawFsuc350_dec20,1354-1356	- AWFKEVSQLQYALQATLFVR -	2399.77	3	758.49	2.03	0.0	368	21/76	1
phagrawFActin_dec23, 1536	- YYNTSERMTSLFIKVTNQMVTACK -	2830.30	3	609.21	1.55	0.2	165	4/23	4
phagrawFsuc150_dec22, 1612	-.TDLTFITVVYLR.-	1441.70	2	219.19	1.16	0.0	184	7/22	1
phagrawFsuc300_dec20, 3594	- ETEGLDFESTTMEVDTNDK.-	2162.23	3	501.60	1.60	0.1	277	2/9	1
jmlag1mnacl0minigg, 374	- AVINVLNVAHSK -	1265.49	3	341.66	1.21	0.1	182	7/22	3
jmlag5minigg600mmnacl, 428	- AVINVLNVAHSK -	1265.49	3	436.44	1.41	0.1	184	7/22	3
jmlag5minigg200mmnacl, 484	- AVINVLNVAHSK -	1265.49	3	336.26	1.23	0.1	188	7/22	3
jmlag5minigg450mmnacl_030527025134, 1142	-.AVINVLNVAHSK -	1265.49	3	933.24	1.44	0.2	309	9/22	3
jmlag5minigg300mmnacl, 1314	- MTSLFIK.-	840.07	2	341.43	1.12	0.1	220	7/12	4
jmlag1mnacl5minigg, 1524	- PMLYTVAFLHSTVQERRK.-	2177.56	3	892.50	1.65	0.1	473	19/68	1
AJRAWpellet1_contr_jun13, 357	- AVINVLNVAHSK -	1265.49	3	359.64	1.29	0.0	272	17/44	3
AJRAWpellet2_contr_jun13, 1028	- GLKNWQAFLDLKK.-	1561.85	3	646.41	1.37	0.2	186	7/24	1
jmbeads450naclrawphag3007, 1036	-.DLDARITDSANESK -	1535.60	2	274.96	1.19	0.1	136	4/13	3
jmlagcont5minbead,1892-1894	- AWFKEVSQLQYALQATLFVR -	2399.77	3	386.44	1.73	0.0	214	17/76	1
rawphag2007chfbead3,304-306	-.LSEDMLSK.-	923.07	2	549.17	1.63	0.1	248	9/14	1
RawPhg2007MeEthmeth3digest, 2184	- TVLSPDHWILRGVALLCDIK.-	2250.69	3	794.52	1.91	0.1	193	9/38	1
jmldl150naclrawphag3007, 1104	- NDVAINSK.-	860.94	2	294.62	1.12	0.1	238	4/7	3
jmldl600naclrawphag3007, 1598	- GLKNWQAFLDLK.-	1433.68	2	348.57	1.38	0.0	249	5/11	1

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, axonemal, heavy chain 8; dynein, axon, heavy chain 8 [Mus musc				**3104.45**	34328061.0	17		
jmrawgg5miniggfreebead, 282	- LSEDMLSK.-	923.07	2	1270.96	1.63	0.1	703	11/14	1
rawextr_250beadigg_Mar04,320-322	- KGVSWSTVR.-	1020.17	3	136.76	1.31	0.0	105	5/16	1
jmrawgg5miniggfreebead, 2382	- PNVFWMTGFFNPQGFLTAMRQEVTR -	2976.43	2	419.97	0.89	0.2	57	7/48	1
rawextr_300beadigg_Mar4, 2544	- GSLVDDESLIGVLRVTK.-	1802.06	2	618.76	1.37	0.0	451	13/32	1
rawextr_350bead_Mar04, 1880	-.TDLTFITVVYLRTVLSPDHWILR -	2760.23	3	657.99	1.86	0.0	353	5/22	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
axonemal dynein heavy chain 8 Dnahc8 [Mus musculus]					**24250.49**	13310482.0	51		
ajrawmedlapbsnocells, 1612	-.KRIDDFSESCPLLEMMTNK.-	2258.63	3	798.94	1.97	0.1	239	2/9	5
AJRAWpelletl_contr_jun13, 800	-.AVSVQGELVQVQPK.-	1482.71	2	151.28	1.11	0.1	85	4/13	3
AJRAWSoluteContr_june13, 2230	-.LVITPLTDRCYITLAQALGMNMGGAPAGPAGTGK.-	3360.96	2	134.91	0.87	0.1	26	5/66	5
AJRAWSoluteContr_june13, 968	-.LTQVIENWTYQNLSFAAFK.-	2274.56	2	1047.33	1.63	0.2	110	5/18	5
jm5minggrawlowionic, 1376	-.EGEKIMLDTPVMAK.-	1562.88	3	257.91	1.23	0.1	84	3/13	5
jmbeads250rawphag3007, 522	-.SWCPDRTVFQARK.-	1594.82	3	1493.06	2.00	0.0	747	5/12	5
jmbeads350rawphag30072nd, 1156	-.IIRTSCGNALLVGVGGSGKQSLSK.-	2346.74	3	309.34	1.26	0.1	198	4/23	5
jmbeadsactinrawphag3007,156-158	-.VKNEVQEVK.-	1073.23	3	151.18	1.43	0.1	68	7/32	5
jmfag_20_minfrench1mnacidttdpi, 848	-.EMRMNPKAITAPQMFGR.-	1979.38	3	301.89	1.30	0.0	218	7/32	6
jmfag1mnacl5mincon, 1840	-.YFRTHLEDSLSLGR.-	1694.87	3	134.48	0.93	0.0	120	5/26	5
jmfag1mnacl5mincon,1314-1316	-.LPRALKDWQAFLDLK.-	1815.15	3	596.87	1.27	0.1	393	17/56	4
jmfag1mnacl5minigg, 1284	-.LPRALKDWQAFLDLK.-	1815.15	3	284.66	1.35	0.0	207	13/56	4
jmfag5mincon450mmnacl, 892	-.KVESVLR.-	831.00	2	413.58	1.30	0.0	317	2/3	5
jmfag5mincont350, 1036	-.SRHVEEAVK.-	1055.17	2	261.06	0.87	0.0	285	1/2	5
jmfag5mincont350, 656	-.AITAPQMFGR.-	1092.30	2	409.44	1.10	0.1	179	4/9	6
jmfag5mincont350, 932	-.QAELDKVQAKFDAAMK.-	1794.07	3	1464.93	1.75	0.2	456	1/3	5
jmfag5mincont400_030531151834, 1058	-.LEVFLRGHGSK.-	1243.44	2	278.20	1.19	0.0	233	1/2	5
jmfag5mintrench1mnacidttdpi, 848	-.EMRMNPKAITAPQMFGR.-	1979.38	3	301.89	1.30	0.0	218	7/32	6
jmfag5minigg150mmnacl, 214	-.SWCPDRTVFQAR.-	1466.65	3	656.60	1.71	0.1	229	4/11	5
jmfag5minigg350mmnacl, 385	-.EKELAVASIK.-	1088.28	2	475.01	1.25	0.1	351	1/2	5
jmfag5minggbead, 1679	-.LQIFQANFDDLWR.-	1666.86	2	306.46	1.18	0.1	192	3/8	5
jmfag5minggbead_030528200105,731-733	-.NIMEAPLLK.-	1029.28	2	789.41	1.62	0.1	455	5/8	6
jmfagcon5min1000mmnacl_030601180404, 1102	-.YFRTHLEDSLSLGR.-	1694.87	2	309.73	1.34	0.0	231	5/13	5
jmfagcont5minbead, 3220	-.KVCGNVAGLLSWTLAMVIFYGINREVLPLK.-	3307.02	2	1754.04	1.15	0.4	117	5/29	5
JMFAGNACL5B21E3, 1240	-.LQIFQANFDDLWR.-	1666.86	2	753.42	1.16	0.2	376	5/12	5
JMFAGNACL5B21E3, 2592	-.LTQVIENWTYQNLSFAAFKGK.-	2459.78	3	573.88	1.46	0.0	374	11/40	5
jmfagtimecon7.5min.582.582.3	-.LEAAKPALEEAEAALNTIK.-	1983.25	0	373.31	1.21	0.1	251	7/36	5
jmIgG250rawphag3007, 3212	-.VFCEDVINFTEAYETEGPMVPNIPPQEASNR.-	3498.84	2	46.02	0.65	0.1	14	1/12	3
jmIggactinrawphag3007,1414-1416	-.ELAVASIK.-	830.99	1	322.55	1.26	0.0	248	4/7	5
jmldl150nacirawphag3007, 3556	-.EKENDLQVTSLNHK.-	1655.79	2	309.70	1.15	0.1	234	9/26	5
jmldl400firstnaclrawphag3007, 1186	-.GPVEIWLLDLLK.-	1398.70	2	637.05	1.02	0.2	282	9/22	5
jmldl400firstnaclrawphag3007, 1380	-.LQSKAVSVQGELVQVQPKFK.-	2214.59	3	1071.38	1.88	0.2	159	21/76	3
jmldlchlfsolblerawphag3007, 1824	-.IWQGMLTVK.-	1076.34	2	179.51	1.09	0.0	165	7/16	5
JMMAGNEGB16D3, 2332	-.ENDLQVTSLNHKYFR.-	1865.04	2	425.09	1.16	0.1	289	9/28	5
jmraw5minigg250mmnaclsyringdnase,1958-1960	-.PEICDMVGNLVSVSRVLWQWTK.-	2562.01	3	430.84	1.75	0.0	222	5/21	5
jmrawigg5min300mmnaclsyringednase, 378	-.IELPVLSVAAQQIYIVLTAR.-	2198.63	3	393.41	1.04	0.0	356	4/19	5
jmrawigg5min350mmnaclsyringednase,737-739	-.KLKNFYPGVAEHK.-	1531.78	3	630.03	1.80	0.0	347	7/24	5
jmrawigg5miniggfreebead, 2166	-.HGLMTLGPSGSGKTTVITILMKSLTECGR.-	2990.56	2	376.34	1.04	0.2	72	1/7	5
jmrawigg5miniggfreebead, 2368	-.LDVPEQAKNLLKLESK.-	1826.13	2	95.54	0.81	0.0	113	3/10	5
jmrawigg5miniggfreebead, 410	-.PILQAWLKKR.-	1253.56	2	564.50	1.09	0.1	455	11/18	5
jmrawminigg200mmnaclsyringdnas, 1666	-.SLKFPGLISGCTMDWFSRWPK.-	2457.90	3	386.84	1.71	0.1	160	17/80	5
phagrawF350_dec20, 2622	-.MLLCRYLNEEYKK.-	1704.05	2	195.49	1.19	0.1	138	1/3	5
phagrawF450_dec20, 572	-.FHYIFNLRDLSR.-	1581.80	3	648.84	1.28	0.2	199	5/22	6
phagrawF600_dec20, 1166	-.LASFIAGYQIFQITLTRSYNVSNLIEDLK.-	3319.80	3	232.60	1.19	0.1	118	15/112	5
phagrawFsuc1000_dec23, 1179	-.WPKEALIAVASYFLLDYNIVCSIETK.-	2988.49	3	306.09	1.32	0.1	158	3/20	5
phagrawFsuc300_dec20, 2820	-.GSQQTMYEFYVTDYGDWEHWNKR.-	2942.13	2	296.42	0.96	0.1	99	2/11	5
phagrawFsucchlf_dec23, 2032	-.FVTYSSGEQLFGLPVTDYEVLHK.-	2630.93	3	552.57	1.68	0.0	289	21/88	5
rawphag2007chfbead2,896-898	-.LSQDLAVK.-	874.02	1	243.60	1.27	0.1	159	1/2	5
rawsucrfp_1000phagigg_Mar04,1297-1300	-.LLFEVHNIENASPATVSR.-	1998.23	3	330.71	1.32	0.0	249	1/4	5
rawsucrfp_400phagigg_Mar04, 1486	-.YIADSLEEKYTEPVILNLEK.-	2368.67	3	252.15	1.54	0.1	123	13/76	5
rawsucrfp_400phagigg_Mar04,945-947	-.KLKNFYPGVAEHK.-	1531.78	3	540.43	1.49	0.1	321	1/3	5

control

axonemal dynein heavy chain 8 Dnahc8 [Mus musculus]					**4168.28**	13310482.0	53		
FPbeads300_Dec19, 108	-.VKFETLITIHVHQRDIFDDLVK.-	2668.09	3	155.47	1.04	0.1	99	5/42	5
FPbeads150_Dec19, 383	-.QIKSFQNNSR.-	1222.34	3	295.71	1.31	0.0	209	13/36	5
rawextr_150bead_Mar04, 457	-.KYDPEVQLSK.-	1207.36	3	362.20	1.78	0.1	178	13/36	5
rawextr_400bead_Mar04, 629	-.ELAVASIK.-	830.99	1	209.78	1.28	0.0	162	1/2	5
rawextr_700beadigg_Mar04, 902	-.LDTATNDWTDGIFSTLWRKTLK.-	2583.88	3	299.15	1.60	0.0	187	17/84	5
rawextr_500bead_Mar04, 1010	-.LQSKAVSVQGELVQVQPKFK.-	2214.59	3	511.11	1.64	0.0	298	9/38	3
FPbeads700_Dec19, 1101	-.KRIDDFSESCPLLEMMTNK.-	2258.63	3	176.48	1.38	0.0	128	13/72	5
rawextr_350bead_Mar04, 1312	-.PEDSELSTVMRGLR.-	1590.79	2	697.97	1.69	0.1	369	6/13	5
rawextr_700beadigg_Mar04,1402-1404	-.FDAAMKEKMDLLNDADMCR.-	2218.59	3	388.40	1.56	0.0	248	1/4	5
rawextr_250bead_Mar04, 1420	-.MLPTPSKFHYIFNLR.-	1865.23	3	281.33	1.38	0.0	187	15/56	5
FPbeads700_Dec19, 1425	-.GTESGEIITLMEDSLMVLGSLLSNR.-	2667.05	3	412.80	1.32	0.0	312	3/16	5
rawextr_800beadigg_Mar04,1666-1668	-.LKNFYPGVAEHK.-	1403.61	2	274.28	1.23	0.0	222	4/11	5
FPbeads600_Dec19, 2592	-.DTINEETVELLQPYFNMDDYTFESAK.-	3114.34	2	103.59	0.91	0.1	43	7/50	5

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, axonemal, heavy polypeptide 9 [Mus musculus]					**29256.48**	38091406.0		14	
jmraw5minbsabeads,1038-1040	-.RPLVAQDVSQK.-	1241.42	3	643.47	1.43	0.1	253	2/5	
jmraw5minbsafreezthaw, 3078	- YYSLIQESGLKIHALVQVTTDRLDTVPR.-	3217.67	2	44.20	0.72	0.1	27	5/54	
phagrawF600_dec20, 414	- TVLEMQPR -	974.16	2	103.71	0.87	0.0	112	5/14	
phagrawF300_dec20, 1013	- LLQAFLDHNAASDPR.-	1668.84	2	154.04	0.91	0.0	159	9/28	1
phagrawFsuc250_dec22,1133-1135	-.SEPPGNHSLR.-	1094.16	2	116.45	1.02	0.0	114	7/18	1
phagrawF250_dec22, 1617	- PLLVVQSGPGGLVVTPGLDAGPEPSRAR.-	2741.14	2	327.70	1.02	0.1	255	13/54	1
phagrawF200_dec22, 1729	-.SLRPAAGTWERCAGTAEAGR.-	2061.27	3	259.88	1.20	0.0	216	17/76	1
phagrawFsuc60MeOH_dec23, 1820	-.SETCEAIVRSIEILQDVGEIGNTRYER -	3082.39	2	51.79	0.72	0.0	56	7/52	
rawsucrfp_350phagigg_Mar04, 1888	- NKYGEELR.-	1009.10	2	878.08	1.07	0.0	819	6/7	
jmfag5miniggbead_030528200105, 963	-.EKFPQEWKNK.-	1334.51	3	333.19	1.72	0.1	168	1/3	
ajrawphagjun20actinDPI, 754	-.AIPADKQDCRSVYACPVYK.-	2128.46	3	886.02	1.65	0.2	194	7/36	
jmfagfrench5minigg1mnacldtt, 761	-.AKITHLNENLAKLTTK.-	1796.11	3	385.11	1.36	0.0	283	1/3	
ajrawphag1MNaCl20, 828	-.VKFVESGQKCK.-	1253.50	3	463.62	1.27	0.0	344	9/20	
jmfag5minigg600mmnacl, 1112	-.EKAIADEEEQK.-	1290.36	2	169.16	1.04	0.0	163	7/20	
jmigg450rawphag3007,1166-1168	-.AKGLFFLRTK.-	1181.46	2	657.34	1.43	0.1	394	11/18	1
jmigg600rawphage3007,1320-1322	-.AKGLFFLRTK.-	1181.46	3	2189.48	1.92	0.0	1138	5/9	1
jmfag5minigg250mmnacl,1356-1358	-.EKFPQEWKNK.-	1334.51	3	189.96	1.40	0.1	92	2/9	
JMFAGNACL15B21E3, 1390	-.TKENPSKWVLAGVALLLQL.-	2081.49	3	122.06	0.94	0.0	130	13/72	
jmfagtrench5minigg1mnacldtt,1425-1427	-.LSPHSGSPHYQGDLEDMADLAGLR.-	2567.78	3	352.46	1.67	0.1	184	4/23	
jmfag5minigg300mmnacl,1558-1560	- EKFPQEWKNK.-	1334.51	3	258.32	1.46	0.1	124	1/4	
jmfag5minigg300mmnacl, 1574	-.AQLPQDSKRFEGIDSDFR.-	2110.27	3	531.23	1.56	0.1	296	21/68	
jmfag5minigg1000mmnacl, 1950	- EQAALAESGDEEPGDPRLRLLGTFVAR.-	2899.17	3	618.20	1.91	0.1	138	19/104	1
jmfag5minigg350mmnacl, 1961	-.YLALIRMFSTELDAVR.-	1899.25	2	597.44	0.99	0.1	416	7/15	
ajrawphagjun20dpi1MNaCl, 2056	-.NIPHLLSRSK.-	1165.37	3	1062.52	1.46	0.2	364	4/9	
JMFAGNACL10_2B21E3, 2194	-.VDSFLDSLIHFDKENIHENCLK.-	2617.92	3	1346.61	1.55	0.2	568	25/84	
jmfag5minigg600mmnacl, 2412	-.LGYTFNNRNFHNVSLGQGQEVVAEAALDLAAK.-	3448.79	2	379.47	1.03	0.2	47	7/62	
JMFAGNACL10_2B21E3, 2560	- LIQVVGVETSKVSR.-	1515.78	2	494.66	1.00	0.2	128	7/26	
jmfag5minigg400mmnacl, 2740	- WSLMFKQHLVDFVTNSLSDLDSFIR.-	3000.42	2	42.08	0.76	0.0	36	5/48	
JMFAGNACL15B21E3, 2744	-.TEGWDYAMQITNSIHDLEQRIQK.-	2891.21	3	1049.90	1.58	0.2	179	15/92	
jmraw5minigg250mmnaclsyringdnase, 3040	-.TFLEEILDRMTDEFNIAELMAKVEER.-	3144.57	2	88.90	0.88	0.1	34	4/25	
jmfag5minigg200mmnacl, 3298	- LDGFLGRVHMVEVERQCAIMWCALVK.-	3005.64	2	522.58	0.98	0.2	93	9/50	
jmfag1mnacl0minigg, 3315	-.PGLTPVFEAQLNLVTPELVFHPSLDSGVK.-	3106.56	2	57.82	0.76	0.0	61	1/8	
jmfagtimecon7.5min,873,873.2	-.AAEETLSWK.-	1035.13	0	322.51	1.03	0.1	203	1/2	
jmbeads1000naclrawphag3007,394-396	-.AKGLFFLRTK.-	1181.46	3	2485.59	2.24	0.1	1031	5/9	
jmbeads300rawphag3007, 576	-.SQYNLSLPLLHR.-	1441.66	2	2166.97	1.62	0.3	552	6/11	
jmbeads400rawphag3007, 675	-.ELWDTIGMVTSSIR.-	1608.84	3	739.10	1.64	0.0	429	4/13	
AJRAWActinContr_june13, 694	-.QQNGFKITLK.-	1177.38	2	369.02	1.04	0.1	145	7/18	
jmfag1mnacl5mincon, 814	-.NMPTMAGGICWAQELRQR.-	2063.42	3	2659.68	1.81	0.3	503	19/68	
jmbeads400rawphag3007, 931	- LGSKYVMGR.-	1011.22	2	198.98	1.08	0.0	180	7/16	
jmfagtimecon10min,1028-1030	-.ALAEYLDTKR.-	1180.34	3	209.57	1.47	0.0	119	11/36	
jmfagcon5minn600mmnacl, 1143	-.EKFPQEWKNK.-	1334.51	3	186.86	1.27	0.0	145	13/36	
jmbeads350rawphag30072nd, 1364	-.AIPADKQDCR.-	1117.26	2	259.22	1.08	0.1	208	1/2	
jmbeads600naclrawphage3007, 1716	-.YVAFFLEEVSSWQKK.-	1862.12	2	1762.55	1.26	0.4	88	1/4	
jmbeads600naclrawphage3007, 1742	-.YGEELRVTQIGQKGCLQTIER.-	2422.75	3	315.10	1.16	0.0	263	17/80	
jmbeads300rawphag3007, 1902	-.VEDLDRRLGTILIQAFDDAPDVEHAFK.-	3085.42	2	58.34	0.80	0.1	46	3/26	
jmidl400naclrawphag3007_030802153313,1316-1318	-.AKGLFFLRTK.-	1181.46	3	1423.87	1.73	0.0	798	1/2	1
jmidl60MeOHrawphag3007, 1856	-.YYSLIQESGLKIHALVQVTTDR.-	2535.88	2	117.52	0.78	0.1	95	5/21	
jmidl150naclrawphag3007, 2768	-.DLTPPMPVMFLK.-	1389.75	2	195.15	1.03	0.0	189	7/22	
ajrawmediapbsnocells, 1264	-.EWPLSLDDQQDHMEK.-	1872.01	2	409.00	2.17	0.0	188	11/28	

control

dynein, axonemal, heavy polypeptide 9 [Mus musculus]					**7589.12**	38091406.0		42	
rawextr_150beadigg2_Mar04, 844	-.ITLKTLEDNLLSR.-	1516.77	2	307.78	1.38	0.0	211	3/8	
rawextr_200beadigg_Mar04, 923	- MTDEFNIAELMAKVEER.-	2027.31	3	256.29	1.39	0.0	185	13/64	
FPbeads600_Dec19, 1096	-.MNILTREIQRSLR.-	1630.94	2	450.86	1.06	0.1	296	5/12	
rawextr_chlfbeadIgG_Mar04, 1130	-.EKAIADEEEQKVALIMLEVQQK.-	2543.92	3	1656.82	2.22	0.2	421	11/42	
rawextr_400beadigg_Mar04, 1264	-.HEMTEGVTAYEEKPR.-	1777.94	3	380.79	1.20	0.0	304	1/4	
FPbeads800_Dec19, 1688	-.FLQNTKNIEPAVK.-	1502.74	2	282.41	1.20	0.1	179	1/3	
rawextr_500beadigg_Mar04, 2001	-.QSSTDDMFEPLKQTIELLK.-	2224.52	3	321.38	1.22	0.0	263	2/9	
rawextr_actinbeadigg_Mar04, 2325	-.GGLYDIVQSLVTRIFAMPSLVPR.-	2534.02	2	769.79	1.02	0.2	220	1/4	
jmbsa400naclrawphag3007_030802153340, 897	-.AKGLFFLRTK.-	1181.46	3	1665.52	1.97	0.1	815	19/36	1
rawextr_350bead_Mar04, 646	-.ALAEYLDTKR.-	1180.34	3	226.02	1.60	0.0	141	1/3	
rawextr_200bead_Mar04, 2034	-.GTEFENDVCEFNKR.-	1688.80	2	1271.45	1.85	0.1	539	1/2	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, axonemal, heavy chain 10 [Mus musculus]					**4217.46**	38080767.0		13	
rawsucrfp_350phagigg_Mar04, 452	-.EPDELNIR.-	986.06	3	281.18	1.48	0.0	177	9/28	
rawsucrfp_actinphagigg_Mar04, 1342	-.WMYLESIFIGGDIRSQLPEEAKK.-	2712.12	3	452.05	1.35	0.1	305	23/88	
phagrawFsuc700_dec23, 2159	-.CCEAPNRLHDLQTISEGLEKCQK.-	2616.98	3	208.31	1.08	0.0	194	9/44	
phagrawFchlfbead_dec23, 2349	-.DIVDSFIRGSILEAREFEWESQLR.-	2897.19	3	261.48	1.09	0.0	240	9/46	
jmfag5minigg150mmnacl, 1310	-.KFDNIDRIFK.-	1296.50	2	234.90	0.94	0.0	245	4/9	
jmfagcont5minbead, 564	-.EPDELNIR.-	986.06	3	828.98	1.31	0.2	222	5/14	
AJRAWpellet2_contr_jun13, 736	-.LNLIMGETLK.-	1132.40	2	1048.60	1.22	0.2	371	1/2	
jmfag5mincont350, 1172	-.EILDTWENMKFTVVK.-	1854.16	2	258.82	1.38	0.0	187	9/28	
jmbeads1000naclrawphag3007, 3051	-.WMYLESIFIGGDIRSQLPEEAKK.-	2712.12	3	569.83	1.31	0.2	182	2/11	
RawPhg2007Etsolutiondigest, 805	-.KYNTVLIIDVHAR.-	1542.81	3	73.31	1.18	0.0	61	5/24	

control

dynein, axonemal, heavy chain 10 [Mus musculus]					**1305.88**	38080767.0		11	
rawextr_500bead_Mar04, 2678	-.GSILEAREFEWESQLR.-	1951.13	3	1156.22	1.66	0.1	539	19/60	
jmbsaactinrawphag3007, 858	-.DLAKALGLLCVVTNCGEGMDYK.-	2314.73	3	149.66	1.40	0.0	98	19/84	1

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, axonemal, heavy chain 11; aitus inversus viscerum; dynein, axon					31116.64	6753652.0		17	
jmrawbas5min1mnacl, 1262	-.MLETAHK -	829.99	2	332.69	1.21	0.0	271	2/3	
rawsucrfp_600phagigg_Mar04, 716	- KIAAMVR.-	789.03	2	412.88	1.27	0.1	300	2/3	
rawsucrfp_450phagigg_Mar04, 742	-.KIAAMVR.-	789.03	2	301.24	1.15	0.0	251	2/3	
rawsucrfp_450phagigg_Mar04, 1096	-.LGTLLCEGLSNCSGLESAFK -	2043.35	3	772.08	1.80	0.0	429	1/4	
rawsucrfp_chlfphagigg_Mar04, 1118	- AGILYVNPQDLGWNPYVASWIDR -	2648.96	3	525.27	1.76	0.0	289	21/88	
phagrawFsuc80MeOH_dec23, 1404	- FYFISSADLLDILSKGAQPK -	2214.55	3	436.21	1.35	0.0	323	1/4	
rawsucrfp_chlfphagigg_Mar04, 1524	- ILRIPQGHALLIGVGGSGKQSLSR.-	2458.89	2	49.01	0.80	0.0	45	7/46	
phagrawFsuc350_dec20, 1564	- SRQRATDELFEPLK.-	1690.88	2	292.42	1.34	0.1	115	5/13	
phagrawFsuc250_dec22, 2127	-.NILDDILERLPEEFNMAELMQK.-	2663.08	3	281.41	1.09	0.1	200	17/84	
phagrawFsucchlf_dec23, 2292	- YNYTTPRSFLEQISLFKSLLK.-	2549.95	3	680.64	1.59	0.1	403	17/80	
rawphag2007chlfbead3, 372	- LVAVLREVK.-	1027.29	2	867.98	1.53	0.0	565	5/8	
RawPhg2007MeEthmeth3digest, 1072	- KIAAMVR -	789.03	2	763.78	1.79	0.1	343	3/4	
RawPhg2007MeEthmeth3digest, 1076	-.KIAAMVR.-	789.03	2	395.32	1.40	0.0	268	3/4	
RawPhg2007MeEthmeth3digest, 1446	- GKPIMLVGNAGVGK.-	1341.65	2	294.37	1.23	0.1	213	5/13	
RawPhag200760MeBeadsdigest, 2722	- VITDVSHTWEALEFSYEAHHRTGTPLLK.-	3239.59	2	23.29	0.69	0.0	18	2/27	
jmfag5minigbead, 142	-.EAALTLDDKGDLFAK.-	1607.79	3	295.09	1.03	0.0	265	2/7	
JMMAGTube1B16E3, 720	- LKELTSMMPVIFAKAVPVDR -	2248.77	3	1362.58	1.96	0.2	422	21/76	
jmraw5minigg500mmnaclsd, 1074	-.WLGTLEKLLEKFSQGSHR.-	2130.44	3	89.32	1.08	0.0	81	3/17	
jmfagfrench20minigg1mnacldtt, 48	- DPEFNPNLIRTKSFAAAGLCAWVINIIR -	3131.84	2	87.99	0.86	0.0	75	4/27	
jmfag1mnacl5minigg, 210	- LTASFEKATAEK -	1296.45	3	1144.52	1.44	0.1	632	19/44	
jmfag5minigg1000mmnacl, 242	- FSQGSHR.-	818.86	2	446.82	1.22	0.0	347	2/3	
jmraw5minigglowionic, 367	- EIWSLDK.-	891.00	2	205.27	1.14	0.0	179	2/3	
jmfag5minigg1000mmnacl, 378	- KGLTSYFTR.-	1073.23	3	184.86	1.55	0.0	119	9/32	
jmfag1mnacl2.5minigg, 512	- ALAEYLETK.-	1038.18	2	607.43	1.56	0.1	353	5/8	1
jmIgG400rawphag3007, 784	-.YFKGVDANALLR.-	1367.58	3	255.98	1.04	0.0	229	13/44	
jmfag1mnacl7.5minigg, 920	- VEDDVRDIVDQAVK.-	1601.74	3	989.83	1.99	0.1	383	19/52	
jmraw5minigg500mmnaclsd, 1074	- WLGTLEKLLEKFSQGSHR.-	2130.44	3	89.32	1.08	0.0	81	3/17	
jmfag5minigg350mmnacl, 1391	- HEVSPLQNAEVTLIR.-	1706.93	2	245.56	1.02	0.0	241	9/28	
jmfagfrench20minigg1mnacldtt, 1464	-.AAAGGHWVILQNVHLVAK.-	1885.21	3	990.47	1.53	0.1	511	5/17	
ajrawphagjun20actinDPI, 1566	-.LRQALRFPEETWGQYLESQDHR -	2747.96	3	1082.43	1.82	0.2	126	17/84	
jmfag5minigg150mmnacl, 1570	- LIDTNDFDLFQR -	1497.64	2	124.17	1.05	0.0	115	7/22	
jmraw5minigg600mmnaclsd, 1572	-.QKQEHLGNGIQK.-	1380.54	2	203.41	0.89	0.1	87	3/11	
jmigg450rawphag3007, 1704	-.DALNTLNRVNLTELK.-	1714.95	2	218.07	1.07	0.0	197	9/28	
jmrawgg5min450mmnaclsd, 1732	-.AVRVWDAYSGLEGTVK.-	1751.96	2	211.75	1.00	0.1	127	3/10	
jmraw5minigg500mmnaclsd,1764-1766	-.PSVGIFITLNPGYAGRTELPENLK.-	2587.96	3	343.24	1.64	0.1	166	4/23	
jmfag1mnacl2.5minigg,1858-1860	-.IGLQTEKVSR.-	1131.31	2	347.65	1.23	0.1	218	4/9	
jmfag5minigg200mmnacl, 2158	-.LVDLDHNLSRLTASFEK.-	1959.19	1	80.90	0.89	0.0	88	7/32	
JMFAGNACL10_2B21E3, 2264	-.PSVGIFITLNPGYAGRTELPENLKALFR.-	3075.55	2	311.95	0.97	0.1	124	5/27	
ajrawphag1MNaCl20, 2266	-.EQIDIYEALYIQMSKFDDFR.-	2525.82	3	706.07	1.73	0.1	202	1/4	
jmfag5minigg200mmnacl, 2558	-.QVTHHLVKLFDSISDLQFEDNLDVSTHK.-	3267.59	2	282.76	1.07	0.1	111	1/6	
jmIgG300rawphag3007, 2574	-.QLCEGDHDGLVDIMGHLLAVRSR.-	2535.89	3	264.38	1.27	0.0	200	17/88	
ajrawphagjun20dpi1MNaCl,2810-2812	-.LVYFIDDLNMPEVDLYGTVQPHALLR.-	3033.49	2	135.65	1.14	0.0	119	9/50	
jmfag5minigg1000mmnacl, 2904	- KLVYFIDDLNMPEVDLYGTVQPHALLR.-	3161.66	2	374.31	1.00	0.2	71	2/13	
jmbeads250rawphag3007, 120	-.QYRQELVDCK.-	1282.45	3	1374.37	1.97	0.1	668	1/2	
jmbeads150rawphag3007, 154	- LVLTKQQNDFK.-	1334.55	2	295.45	0.93	0.1	273	9/20	
jmfagcon5minn600mmnacl, 161	-.KIAAMVR.-	789.03	2	275.34	1.35	0.0	191	7/12	
jmfag5mincon450mmnacl,206-208	- GDLFAKK.-	778.92	2	277.87	1.05	0.0	264	2/3	
jmfag5mincon1150mmnacl, 1307	-.LVDLDHNLSRLTASFEK -	1959.19	3	160.96	1.08	0.0	148	3/16	
jmfag5mincon1200mmnacl, 2248	-.LETTKATAAEIEHKVTEAR.-	2099.33	3	813.46	1.51	0.1	418	1/4	
jmbeadsactinrawphag3007,2624-2626	-.DIVDQAVKELGTEK.-	1545.72	2	216.85	1.08	0.0	193	9/26	
jmbeadsactinrawphag3007, 2790	-.LEFGGSKGAVLNAQIHSTSEEFIECCK.-	2899.25	3	159.37	1.23	0.0	128	2/13	
jmldl350naclrawphag3007, 1090	- WWHKEMKAVK.-	1343.83	2	255.34	0.76	0.1	250	4/9	
jmldlactinrawphag3007, 1276	-.KVAAIQTEASQKQR -	1558.77	3	563.59	1.57	0.1	206	1/4	
jmldlactinrawphag3007, 1802	- ILRIPQGHALLIGVGGSGKQSLSR.-	2458.89	3	265.39	1.35	0.1	31	7/46	
jmldl400firstnaclrawphag3007, 1916	-.EIWSLDKAVRVWDAYSGLEGTVK.-	2623.95	3	294.79	1.28	0.1	197	2/11	
jmldl60MeOHrawphag3007, 2118	- VQRFALDPRVCFLGGR.-	1835.17	2	792.35	1.83	0.1	217	11/30	
jmldl600naclrawphag3007, 2152	- VQRFALDPRVCFLGGR.-	1835.17	2	1950.09	1.99	0.3	305	2/5	
jmldl1000naclrawphag3007, 2368	- VQRFALDPRVCFLGGR.-	1835.17	2	3132.37	1.93	0.4	264	2/5	
jmldl150naclrawphag3007, 2950	-.VTFPRFYFISSADLLDILSKGAQPK -	2815.26	2	227.67	1.24	0.1	119	11/48	
jmrawgg5miniggfreebead, 192	-.AGRNYGPKGNK -	1162.28	2	979.43	1.29	0.2	382	1/2	
ajrawmediapbsnocells, 944	-.QALAQTNLDLAAATEK -	1658.84	3	991.59	1.89	0.0	524	19/60	

control

dynein, axonemal, heavy chain 11; aitus inversus viscerum; dynein, axon					8179.05	6753652.0		73	
rawextr_1000bead_Mar04,744-746	-.KIAAMVR -	789.03	2	331.50	1.64	0.0	200	7/12	
rawextr_600bead_Mar04, 758	-.KIAAMVR.-	789.03	2	305.53	1.46	0.0	207	7/12	
rawextr_700bead_Mar04, 883	-.IPQGHALLIGVGGSGK.-	1504.76	2	289.53	1.37	0.1	167	1/3	
rawextr_150beadigg2_Mar04, 894	-.RFIEEIEGIEPQHKDSISLFMAHVHTSVK.-	3379.84	2	69.07	0.99	0.1	44	1/7	
rawextr_450bead_Mar04, 940	-.LSPSEQEDEEDEEAAAAR.-	1978.94	3	1376.91	1.71	0.2	546	21/68	
FPbeads200_Dec19, 971	-.VMTICTIDVHAR.-	1359.65	2	119.93	0.77	0.1	124	7/22	
rawextr_150bead_Mar04, 1601	-.VDAEFKELMFETAKVK.-	1886.20	3	862.74	1.74	0.1	416	19/60	
rawextr_350beadigg2_Mar04, 1630	-.LIDTNDFDLFQR.-	1497.64	2	288.61	1.07	0.0	269	5/11	
FPbeads250_Dec19, 1752	- IPQGHALLIGVGGSGK.-	1504.76	2	225.47	1.11	0.0	204	3/10	
rawextr_250bead_Mar04, 1848	-.QLKPTPFFQAQMLLMPPEIVFK.-	2605.20	3	754.34	1.54	0.1	435	5/21	
FPbeads300_Dec19, 2046	-.LPEEFNMAELMQK.-	1580.85	2	289.32	1.00	0.1	237	3/8	
rawextr_450beadigg_Mar04,2074-2076	-.PCAMVAPDTELICEIMLVAEGFVDARSLARK.-	3350.99	3	1062.11	1.29	0.3	138	17/120	
rawextr_chlfbeadigG_Mar04, 2136	-.PPLEKEAGDGFYDLVEEMLCGSFR.-	2704.03	3	360.18	1.25	0.1	252	4/23	
rawextr_300bead_Mar04, 2162	-.FSPINGLLSVNFDPKLVAVLREVK.-	2657.15	2	65.83	0.96	0.0	63	7/46	
rawextr_chlfbead_Mar04, 2428	-.TFPNPPNAVTNVTAAVMVLLAPR.-	2394.82	2	232.84	1.34	0.1	142	1/4	
FPbeads800_Dec19, 2508	-.TLDFDRRLGTLLCEGLSNCSGLESAFK.-	2947.34	2	246.81	0.98	0.1	80	2/13	
jmbsaactinrawphag3007, 425	-.VVNEQYLK -	993.14	2	402.07	1.33	0.1	257	4/7	
jmbsaactinrawphag3007, 1681	-.IHNLVEENRKLFR.-	1668.93	2	896.25	1.23	0.2	315	3/8	

Fc complex

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, cytoplasmic, heavy chain 1; dynein heavy chain, retrograde tra				36601.91	13384736.0		72	
ajrawmediapbsnocells, 950								
ajrawphagactin20, 1588	- AKEALELTDTGLLSGSEER -	2020.19	3	647.28	1.70	0.1	156	17/72
ajrawphagactin20, 1970	- EGLMLDSHEELYK -	1564.74	2	420.75	1.32	0.1	157	7/24
ajrawphagactin20, 542	- LALESICLLLGESTTDWK -	1993.31	3	1230.80	1.42	0.2	334	4/17
jmbeads150rawphag3007, 2036	- VEPLRNELQK -	1228.41	2	222.35	0.91	0.1	217	7/18
jmbeadsactinrawphag3007, 2374	-.GKEIVLSAGSTPK -	1287.49	1	334.52	1.10	0.1	205	5/12
jmfag1mnacl2.5minigg, 1954	- RWVYLEGIFTGSADIK.-	1856.11	2	270.91	1.15	0.0	234	1/3
jmfag1mnacl5mincon, 220	- RWVYLEGIFTGSADIK.-	1856.11	2	337.27	1.19	0.1	252	1/3
jmfag1mnacl5mincon, 888	- AVIVRVLR.-	926.19	2	289.99	1.12	0.0	258	4/7
jmfag5mincon250mmnacl, 1084	- QELEQHSVDTASTSDAVTFITYVQSLKRK.-	3283.59	3	403.59	1.52	0.1	202	5/28
jmfag5mincon450mmnacl, 1606	- SNLPDNLKK -	1029.17	2	134.05	0.99	0.1	104	1/2
jmfag5mincont150mmnacl, 1791	- SPLVMDVLNIQGVQRSLER -	2155.51	3	352.52	1.41	0.1	201	2/9
jmfag5minigg1000mmnacl, 1560	- LSPYYKVFEEDALSWEDK -	2220.42	3	861.72	1.58	0.1	459	21/68
jmfag5minigg200mmnacl, 1164	- RWVYLEGIFTGSADIK -	1856.11	3	735.18	1.53	0.1	413	17/60
jmfag5minigg300mmnacl, 1452	-.VTFVNFTVTRSSLQSQCLNEVLK.-	2615.00	3	495.59	1.62	0.1	219	17/88
jmfag5minigg400mmnacl, 642	-.LRQYASYEFVQRLLK -	1915.23	3	374.28	1.16	0.1	292	9/28
jmfag5minigg450mmnacl_030527025134, 1444	- SVLVSAGNVKR -	1130.32	2	211.98	1.21	0.0	154	9/20
jmfag5minigg450mmnacl_030527025134, 758	- LKVNFLPEITLSK -	1615.98	3	506.39	1.49	0.1	277	4/13
jmfag5minigg500mmnacl, 1010	- PDVDEKRSDLLK -	1415.58	3	484.88	1.28	0.1	339	7/22
jmfag5minigg500mmnacl, 2586	- NLQVSGRIFTIESAR -	1620.84	2	866.75	1.29	0.2	178	9/28
jmfag5minigbead_030528200105, 1643	-.SRQELEQHSVDTASTSDAVTFITYVQSLKR.-	3398.68	3	368.68	1.43	0.1	99	19/116
jmfagcon5min1000mmnacl_030601180404, 1540	-.DQLGTAKNANEMFR.-	1595.76	3	349.21	1.19	0.1	245	4/13
jmfagcon5minn600mmnacl, 2233	-.LFLTMEINPK.-	1205.48	1	938.31	1.72	0.1	434	1/2
jmfagcon5minn600mmnacl, 2447	- AISKDHLYGTLDPNTR.-	1801.98	2	396.42	1.46	0.1	237	1/3
jmfagcont5minbead, 1432	-.LRQNLDGLLNQLK.-	1525.78	2	83.30	0.81	0.0	99	1/4
jmfagcont5minbead, 1554	-.MVVLSLPR.-	915.18	2	245.76	0.95	0.1	189	3/7
jmfagcont5minbead, 930	-.KARTDSTSDGR.-	1194.24	2	162.35	0.98	0.1	121	2/5
jmfagfranch20minigg1mnacldit, 834	-.SLETCMYDHK.-	1227.39	2	347.90	1.27	0.1	228	1/2
JMFAGNACL10_1B21E3, 200	-.EKCAKAK.-	777.96	2	313.87	0.98	0.0	318	2/3
JMFAGNACL10_1B21E3, 228	- QNLFTTWSHHLQQANIQFR.-	2370.61	3	986.92	2.16	0.1	415	7/24
JMFAGNACL10_2B21E3, 344	- NIHVCLGGLFVPEAYITATR -	2175.54	3	805.29	1.32	0.0	457	5/19
JMFAGNACL15B21E3, 2924	- QNLFTTWSHHLQQANIQFR.-	2370.61	3	1064.14	2.28	0.1	410	5/18
JMFAGNACL5B21E3, 1676	-.VFEEDALSWEDK -	1468.55	2	52.84	0.81	0.0	63	5/22
JMFAGNACL5B21E3, 3074	- LERIQFVGACNPPTDPGRK -	2099.40	3	208.94	1.24	0.0	168	17/72
jmfagtimacon10min, 2282	- IDLEVRSLETCMYDHKTFSEILNR -	2914.31	2	144.69	0.71	0.1	39	7/46
jmfagtimacon7.5min.1552.1552.3	-.YPLIIDPSGQATEFIMNEYK -	2330.64	3	559.83	1.69	0.1	247	9/38
jmfagtimacon7.5min.2268.2268.2	-.SACDTVDTWLDDTAK.-	1641.74	0	759.90	1.85	0.0	461	17/56
jmfagtimacont0min_030601230741,1888-1888	-.WVYLEGIFTGSADIK -	1699.93	0	937.33	1.41	0.2	326	3/7
jmfagtimacont10min_030601202502, 1112	-.IFTIESARVR.-	1192.39	2	815.85	1.07	0.2	449	5/9
jmIgG150rawphag3007, 1254	-.QNLFTTWSHHLQQANIQFR.-	2370.61	3	666.10	1.72	0.1	179	17/72
jmIgG150rawphag3007, 1894	-.LGGSPFGPAGTGKTESVKALGHQLGR.-	2523.83	3	305.41	1.48	0.0	206	4/25
jmIgG300rawphag3007, 1236	- EFISYNINIDIHYGVKSNSLAFIKR.-	2943.35	3	363.46	1.42	0.0	242	19/96
jmIgG500rawphag3007,1785-1787	-.KLEHLITELVHQR.-	1616.88	3	377.28	1.68	0.0	209	7/24
jmldl150nacirawphag3007,1120-1122	-.TVENIKDPLFR.-	1332.53	2	237.67	1.11	0.1	178	7/20
jmldl450nacirawphag3007, 2276	-.GRQNISPDK.-	1015.11	2	524.97	1.19	0.1	393	11/16
jmldl500nacirawphag3007, 1891	-.VFYEEELDVPLVLFNEVLDHVLR.-	2789.18	3	446.35	1.24	0.1	148	7/44
JMMAGNEGB16D3, 1200	-.KDSAIQQQVANLQMKIVQEDR.-	2443.77	2	107.15	0.85	0.1	49	1/5
JMMAGTube1B16E3, 2882	-.IKLKGTVGEPTYDAEFQHFLR.-	2450.78	3	472.94	1.55	0.0	304	17/80
jmraw5minigg500mmnaclsd, 1034	-.LLAESVTEVEIFGKATSIDPNTYITWIDK -	3255.66	2	1045.68	1.16	0.3	48	1/8
jmraw5minigg500mmnaclsd, 2458	-.GRILVDDTIITTLENLK.-	1915.22	2	618.52	1.84	0.0	316	3/8
jmraw5minigg500mmnaclsd,1606-1608	-.GYMKINMLVIELK.-	1552.97	3	156.23	1.13	0.1	108	11/48
jmraw5miniggiowionic, 463	-.GVWSELSKVWEQIDQMK.-	2064.35	3	1540.64	1.70	0.2	343	9/32
jmrawbas5min1mnact, 1460	-.VAAPDVVVPTLDTVR.-	1552.80	3	557.93	1.46	0.0	383	2/7
jmrawgg5min150mmnacl, 1042	-.KNLESALR.-	931.07	2	342.79	0.90	0.0	375	9/14
jmrawgg5min150mmnacl, 1334	-.TLHTTASNWLHLIPQTLSPLKR.-	2528.94	3	1125.56	1.77	0.1	526	5/21
jmrawgg5min150mmnacl, 964	-.ADLAAVEAKVNRSTALLK.-	1871.17	2	609.18	1.87	0.0	307	6/17
jmrawgg5min1mnacl, 849	-.IWAHEALR.-	996.15	2	236.57	1.05	0.0	224	1/2
jmrawgg5min300mmnaclsyringednase, 2303	-.TVENIKDPLFR.-	1332.53	2	1138.33	1.38	0.2	400	11/20
jmrawgg5min400mmnaclsd,1033-1035	-.AVDDLNLHSYSNLPIWVNKLDMEIER.-	3086.47	2	179.01	0.87	0.1	86	7/50
jmrawgg5min450mmnaclsd, 463	-.DRAATSPALFNR.-	1319.45	1	151.24	1.13	0.1	74	7/22
jmrawgg5min450mmnaclsd, 515	-.GYMKINMLVIELK.-	1552.97	3	240.02	1.18	0.1	108	1/4
jmrawgg5minbeadsfreezethaw, 650	-.FGSISTEFLALMK.-	1515.80	3	993.41	1.68	0.1	390	17/48
jmrawminigg200mmnaclsyringdnas, 2134	-.SQELEVKNAAANDK.-	1517.62	3	329.37	1.38	0.0	231	7/26
phagrawF250_dec22, 1033	-.LVPLLLEDGGDAPAALEAALEEK.-	2335.64	3	1731.55	1.72	0.2	505	23/88
phagrawF400_dec20, 1146	-.KNYMSNPSYNYEIVNR.-	1993.19	3	185.13	1.29	0.0	131	13/60
phagrawFsuc500_dec20, 2936	-.QTSAEKKASVVTLPVYLNFTR -	2353.70	3	1149.35	1.80	0.2	324	11/40
phagrawFsuc700_dec23, 1523	-.RQWIVFDGDVDPEWVENLNSVLDDNK.-	3104.33	2	237.18	1.11	0.1	67	4/25
rawphag2007chfbead1, 1470	-.LLNTFLERLFTTR.-	1624.91	2	120.40	0.90	0.0	125	7/24
rawphag2007chfbsol2, 2126	-.GKEIVLSAGSTPKIQGLTVEQAEAVVR.-	2782.19	3	559.89	1.63	0.1	233	17/104
rawsucrfp_100cphagigg_Mar04, 2310	- KVMSQEIQEQLHK.-	1598.85	2	100.71	0.92	0.0	97	7/24
rawsucrfp_150phagigg_Mar04, 1533	- QRFQFPPSWLYIDNIEGEWGAFNDIMR.-	3331.71	2	27.21	0.91	0.0	30	7/52
rawsucrfp_150phagigg_Mar04, 916	- DAATIMQPYFTSNGLVTK.-	1958.23	2	78.24	1.07	0.0	70	3/17
rawsucrfp_250phagigg_Mar04, 1852	- LERIQFVGACNPPTDPGR.-	1971.23	3	220.78	1.58	0.0	139	4/17
rawsucrfp_actinphagigg_Mar04,678-680	-.DPASGTALQEISFWLNLERALYR.-	2651.96	3	245.12	1.27	0.0	190	9/44
	-.QNLFTTWSHHLQQANIQFR -	2370.61	3	658.23	1.98	0.1	264	17/72

control

Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
dynein, cytoplasmic, heavy chain 1; dynein heavy chain, retrograde tra				10833.98	13384736.0		90	
FPbeads250_Dec19, 86	-.LYFLLAWFHAIIQERLRYAPLGWSK.-	3093.86	2	63.36	0.80	0.0	66	7/48
rawextr_250beadigg_Mar04, 130	-.TSAPITCELLNK.-	1290.51	3	278.29	1.81	0.0	150	7/22
rawextr_800bead_Mar04, 452	-.TDIARTEYLSNADER.-	1754.84	3	454.51	1.51	0.0	285	3/8
rawextr_200beadigg_Mar04, 477	-.KIRNTK.-	759.92	2	131.78	1.11	0.1	83	3/5
rawextr_350beadigg2_Mar04, 568	-.ARTDSTSQGR.-	1066.06	3	298.96	1.21	0.0	227	13/36
rawextr_chfbeadigG3_Mar04, 600	-.QNLFTTWSHHLQQANIQFR.-	2370.61	3	863.58	1.95	0.0	422	5/18
rawextr_500beadigg_Mar04, 648	-.QNLFTTWSHHLQQANIQFR -	2370.61	3	1034.89	1.85	0.2	287	19/72
rawextr_chfbead_Mar04, 962	-.TTDLLTDWEKTKPVTGNLR.-	2189.48	2	360.25	1.38	0.1	156	5/18
rawextr_500bead_Mar04, 982	-.PVTGNLRPEEALQALTIYEGKFGR.-	2661.01	3	247.60	1.67	0.0	132	19/92
rawextr_700bead_Mar04, 1015	-.ITARLRDQLGTAK.-	1443.68	2	464.42	1.45	0.1	257	5/12
rawextr_actinbeadigg_Mar04, 1039	-.SFEWLSQMR.-	1184.35	2	302.01	1.24	0.1	175	1/2
rawextr_150bead_Mar04, 1149	-.EGTEAWEAAMK.-	1223.34	2	94.78	0.82	0.0	96	7/20
rawextr_500bead_Mar04, 1218	-.IQQLTVEQAEAVVR.-	1513.72	2	374.63	1.43	0.1	155	9/26
rawextr_500beadigg_Mar04, 1348	-.ALPDMEVVGLNFSSATTPELLLK.-	2446.85	3	244.91	1.16	0.0	208	2/11
rawextr_350bead_Mar04, 1546	-.SNLPDNLKKLFR.-	1445.69	2	147.52	1.03	0.1	84	7/22
rawextr_700bead_Mar04, 1549	-.CRLIRGWDDLFNK.-	1636.90	2	117.65	1.03	0.0	104	1/3
rawextr_250beadigg_Mar04, 1920	-.LEGVEGVAHIIDPK.-	1477.69	2	891.87	1.34	0.1	529	6/13
FPbeads250_Dec19, 1952	-.LEDDAKDNQQKANEVEQMIR.-	2375.56	3	421.94	1.13	0.1	227	4/19
rawextr_actinbeadigg_Mar04, 1967	-.VSKSPLVMDVLNIQGVQRSLER.-	2469.89	3	192.04	1.53	0.0	112	4/21
rawextr_actinbeadigg_Mar04, 1985	-.KVMSQEIQEQLHK.-	1598.85	2	139.00	1.00	0.0	138	1/3
rawextr_60MeOHbeadigg_Mar04, 2048	-.KLRQNLDGLLNQLK.-	1653.95	2	94.35	0.91	0.0	103	7/26
rawextr_250bead_Mar04, 2060	-.TKPVTGNLRPEEALQALTIYEGK.-	2529.88	3	210.55	1.12	0.0	176	7/44
rawextr_250bead_Mar04, 2144	- VFYEEELDVPLVLFNEVLDHVLR.-	2789.18	3	774.26	1.65	0.1	330	17/88
rawextr_350beadigg2_Mar04, 2234	-.YPLIIDPSGQATEFIMNEYKDRK.-	2730.09	3	1000.28	2.22	0.1	285	19/88
FPbeads300_Dec19, 2270	-.LRWQASSLPADDLCTENAIMLKR.-	2633.04	3	448.98	1.18	0.1	209	9/44
FPbeads250_Dec19,3498-3500	-.GTFDNAETKKEFGPVVIDYGK.-	2316.55	3	430.00	1.19	0.1	221	17/80
jmbsa250nacirawphag3007, 557	-.INMLVIELKSEALK.-	1601.98	3	448.42	1.38	0.0	325	4/13
jmraw5minbsafreezthaw, 1788	-.LSPYYKVFEEDALSWEDKLNR.-	2603.87	3	303.13	1.66	0.1	138	17/80

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to Sl:zC220F6.1 (novel protein similar to human dynein heavy c					35097.83	38084535.0	64		
phagrawFsuc200_dec22, 611	- PKAKEVGISEGNR -	1385.55	3	461.02	1.22	0.1	226	1/3	
phagrawFchfbead_dec23, 1263	- LLEYDKENIKPQILLK -	1958.33	3	105.07	0.94	0.0	109	3/20	
phagrawFsuc500_dec20, 1320	-.MAFQGTEDEIDLK.-	1497.65	2	753.62	1.81	0.1	320	5/12	
rawsucrfp_60MeOHphagigg_MAr04, 1372	- WPLMIDPQDQANR -	1584.78	2	284.49	1.45	0.0	195	3/8	
rawsucrfp_60MeOHphagigg_MAr04, 1418	- AGTLSTTASFGQKRAFK -	1772.00	2	1889.95	1.89	0.2	390	13/32	
phagrawFchfbead_dec23, 1511	- VTIINFTVTKSGLEDQLLSDVVR.-	2548.92	3	1228.31	2.32	0.0	530	21/88	
rawsucrfp_60MeOHphagigg_MAr04, 1568	- YFKQLFNTTIETSEKSDNLHER.-	2701.93	3	1769.05	2.32	0.1	715	1/4	
rawsucrfp_250phagigg_Mar04, 1590	- QERGNALLVGVGGTGKQSLTR -	2142.41	3	648.38	1.59	0.1	187	1/5	
rawsucrfp_250phagigg_Mar04, 1632	-.LAAHICGYKCMQIELSR -	1937.34	3	811.20	1.35	0.1	525	9/32	
phagrawFchfbead_dec23,1703-1705	- KVLLDDSTINIATIASSR.-	1918.18	2	518.52	1.40	0.1	155	9/34	
phagrawF400_dec20, 1798	-.KVLLDDSTINIATIASSR.-	1918.18	2	441.81	1.23	0.1	169	5/17	
phagrawF600_dec20, 1802	-.QEEPDVQFFSSQLEKYHK.-	2240.41	2	237.85	1.12	0.0	207	9/34	
phagrawFsuc250_dec22,1805-1807	-.KVLLDDSTINIATIASSR -	1918.18	2	499.92	1.87	0.1	224	11/34	
phagrawFsuc800_dec23,1916-1918	- KVLLDDSTINIATIASSR -	1918.18	2	548.40	1.54	0.1	153	9/34	
rawsucrfp_250phagigg_Mar04, 1966	-.KVLLDDSTINIATIASSR.-	1918.18	2	443.90	1.44	0.1	214	5/17	
phagrawF200_dec22,2009-2011	-.KVLLDDSTINIATIASSR.-	1918.18	2	282.82	1.30	0.0	195	11/34	
phagrawF250_dec22, 2491	- DHVWGLDFSSFHK.-	1575.71	2	925.12	1.09	0.3	210	3/8	1
phagrawFsuc400_dec20, 2572	-.LIFGICFFHAIIQVYLGNTIAQER.-	2768.27	2	131.01	0.86	0.1	97	9/46	
phagrawFsuc400_dec20, 2784	-.KVLLDDSTINIATIASSR.-	1918.18	2	162.29	1.24	0.1	90	4/17	
phagrawFsuc600_dec20, 3284	-.VKAEETQAIADDAQRDLEEALPALEAANK.-	3111.37	2	111.43	0.96	0.1	76	9/56	
jmfag1mnacl5mincon, 2104	-.AIAGLVVMSEEMEK.-	1507.80	2	698.87	1.07	0.2	226	5/13	1
JMMAGTube1B16E3, 3330	-.ASIISLEAQEAVKRK.-	1643.91	2	255.30	1.03	0.1	127	9/28	
JMFAGNACL15B21E3, 180	-.WKAFSVWR.-	1080.27	2	618.70	1.01	0.2	381	4/7	
ajrawphagjun20dpi1MNaCl, 456	-.VTTLCCLLESLLLSK.-	1637.04	3	291.90	1.18	0.0	228	15/56	
ajrawphagjun20actinDPI, 462	- PSADVFSPSPTKLPR.-	1599.81	3	1424.76	1.68	0.2	604	5/14	
ajrawphagjun20dpi1MNaCl, 482	-.VTTLCCLLESLLLSK.-	1637.04	3	430.48	1.43	0.1	217	2/7	
jmfagfrench5minigg1mnackdtt, 803	- SVLVMAGSLKR.-	1161.44	3	850.83	1.45	0.2	152	7/20	
jmrawigg5minbeadsfreezethaw,724-726	-.PLGSWVKDLILR.-	1397.69	3	307.76	1.42	0.0	206	7/22	1
jmrawigg5min1mnacl, 973	-.VEEAMFTSLRR.-	1339.55	2	732.39	1.47	0.1	363	1/2	
jmfagfrench5minigg1mnackdtt, 1137	-.LQEVTERLEVFRCAAK.-	1893.20	2	219.40	1.21	0.0	158	3/10	
jmfgG350naclrawphag3007, 1153	- LPSSGDLWSIHIDFDTK.-	1932.12	3	537.43	1.38	0.0	381	19/64	
ajrawphagjun20actinDPI,1336-1338	- ELIPVPK.-	795.99	1	382.98	1.18	0.0	313	3/4	
jmfagfrench20minigg1mnackdtt, 1692	- QVHRPSADVFSPSPTK -	1753.94	3	381.18	1.36	0.0	260	1/4	
jmfag5minigg450mmnacl_030527025134, 1938	-.PRTEWVIAGHPSQVILTISQIMWCR.-	2923.45	3	72.36	0.96	0.0	69	11/96	
ajrawphagactin20,2168-2170	- ELIPVPK.-	795.99	1	1023.81	1.69	0.2	302	3/4	
jmfag5minigg250mmnacl, 2320	- KKFGPLGWNICYEFNDSDR.-	2290.54	3	472.19	1.43	0.0	319	1/4	1
jmraw5minigg500mmnaclsd, 2466	-.DLSKCVQGTIREELQIFR.-	2136.46	3	423.85	1.29	0.1	204	15/68	
jmfag5minigg500mmnacl, 2598	-.PSPSTADRASIISLEAQEAVKR.-	2327.58	3	429.50	1.44	0.1	140	13/84	
jmfag5minigg200mmnacl, 2744	- LMSSGILKPSPSTADRASIISLEAQEAVK -	3001.45	2	177.40	1.00	0.1	125	5/28	
jmfag1mnacl7,5minigg, 3114	-.SRCRMFPSLVNCCTIDWFVQWPR -	2846.37	2	843.67	1.17	0.2	168	5/22	
jmfag5minigg1000mmnacl, 3126	- YSRDVPFFEMLVPTTDTVRYGYLMEK.-	3159.62	2	328.94	0.98	0.2	44	3/25	
jmfagtimecon2.5min.2768.2768.2	-.SCRFALRAAGFIPDDCEVETYEDYFK.-	3047.37	0	794.49	1.05	0.2	135	11/50	
jmfagcon5min1000mmnacl_030601180404, 1042	-.VDSADSFDWQR.-	1326.35	2	449.24	1.46	0.0	298	11/20	
jmfagcon5min1000mmnacl_030601180404, 1132	-.FIRHFSMLCLPMPSEHSLK.-	2274.76	3	419.51	1.46	0.0	287	7/24	
jmbeads350rawphag30072nd, 1158	-.VIKLTDTNFLR.-	1320.56	3	1051.86	1.50	0.0	686	17/40	
jmfag5mincont150mmnacl, 1325	-.HTTKAQERTR.-	1228.34	2	351.95	0.97	0.0	354	1/2	
jmfagtimecont0min_030601230741,1702-1704	-.VIKLTDTNFLR.-	1320.56	2	234.73	1.17	0.1	161	7/20	
jmfag1mnacl5mincon, 2104	- AIAGLVVMSEEMEK.-	1507.80	2	698.87	1.07	0.2	226	5/13	1
jmfag5mincont150mmnacl, 2499	-.TCGPGPNLSAVFEDDRNFLTIIMQIK.-	2881.32	3	974.04	1.45	0.2	401	1/5	
jmfag5mincon300mmnacl, 2816	-.CTQAIPQVDISKVTTLCCLLESLLLSK.-	2921.53	3	438.42	1.29	0.1	287	21/104	
rawphag2007chfbead2, 278	-.YINNPDFVPEKVEK.-	1692.89	3	544.65	1.47	0.0	370	15/52	
rawphag2007chfbead3, 669	-.SVIAKGLLNR.-	1071.30	2	186.84	1.25	0.1	122	4/9	
phagrawFchfbead_dec23, 1263	-.LLEYDKENIKPQILLK.-	1958.33	3	105.07	0.94	0.0	109	3/20	
rawsucrfp_60MeOHphagigg_MAr04, 1372	-.WPLMIDPQDQANR.-	1584.78	2	284.49	1.45	0.0	195	3/8	
rawsucrfp_60MeOHphagigg_MAr04, 1418	- AGTLSTTASFGQKRAFK.-	1772.00	2	1889.95	1.89	0.2	390	13/32	
phagrawFchfbead_dec23, 1511	-.VTIINFTVTKSGLEDQLLSDVVR.-	2548.92	3	1228.31	2.32	0.0	530	21/88	
rawsucrfp_60MeOHphagigg_MAr04, 1568	-.YFKQLFNTTIETSEKSDNLHER.-	2701.93	3	1769.05	2.32	0.1	715	1/4	
phagrawFchfbead_dec23,1703-1705	-.KVLLDDSTINIATIASSR.-	1918.18	2	518.52	1.40	0.1	155	9/34	

control

similar to Sl:zC220F6.1 (novel protein similar to human dynein heavy c					5077.14	38084535.0	61		
rawextr_350beadigg2_Mar04, 642	-.QLLGDSNFLR.-	1163.31	2	272.84	1.06	0.1	100	1/2	
rawextr_actinbeadigg_Mar04,703-705	-.YINNPDFVPEKVEKVSK.-	2007.28	3	435.46	1.77	0.1	210	17/64	
rawextr_200bead_Mar04, 1148	-.LDPWERIIPTFKYSR -	1922.22	3	488.03	1.79	0.1	236	1/4	
rawextr_60MeOHbeadigg_Mar04, 1172	-.ELTKIPIFALFRK.-	1576.95	2	281.65	1.41	0.0	191	5/12	
rawextr_300bead_Mar04, 1476	-.ALAIQCVVFNCSDGLDYK.-	1960.27	2	115.41	0.99	0.0	112	9/34	1
rawextr_500beadigg_Mar04, 1754	-.IPWDALIYITGIYFAPLADSLQDFK.-	2872.30	3	349.14	1.69	0.1	151	5/32	
rawextr_250bead_Mar04, 1910	-.VLLDDSTINIATIASSRYVGPLK -	2447.81	3	438.97	1.56	0.1	208	17/88	
rawextr_350beadigg2_Mar04, 2084	-.DSVALRPTRNVGLLLIDTK.-	2082.43	3	522.56	1.48	0.0	353	1/4	
FPbeads450_Dec19, 2258	-.EVLDPALEPILLKQTFMSGGR.-	2315.72	2	396.97	1.24	0.0	313	3/10	
FPbeads450_Dec19,2522-2524	-.KVLLDDSTINIATIASSR.-	1918.18	2	328.96	1.15	0.1	187	5/17	
rawextr_350bead_Mar04, 2574	-.FQEELANIVGNVFIAAACVAYYGAFTAQYR.-	3301.72	2	194.41	0.92	0.1	62	9/58	
jmbsa600naclrawphag3007, 1110	-.SIEHQAEENPILAR.-	1607.75	3	839.12	1.34	0.2	275	7/26	
jmbsa150naclrawphag3007, 1315	- LNTDNPFYQPVK.-	1436.59	2	413.61	1.33	0.1	257	5/11	

Fc complex

	Peptide Sequence	MH+	Charge	Score	Score XC	Accession Delta CN	Sp	Peptides Ions	Count
similar to dynein, cytoplasmic, heavy chain 2; cytoplasmic dynein heav					2644.67	38094558.0	2		
ajrawphagactin20,2464-2466	-.ASSALIQDSLKESYK.-	1640.82	3	1902.85	2.01	0.1	790	3/8	
phagrawFsucchlf_dec23, 2672	-.KIQLARLEESLLETLATSQGNILENK.-	2913.32	2	363.38	1.21	0.1	80	9/50	
phagrawFsuc200_dec22,1237-1239	-.LKQRIAEEVVK.-	1313.57	2	161.22	0.93	0.0	169	7/20	
jmfag5minigg200mmnacl, 2206	-.MGGSARTELFSTVGAQK.-	1740.96	2	217.23	0.90	0.0	241	11/32	

control

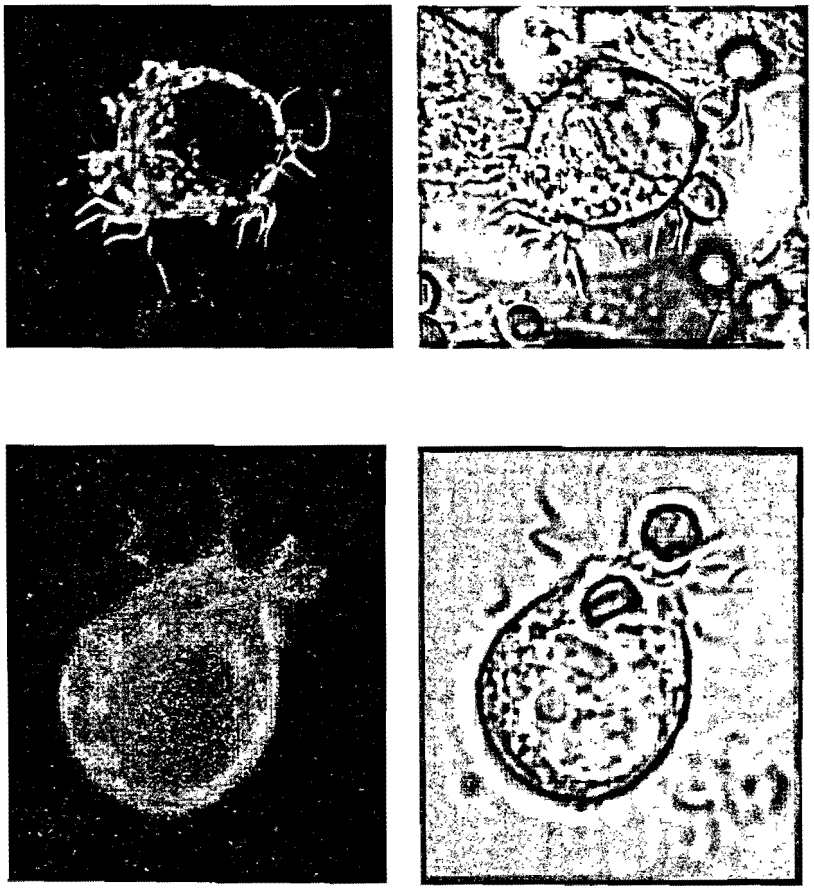
similar to dynein, cytoplasmic, heavy chain 2; cytoplasmic dynein heav					983.02	38094407.0	2		
rawextr_450beadigg_Mar04, 1228	-.EVQPLVNEAKLAVGNIR.-	1851.14	3	614.12	1.41	0.1	363	17/64	
FPbeads800_Dec19, 1882	-.LEAEVSKAQETIK.-	1446.63	2	199.04	0.99	0.0	200	1/3	
jmbsa300naclrawphag3007, 109	-.AFQMSSSIDPADA.-	1340.44	3	169.87	1.13	0.0	132	1/4	

APPENDIX M – ADDITIONAL GFP IMAGES

Additional GFP images are shown below of RAW 264.7 macrophage cells transfected with pEGFP-PLC-β_3 (Panel A), pEGFP-PLC-β_4 (Panel B), pEGFP-PLC-γ_1 (Panel C), $PH^{PLC-\delta 1}$-GFP (Panel D) or dominant negative PLC-δ_1 (E341R/D343R) (Panel E). Dominant negative PLC-δ_1 (E341R/D343R) transfectants surrounded by non-transfected cells displays the dominant negative PLC-δ_1 eating less IgG coated beads compared to neighbouring non-transfected cells (Panel F).

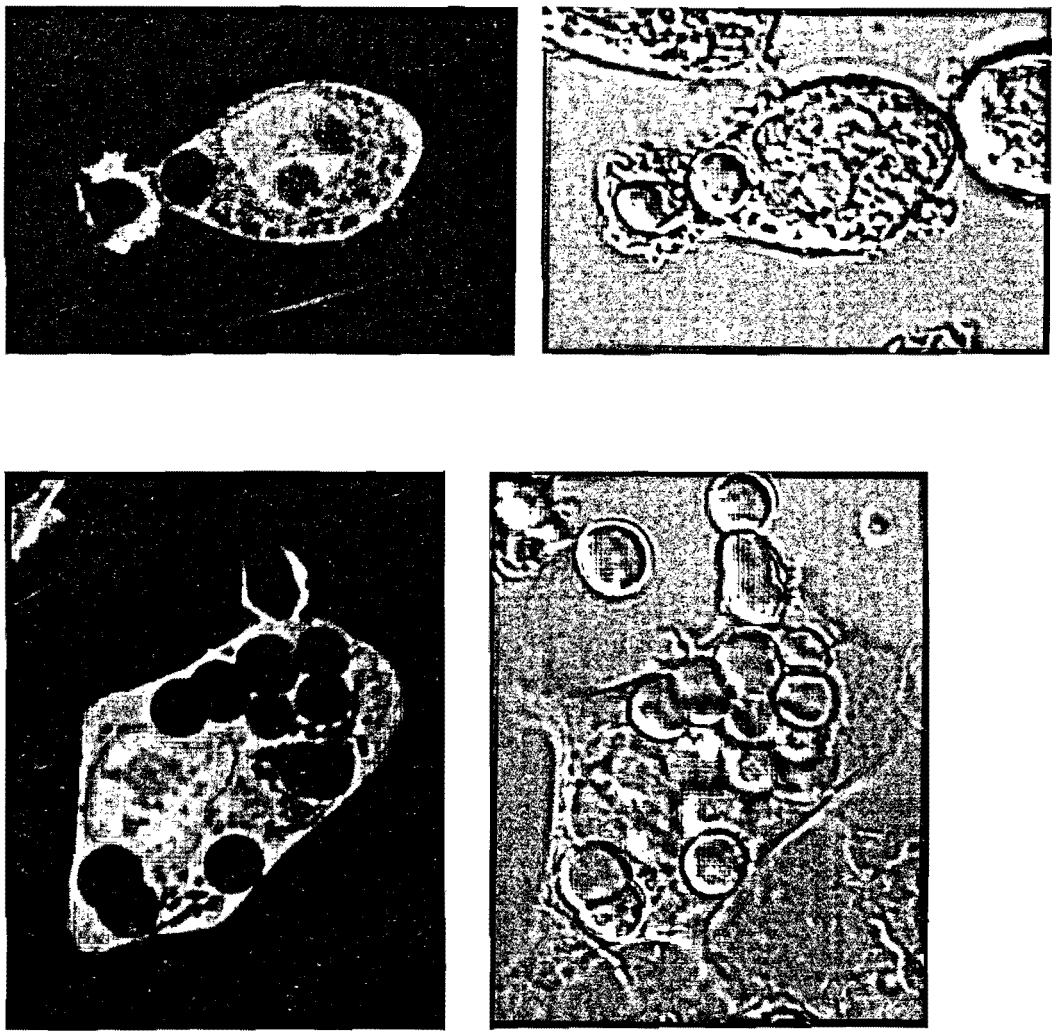
Panel A pEGFP-PLC-β_3

RAW 264.7 macrophage cells transfected with pEGFP-PLC-β_3.



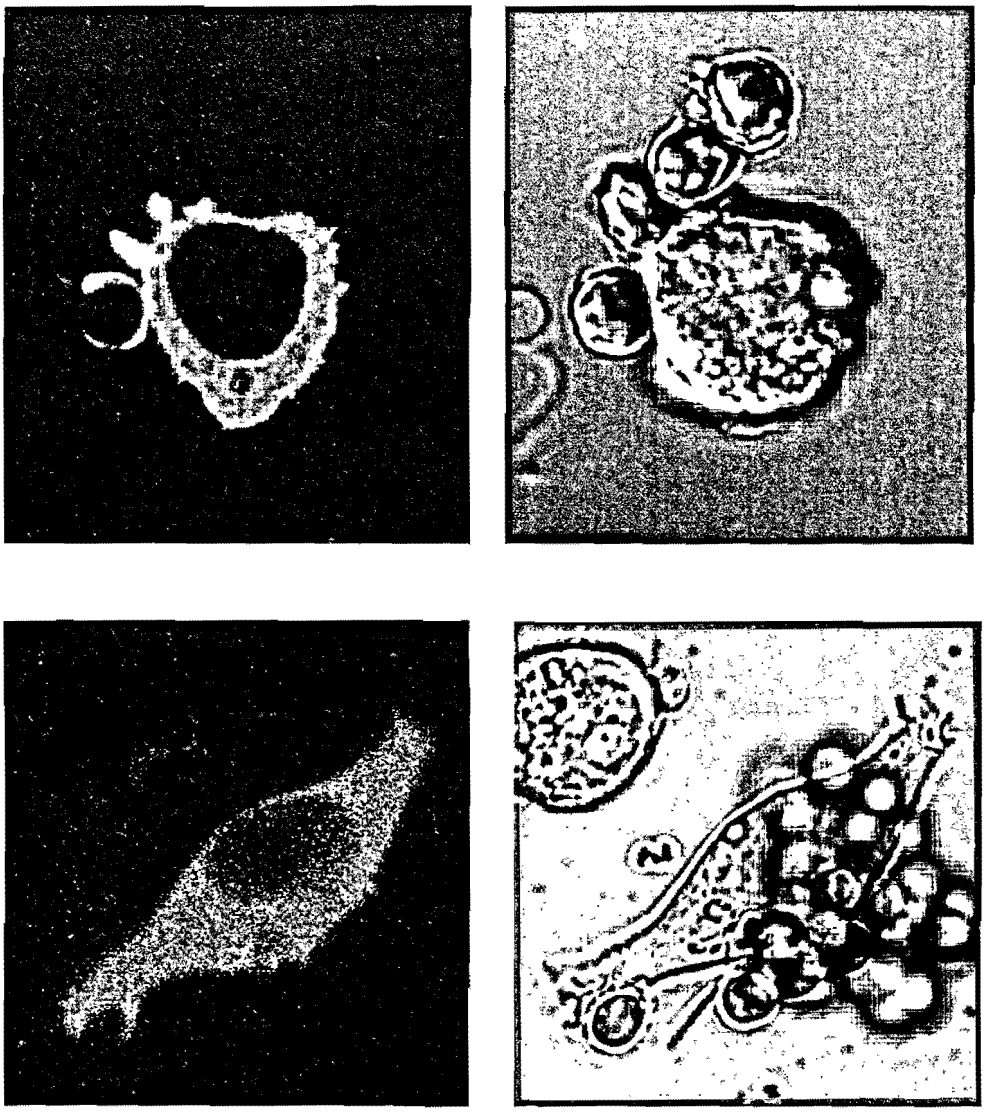
Panel B **pEGFP-PLC-β_4**

RAW 264.7 macrophage cells transfected with pEGFP-PLC-β_4.



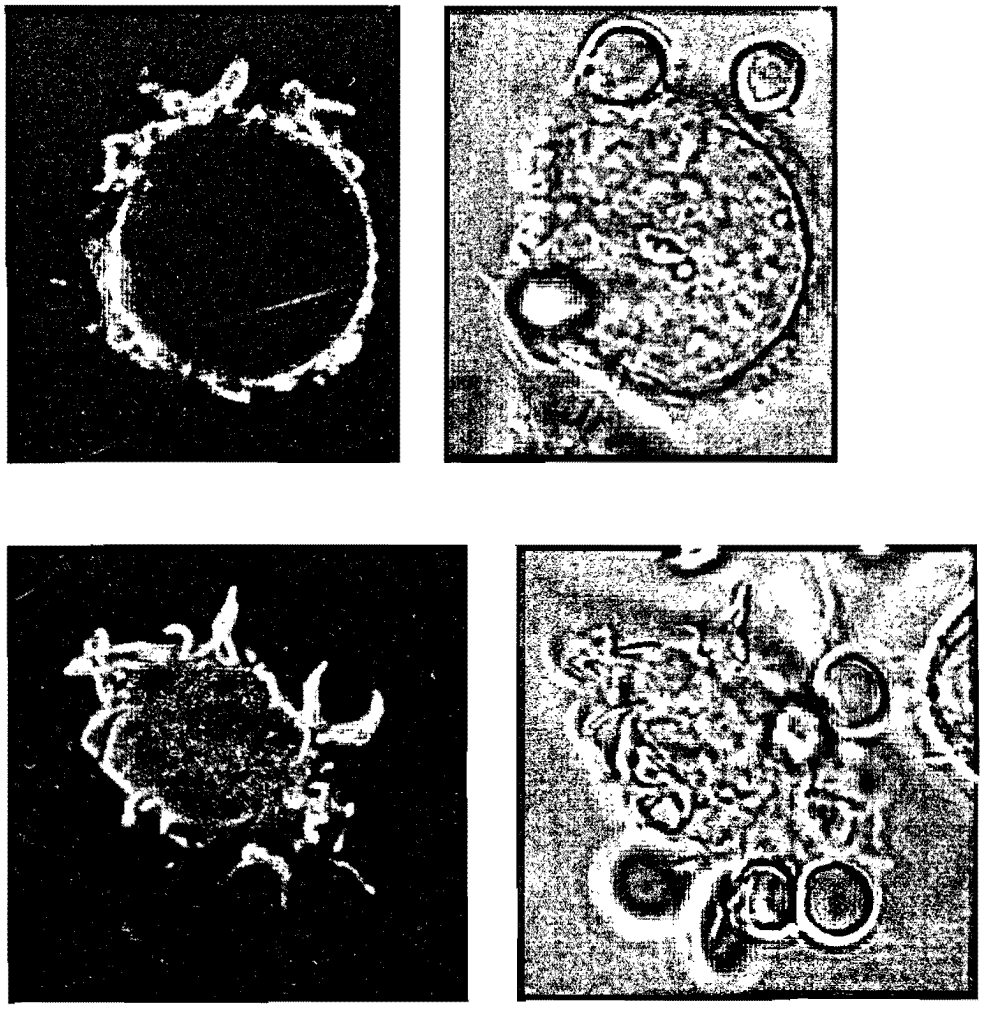
Panel C **pEGFP-PLC-γ_1**

RAW 264.7 macrophage cells transfected with pEGFP-PLC-γ_1.



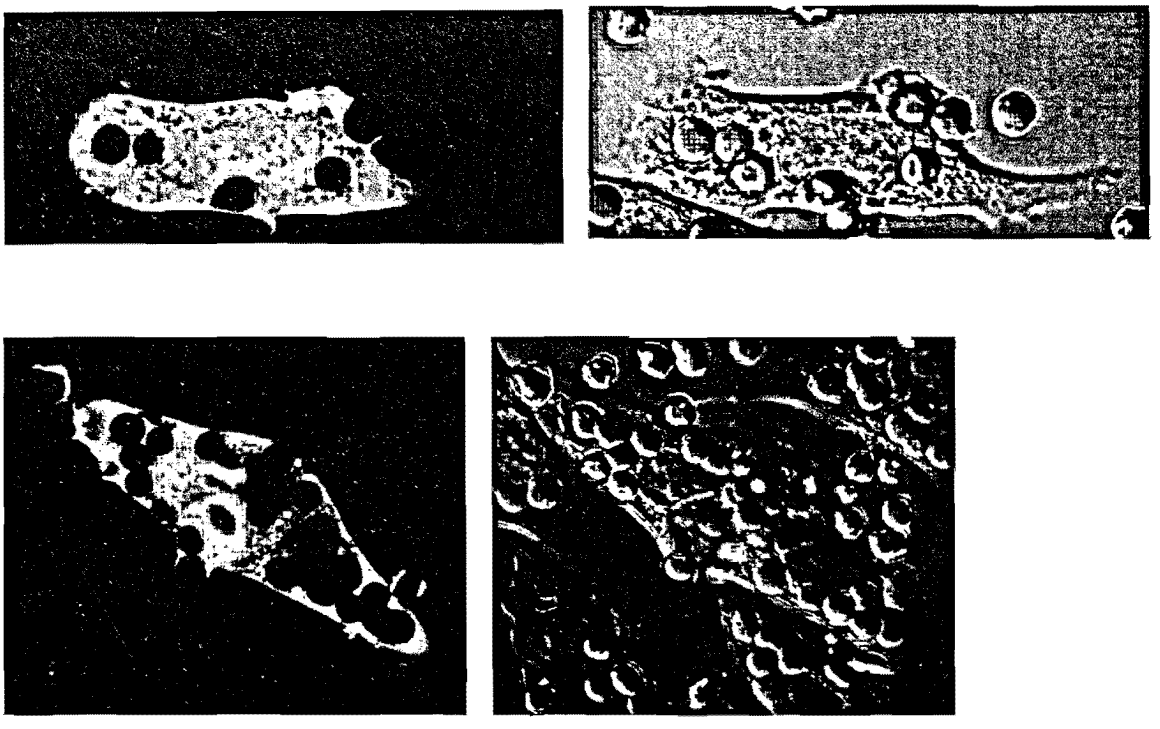
Panel D **$PH^{PLC-\delta 1}$-GFP**

RAW 264.7 macrophage cells transfected with $PH^{PLC-\delta 1}$-GFP.



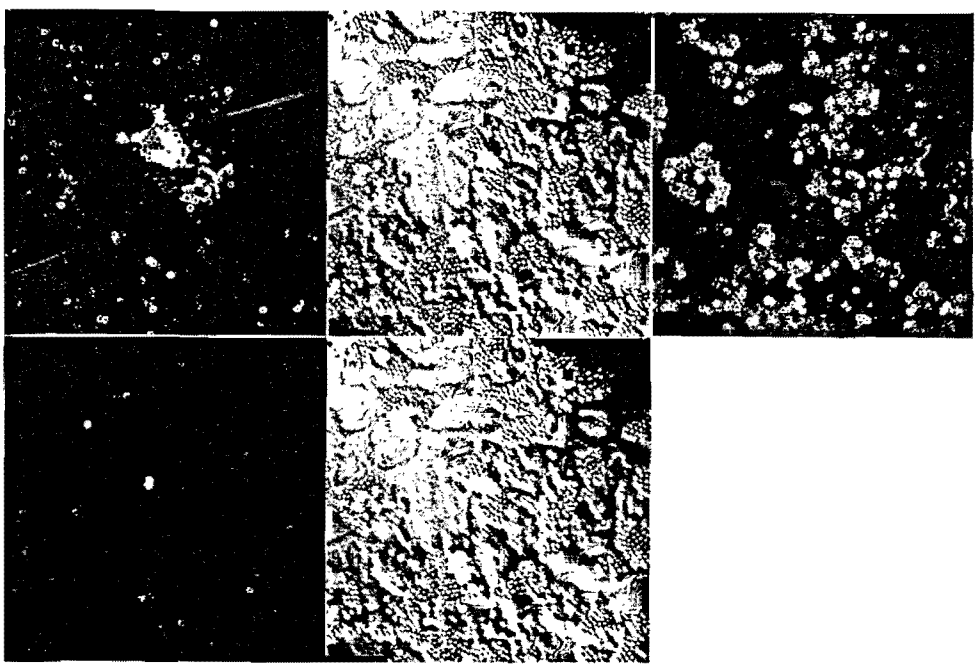
Panel E **Dominant negative PLC-δ_1 (E341R/D343R)**

RAW 264.7 macrophage cells transfected with dominant negative PLC-δ_1 (E341R/D343R).



Panel F Dominant negative PLC-δ_1 (E341R/D343R) and neighbouring non-transfected cells

Dominant negative PLC-δ1 (E341R/D343R) transfectants surrounded by non-transfected cells displays the dominant negative PLC-δ1 eating less IgG coated beads compared to neighbouring non-transfected cells. Beads inside the cells are shown in red (what cell has consumed), beads outside the cell are shown in blue, and the transfected dominant negative is displayed by the green cell (image of cells after eating for 2 hours). A summary of the dominant negative data is shown in the table below.

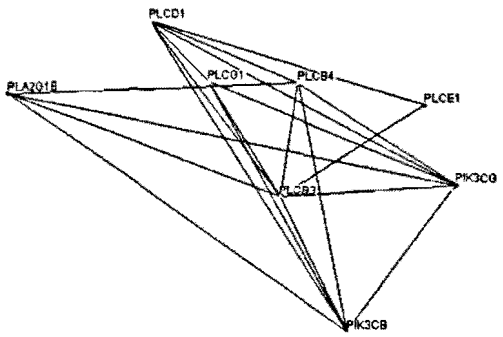


Average Number of Beads Consumed by Transfected Cells with eGFP, PLCd1-GFP or PLCd1-GFP-DN at 7.5, 10 and 30 minutes, as well as 2 hours					
Average beads comsumed by cell transfected with empty GFP at 7.5 minutes	red beads	4	Average beads comsumed by cell transfected with empty GFP at 30 minutes	red beads	18
Average beads comsumed by cell transfected with wild type PLCd1-GFP at 7.5 minutes	red beads	2	Average beads comsumed by cell transfected with wild type PLCd1-GFP at 30 minutes	red beads	21
Average beads comsumed by cell transfected with dominant negative PLCd1-GFP at 7.5 minutes	red beads	1	Average beads comsumed by cell transfected with dominant negative PLCd1-GFP at 30 minutes	red beads	13
Average beads comsumed by cell transfected with empty GFP at 10 minutes	red beads	4	Average beads comsumed by cell transfected with empty GFP at 2 hours	red beads	33
Average beads comsumed by cell transfected with wild type PLCd1-GFP at 10 minutes	red beads	6	Average beads comsumed by cell transfected with wild type PLCd1-GFP at 2 hours	red beads	37
Average beads comsumed by cell transfected with dominant negative PLCd1-GFP at 10 minutes	red beads	6	Average beads comsumed by cell transfected with dominant negative PLCd1-GFP at 2 hours	red beads	29

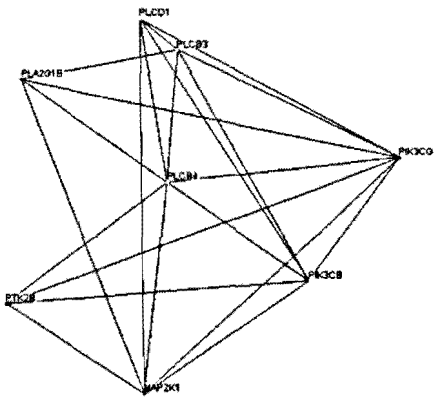
APPENDIX N – PHOSPHOLIPASE MODELS

Additional models visualized by Osprey show the direct interactions with the family of Phospholipase's, specifically PLC-β_3 (A), PLC-β_4 (B), PLC-γ_1 (C), PLC-δ_1 (D), PLC- ε_1 (E) and PLC like-2 (F).

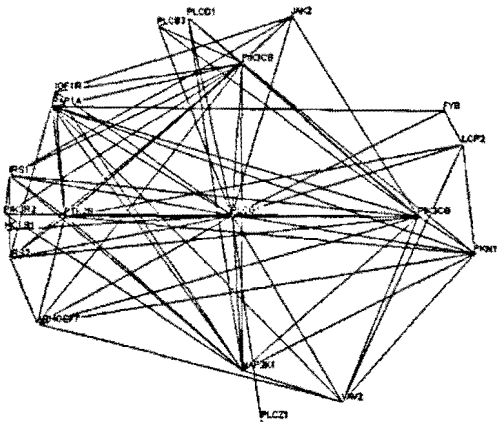
(A) PLC-β_3



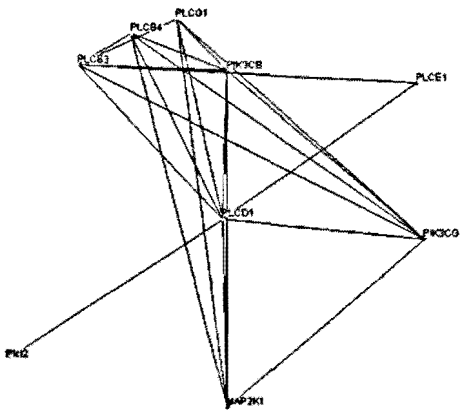
(B) PLC-β_4



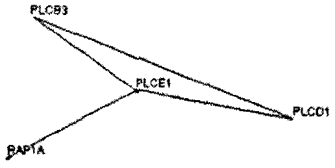
(C) PLC-γ_1



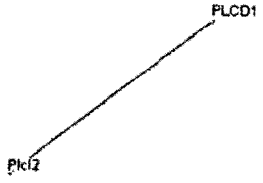
(D) PLC-δ_1



(E) PLC- ε_1



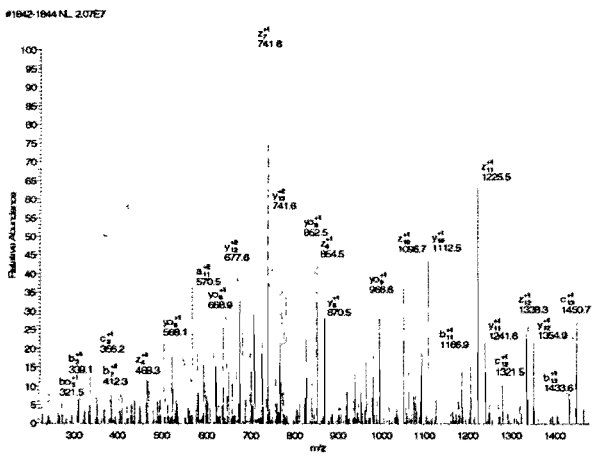
(F) PLC like-2



APPENDIX O – ADDITIONAL MASS SPECTRA (MAIN INTERACTORS)

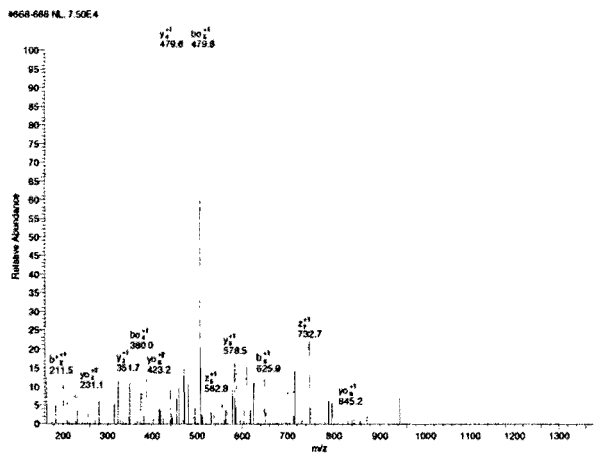
Additional mass spectra for the main interactors of Fcγ receptor-mediated phagocytosis as predicted by Cytoscape, Osprey and STRING. LC-MS/MS peptide sequences include Tyrosine-protein kinase SYK (SYK) for the 2+ -.NVLLVTQHYAK.- (MH+ 1286.51), Protein tyrosine kinase 2 beta (PTK2β) for the 2+-.INVAVKTCK.- (MH+ 976.22), Phosphatidylinositol 3-kinase, catalytic, beta polypeptide (PI3-Kcβ) for the 2+ -.RIGQFLFWHLR.- (MH+ 1473.75), Phosphatidylinositol 3-kinase, catalytic, gamma polypeptide (PI3-Kcγ) for the 3+ -.KGQWYEIYDRYQVVQTLDCLHYWK.- (MH+ 3136.53), Phospholipase C, beta 3 (PLC-β3) for the 2+ -.KAVLTR.- (MH+ 758.93), Phospholipase C, gamma 1 (PLC-γ1) for the 2+ -.HPLYRK.- (MH+ 813.97), Vinculin (VCL) for the 3+ -.GALAEARKIAELCDDPK.- (MH+ 1801.06), Mitogen activated protein kinase kinase 1 (MAP2K1) for the 2+ -.ISELGAGNGGVVFK.- (MH+ 1348.53), RAP1A, member of RAS oncogene family (RAP1A) for the 3+ -.SKINVNEIFYDLVR.- (MH+ 1710.96), Coronin, actin binding protein 1A (Coro1A) for the 2+ -.NLNAIVQK.- (MH+ 900.06), Protein-tyrosine kinase (EC 2.7.1.112) JAK2 (JAK2) for the 3+ -.WSFGTTLWEICSGGDKPLSALDSQR.- (MH+ 2756.04) and Vav2 oncogene (VAV2) for the 3+ -.FGLRNSELFDPFDLFDVRDFGK.- (MH+ 2635.91). The fragmentation spectra were obtained from LC-MS/MS in conjunction with the SEQUEST algorithm.

SYK



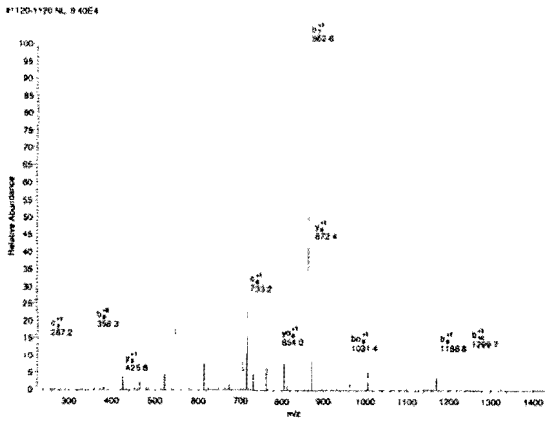
2+ -.NVLLVTQHYAK.-

PTK2β



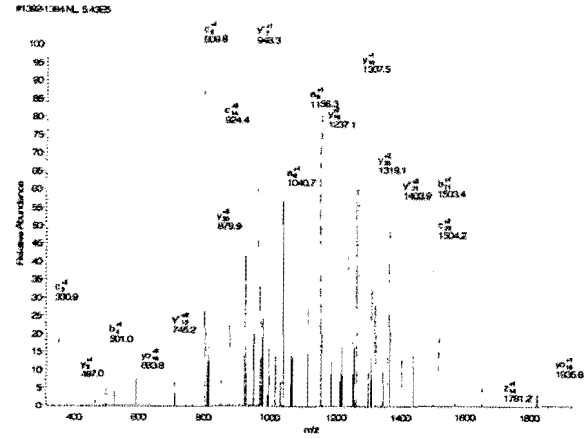
2+ -.INVAVKTCK.-

PI3-Kcβ



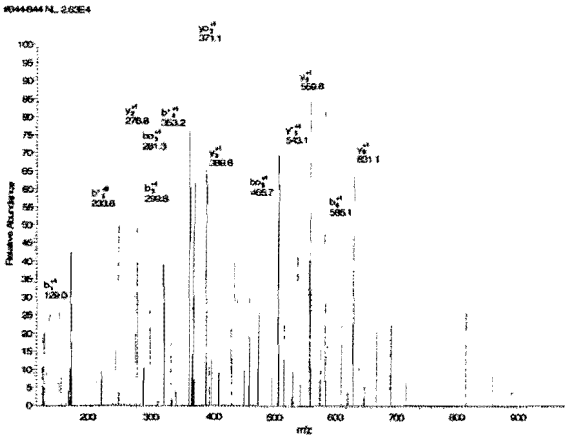
2+ -.RIGQFLFWHLR.-

PI3-Kcγ



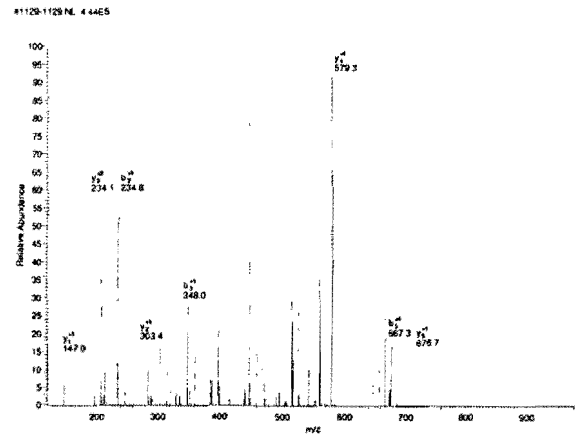
3+ -.KGQWYEIYDRYQVVQTLDCLHYWK.-

PLC-β3



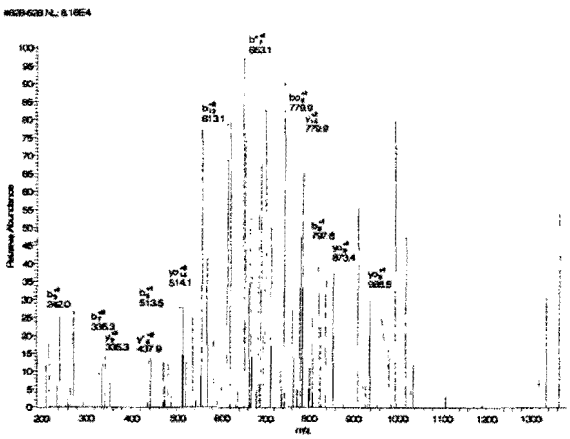
2+ -.KAVLTR.-

PLC-γ1



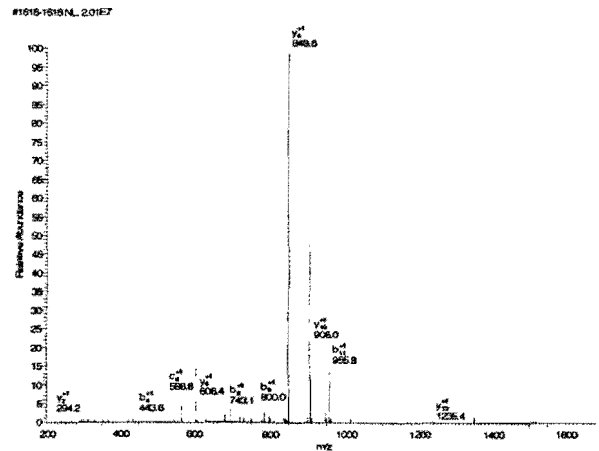
2+ -.HPLYRK.-

VCL



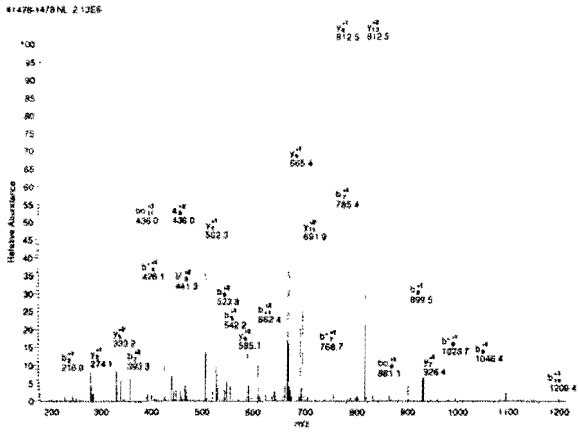
3+ -.GALAEARKIAELCDDPK.-

MAP2K1



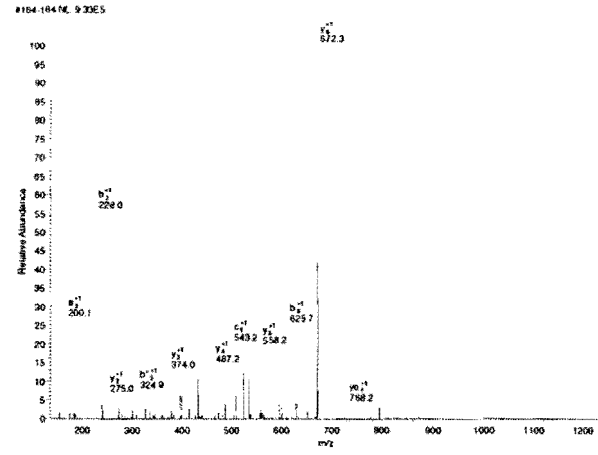
2+ -.ISELGAGNGGVVFK.-

RAP1A



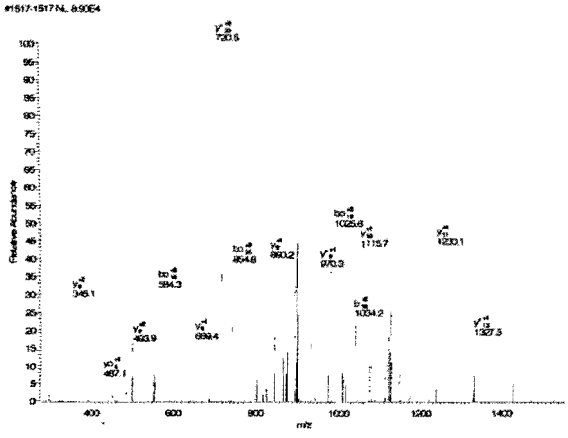
3+ -.SKINVNEIFYDLVR.-

Coro1A



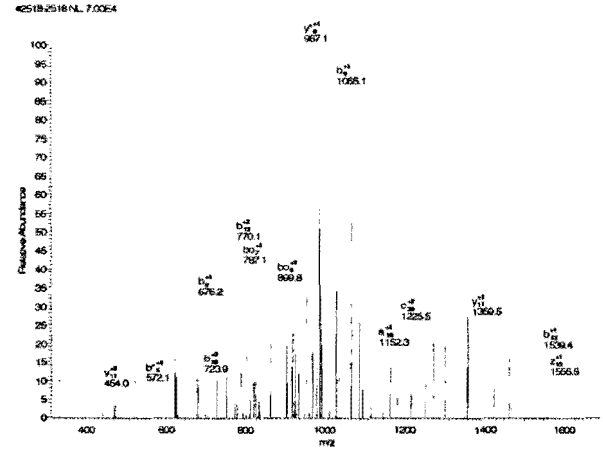
2+ -.NLNAIVQK.-

JAK2



3+ -.WSFGTTLWEICSGGDKPLSALDSQR.-

VAV2

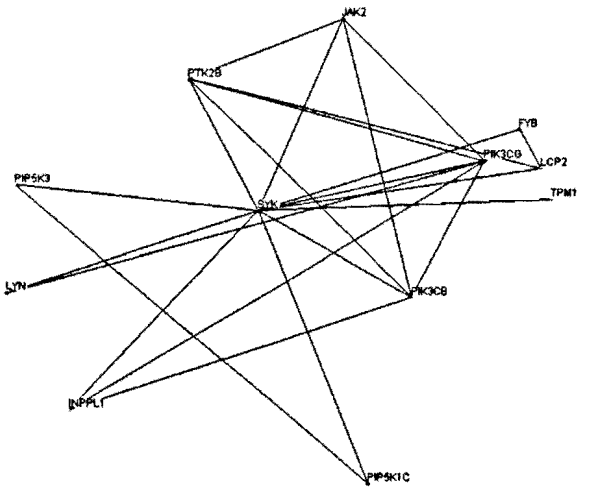


3+ -.FGLRNSELFDPFDLFDVRDFGK.-

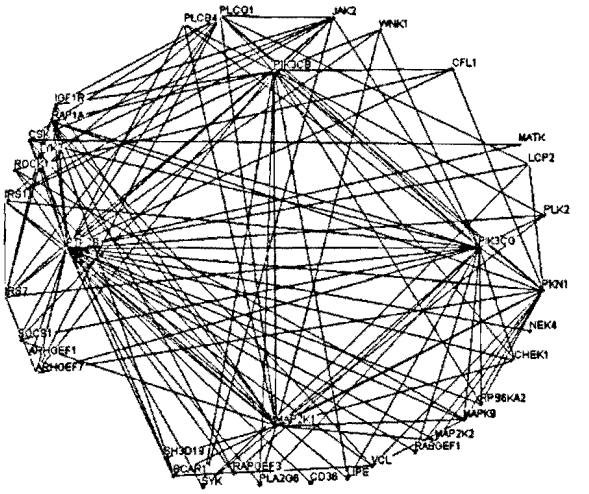
APPENDIX P – ADDITIONAL MODELS (MAIN INTERACTORS)

Additional models visualized by Osprey show the direct interactions with main interactors of Fcγ receptor-mediated phagocytosis as predicted by Cytoscape, Osprey and STRING. Main proteins identified include Tyrosine-protein kinase SYK (SYK), Protein tyrosine kinase 2 beta (PTK2β), Phosphatidylinositol 3-kinase, catalytic, beta polypeptide (PI3-Kcβ), Phosphatidylinositol 3-kinase, catalytic, gamma polypeptide (PI3-Kcγ), Phospholipase C, beta 3 (PLC-β_3), Phospholipase C, gamma 1 (PLC-γ_1), Vinculin (VCL), Mitogen activated protein kinase kinase 1 (MAP2K1), RAP1A, member of RAS oncogene family (RAP1A), Coronin, actin binding protein 1A (Coro1A), Protein-tyrosine kinase (EC 2.7.1.112) JAK2 (JAK2) and Vav2 oncogene (VAV2).

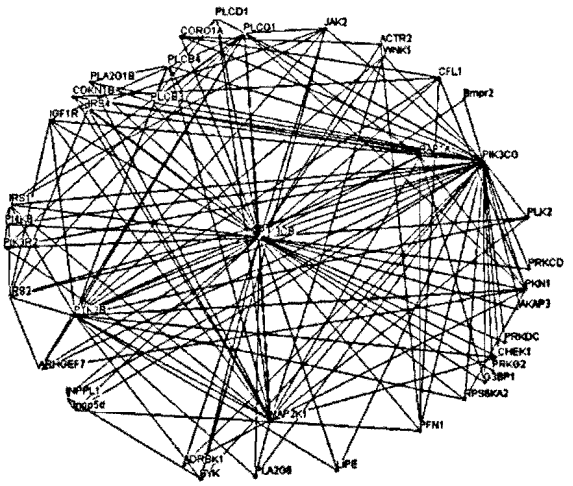
SYK



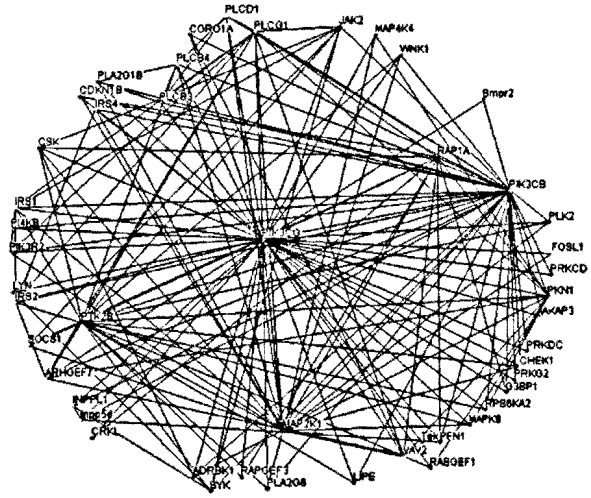
PTK2β



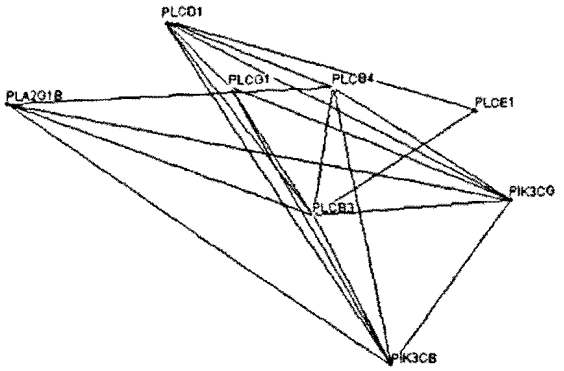
PI3-Kcβ



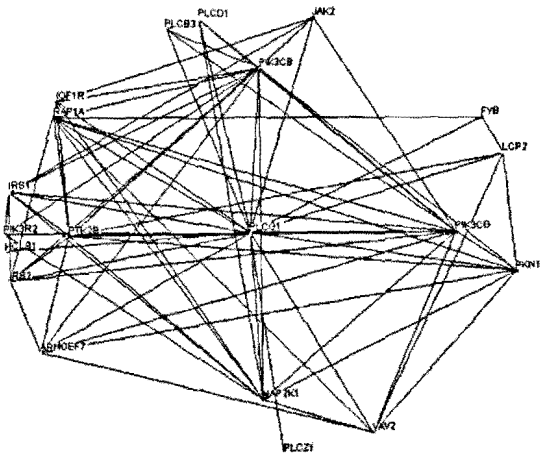
PI3-Kcγ



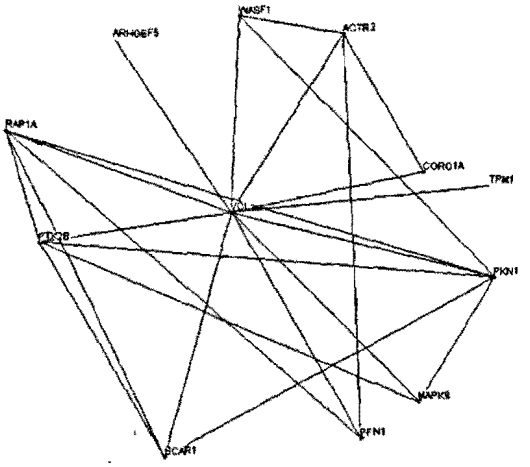
PLC-β_3



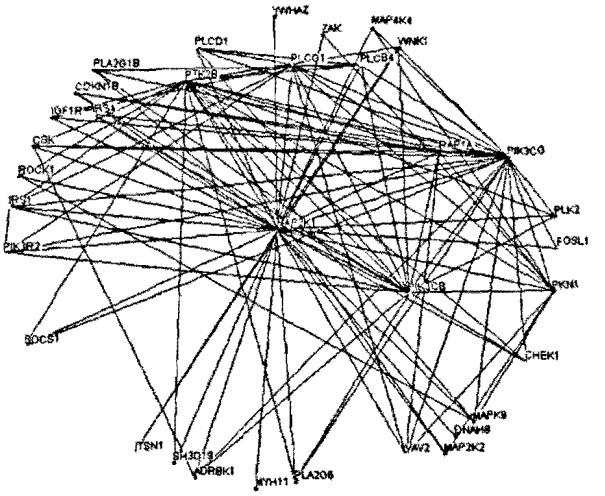
PLC-γ_1



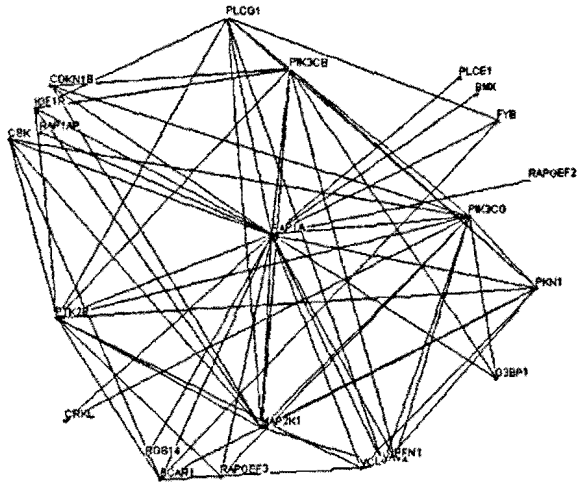
VCL



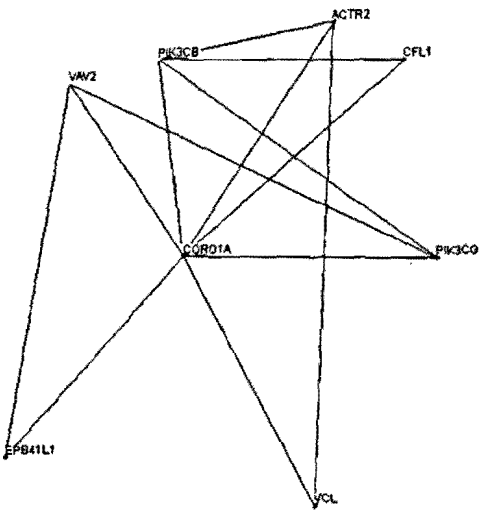
MAP2K1



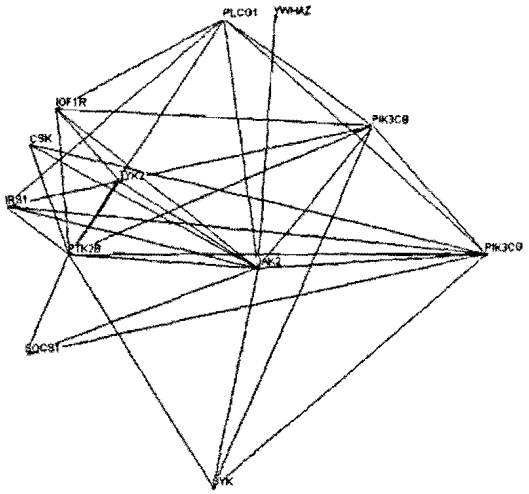
RAP1A



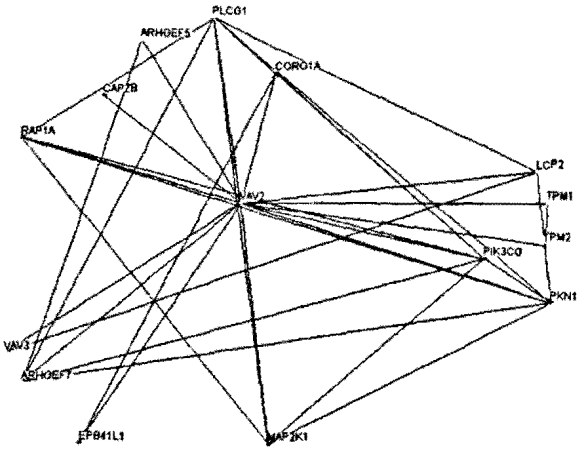
Coro1A



JAK2


PLCG1
YWHAZ
IGF1R
PIK3CB
CSK
LYN
IRS1
PTK2B
JAK2
PIK3CG
SOCS1
SYK

VAV2


PLCG1
ARHGEF5
CORO1A
CAP2B
RAP1A
LCP2
VAV2
TPM1
TPM2
PIK3CG
PKN1
VAV3
ARHGEF7
EPB41L1
MAP2K1