QP
S52
A27
F56
2008

**AFFINITY INTERACTIONS OF ACTIN WITH HS1 AND
Annexin I, II, IV, V AND VI IN RAW264.7 MACROPHAGES
IN VITRO AND IN THE Fc-RECEPTOR COMPLEX**

by

Angelica Kirsten Florentinus

Bachelor of Applied Science, Master of Science

(Ryerson University , 2008)

A thesis

presented to Ryerson University

in partial fulfillment of the

requirements for the degree of

Master

in the program of

Molecular Science

Toronto, Ontario, Canada, 2008

© Angelica Kirsten Florentinus, 2008

AUTHOR'S DECLARATION

"I, Angelica Kirsten Florentinus, hereby declare that I am the sole author of this thesis that is comprised entirely of my original scholarly work.

I authorize Ryerson University to lend this thesis to other institutions or individuals for the purpose of scholarly research.

Signature:

I further authorize Ryerson University to reproduce this thesis by photocopying or by other means, in total or in part, at the request of other institutions for the purpose of scholarly research

Signature:

Affinity Interactions of Actin with HS1 and Annexin I, II, IV, V and VI in RAW264.7 Macrophages *in vitro* and in the Fc-Receptor Complex

© Angelica Kirsten Florentinus, B SC, M Sc, 2008, Molecular Science, Ryerson University

ABSTRACT

Actin binding proteins HS1 and Annexin I, II, IV, V and VI proteins were examined in RAW macrophages *in vitro* using affinity chromatography, LC-MS/MS, western blot, cell staining and expression of fluorescent proteins. Actins and many related actin isoforms were observed in the phagosome. However, actins were also observed on polystyrene beads incubated with crude extracts readily bound to NHS affinity chromatography beads in the absence of anti-actin antibodies. Annexin II and V and the haematopoietic specific proteins HS1 (also called Lyn substrate) were prominently observed in isolated phagosomes and not observed in control beads incubated with crude extracts of RAW macrophages. Annexin II and V as well as G3BP, FLT1, FARP2, STARD13, RAB25 and FRAP1 were observed to bind actin in affinity chromatography experiments using LC-MS/MS and western blot. Cell staining and/or expression of GFP constructs showed that actin, HS1 and Annexin V prominently accumulate at the nascent Fc-receptor complex of RAW macrophages.

ACKNOWLEDGEMENTS

I would like to take this opportunity to express my sincere gratitude and appreciation to a variety of people who made this master's thesis possible.

Firstly, I would like to thank my supervisor Dr John Marshall for his knowledge, continued support and encouragement throughout my thesis project. I am grateful for the many opportunities that he has provided me to complete my undergraduate career in the Netherlands and during my graduate studies at Ryerson University.

Many thanks go to all my colleagues in the Protein Biochemistry laboratory at Ryerson University for their advice and support.

I am indebted to the School of Graduate Studies at Ryerson University for scholarship funding, which made my thesis financially possible.

Finally, special thanks go to Tommy, my friends and family for their strong support and understanding throughout all these years.

TABLE OF CONTENTS

AUTHOR'S DECLARATION	II
ABSTRACT	IV
ACKNOWLEDGEMENTS	V
LIST OF FIGURES	VIII
LIST OF TABLES	VIII
ABBREVIATIONS	IX
INTRODUCTION	1
HYPOTHESIS	10
OBJECTIVES	10
MATERIALS AND METHODS	12
Cell culture	12
Antibodies	12
DNA constructs	12
Immuno fluorescence staining.....	13
Competent cells (RbCl)	15
Transformation of competent DH5 α with GFP constructs.....	15
GFP transfections	16
Affinity chromatography	17
-Protein G/ Sepharose, Fast Flow column (1)	17
-N-hydroxysuccinimide (NHS)-activated Sepharose 4 Fast Flow	18
SDS-PAGE and Western Blotting.....	19
Blue Silver Stain.....	21
Silver Stain (Hahn's lab protocols)	21
Capturing of the Fc-receptor complex (LARC)	22
Liquid Chromatography Mass Spectrometry (LC-MS/MS)	22
Peptide correlation.....	23
Generation of protein-protein interaction model using iHOP	24
RESULTS	25
Capturing the Fc-receptor complex (LARC).....	26
Mass spectrometry of captured Fc-receptor complexes	27
Affinity Chromatography	31
-Protein G/ Sepharose, Fast Flow column	31
-N-hydroxysuccinimide (NHS)-activated Sepharose 4 Fast Flow	31
LC-MS/MS of proteins observed in affinity chromatography pull downs	38
Confocal microscopy	41

-Immuno fluorescent staining	41
-GFP transfection.....	42
Protein-protein interaction models (iHOP)	43
DISCUSSION.....	48
Capturing the Fc-receptor complex.....	48
Mass spectrometry of captured Fc-receptor complexes	48
Affinity Chromatography	50
LC-MS/MS of proteins observed in affinity chromatography pull downs	50
Confocal microscopy.....	51
-Immuno fluorescent staining.....	51
-GFP transfection.....	51
Protein-protein interaction models (iHOP)	52
CONCLUSION.....	53
REFERENCES	55
APPENDIX	60

List of figures

<i>FIGURE 1.</i> FC-RECEPTOR MEDIATED PHAGOCYTOSIS AND ACTIN REMODELING.....	2
<i>FIGURE 2.</i> CONSERVED DOMAINS OF HAEMATOPOIETIC CELL SPECIFIC LYN SUBSTRATE 1.....	3
<i>FIGURE 3.</i> CONSERVED DOMAINS FOR ANNEXINS.	4
<i>FIGURE 4.</i> FLOW CHART OF THE CONDUCTED EXPERIMENTS.....	9
<i>FIGURE 5.</i> CAPTURING THE FC-RECEPTOR COMPLEX.	26
<i>FIGURE 6.</i> CAPTURING THE FC-RECEPTOR COMPLEX.	27
<i>FIGURE 7A.</i> SPECTRA OF ACTIN, HS1 AND ANNEXINS OBSERVED IN THE CAPTURED FC-RECEPTOR COMPLEX BY LC-MS/MS.	29
<i>FIGURE 7B.</i> SPECTRA OF ACTIN BINDING PROTEINS OBSERVED IN THE CAPTURED FC-RECEPTOR COMPLEX.....	30
<i>FIGURE 8.</i> WESTERN BLOT ANALYSIS OF A PROTEIN G-HS1 AFFINITY CHROMATOGRAPHY IN THE PRESENCE OF NA-DEOXYCHOLATE AND N-OCTYL GLUCOSIDE.....	32
<i>FIGURE 10.</i> WESTERN BLOT ANALYSIS OF A NHS-ANTI-ACTIN AFFINITY CHROMATOGRAPHY COLUMN.....	34
<i>FIGURE 11.</i> FARP2, G3BP, RAB25, FRAP1, FLT1 AND STARD13 OBSERVED IN THE NHS AFFINITY CHROMATOGRAPHY PULLDOWNS BY LC-MS/MS.....	40
<i>FIGURE 12.</i> FARP2, G3BP, RAB25, FRAP1, FLT1 AND STARD13 OBSERVED IN CAPTURED FC-RECEPTOR COMPLEX BY LC-MS/MS.....	41
<i>FIGURE 13.</i> IMMUNO FLUORESCENCE STAINING OF ACTIN, HS1, ANXA1, ANXA2, ANXA4, ANXA5 AND ANXA6 IN RAW264.7 MACROPHAGES.	42
<i>FIGURE 14.</i> IMMUNO FLUORESCENCE STAINING OF RAB25, FERM, RHOGEF AND PLECKSTRIN DOMAIN PROTEIN 2 AND RHOGTPASE ACTIVATING PROTEIN IN RAW264.7 MACROPHAGES.	43
<i>FIGURE 15.</i> EXPRESSION OF GFP FUSION PROTEINS IN RAW 264.7 MACROPHAGES.	44
<i>FIGURE 16.</i> PROTEIN-PROTEIN INTERACTIONS OBSERVED FROM LITERATURE.....	45

List of tables

<i>TABLE 1.</i> PROTEIN-PROTEIN INTERACTIONS OBSERVED FROM LITERATURE.....	46
<i>TABLE 2.</i> NOVEL PROTEIN-PROTEIN INTERACTIONS OBSERVED FROM NHS AFFINITY CHROMATOGRAPHY COLUMNS.	47

Keywords: Fc-receptor complex, affinity capture, LC-MS/MS, Live-cell Affinity Receptor Chromatography, LARC, confocal microscopy, Actin, protein-protein interactions

ABBREVIATIONS

ADP	adenosine diphosphate
AnXA1	Annexin 1
AnXA2	Annexin 2
AnXA4	Annexin 4
AnXA5	Annexin 5
AnXA6	Annexin 6
APS	ammonium persulfate
Arp2/3 complex	Actin related protein 2/3 complex
ATP	adenosine triphosphate
DN	Dominant negative
EtOH	Ethanol
FARP2	FERM, RhoGEF and pleckstrin domain protein 2
Fc-receptor	Fragment crystallizable receptor
FBS	Fetal bovine serum
FLT1	FMS-like tyrosine kinase 1
FRAP1	FK506 binding protein 12-rapamycin associated protein 1
G3BP	ras-GTPase activating protein SH3-domain binding protein
GFP	green fluorescent proteins
HCl	hydrochloric acid
HS1	Hematopoietic lineage cell specific protein 1
GTPases	guanosine triphosphates
LARC	Live-cell affinity receptor chromatography
LC-MS/MS	liquid chromatography tandem mass spectrometry
NaCl	Sodium chloride
NHS	N-hydroxysuccinimide-activated Sepharose 4 Fast Flow
PIP2	phosphatidyl inositol biphosphate
RAB25	RAB25, member RAS oncogene family
Scar	Wasp related protein
SDS	sodium dodecyl sulfate
sRBC	sheep red blood cells
sRNAi	short interference double stranded RNA
STARD13	Rho GTPase-activating protein
Tris	tris(hydroxymethyl)aminomethane
WASp	Wiskott-Aldrich Syndrome protein

INTRODUCTION

Innate immunity is a significant first line of defense against infection. The innate immune system kills pathogens in a non-specific manner to protect the host and includes physical or chemical barriers such as the skin or stomach acid. The cells of the adaptive immune system also defend against infection (1, 2).

Phagocytosis involves the internalization of foreign particles by specialized cells and is a crucial component of the innate immune system (3). In Fc-receptor mediated phagocytosis, the receptor becomes activated upon binding to foreign particles that are opsonized with IgG (4). Clustering of activated Fc-receptors to the contact site stimulates cell signaling, local rearrangement of the actin cytoskeleton and remodeling of the membrane (5). Actin filaments are assembled at the contact site and push the cell membrane around the opsonized particle and engulf the foreign body (6). The formation of filamentous actin stimulates the production of superoxide by NADPH oxidase and intracellular vesicles will transport superoxide to the phagosome. The vesicles fuse with the phagosome and superoxide degrades the internalized particle (7).

Upon stimulation of the Fc-receptor, the production of active GTPases and PIP2 activates WASp/Scar. WASp/Scar are nucleation promoting factors that transport actin monomers and the Arp2/3 complex to the elongating barbed end of the actin filaments. WASp/Scar activates the Arp2/3 complex, which is responsible for the formation of actin filaments. The Arp2/3 complex connects actin monomers bound to ATP to the barbed ends of

the actin filaments. Upon binding, ATP hydrolyzes to ADP. The filaments grow and push the membrane forward until the barbed end is capped by capping proteins. At the pointed ends of the elongating actin filaments, Actin Depolymerizing Proteins (ADP) such as cofilin bind to the filaments and depolymerize the pointed end and cofilin catalyzes the exchange of ADP for ATP (8) (Figure 1).

Figure 1. Fc-receptor mediated phagocytosis and actin remodeling.
The Fc-receptor located on the surface of the cell binds to an opsonized particle, resulting in the phosphorylation of the Fc-receptor and activation of a cascade of intracellular events including remodeling of the actin cytoskeleton, vesicle fusion and oxidative burst.

Actin, expressed in all eukaryotic cells, is found in two states: monomeric actin or globular actin (G-actin), and filamentous actin (F-actin). Actin is a highly abundant protein of 42 kDa (9). Filaments form the actin cytoskeleton, which is responsible for cellular shape, resisting tension and cell motility (10). Rearrangement of the actin cytoskeleton is tightly

regulated by a large variety of proteins and is not completely understood yet (11). This paper will concentrate on actin-protein interactions mediated by Fc-receptor activation.

Haematopoietic cell specific Lyn substrate 1 (HS1) is a 486 amino acid, 75 kDa intracellular protein only expressed in haematopoietic cells (12). The conserved domains of HS1 consist of three and a half HS1 repeats and a SH3 domain (Figure 2). HS1 contains an acidic region (NTA) that binds and activates the Arp2/3 complex, promoting modest actin polymerization. HS1 also includes a coiled-coil domain and a helix-turn-helix domain that can both bind F-actin directly (13). HS1 connects the Arp2/3 complex with F-actin and therefore stabilizes the actin filaments (14). Inactive HS1 resides in the cytoplasm and translocates to the plasma membrane upon activation. HS1 is activated by phosphorylated Syk, which binds to HS1 and in turn phosphorylates at tyrosine residues 397 and 378 (15). Syk detaches from HS1, allowing Src to bind to the Src homology 2 (SH2) or 3 (SH3) domain of HS1 and phosphorylates at tyrosine residue 222, resulting in the activation of HS1 (16).

Figure 2. Conserved domains of Haematopoietic cell specific Lyn substrate 1. HS1 consists of three and a half HS1 repeats and a SH3 domain.

Members of the Annexin family are comprised of four annexin repeats (except annexin 6, which has eight repeats) (Figure 3), each of 70 amino acids in length, which form the annexin core. The core forms a tightly packed, α -helical, slightly curved disk with two distinct sides. The more spherical side contains the COOH-terminus contains Ca^{2+} binding sites that interact with the cell membrane through phospholipid binding, activation and phosphorylation

of annexins (17, 18). The more concave side remains open for the interaction of proteins with the NH₂-terminus (17). Each annexin has a structurally unique N-terminus, which is variable in length and establishes the different functions of the isoforms. Activation of annexins occurs upon binding of the N-terminus and phosphorylation of the protein. Annexins have been observed to be involved in intracellular events such as signal transduction and during endocytosis for membrane fusion (18) as well as ion channel activities (17), cell differentiation and growth (19). The presence of AnXA1-AnXA5 has previously been shown in phagosomes isolated from J774 macrophages (20).

Figure 3. Conserved domains for annexins.

A; The annexin core for annexin A1, A2, A4 and A5 consists of 4 annexin repeats each of 70 amino acids in length. B; Annexin A6 is the only member of the annexin family that has 8, instead of 4, annexin repeats.

Annexin A1 (AnXA1) is a 346 amino acid, 35kDa intracellular protein found in most eukaryotic cells. AnXA1, as well as AnXA2, are able to cross-link membranes due to their ability to aggregate membrane vesicles (21). AnXA1 contains 4 Ca²⁺-binding sites and interacts with the epidermal growth factor receptor protein kinase when Ca²⁺ concentrations are elevated. Upon binding, AnXA1 becomes tyrosine phosphorylated at residue 21 (22). AnXA1 becomes serine and threonine phosphorylated upon binding to protein kinase C at residue 24 (threonine), 27 and 28 (serine) (23) and forms a complex with its substrate S100A11 in a Ca²⁺-

dependent manner, which binds and inactivates cytosolic phospholipase A (cPLA) (24). AnXA1 has been demonstrated to interact with actin as well as selectin, integrin A4, epithelial growth factor receptor and formyl peptide receptor (25).

Annexin A2 (AnXA2) is a 338 amino acid, 34kDa intracellular protein and exists in monomeric and heteromeric forms. Monomeric AnXA2 is located in the cytosol and the heterotetramer is found at the membrane cytoskeleton. The heterotetramer consists of two AnXA2 and two S100A10 (S100 calcium binding protein A10) molecules, which are bound to the NH₂-terminus of AnXA2, and interacts with other proteins (26). In response to extracellular stimulation, AnXA2 is tyrosine phosphorylated by pp60^{src} (27) and protein kinase C (28). AnXA2 has been shown to be associated with the regulation of contact between cells through complex formation with cadherin and Rac1/p21-associated kinase (29). AnXA2 has been observed to be involved in the assembly of actin-rich tight junctions (30) as well as to directly bind actin and interact with the actin cytoskeleton (31). AnXA2 is also known to bind insulin receptors, caveolin 1, tissue plasminogen activator, tenascin C and angiostatin (25).

Annexin A4 (AnXA4) is a 321 amino acid, 35 kDa intracellular, cytosolic protein. AnXA4 has been demonstrated to regulate vesicle aggregation and trafficking in a Ca²⁺-dependent and phospholipid binding dependent manner. AnXA4 becomes inactivated when phosphorylated by protein kinase C (32). In the cytoplasm, soluble, monomeric AnXA4 interacts with other AnXA4 monomers to form a trimer that binds to the inner leaflet of the cell membrane (33). Upon extracellular stimulation, AnXA4 is translocated from the cytosol to the plasma membrane. AnXA4 is known to inhibit Ca²⁺-activated regulation of the chloride ion

efflux (32) (34). In a study by Diakonova *et al* (1997), AnXA4 levels were demonstrated to increase during the maturation of phagosomes in J774 macrophages, suggesting a role for AnXA4 in phagocytosis (20). AnXA4 is also known to interact with glycoprotein 2 and lectins (25).

Annexin A5 (AnXA5) is a 320 amino acid, 36 kDa intracellular protein. AnXA5 binds and stabilizes the plasma membrane by binding to the membrane more tightly as a result of elevations of Ca^{2+} levels (35) and is involved in membrane aggregation. Binding of the N-terminus of AnXA1 to the core of AnXA5 stimulates the activation of AnXA5 (36) and this results in an interaction between repeat I/IV and II/III in AnXA5. Activated AnXA5 is translocated to the cortical membrane cytoskeleton where it interacts with the plasma membrane and γ -actin (37). Ca^{2+} activity of AnXA5 is inhibited by benzothiazepine K201, which suppresses the joining of the two lobes formed by AnXA5 repeat I/IV and II/III (38). Conserved arginine, serine and threonine residues and unique tryptophan are proven to be crucial for AnXA5 activities (39). AnXA5 inhibits protein kinase C activity, whereas most annexins are phosphorylated by protein kinase C (40). AnXA5 has also been shown to interact with vascular endothelial growth factor receptor 2, collagen type 2, integrin B5, helicase, DNA (cytosine-5-)methyltransferase 1 and modulator of immune recognition (25).

Annexin A6 (AnXA6) is a 673 amino acid, 67 kDa intracellular protein and is so far the only member of the annexin family with eight, rather than four, annexin repeats. Like many annexins, AnXA6 promotes aggregation of membrane vesicles in a Ca^{2+} -dependent manner. Because of the longer and more flexible double annexin core of AnXA6, it contains a second

module for Ca^{2+} -dependent phospholipid binding for membrane interactions (41) such as budding of clathrin coated vesicles. AnXA6 interacts with cysteine proteases during the final stages of vesicle budding, resulting in separation of the vesicle from the spectrin membrane (42). Complex formation of AnXA6 with its substrates S100A1 and S100B result in the inactivation of S100A1 and S100B. S100A1 and S100B are known to inhibit the assemblage of intermediate filaments composed of glial fibrillary acidic protein and desmin (43). AnXA6 is also known to form a complex with membranes and the actin cytoskeleton (44) and is involved in the regulation of low density lipoprotein (LDL) receptor-mediated endocytosis and degradation of LDL (45). Activation of the Ras signaling pathway is initiated by AnXA6 which promotes accumulation of GTPase-activating protein p120GAP and protein kinase C to the cell membrane (46).

Remodeling of the actin cytoskeleton plays an important role in phagocytosis. Rearrangement of the actin cytoskeleton is tightly regulated by a large variety of different proteins and is not completely understood yet (11). Before complex protein-protein interactions that are involved during Fc-receptor mediated phagocytosis can be examined, the basic and fundamental interactions between actin and actin binding proteins need to be understood first. Therefore, six proteins (HS1 and Annexin A1, A2, A4, A5 and A6) that are known to interact with actin were selected for further characterization and localization of these proteins during Fc-receptor mediated phagocytosis.

Figure 4 shows the flow chart of the experiments that were conducted. RAW 264.7 macrophages were grown in AMEM complemented with 5% FBS and were exposed to

opsonized latex beads to activate the Fc-receptor. Isolated Fc-receptor complexes were used for SDS-PAGE and Western blotting as well as for Mass spectrometry. For another experiment, RAW cells were lysed using a French press or by freeze/thaw cycles. Lysates were used for affinity chromatography and collected elution fractions were subjected to Mass spectrometry. Mass spectrometry results were used to generate protein-actin or protein-protein interaction models using I-Hop. RAW cells were also cultured on glass microscope slide cover slips and incubated with latex beads or sheep red blood cells to activate the Fc-receptor, fixed and stained with specific antibodies and imaged by using a laser confocal microscope. Live cells expressing fluorescent proteins were also incubated with latex beads or sheep red blood cells to activate the Fc-receptor and the accumulation of Actin, HS1 and AnXAs at the nascent Fc-receptor complex were imaged using a laser confocal microscope.

Figure 4. Flow chart of the conducted experiments.

1, RAW cells are exposed to opsonized particles to stimulate phagocytosis. Once Fc-receptor complexes were formed, the Fc-receptor complexes were isolated and subjected to SDS-PAGE and Western blot or Mass spectrometry. 2, RAW cells were lysed and used for affinity chromatography experiments. Proteins that were eluted from the columns were analyzed by SDS-PAGE and Western blot or Mass spectrometry. Mass spectrometry results were compared to the literature in order to generate a protein-protein interaction model.

HYPOTHESIS

The hypothesis of this thesis is that actin and actin binding proteins participate in the formation of the Fc-receptor complex prior to internalization. Actin and actin binding proteins are predicted to accumulate at the site of the nascent Fc-receptor complex by LC-MS/MS and confocal microscopy.

OBJECTIVES

- Show the presence of actin binding proteins at the Fc-receptor complex by LC-MS/MS
- Examine the interaction with actin *in vitro*
- Confirm the presence and localization of these proteins to the Fc-receptor by immuno staining and GFP

This document reports the presence of actin binding proteins at the Fc-receptor complex by LC-MS/MS and the interactions of actin *in vitro*. Immuno stain and GFP fusion proteins was used to confirm the presence and localization of actin binding proteins to the Fc-receptor. A method to analyze protein-protein interactions in buffers directly compatible with mass spectrometry was used.

Standard biochemical techniques were used to approach the objectives. The novel LARC method was used to isolate the captured Fc-receptor complex prior to LC-MS/MS and Western blot analysis. Standard and novel approaches were used for the protein-protein interactions *in vitro* using standard buffers (containing detergents) and novel buffers (without

detergents) as loading and elution buffers for the affinity chromatography columns. The purpose of the novel approach was to develop a method for purifying proteins over an affinity chromatography column with mass spectrometry compatible buffers.

MATERIALS AND METHODS

Cell culture

RAW 264.7 cells derived from mice were obtained from ATTC and grown in Alpha Modification of Eagle's Medium 1x (AMEM Multicell, Wisent Bioproducts, St-Bruno, Quebec, Canada) supplemented with 5% Fetal Bovine Serum in an incubator at 7% CO₂ at 37°C.

Antibodies

Monoclonal mouse anti- β -actin antibodies were purchased from Ambion (Austin, TX, USA). Monoclonal mouse anti-HS1 antibodies were obtained from Stressgen (Michigan, USA). Polyclonal goat anti-Annexin A1 antibodies were from Santa Cruz Biotechnology (Santa Cruz, CA, USA). Monoclonal mouse anti-Annexin A2 and monoclonal mouse anti-Annexin A6 antibodies were purchased from BD Biosciences Pharmingen (Franklin Lakes, NJ, USA). Polyclonal rabbit anti-Annexin A4 and polyclonal rabbit anti-Annexin A5 were obtained from Abcam (Cambridge, MA, USA).

DNA constructs

A plasmid encoding β -actin-GFP was a gift from Dr B. Wehrle-Haller (Centre Médical Universitaire, Geneva, Switzerland). A plasmid encoding HS1-GFP was provided by Xi Zhan (Dept. of Pathology, Baltimore, MD, USA). A plasmid encoding Annexin A1-GFP was a gift from Dr. U. Rescher (Center for Molecular Biology of Inflammation, Institute for Medical Biochemistry, Münster, Germany). A plasmid encoding Annexin A2-GFP was provided by Dr. S.M. Nielsen-Preiss (University of Colorado Health Sciences Center, Department of

Orthopaedics, Denver, CO, USA). A plasmid encoding Annexin A4-GFP was a gift from Dr. R. Walther (Klinikum der Ernst-Moritz-Arndt-Universität, Institut für Medizinische Biochemie und für Molekularbiologie, Greifswald, Germany). A plasmid encoding Annexin A5-GFP was provided by Dr. C. Broaddus (University of California, San Francisco, CA, USA). Plasmids encoding Annexin A6-1-GFP and Annexin A6-2 were a gift from Dr. J. Bandorowicz-Pikuła (Department of Biochemistry, Nencki Institute of Experimental Biology, Polish Academy of Sciences, Warsaw, Poland).

Immuno fluorescence staining

Antibody staining with specific primary antibodies and Cy3 labeled secondary antibody was performed on fixed RAW 364.7 macrophages in order to determine the localization of actin, HS1 and the annexins. Images were obtained using a 510 zeta laser confocal microscope with a 543 nm He/Ne laser (Zeiss). Prior to fixation, cells were incubated with sRBC or micro beads to induce phagocytosis. Antibody staining confirmed the localization of the proteins of interest during Fc-receptor mediated phagocytosis. RAW 264.7 cells were grown on glass cover slips (Fisher Scientific, Pittsburgh, PA, USA) in a 6 well plate (BD Biosciences Pharmingen, Franklin Lakes, NJ, USA) for 48 hours in AMEM with 5% FBS. Cells were then incubated with sheep red blood cells (sRBC) (MP Biomedicals, LLC, Solon, OH, USA) coated with rabbit anti-sRBC antibodies (ICN Biomedicals Inc, Aurora, OH, USA) for cell staining with primary antibody derived from mouse or goat, or with latex beads (2µm, Bangs Laboratories Inc, Fisher, IN, USA) opsonized with human immunoglobulin G (hIgG) were used for cell staining (3) with primary antibodies derived from rabbit. 50 µl sRBC plus 5 µl rabbit anti-sRBC was resuspended in 150 µl PBS (Bioshop, Burlington, ON, Canada) and

incubated at 37°C for 30 minutes. 5 µl latex beads with 4 µl hIgG were suspended in PBS and incubated at room temperature for 10 minutes. Cells were incubated with 30 µl of the sRBC suspension or latex beads at 37°C for 5 and 7.5 minutes to induce phagocytosis. After incubation with sRBC or latex beads, the 6 well plate was placed on ice and cells were fixed with 4% paraformaldehyde (Canemco, St. Laurent, Quebec, Canada) for 2 hours at room temperature. Cover slips were washed twice with 5% glycine in PBS (Bioshop, Burlington, ON, Canada) for 10 minutes prior to permeabilizing and blocking with 5% skim milk and 1% donkey serum in PBS-0.1% Triton X100 (Bioshop, Burlington, ON, Canada) at room temperature for 1 hour with constant gentle agitation. Cells were incubated with the primary antibody (1 in 25 dilution in PBS-0.1% Triton X100) at room temperature for 1 hour. Cover slips were washed 3 times for 10 minutes each with 2 ml PBS-0.1% Triton X100 per well at room temperature with constant gentle agitation. Cells were incubated with 2 ml secondary Cy3-labeled antibody (1 in 20,000 dilution in PBS-0.1% Triton X100) (Jackson ImmunoResearch Laboratories Inc, Hornby, ON, Canada) per well in the dark at room temperature for 1 hour with constant gentle agitation. Cover slips were washed 3 times for 10 minutes each with PBS at room temperature in the dark with constant gentle agitation prior to mounting the cover slips on microscope slides (Fisher Scientific, Pittsburgh, PA, USA) using Dako Cytomation Fluorescent Mounting Medium (Dako North America Inc, Carpinteria, CA, USA). Slides were dried at room temperature in the dark for 24 hours and stored at -20°C. Images were recorded using a 510 zeta laser confocal microscope with a He/Ne 543 nm laser (Zeiss).

Competent cells (RbCl)

Competent bacterial cells were prepared according to the following procedure. A pipette tip was dipped into an *E. coli DH5α* stock and resuspended into 5 ml of sterile Difco LB broth (Becton, Dickinson and Company, Sparks, MD, USA) and incubated over night (O/N) at 37°C at 300 rpm. A streak plate (Difco LB broth with agar (Becton, Dickinson and Company, Sparks, MD, USA)) was made from the O/N culture and incubated (O/N) at 37°C. A single colony was inoculated into 5 ml LB broth and incubated for 2 hours at 37°C at 300 rpm until the cell suspension had reached an Optical Density of 0.3 (OD₅₅₀ 0.3). 100 ml pre-warmed LB broth was inoculated and incubated for 2-3 hours at 37°C at 300 rpm until the cell suspension had reached an OD₅₅₀ 0.45. The cell suspension was chilled on ice and centrifuged for 5 minutes at 4°C at 3500 rpm or 6000g. The pellet was resuspended in 40 ml (2/5 of the original volume) TfbI buffer (30 mM potassium acetate, 10 mM CaCl₂·2H₂O, 100 mM RbCl₂, 50 mM MnCl₂·4H₂O, add glycerol to 15% (v/v) in H₂O, adjust pH to pH 5.8 with 10% acetic acid) and left on ice for 5 minutes. The cell suspension was centrifuged for 5 minutes at 4°C at 3500 rpm or 6000g. The pellet was resuspended in 4 ml (1/25 of the original volume) TfbII buffer (10 mM MOPS, 75 mM CaCl₂·2H₂O, 10 mM RbCl₂, 15% glycerol (v/v), adjust pH to pH 6.5 with KOH) and left O/N at 4°C. 10% sterile DMSO was added to the cell suspension and 200 µl aliquots were stored at -80°C.

Transformation of competent DH5α with GFP constructs

Competent bacterial cells were thawed on ice. 100 µl cells were incubated with 1 µl DNA for 30 minutes on ice. Cells were heat shocked for 90 seconds at 42 °C and placed on ice for 2 minutes. Cells were then suspended in 1 ml LB broth and incubated for 1 hour at 37°C at

300 rpm. 150 μ l of the cell suspension was plated on LB plates containing no antibiotics, kanamycin (50 μ g/ml) (Cellgro, Herndon, VA, USA) or ampicillin (50 μ g/ml) (VWR international, Mississauga, ON, Canada) and incubated O/N at 37°C. A single colony was inoculated in 2 ml pre-warmed LB broth containing the appropriate antibiotic (50 μ g/ml) and incubated for 8 hours at 37°C at 300 rpm. 20 μ l of the cell suspension was resuspended in 5 ml LB broth containing the appropriate antibiotic (50 μ g/ml) and incubated O/N at 37°C at 300 rpm. 20 μ l of the cell suspension was resuspended in 100 ml LB broth containing the appropriate antibiotic (50 μ g/ml) and incubated for 10 hours at 37°C at 300 rpm. 850 μ l of the cell suspension was resuspended in 150 μ l sterile glycerol and stored at -80°C. The rest of the cell suspension was centrifuged for 15 minutes at 4°C at 6000g. MaxiPrep kits (Qiagen, Mississauga, ON, Canada) were used to isolate the DNA. DNA concentrations were determined with a DNA spectrometer (VWR international, Mississauga, ON, Canada).

GFP transfections

Expression of GFP fusion proteins in live cells was also imaged using a 510 zeta laser confocal microscope with a 543 nm He/Ne laser (Zeiss). Transfected cells were incubated with sRBC or opsonized micro beads to induce phagocytosis and localization of the proteins was monitored.

RAW 264.7 cells were grown on glass cover slips in a 6 well plate for 36 hours in AMEM with 5% FBS. 3 μ l Fugene6 HD Transfection Reagent (Roche, Mississauga, ON, Canada) was mixed with 100 μ l AMEM and added to 1 μ g of DNA and incubated at room temperature for 6-8 hours. 100 μ l of the DNA/Fugene6/AMEM mixture was added to one well and incubated O/N at 37°C. Opsonized sRBC (30 μ l sRBC, 150 μ l PBS, 5 μ l rabbit-anti-sRBC)

or latex beads (30 μ l latex beads, 150 μ l PBS, 5 μ l hIgG) were added to the cells to induce phagocytosis and images were recorded using a 510 zeta laser confocal microscope with an Ar 488 nm laser (Zeiss).

Affinity chromatography

Affinity chromatography columns were constructed and run under various conditions to optimize binding and elution. Antibodies or pure protein were linked to NHS beads and RAW lysates were run through the column. Fractions were collected and analyzed using Western blotting or by LC-MS/MS. 9% SDS-PAGE gels were prepared and used to separate proteins and gels were stained with either Blue Silver Stain or Silver nitrate Stain. For other experiments, the separated proteins in the gels were transferred to a Polyvinylidene Fluoride (PVDF) membrane for Western blotting.

Elution fractions from the NHS affinity columns as well as the captured Fc-receptor complexes using the novel LARC method were analyzed by LC-MS/MS. Spectra for the proteins of interest were collected from this data.

-Protein G/ Sepharose, Fast Flow column (1)

RAW 264.7 cells were grown, harvested and collected. Protease inhibitors such as 4-(2-aminoethyl)-benzene-sulfonyl fluoride hydrochloride (Sigma, St. Louis, MO, USA) and a protease inhibitor cocktail for use with mammalian cells and tissues (Sigma, St. Louis, MO, USA) were added to the cell suspension. Cells were lysed using a French press. A Protein G/ Sepharose, Fast Flow (Sigma, St. Louis, MO, USA) column was made in a pipette tip with glass wool. 40 μ l 50% slurry was used to prepare one column and left on ice for 1 hour to

settle. The column was washed with 1 ml RIPA buffer (10 mM Tris-HCl pH 7.4, 15 mM potassium chloride, 1% sodium deoxycholate (w/v), 1% Triton X-100 (v/v), 0.1% SDS (w/v) in PBS). 80 μ l Monoclonal mouse anti-HS1 was diluted in PBS (1 in 4) and run through the column by gravity on ice 3 times. The column was washed with 2 ml RIPA buffer on ice. 200 μ l cell lysates were diluted (1 in 10) in RIPA buffer and run through the column by gravity on ice 3 times. The column was washed with 0.5 ml RIPA buffer and protein complexes were eluted off the column with 100 μ l 2% SDS. The experiment was repeated with a RIPA buffer without Triton X-100 and 0.1% SDS. All fractions that came off the column were collected and used for Western blotting.

-N-hydroxysuccinimide (NHS)-activated Sepharose 4 Fast Flow

RAW 264.7 cells were grown, harvested and collected. Protease inhibitors such as 4-(2-aminoethyl)-benzene-sulfonyl fluoride hydrochloride (Sigma, St. Louis, MO, USA) and a protease inhibitor cocktail for use with mammalian cells and tissues (Sigma, St. Louis, MO, USA) were added to the cell suspension. Cells were lysed using a French press or by freeze/thaw cycles. 100 μ l NHS-activated Sepharose 4 Fast Flow was used to prepare one column. Preparation of the resin was performed on ice. The resin was washed with 5 ml H₂O and incubated with 10-15 medium volumes (1 ml) ice cold 1 mM HCl for 15 minutes. The resin was mixed with 50 μ g antibody or protein and incubated O/N at 4°C. Non-specific binding sites were blocked with 0.5 M ethanolamine, 0.5 M NaCl pH 8.3 at 4°C for 3 hours. The resin was washed with 300 μ l 100 mM Tris pH 8.0 followed by a wash with 300 μ l 100 mM acetate. This was repeated 6 times before storing the resin in 20% EtOH in PBS. The column was made in a pipette tip with glass wool and washed with 3 ml H₂O. 100 μ l cell lysate

was diluted in loading buffer (1 in 10) and run through the column. The column was washed with 5 ml loading buffer prior to elution with 1 M NaCl followed by 0.2% formic acid. Different loading buffers such as RIPA; RIPA without Triton X100 and SDS; 20 mM Tris pH 8.0; 20 mM Tris with 0.1% sodium deoxycholate and 0.1% N-octylglucoside pH<8.0; 20 mM Tris with 0.5% sodium deoxycholate and 0.5% N-octylglucoside pH<8.0; 20 mM Tris with 1% sodium deoxycholate and 1% N-octylglucoside pH<8.0 were used to optimize binding conditions. All fractions that came off the column were collected and used for Western blotting or mass spectrometry.

SDS-PAGE and Western Blotting

Column fractions as well as a molecular weight standards, RAW 364.7 lysates and the appropriate antibody were mixed with 2x Sample Buffer (10 ml 4xTris-HCl/SDS, pH 6.8, 12 ml glycerol, 4.0 g SDS, 1.55 g DTT, 10 mg Coomassie Brilliant Blue G-250) or 10x Sample Buffer (10 ml 4xTris-HCl/SDS, pH 6.8, 2.0 g sucrose, 4.0 g SDS, 1.55 g DTT, 10 mg Coomassie Brilliant Blue G-250) and heated at 96°C for 5 minutes prior to loading onto a 9% SDS-PAGE gel. 9% SDS-PAGE gels were prepared following SynX Standard Operating Procedures for Biochemistry SOP-BM-011-GN (47) (Separating gel: 4.5 ml 30% Acryl/ 0.8% bis, 4.5 ml 3 M Tris-HCl/0.3%SDS, 4.5 ml H₂O, 1.5 ml glycerol, 20 µl TEMED, 50 µl 20% APS; Stacking gel: 1.62 ml 30% Acryl/ 0.8% bis, 3.10 ml 3 M Tris-HCl/0.3%SDS, 7.78 ml H₂O, 20 µl TEMED, 50 µl 20% APS). A cathode buffer was used to fill the inner chamber of the gel apparatus and an anode buffer was used to fill the outer chamber. Gels were run at 30 Volts for 30 minutes, then at 125 Volts until the tracking dye had reached the bottom of the gel. Gels were stained with Coomassie Brilliant Blue or Silver stained or used unstained for

Western Blotting (48). Proteins were transferred to a Polyvinylidene fluoride (PVDF) membrane (Millipore, Bedford, MA, USA) at 100 Volts for 1 hour. Membranes were stained with Coomassie Brilliant Blue G-250 (0.5 g /l Coomassie Brilliant Blue G-250, 500 ml methanol, 400 ml H₂O) and destained with 50% methanol to ensure that proteins were transferred onto the PVDF membrane. Membranes were then completely destained with 100% methanol and rinsed in H₂O prior to blocking with 5% skim milk and 1% goat serum in 10 ml PBS-0.1% Tween-20 at room temperature for 30 minutes. Blots were then rinsed with 10 ml PBS-0.1% Tween-20 and washed for 5 minutes with 10 ml PBS-0.1% Tween-20 followed by another rinse with 10 ml PBS-0.1% Tween-20. Blots were incubated with the primary antibody diluted into 2 ml (1 in 1000) at room temperature for 30 minutes with constant gentle agitation. Unbound primary antibody was washed away with 3x5 minutes washes with 10 ml PBS-0.1% Tween-20 prior to incubating the blot with the secondary HRP-labeled antibody (Jackson Immuno Research Laboratories Inc, Hornby, ON, Canada) diluted into 5 ml (1 in 10,000) at room temperature for 30 minutes with constant gentle agitation. After washing the blots with 3x5 minute with 10 ml PBS-0.1% Tween-20 at room temperature with constant gentle agitation, blots were incubated with 10 ml Enhanced Chemiluminescence (ECL) solution III for 1 minute at room temperature with constant gentle agitation. ECL solution I (9 ml H₂O, 1 ml 1 M Tris-HCl pH 8.8, 4.5 µl p-coumaric acid (0.015 g in 1 ml DMSO), 100 µl luminol (0.04 g in DMSO)) and ECL solution II (9 ml H₂O, 1 ml 1 M Tris-HCl pH 8.8, 6 µl H₂O₂) were mixed in a 1:1 ratio to prepare solution III. Blots were then wrapped in Saran Wrap and an autoradiography film (Denville, Metuchen, NY, USA) was exposed to the blot in a dark room for 1 minute. The autoradiography film was developed using GBX developer and replenisher

(Kodak, Rochester, NY, USA), rinsed with water and fixed using GBX fixer and replenisher (Kodak, Rochester, NY, USA).

Blue Silver Stain

9% SDS-PAGE gels were run and stained with Blue Silver Stain (0.12% Coomassie Brilliant Blue G-250, 10% ammonium sulphate, 10% phosphoric acid, 20% methanol) for 1 hour at room temperature with constant gentle agitation to visualize the separated protein bands. Gels were destained with 5% methanol, 7% acetic acid O/N at room temperature with constant gentle agitation (49).

Silver Stain (Hahn's lab protocols)

9% SDS-PAGE gels were run and soaked in 100 ml 7% acetic acid at room temperature for 7 minutes with constant gentle agitation. Prior to incubating the gels at room temperature O/N in 100 ml 50% methanol, gels were washed in 100 ml 50% methanol at room temperature for 10 minutes with constant gentle agitation. Gels were rinsed twice in 100 ml H₂O at room temperature for 10 minutes with constant gentle agitation followed by soaking the gels in staining solution (Solution A: 0.8 g silver nitrate (VWR, West Chester, PA, USA) was dissolved in 4 ml H₂O and added drop wise to Solution B: 21 ml H₂O, 250 µl 30% NaOH (Bioshop, Burlington, ON, Canada), 1.4 ml 14.8 M ammonium hydroxide (Caledon, Georgetown, ON, Canada). 76 ml H₂O was added to the solution) at room temperature for 15 minutes with constant gentle agitation. Gels were rinsed twice in 100 ml H₂O at room temperature for 5 minutes with constant gentle agitation prior to rinsing the gels in the developing solution (200 ml H₂O, 1% citric acid, 100 µl 27% formaldehyde (Sigma, St Louis,

MO, USA)) for 2-15 minutes with constant gentle agitation until bands are visible. The development reaction was stopped by rinsing the gels 3 times in 5% methanol, 7% acetic acid in H₂O.

Capturing of the Fc-receptor complex (LARC)

The Fc-receptor's cognate ligand IgG was bound to the surface of micro beads. RAW 264.7 macrophages were incubated with the opsonized beads to activate the Fc-receptor on the surface of the macrophages. Assembled receptor complexes were isolated using the novel Live-cell Affinity Receptor Chromatography (LARC) approach (61) and analyzed by LC-MS/MS and Western blotting.

RAW 264.7 macrophages were grown and incubated with polystyrene coated with IgG beads (3) on ice for 30 minutes to activate the Fc-receptor and formation of the Fc-receptor complex. Free beads were washed away 3 times with ice cold medium. Cells were warmed to 37°C to completely activate the Fc-receptor prior to scraping the cells with ice cold medium. A French press was used to disrupt the cells and Fc-receptor complexes attached to the micro beads were isolated through a sucrose gradient.

Liquid Chromatography Mass Spectrometry (LC-MS/MS)

Elution fractions from the NHS affinity columns as well as the captured Fc-receptor complexes using the novel LARC method were analyzed by LC-MS/MS. Spectra for the proteins of interest were collected from this data.

69 μ l of each elution fraction from the affinity chromatography columns was digested with 3 μ l 0.5 mg/ml trypsin in 1% acetic acid (Calbiochem, Gibbstown, NY, USA) in 10 μ l 10x digestion buffer (50% Acetonitrile (Caledon, Georgetown, ON, Canada), 2 M UREA, 1 M Tris-HCl pH 8.8), 18 μ l 10 M UREA O/N at 37 °C. 1 mM DTT and 1 μ l trypsin was added the next day and the sample was incubated for 3 hours at 37 °C. The sample was acidified with 5% Formic acid to pH 3-4. A C₁₈ resin (Millipore, Billerica, MA, USA) was wetted with 65% acetonitrile containing 0.2% formic acid and then equilibrated with 5% acetonitrile with 0.2% formic acid. Polypeptides were collected and the resin was washed with 0.2% formic acid prior to elution with acetonitrile in 0.2% formic acid. Peptides were analyzed over a 90 minute gradient from 5% to 65% acetonitrile at a flow rate of 2 μ l per minute with a an Agilent 1100 series capillary pump via a metal needle to form an electrospray into a Deca XP-100 ion trap (50). The MS/MS data files from the LC-ESI-ion trap runs were searched against a non-redundant library of proteins, cDNAs, EST and genomic DNA using SEQUEST. A cut off score of 10^{-3} was applied to obtain results with expectation values of 0.0001 (E-4) or less. The peptides found in the control columns were removed from the list of proteins found in the antibody or protein columns.

Peptide correlation

The manufacturer's software with the manufacturer's recommended settings and conditions were used and resulted in the peptide spectra (50) (51) and described in Jankowski *et al.* (61) using SEQUEST and BOWWORKS (Thermo Electron Corporation) to identify the peptides.

Generation of protein-protein interaction model using iHOP

Proteins observed in the LC-MS/MS results of the NHS-control column were omitted from the LC-MS/MS results of the NHS-protein/antibody affinity columns. The LC-MS/MS results from the NHS affinity columns were compared to the literature and a protein-protein interaction model generated using iHOP. Protein-protein interactions from the literature were combined in iHOP to generate a protein-protein interaction model (60).

RESULTS

Figure 1 shows a proposed phagocytosis pathway. A large variety of proteins involved in phagocytosis has been studied and added to the model. The Fc-receptor, located on the surface of macrophages, is activated through binding to opsonized particles. Activation of the Fc-receptor results in the phosphorylation of the receptor and initiates a cascade of intracellular events such as remodeling of the actin cytoskeleton, vesicle fusion and oxidative burst. Our lab is focused on protein-protein interactions but before those can be studied, the basic, fundamental interactions need to be understood first. Therefore, in this thesis the baseline of protein-actin interactions was examined using different methods to support the findings. HS1 (Haematopoietic cell specific Lyn substrate 1) and members of the annexin family have previously been demonstrated to interact with actin and are here proposed to be involved in phagocytosis.

The conserved domains of HS1 and AnXAs are shown in Figure 2 and 3. HS1 contains 3.5 37 amino acid tandem repeats and a SH3-domain at the C-terminus as well as an acidic region (NTA), a coiled-coil domain and a helix-turn-helix domain (13). AnXAs are comprised of 4 annexin repeats (except AnXA6, which comprises of eight annexin repeats), each of 70 amino acids in length. The COOH-terminus is responsible for Ca^{2+} and phospholipid binding (17). Annexins have a structurally unique N-terminus, variable in length, which is responsible for binding, activation and phosphorylation of annexins (18).

Capturing the Fc-receptor complex (LARC)

Figure 5 shows a 9% gel stained with Blue Silver Stain. Lane 1 shows the molecular weight marker and lane 2 displays a specific band pattern of the proteins present in the crude extract of RAW macrophages. Lane 3 represents a specific band pattern of proteins that were captured in the isolated Fc-receptor complex and lane 4 shows a specific band pattern of proteins in the growth media.

Figure 5. Capturing the Fc-receptor complex. Lysates of RAW macrophages, isolated Fc-receptor complexes and growth media were run on a 9% gel and stained with Blue Silver Stain to determine the presence of proteins in the respective solutions. Lane 1: Molecular weight marker, lane 2: crude extract of RAW macrophages, lane 3: Fc-receptor complex, lane 4: DMEM with 10% FBS.

Figure 6 shows the results of a Western blot using specific antibodies against β -Actin, AnXA1, AnXA2 and AnXA5. β -Actin was detected in the crude extract of RAW macrophages as well as in the captured Fc-receptor complex. AnXA1 was not observed in the crude extract of RAW macrophages or in the captured Fc-receptor complex. AnXA2 was detected by two independent anti-AnXA2 antibodies in the isolated Fc-receptor complex but not in the crude extract from RAW macrophages. AnXA5 was observed in the both the crude extract of RAW macrophages and in the captured Fc-receptor complex.

Figure 6. Capturing the Fc-receptor complex.

Lysates of RAW macrophages, isolated Fc-receptor complexes and growth media were run on a 9% gel and transferred to a PVDF membrane for Western blotting. Blots were probed with anti- β -Actin (lane 1-3), anti-Annexin A1 (lane 4-6), anti-Annexin A2 (lane 7-9 for anti-Annexin A2 from BD Biosciences, lane 10-12 for anti-Annexin A2 from Zymed), and anti-Annexin A5 (lane 13-15). Lane 1, 4, 7, 10 and 13: crude extract of RAW macrophages, lane 2, 4, 8, 11 and 14: Fc-receptor complex, lane 3, 5, 9, 12 and 15: DMEM with 10% FBS, lane 4: crude extract of RAW macrophages.

Mass spectrometry of captured Fc-receptor complexes

Fc-receptor complexes were isolated under different physiological conditions, digested with trypsin and analyzed using mass spectrometry to determine which proteins participate in the Fc-receptor complex. Figure 7a shows the detection of β -Actin, HS1, AnXA1, AnXA2, AnXA4, AnXA5 and AnXA6 by LC-MS/MS analysis of purified Fc-receptor complexes. In MS/MS analysis, scores of 10^3 or higher were considered to be significant. Appendix Table 1 shows all the different peptides and scores for Actin and many related isoforms, HS1 and the annexins detected by LC-MS/MS. Figure 7a shows the spectrum of peptide -.KDLYANTVLSGGTTMYPGIADR.- of β -Actin with a score of 37,139.96 and a total score of 3,626,521.98. The spectrum of peptide -.SAVGHEYVADVEK.- of HS1 with a score of

4,792.167 and a total score of 15,588.70 is shown in Figure 7a. AnXA1 peptides were also detected by LC/MS/MS with peptide **-.GVDEATHIDILTK.-** having the highest score of 13,791.86 and a charge of +2 (Figure 7a; Appendix Table 1). Peptide **-.WISIMTER.-** was detected for AnXA2 (Figure 7a; Appendix Table 1) and peptide **-.SETSGSFEDALLAIVK** was detected for AnXA4 by LC-MS/MS.- (Figure 7a; Appendix Table 1). LC-MS/MS detected AnXA5 with peptide **-.GLGTDEDSILNLLTSR.-** having a score of 24,558.30 and total score of 2,008,443.14 and peptide **-.GSVHDFPEFDANQDAEALYTAMK.-** was detected by LC-MS/MS for AnXA6 with a score of 6,334.528 and a total score of 10,383.01 (Figure 7a; Appendix Table 1).

Other known actin binding proteins that are involved in the rearrangement of the actin cytoskeleton such as gelsolin, profilin, Arp2/3 complex, WASp, cofilin, WAVE, LIM kinase and PAK (8) and many associated isoforms were also detected by LC-MS/MS (Figure 7b) (these spectra are also found in Appendix Figure 16 and Appendix Table 1). Peptide **-.TFVSITPAEVGVLVGK.-** with a score of 14,304.61 and a total score of 232,299.98 and a charge of +2 was detected for profilin (Figure 7b). Gelsolin peptide **-.EGNPEEDITADQTNAQAAALYK.-** with a score of 12,680.59 and a total score of 80,477.06 and a charge of +2 was detected for gelsolin (Figure 7b). Peptide **-.ALAAGGVGSIVR.-** with a score of 10,421.79 and a total score of 28,902.90 and charge of +2 was detected for Arp2/3 complex (Figure 7b). WASp peptide **-.PPFPGNRGA AFGAGSARQNPSGSSSPFPR.-** with

Figure 7a. Spectra of actin, HS1 and annexins observed in the captured Fc-receptor complex by LC-MS/MS.

a score of 1,396.371 and a total score of 3,755.01 and charge of +2 was detected (Figure 7b). Peptide -.HELQANCYEEVK.- with a score of 19,696.62 and a total score of 34,282.87 and a charge of +2 was detected for cofilin (Figure 7b). Peptide -.YAEDIFGELFNEAHSFSFR.- with a score of 1,396.371 and a total score of 3,755.01 and a charge of +3 was detected for WAVE (Figure 7). Peptide -.KRYTVVGPNPYWMAPEMINGR.- with a score of 691.0541 and a total score of 1,433.95 and a charge of +3 was detected for LIM kinase (Figure 7b). PAK peptide -.IGQGASGTVYTAMDVATGQEVAIKQMNLLQQQPK.- with a score of 396.4179 and a charge of +2 was detected (Figure 7b).

Figure 7b. Spectra of actin binding proteins observed in the captured Fc-receptor complex. Proteins that are involved in the rearrangement of the actin cytoskeleton such as gelsolin, profilin, Arp2/3 complex, WASp, cofilin, WAVE, LIM kinase and PAK were detected in the captured Fc-receptor complex by LS-MS/MS.

Affinity Chromatography

-Protein G/ Sepharose, Fast Flow column

Protein G columns were run to optimize binding and elution conditions. Anti-HS1 antibodies were linked to Protein G beads and RAW lysates were run over the affinity columns. The column was washed with PBS and eluted with 0.1% Na-Deoxycholate and 0.1% N-Octyl Glucoside prior to elution with 2% SDS. Figure 8 shows a Western blot of the elution fractions of the Protein G-HS1 column versus a control column (NHS beads alone). Other controls included the HS1 antibody alone, represented in lane 3. The blot shows the presence of HS1 in the crude sample (lane 1) and in the Flow Through of the control column (lane 3). HS1 was observed in the Flow Through of the NHS-anti-HS1 column (lane 6) as well as the control column (lane 7). HS1 was eluted from the NHS-anti-HS1 column with 0.1% Na-Deoxycholate and 0.1% N-Octyl Glucoside (lane 10) but not in the control column (lane 11). More HS1 eluted from the NHS-anti-HS1 column with 2% SDS (lane 12) but no HS1 was detected for the control column (lane 13).

The same experiment was performed with a RIPA buffer without Triton X-100 and 0.1% SDS, results are shown in Figure 9. Buffers without detergents were used to create mass spectrometry friendly conditions so that the elutions from the affinity chromatography could be directly prepared for the mass spectrometer.

-N-hydroxysuccinimide (NHS)-activated Sepharose 4 Fast Flow

NHS columns were prepared with 7 different columns: NHS-Actin, NHS-anti-Actin, NHS-anti-HS1, NHS-anti-AnXA1, NHS-anti-AnXA2, NHS-anti-AnXA4, NHS-anti-AnXA5

and a control column with no antibodies linked to NHS beads. A NHS-Actin column was used to optimize the binding conditions with different loading buffers such

Figure 8. Western blot analysis of a protein G-HS1 Affinity chromatography in the presence of Na-Deoxycholate and N-Octyl Glucoside. Protein G-HS1 Affinity chromatography fractions were run on a 9% gel and transferred to a PVDF membrane or Western blotting. The blot was probed with anti-HS1. Lane 1: crude extract of RAW macrophages, lane 2: Flow through control column, lane 3: anti-HS1 antibody, lane 4: Protein G-HS1 column wash, lane 5: Control column wash, lane 6: Protein G-HS1 column flow through, lane 7: Control column (beads alone) flow through, lane 8: Protein G-HS1 column wash, lane 9: Control column (beads alone) wash, lane 10: Protein G-HS1 column elution with Na-Deoxycholate and N-Octyl Glucoside, lane 11: control column elution with Na-Deoxycholate and N-Octyl Glucoside, lane 12: Protein G-HS1 column elution with SDS, lane 13: control column elution with SDS.

as 20 mM Tris pH 8.0 (Appendix Figure 1); 20 mM Tris with 0.1% sodium deoxycholate and 0.1% N-octylglucoside pH<8.0 (Appendix Figure 2); 20 mM Tris with 0.5% sodium deoxycholate and 0.5% N-octylglucoside pH<8.0 (Appendix Figure 3); 20 mM Tris with 1%

sodium deoxycholate and 1% N-octylglucoside pH<8.0 (Appendix Figure 4). Proteins were eluted with 1M NaCl and any remaining proteins were eluted with 0.2% Formic Acid.

Figure 9. Western blot analysis of a protein G-HS1 affinity column using RIPA without SDS or Triton X-100. Protein G-HS1.

Affinity chromatography fractions were run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-HS1. Lane 1: crude extract of RAW macrophages, lane 2: Flow through control column, lane 3: anti-HS1 antibody, lane 4: Protein G-HS1 column wash, lane 5: Control column wash, lane 6: Protein G-HS1 column flow through, lane 7: Control column (beads alone) flow through, lane 8: Protein G-HS1 column wash, lane 9: Control column (beads alone) wash, lane 10: Protein G-HS1 column elution with Na-Deoxycholate and N-Octyl Glucoside, lane 11: control column elution with Na-Deoxycholate and N-Octyl Glucoside, lane 12: Protein G-HS1 column elution with SDS, lane 13: control column elution with SDS.

Figure 10 shows the results of a Western blot of all the collected fractions from a NHS-Actin column using 20 mM Tris pH 8.0 as loading buffer as well as a control column (NHS beads alone). Western blot was performed using a monoclonal anti-Actin antibody. Actin was observed in the crude sample (lane 1). Lane 2 displays another control, the anti-Actin antibody alone. Furthermore, actin was present in the Flow Throughs of the NHS-Actin column (lane 3) as well as in the Flow Through of the control column (lane 4). Actin was also detected in the

Figure 10. Western blot analysis of a NHS-anti-Actin affinity chromatography column. 50 µg anti-Actin was bound to 100 µl NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-Actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-Actin antibody, lane 3: Flow trough of 100 µl RAW cell lysate in 1 ml binding buffer of anti-Actin column, lane 4: Flow trough of 100 µl RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: anti-Actin column wash, lane 6: control column wash, lane 7: elution 1 of anti-Actin column with 100 µl 1 M NaCl, lane 8: elution 1 of control column with 100 µl 1 M NaCl, lane 9: elution 2 of anti-Actin column with 100 µl 1 M NaCl, lane 10: elution 2 of control column with 100 µl 1 M NaCl, lane 11: elution 3 of anti-Actin column with 100 µl 1 M NaCl, lane 12: elution 3 of control column with 100 µl 1 M NaCl, lane 13: elution of anti-HS1 column with 500 µl 0.2% FA, lane 14: elution of control column with 500 µl 0.2% FA.

washes of the NHS-Actin column (lane 5) and the control column (lane 6) with 20 mM Tris pH 8.0. Actin eluted from the NHS-Actin column with 1 M NaCl (lane 7) and the control column (lane

8) as well as with 0.2% FA from the NHS-Actin column with 1 M NaCl (lane 9) and the control column (lane 10).

In another experiment, NHS beads were activated and non-specific binding sites were blocked according to manufacturer's instructions. To optimize the binding conditions, RAW lysates were diluted 1 in 10 in different loading buffers and run through columns with no antibodies linked to the NHS beads. Flow Throughs were collected and run on a 9% SDS-PAGE gel and the gel was stained with Blue Silver Stain. Results are shown in Appendix Figure 5. Proteins that did not bind to the beads when using 20 mM Tris pH 8.0 as binding buffer are shown in lane 3. The proteins in the Flow Through of a column where 20 mM Tris, 0.1% N-octyl glucoside pH 8.0 was used as binding buffer are seen in lane 4. Proteins that did not bind to the beads when using 20 mM Tris, 0.5% N-octyl glucoside pH 8.0 as binding buffer are represented in lane 5. Lane 6 reveals the presence of proteins that flowed through the column where 20 mM Tris, 1% N-octyl glucoside pH 8.0 was used as binding buffer. Proteins that did not bind to the beads when using 20 mM Tris, 0.1% Na-deoxycholate pH 8.0 as binding buffer is shown in lane 7. The proteins in the Flow Through of a column where 20 mM Tris, 0.5% Na-deoxycholate pH 8.0 was used as binding buffer are represented in lane 8. Lane 9 reveals the presence of proteins that flowed through the column where 20 mM Tris, 1% Na-deoxycholate pH 8.0 was used as binding buffer. Proteins that did not bind to the beads when using 20 mM Tris, 0.1% N-octyl glucoside, 0.1% Na-deoxycholate pH 8.0 as binding buffer are shown in lane 10. The proteins in the Flow Through of a column where 20 mM Tris, 0.5% N-octyl glucoside, 0.5% Na-deoxycholate pH 8.0 was used as binding buffer are observed in lane 11 and lane 12 reveals the presence of proteins that flowed through the column where 20 mM Tris, 1% N-octyl glucoside, 1% Na-deoxycholate pH 8.0 was used as binding buffer. 20

mM Tris, 40mM NaCl pH 8.0 was also used as binding buffer and the proteins that flowed through the column are observed in lane 13.

Appendix Figure 6 shows a Blue silver stained gel of the elutions of a NHS-anti-actin column. Anti-actin was bound to 25 μ l NHS resin and washed 5 times with 100 μ l 20 mM Tris pH 8.0 and incubated with 50 μ l RAW cell lysate in 1 ml binding buffer for 1 hour. Actin was eluted off the column in different fractions with anti-Actin, 1M NaCl and FA. Proteins present in the crude extract of RAW macrophages are represented in lane 2. The anti-Actin antibody was run on the gel to serve as an additional control. RAW lysates were run through the column and the column was washed with 20 mM Tris pH 8.0. Proteins were eluted from the NHS-anti-actin column with the anti-actin antibody (lane 4). Proteins remaining on the column were eluted with 5 fractions of 100 μ l 1M NaCl (lane 5-9) and lane 10 shows the elution of proteins from the control column (beads alone) with 500 μ l 1M NaCl. Remaining proteins were eluted from the column using 500 μ l 0.2% FA for the NHS-anti-Actin column (lane 11) and the control column (lane 12).

Appendix Figure 7 shows a SDS-PAGE gel of the optimization of the binding and elution conditions of a NHS-anti-Actin affinity column versus a control column stained with Silver nitrate. Anti-Actin was bound to 25 μ l NHS resin washed 5 times with 100 μ l 20 mM Tris pH 8.0 and incubated with 50 μ l RAW cell lysate in 1 ml binding buffer for 1 hour. Lane 2 shows the presence of different proteins present in the crude extract of RAW macrophages. The anti-Actin antibody was run on a gel to serve as an additional control (lane 3). Proteins that did not bind to the NHS-anti-Actin affinity column (lane 4) or the control column (lane 5)

ran through the column. The NHS-anti-Actin affinity column (lane 6) and the control column (lane 7) were washed with the 20 mM Tris pH 8.0 prior to eluting the proteins from the NHS-anti-Actin affinity column (lane 8) and the control column (lane 9) 500 μ l 1M NaCl. Remaining proteins were eluted from the NHS-anti-Actin affinity column (lane 10) and the control column (lane 11) with 500 μ l 0.2% FA.

Appendix Figure 8 shows a Western blot of a NHS-anti-HS1 affinity chromatography column, blotted with anti-Actin. 50 μ g anti-HS1 was bound to 100 μ l NHS resin and 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% SDS-PAGE gel and transferred to a PVDF membrane for Western blotting. Lane 1 shows the presence of actin in the crude extract of RAW macrophages and the anti-HS1 antibody (lane 2) and anti-Actin antibody (lane 3) were run on the gel as additional controls. 100 μ l RAW cell lysate in 1 ml binding buffer was run through the NHS-anti-HS1 column (lane 4) and the control column (lane 5) prior to washing the NHS-anti-HS1 column (lane 6) and the control column (lane 7) with 20 mM Tris pH 8.0. Proteins were eluted from the NHS-anti-HS1 column (lane 8) and the control column (lane 9) with an anti-Actin antibody. Remaining proteins were eluted of the NHS-anti-HS1 column (lane 10) and the control column (lane 11) with 500 μ l 1 M NaCl.

A similar experiment was performed using the elutions of a NHS-anti-HS1 affinity chromatography column for Western blotting with anti-HS1 antibodies (Appendix Figure 9).

In a comparable study, NHS-Actin (Appendix Figure 10), NHS-anti-Actin (Appendix Figure 11), NHS-anti-HS1 (Appendix Figure 12), NHS-anti-AnXA1 (Appendix Figure 13),

NHS-AnXA2 (Appendix Figure 14) and NHS-anti-AnXA5 (Appendix Figure 15) affinity columns were run and collected elution fractions were run on 9% gels and transferred to PVDF for Western blotting. Blots were probed with anti-Actin to detect the presence of Actin in the elution fractions. 50 μ g anti-AnXA5 was bound to 100 μ l NHS resin and 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-actin. In Appendix Figure 10-14, lane 1 represents the presence of actin in the crude extract of RAW macrophages and lane 2 shows the antibody alone for the corresponding antibody column. Proteins that did not bind to the NHS-antibody columns (lane 3) or control columns (lane 4) flowed through the columns. NHS-antibody columns (lane 5) and control columns (lane 6) were washed with 20 mM Tris pH 8.0 prior to eluting the proteins from the NHS-antibody columns (lane 7) and control columns (lane 8) with 500 μ l 1 M NaCl. Remaining proteins were eluted from the NHS-antibody columns (lane 9) and control columns (lane 10) with 500 μ l 0.2% FA.

LC-MS/MS of proteins observed in affinity chromatography pull downs

After running the NHS affinity chromatography columns, the collected elution fractions with NaCl and FA were prepared for LC-MS/MS. Elution fractions were digested with trypsin and ziptipped using C18 tips. Proteins that were detected in the control columns were omitted from the protein/antibody affinity column results. NHS affinity chromatography using Actin, anti-Actin, anti-Annexin I, II, IV and V and anti-HS1 revealed the presence of more than 50 proteins not found in control beads alone that showed expectation values of 0.0001 (E-4) or less (Appendix Table 1). Six proteins were selected from the result list: Ras-GTPase-activating SH3-domain binding protein (G3BP), FMS-like tyrosine kinase 1 (FLT1), FERM RhoGEF

pleckstrin domain protein 2 (FARP2), RhoGTPase-activating protein (STARD13), RAB25, member RAS oncogene family (RAB25) and FKBP-rapamycin (FRAP1) and their spectra are shown in Figure 11. Peptide LPNFGFVVFDDSEPVQK was detected for Ras-GTPase-activating SH3-domain binding protein (Appendix Table 1) and peptide SFILDPSSNLGNRIESISQR was detected for FMS-like tyrosine kinase 1, also known as the vascular endothelial growth factor receptor (Appendix Table 1). Peptides associated with FERM RhoGEF pleckstrin domain protein 2 and peptides associated with RhoGTPase-activating protein were observed (Appendix Table 1). Peptide STNVELAFQTVLKEIFAK for RAB25 was detected as shown in Appendix Table 1 as well as the peptides that were found to be associated with FKBP-rapamycin.

G3BP, FLT1, FARP2, STARD13, RAB25 and FRAP1 were also detected in the captured Fc-receptor complex. Figure 12 (these spectra are also found in Figure 16 of the appendix) shows the LC-MS/MS results of these proteins. Peptide LPNFGFVVFDDSEPVQK was detected for Ras-GTPase-activating SH3-domain binding protein with a score of 18,803.69 and a total score of 26,117.53 (Appendix Table 2) and peptide SFILDPSSNLGNRIESISQR with a score of 1,785.737 and a total score of 3,622.36 was detected for FMS-like tyrosine kinase 1, also known as the vascular endothelial growth factor receptor (Appendix Table 2). Peptide -.LTELQRDLVGVENLIAPGREFIR.- with a score of 2,822.381 and a total score of 13,282.41 was detected for FERM RhoGEF pleckstrin domain protein 2 (Appendix Table 2) and peptide -.SVPISRTEVPPDDEPAYCPRPVYQYK.- with a score of 1,050.46 was detected for RhoGTPase-activating protein (Appendix Table 1). Peptide -.STNVELAFQTVLKEIFAK.- was detected for RAB25 with a score of 781.4144 and peptide -.YHPQALIYPLTVASK.- was

found to be associated with FKBP-rapamycin with a score of 1,114.9 and a total score of 6,210.96.

Figure 11. FARP2, G3BP, RAB25, FRAP1, FLT1 and STARD13 observed in the NHS affinity chromatography pulldowns by LC-MS/MS.

RAW lysates were run through NHS-affinity chromatography columns and eluted with NaCl and formic acid. FARP2, G3BP and RAB25 were shown to interact with the NHS-anti-HS1 column, FRAP1 eluted from the NHS-anti-AnXA4 column, FLT1, G3BP was shown to interact with the NHS-actin column and STARD13 was observed to interact with the NHS-anti-AnXA5 column by LS-MS/MS.

Figure 12. FARP2, G3BP, RAB25, FRAP1, FLT1 and STARD13 observed in captured Fc-receptor complex by LC-MS/MS.

Fc-receptor complexes were isolated and analyzed by LC-MS/MS.

Confocal microscopy

-Immuno fluorescent staining

Laser confocal microscopy confirmed the recruitment of proteins to the Fc-receptor complex in RAW 264.7 macrophages. Cells were grown on cover slips, incubated with opsonized sRBC or latex beads, fixed and stained with specific antibodies. Proteins accumulated to the site of the plasma membrane where the activated Fc-receptor complex was formed by contact to opsonized particles. Actin and HS1 were observed to strongly accumulate to the site of the activated Fc-receptor complex, as shown in Figure 13. Specific anti-AnXA1

and anti-AnXA2 antibodies revealed the presence of AnXA1 and AnXA2 in the cells although no strong accumulation was observed. AnXA4 and

Figure 13. Immuno fluorescence staining of actin, HS1, AnXA1, AnXA2, AnXA4, AnXA5 and AnXA6 in RAW264.7 macrophages. Arrows indicate the protein accumulation at the site of the nascent Fc-receptor complex.

AnXA5 strongly accumulate at the site of the activated Fc-receptor complex as well as AnXA6. Figure 14 shows accumulation of RAB25, FRAP1 and STARD13 in RAW macrophages.

-GFP transfection

In another experiment, cells were grown on cover slips and transfected with GFP fusion proteins. Cells were incubated with opsonized sRBC or latex beads to activate the Fc-receptor.

Figure 15 shows the localisation of β -Actin at the active receptor site. Expression of the HS1-GFP fusion proteins accumulated to the nascent Fc-receptor

Figure 14. Immuno fluorescence staining of RAB25, FERM, RhoGEF and pleckstrin domain protein 2 and RhoGTPase activating protein in RAW264.7 macrophages. Arrows indicate the protein accumulation at the site of the nascent Fc-receptor complex.

complex. The presence of AnXA2 to the site of receptor activation was confirmed by the expression of the AnXA2 coding sequence fused to GFP. AnXA5-GFP was observed to strongly accumulate at the active receptor site and AnXA6-GFP was found to be recruited to the plasma membrane at the site of the activated Fc-receptor.

Protein-protein interaction models (iHOP)

Proteins observed in the LC-MS/MS results of the NHS-control column were omitted from the LC-MS/MS results of the NHS-protein/antibody affinity columns. The proteins that eluted from the NHS affinity chromatography columns and that were detected by LC-MS/MS

were compared to the literature in order to compose a protein-protein interaction model. Figure 16 and Table 1 show the protein-protein interactions

Figure 15. Expression of GFP fusion proteins in RAW 264.7 macrophages. Arrows indicate the protein accumulation at the site of the nascent Fc-receptor complex.

between Actin and the Annexins and the interacting proteins from the literature with Appendix Table 2 showing the abbreviations of the proteins represented in the model. Although HS1 is known to interact with actin directly, the software used did not show this interaction. MAP4K1, RAB25 and RAB11FIP5 also showed no direct interaction with Actin or the Annexins. Furthermore, over 50 other proteins that were observed in the NHS affinity chromatography columns were found to have no direct interaction with Actin, HS1 or the Annexins (Table 2).

Proteins that eluted from the NHS affinity chromatography columns were subjected to a literature review using the iHOP computer software program (60) and combined to a protein-protein interaction diagram.

Table 1. Protein-protein interactions observed from literature.

Proteins that eluted from the NHS affinity chromatography columns were subjected to a literature review using the iHOP computer software program (60) and combined to a protein-protein interaction table.

	ACTB	ANKA1	ANKA2	ANKA4	ANKA5	ANKA6	PFN1	PKM2	SCIN	MAP4K1	YWHAE	RAB25	HSP90B1	CCRO1A	HINT1	PLAU	RANBP1	FRAP1
ACTB			x		x		x							x				
HCLS1										x								
ANKA1			x	x	x	x	x						x					
ANKA2	x	x		x	x	x		x	x				x			x		
ANKA4		x	x		x	x	x											x
ANKA5	x	x	x	x		x								x		x		
ANKA6		x	x	x	x			x	x									
PGK1	x		x				x	x									x	
TUBB	x	x	x			x												
MYH9	x	x							x									
RAB11FIP5												x						
PLAU			x		x										x			
TPM4		x									x							
CFL1	x	x	x				x	x	x				x	x				
FLT1	x												x			x		x
MYBBP1A						x												
PTBP1			x											x			x	
C2orf18															x			
FRAP1				x			x							x				
PFN1	x	x		x									x					x
C1QBP		x	x	x												x		
MLL1					x													x
DUSP8					x													

Table 2. Novel protein-protein interactions observed from NHS affinity chromatography columns. Proteins that eluted from the NHS affinity chromatography columns were subjected to a literature review using the iHOP computer software program (60). Over 50 proteins that were observed in the NHS affinity chromatography columns were found to have no direct interaction with Actin, HS1 or the Annexins.

	ACTB	anti-ACTB	HCLS1	ANXA1	ANXA2	ANXA4	ANXA5
WDR70			x				
HSPA1L		x	x			x	x
FARP2			x				
DNAJC8		x	x	x	x		x
ITGBP3BP		x					
PPFIA2		x		x			
CCT	x	x			x		
CASZ1		x					x
INPP1		x					
INPP5F				x			
SNF1LK2	x						
RBPSUH	x						
RRBP1	x						
CCNK	x						
FN3K	x						
PA2G4					x		
SYT15					x		
PRF1				x	x	x	x
TTLL12					x		
HIPK4					x		
FAT					x		
TAGAP							x
PDRG1							x
DDX3Y		x					x
STARD13							x
PIK3R5						x	
CDH15						x	
ZBPB2						x	
PSTPIP2						x	
TOPBP1		x					
HD		x					
PTPRE		x					
DDX46		x					
RAB25			x				
MFI2			x				
ARHGAP5				x			
WDR40A				x			

DISCUSSION

Capturing the Fc-receptor complex

RAW 264.7 macrophages were incubated with opsonized microbeads to activate the Fc-receptor and formed complexes were isolated using the LARC approach and analyzed by LC-MS/MS and Western blotting. LC-MS/MS confirmed the presence of Actin, HS1 and AnXA1, AnXA2, AnXA4, AnXA5 and AnXA6 in the captured Fc-receptor complex (Figure 6). Actin and HS1 were observed in the crude as well as in the isolated Fc-receptor complex by Western blot but not in the culture media. However, Western blot did not show the presence of AnXA1 in the crude, Fc-receptor complex or the culture media. AnXA2 was observed in the Fc-receptor complex and in the crude extract from RAW 264.7 macrophages but not in the culture media. AnXA5 was also present in the crude extract and the isolated Fc-receptor complex but not in the culture media (Figure 5). Because HS1 (13), AnXA1 (25), AnXA2 (30), AnXA4 (20), AnXA5 (37) and AnXA6 (44) are known to interact with actin and the actin cytoskeleton, these proteins were expected to be observed in the captured Fc-receptor complex. Other proteins that are known to interact with actin such as Arp2/3 complex, cofilin, gelsolin, profilin, WASp, LIK kinase, PAK and WAVE were also observed in the captured Fc-receptor complex.

Mass spectrometry of captured Fc-receptor complexes

Isolated Fc-receptor complexes were analyzed by LC-MS/MS and a large variety of proteins associated with the rearrangement of the actin cytoskeleton were observed. These proteins include gelsolin, profilin, Arp2/3 complex, WASp, cofilin, WAVE, LIM kinase and PAK (8) as well as HS1 (13), AnXA1 (25), AnXA2 (30), AnXA4 (20), AnXA5 (37) and

AnXA6 (44). G3BP, FLT1, FARP2, STARD13, RAB25 and FRAP1 were observed in the elution of the NHS affinity chromatography columns detected by LC-MS/MS and were also present in the captured Fc-receptor complexes. G3BP (Ras-GTPase-activating SH3-domain binding protein) regulates the assembly of cytoplasmic stress granules (52) and was shown to bind to the tumor suppressor p53. G3BP redistributes p53 from the nucleus to the cytoplasm and inhibits its activity (53). The oncogene FLT1 (FMS-like tyrosine kinase 1 or vascular endothelial growth factor/vascular permeability factor receptor) is a member of the scr family and has a key role in cell proliferation and differentiation (54) whereas the tumor suppressor FRAP1 (FKBP-rapamycin) is associated with the phosphatidyl-inositol 3-kinase signal transduction pathway (55). It was therefore no surprise that these known actin interacting proteins were observed in the captured Fc-receptor complex.

However, to date there is no genetic or biochemical evidence that FARP2, STARD13 or RAB25 are involved in the rearrangement of the actin cytoskeleton or the function of the Fc-receptor. FARP2 (FERM RhoGEF pleckstrin domain protein 2) has a key role in neuronal growth cone responses and in Sema3A-stimulated axonal repulsion. FARP2 is also known to activate Rac and down regulate R-Ras as well as to suppress focal adhesion (56). STARD13 is a member of the Ras superfamily and are involved in the Rho mediated signaling pathway (57). RAB25 is a member of the small RAB GTPases and are associated with hydrolysis, nucleotide binding (58) and membrane trafficking (59).

Affinity Chromatography

RAW lysates were run through NHS-protein/antibody columns using different binding and elution buffers. Buffers containing small amounts of detergents such as Triton X-100, sodium deoxycholate and N-octylglucoside were observed to be the optimal conditions to bind proteins to the column, wash away unbound proteins and elute proteins from the affinity columns. High concentrations of detergents inhibited NHS-protein/antibody-protein binding. However, detergents are not mass spectrometer compatible therefore binding and elution buffers without detergents were used in order to analyze the elution fractions from the columns by LC-MS/MS and Western blotting. In addition to the NHS-protein/antibody columns, a control column without any antibodies linked to the NHS beads was also run and analyzed. The mass spectrometer compatibility binding buffer used, 20 mM Tris pH8.0, was not always able to wash away all unbound proteins resulting in non-specific binding in the control column. However, LC-MS/MS did show differences between NHS-protein/antibody columns and the control column and revealed at least 51 protein-protein interactions with Actin, HS1 and the Annexins which to date have not been addressed in the literature (Table 2).

LC-MS/MS of proteins observed in affinity chromatography pull downs

Proteins observed in the LC-MS/MS results of the NHS-control column were omitted from the LC-MS/MS results of the NHS-protein/antibody affinity columns. G3BP, FLT1, FARP2, STARD13, RAB25 and FRAP1 were detected by LC-MS/MS in the NHS affinity columns as well as in the captured Fc-receptor complex. However, to date there is no genetic or biochemical evidence that FARP2, STARD13 or RAB25 are involved in the rearrangement of the actin cytoskeleton or the function of the Fc-receptor. Confocal microscopy showed weak

staining of these proteins and needs to be further examined. LC-MS/MS revealed at least 51 protein-protein interactions with Actin, HS1 and the Annexins which to date have not been addressed in the literature (Table 2).

Confocal microscopy

-Immuno fluorescent staining

Laser confocal microscopy confirmed the recruitment of proteins to the Fc-receptor complex in RAW 264.7 macrophages. Staining with specific antibodies was used to image the localization of Actin, HS1, AnXA1, AnXA2, AnXA4, AnXA5 and AnXA6 to the site of activated Fc-receptor. Laser confocal images of antibody staining were found to be in agreement with the LC-MS/MS results. Actin, HS1, AnXA4, AnXA5 and AnXA6 were found to strongly accumulate at the site of phagocytosis. However, AnXA1 and AnXA2 were not found to be particularly associated with the Fc-receptor complex. Because HS1 (13), AnXA1 (25), AnXA2 (30), AnXA4 (20), AnXA5 (37) and AnXA6 (44) are known to interact with actin and the actin cytoskeleton, these proteins were expected to accumulate at the site of the activated Fc-receptor.

-GFP transfection

In an additional experiment using GFP fusion proteins, laser confocal microscopy confirmed the recruitment of proteins to the Fc-receptor complex in RAW 264.7 macrophages. Transfecting RAW 264.7 macrophages with GFP fusion proteins allowed imaging of the localization of Actin, HS1, AnXA2, AnXA5 and AnXA6 to the site of the activated Fc-receptor in live cells. Laser confocal images of GFP fusion proteins were found to be in

agreement with the LC-MS/MS results. Actin, HS1, AnXA2, AnXA5 and AnXA6 were found to strongly accumulate at the site of phagocytosis.

Protein-protein interaction models (iHOP)

LC-MS/MS results from the NHS affinity chromatography columns were compared to the literature to generate a protein-protein interaction model (Figure 16, Table 1). To date, there is no genetic or biochemical evidence showing that CCT, SNF1LK2, RBPSUH, RRBPI, CCNK, FN3K, HSPA1L, DNAJC8, ITGBP3BP, PPFIA2, CASZ1, INPP1, DDX3Y, TOPBP1, HD, PTPRE or DDX46 interact with Actin. However, these proteins eluted from the NHS-Actin and NHS-anti-Actin affinity columns (Appendix Table 1).

HS1 was observed to interact with WDR70, HSPA1L, FARP2, DNAJC8, RAB25 and MFI2 although there is no biochemical or genetic evidence of interaction between HS1 and these proteins (Table 2).

AnXA1 was observed to interact with DNAJC8, PPFIA2, INPP5F, PRF1, ARHGAP5 as well as WDR40A but no evidence was found for interactions between AnXA1 and these proteins (Table 2).

DNAJC8, CCT, PA2G4, SYT15, PRF1, TTLL12, HIPK4 and FAT eluted off the NHS-anti-AnXA2 suggesting interactions of these proteins with AnXA2 (Table 2).

AnXA4 was observed to interact with HSPA1L, PRF1, PIK3R5, CDH15, ZBP2 and PSTPIP2 but no biochemical or genetic evidence was found for interactions between AnXA4 and these proteins (Table 2).

HSPA1L, DNAJC8, CASZ1, PRF1, TAGAP, PDRG1, DDX3Y and STARD13 eluted off the NHS-anti-AnXA5 suggesting interactions of these proteins with AnXA5 (Table 2).

CONCLUSION

Standard biochemical techniques were used to approach the objectives. The novel LARC method was used to isolate the captured Fc-receptor complex prior to LC-MS/MS and Western blot analysis. Standard and novel approaches were used for the protein-protein interactions *in vitro* using standard buffers (containing detergents) and novel buffers (without detergents) as loading and elution buffers for the affinity chromatography columns. The purpose of the novel approach was to develop a method for purifying proteins over an affinity chromatography column with mass spectrometry compatible buffers. The classic technique for affinity chromatography uses buffers that contain detergents. Proteins eluted from the columns are separated on SDS-PAGE gels and stained with either Coomassie Brilliant Blue or Silver nitrate. A band of interest is cut from the gel and prepared for mass spectrometry. With the novel approach, purified proteins from the affinity chromatography columns can be directly analyzed by mass spectrometry, eliminating SDS-PAGE and resulting in a faster analysis of the sample.

Actin, HS1 and AnXA1, AnXA2, AnXA4, AnXA5 and AnXA6 were found to participate in the formation of the Fc-receptor complex prior to internalization.

Actin and actin binding proteins accumulated at the site of the nascent Fc-receptor complex confirmed by LC-MS/MS and confocal microscopy. NHS affinity columns revealed at least 51 protein-protein interactions with Actin, HS1, AnXA1, AnXA2, AnXA4 and AnXA5 with 36 different proteins, which have not been reported in the literature yet. Furthermore, G3BP, FLT1, FARP2, STARD13, RAB25 and FRAP1 were detected by LC-MS/MS and affinity chromatography, however, to date there is no biochemical or genetic evidence of STARD13,

RAB25 and FRAP1 being associated with the rearrangement of the actin cytoskeleton or the function of the Fc-receptor.

Affinity chromatography columns work best with binding/elution buffers that contain a small amount of detergent to reduce non-specific binding. However, such conditions are not mass spectrometer compatible.

REFERENCES

- (1) Nakatani Y, Ogryzko V. Immunoaffinity purification of mammalian protein complexes. *Methods Enzymol.* 2003;370:430-444.
- (2) Janeway CA, Jr, Medzhitov R. Innate immune recognition. *Annu.Rev.Immunol.* 2002;20:197-216.
- (3) Marshall JG, Booth JW, Stambolic V, Mak T, Balla T, Schreiber AD, et al. Restricted accumulation of phosphatidylinositol 3-kinase products in a plasmalemmal subdomain during Fc gamma receptor-mediated phagocytosis. *J.Cell Biol.* 2001 Jun 25;153(7):1369-1380.
- (4) Swanson JA, Hoppe AD. The coordination of signaling during Fc receptor-mediated phagocytosis. *J.Leukoc.Biol.* 2004 Dec;76(6):1093-1103.
- (5) Corbett-Nelson EF, Mason D, Marshall JG, Collette Y, Grinstein S. Signaling-dependent immobilization of acylated proteins in the inner monolayer of the plasma membrane. *J.Cell Biol.* 2006 Jul 17;174(2):255-265.
- (6) Niedergang F, Chavrier P. Regulation of phagocytosis by Rho GTPases. *Curr.Top.Microbiol.Immunol.* 2005;291:43-60.
- (7) Adachi R, Takeuchi K, Suzuki K. Antisense oligonucleotide to cofilin enhances respiratory burst and phagocytosis in opsonized zymosan-stimulated mouse macrophage J774.1 cells. *J.Biol.Chem.* 2002 Nov 22;277(47):45566-45571.
- (8) Pollard TD. Regulation of actin filament assembly by Arp2/3 complex and formins. *Annu.Rev.Biophys.Biomol.Struct.* 2007;36:451-477.
- (9) Reisler E, Egelman EH. Actin structure and function: what we still do not understand. *J.Biol.Chem.* 2007 Dec 14;282(50):36133-36137.
- (10) Pollard TD, Borisy GG. Cellular motility driven by assembly and disassembly of actin filaments. *Cell* 2003 Feb 21;112(4):453-465.
- (11) Kodama A, Lechler T, Fuchs E. Coordinating cytoskeletal tracks to polarize cellular movements. *J.Cell Biol.* 2004 Oct 25;167(2):203-207.
- (12) Kitamura D, Kaneko H, Miyagoe Y, Ariyasu T, Watanabe T. Isolation and characterization of a novel human gene expressed specifically in the cells of hematopoietic lineage. *Nucleic Acids Res.* 1989 Nov 25;17(22):9367-9379.
- (13) Hao JJ, Zhu J, Zhou K, Smith N, Zhan X. The coiled-coil domain is required for HS1 to bind to F-actin and activate Arp2/3 complex. *J.Biol.Chem.* 2005 Nov 11;280(45):37988-37994.

- (14) Uruno T, Zhang P, Liu J, Hao JJ, Zhan X. Haematopoietic lineage cell-specific protein 1 (HS1) promotes actin-related protein (Arp) 2/3 complex-mediated actin polymerization. *Biochem.J.* 2003 Apr 15;371(Pt 2):485-493.
- (15) Yamanashi Y, Fukuda T, Nishizumi H, Inazu T, Higashi K, Kitamura D, et al. Role of tyrosine phosphorylation of HS1 in B cell antigen receptor-mediated apoptosis. *J.Exp.Med.* 1997 Apr 7;185(7):1387-1392.
- (16) Yamanashi Y, Okada M, Semba T, Yamori T, Umemori H, Tsunasawa S, et al. Identification of HS1 protein as a major substrate of protein-tyrosine kinase(s) upon B-cell antigen receptor-mediated signaling. *Proc.Natl.Acad.Sci.U.S.A.* 1993 Apr 15;90(8):3631-3635.
- (17) Gerke V, Moss SE. Annexins: from structure to function. *Physiol.Rev.* 2002 Apr;82(2):331-371.
- (18) Gerke V, Creutz CE, Moss SE. Annexins: linking Ca²⁺ signalling to membrane dynamics. *Nat.Rev.Mol.Cell Biol.* 2005 Jun;6(6):449-461.
- (19) Mailliar WS, Haigler HT, Schlaepfer DD. Calcium-dependent binding of S100C to the N-terminal domain of annexin I. *J.Biol.Chem.* 1996 Jan 12;271(2):719-725.
- (20) Diakonova M, Gerke V, Ernst J, Liautard JP, van der Vusse G, Griffiths G. Localization of five annexins in J774 macrophages and on isolated phagosomes. *J.Cell.Sci.* 1997 May;110 (Pt 10)(Pt 10):1199-1213.
- (21) Fan X, Krahling S, Smith D, Williamson P, Schlegel RA. Macrophage surface expression of annexins I and II in the phagocytosis of apoptotic lymphocytes. *Mol.Biol.Cell* 2004 Jun;15(6):2863-2872.
- (22) Schlaepfer DD, Haigler HT. Characterization of Ca²⁺-dependent phospholipid binding and phosphorylation of lipocortin I. *J.Biol.Chem.* 1987 May 15;262(14):6931-6937.
- (23) Schlaepfer DD, Haigler HT. In vitro protein kinase C phosphorylation sites of placental lipocortin. *Biochemistry* 1988 Jun 14;27(12):4253-4258.
- (24) Sakaguchi M, Murata H, Sonogawa H, Sakaguchi Y, Futami J, Kitazoe M, et al. Truncation of annexin A1 is a regulatory lever for linking epidermal growth factor signaling with cytosolic phospholipase A2 in normal and malignant squamous epithelial cells. *J.Biol.Chem.* 2007 Dec 7;282(49):35679-35686.
- (25) Moss SE, Morgan RO. The annexins. *Genome Biol.* 2004;5(4):219.
- (26) van de Graaf SF, Hoenderop JG, Gkika D, Lamers D, Prenen J, Rescher U, et al. Functional expression of the epithelial Ca(2+) channels (TRPV5 and TRPV6) requires association of the S100A10-annexin 2 complex. *EMBO J.* 2003 Apr 1;22(7):1478-1487.

- (27) Glenney JR, Jr, Tack BF. Amino-terminal sequence of p36 and associated p10: identification of the site of tyrosine phosphorylation and homology with S-100. *Proc.Natl.Acad.Sci.U.S.A.* 1985 Dec;82(23):7884-7888.
- (28) Gould KL, Woodgett JR, Isacke CM, Hunter T. The protein-tyrosine kinase substrate p36 is also a substrate for protein kinase C in vitro and in vivo. *Mol.Cell.Biol.* 1986 Jul;6(7):2738-2744.
- (29) Hansen MD, Ehrlich JS, Nelson WJ. Molecular mechanism for orienting membrane and actin dynamics to nascent cell-cell contacts in epithelial cells. *J.Biol.Chem.* 2002 Nov 22;277(47):45371-45376.
- (30) Lee DB, Jamgotchian N, Allen SG, Kan FW, Hale IL. Annexin A2 heterotetramer: role in tight junction assembly. *Am.J.Physiol.Renal Physiol.* 2004 Sep;287(3):F481-91.
- (31) Hayes MJ, Shao D, Bailly M, Moss SE. Regulation of actin dynamics by annexin 2. *EMBO J.* 2006 May 3;25(9):1816-1826.
- (32) Piljic A, Schultz C. Annexin A4 self-association modulates general membrane protein mobility in living cells. *Mol.Biol.Cell* 2006 Jul;17(7):3318-3328.
- (33) Ponnampalam AP, Rogers PA. Cyclic changes and hormonal regulation of annexin IV mRNA and protein in human endometrium. *Mol.Hum.Reprod.* 2006 Nov;12(11):661-669.
- (34) Chan HC, Kaetzel MA, Gotter AL, Dedman JR, Nelson DJ. Annexin IV inhibits calmodulin-dependent protein kinase II-activated chloride conductance. A novel mechanism for ion channel regulation. *J.Biol.Chem.* 1994 Dec 23;269(51):32464-32468.
- (35) Goossens EL, Reutelingsperger CP, Jongsma FH, Kraayenhof R, Hermens WT. Annexin V perturbs or stabilises phospholipid membranes in a calcium-dependent manner. *FEBS Lett.* 1995 Feb 13;359(2-3):155-158.
- (36) Bitto E, Cho W. Structural determinant of the vesicle aggregation activity of annexin I. *Biochemistry* 1999 Oct 19;38(42):14094-14100.
- (37) Tzima E, Trotter PJ, Orchard MA, Walker JH. Annexin V relocates to the platelet cytoskeleton upon activation and binds to a specific isoform of actin. *Eur.J.Biochem.* 2000 Aug;267(15):4720-4730.
- (38) Kaneko N, Ago H, Matsuda R, Inagaki E, Miyano M. Crystal structure of annexin V with its ligand K-201 as a calcium channel activity inhibitor. *J.Mol.Biol.* 1997 Nov 21;274(1):16-20.
- (39) Campos B, Wang S, Retzinger GS, Kaetzel MA, Seaton BA, Karin NJ, et al. Mutation of highly conserved arginine residues disrupts the structure and function of annexin V. *Arch.Med.Res.* 1999 Sep-Oct;30(5):360-367.

- (40) Russo-Marie F. Annexin V and phospholipid metabolism. *Clin.Chem.Lab.Med.* 1999 Mar;37(3):287-291.
- (41) Avila-Sakar AJ, Kretsinger RH, Creutz CE. Membrane-bound 3D structures reveal the intrinsic flexibility of annexin VI. *J.Struct.Biol.* 2000 May;130(1):54-62.
- (42) Kamal A, Ying Y, Anderson RG. Annexin VI-mediated loss of spectrin during coated pit budding is coupled to delivery of LDL to lysosomes. *J.Cell Biol.* 1998 Aug 24;142(4):937-947.
- (43) Garbuglia M, Verzini M, Donato R. Annexin VI binds S100A1 and S100B and blocks the ability of S100A1 and S100B to inhibit desmin and GFAP assemblies into intermediate filaments. *Cell Calcium* 1998 Sep;24(3):177-191.
- (44) Babiychuk EB, Palstra RJ, Schaller J, Kampf U, Draeger A. Annexin VI participates in the formation of a reversible, membrane-cytoskeleton complex in smooth muscle cells. *J.Biol.Chem.* 1999 Dec 3;274(49):35191-35195.
- (45) Grewal T, Heeren J, Mewawala D, Schnitgerhans T, Wendt D, Salomon G, et al. Annexin VI stimulates endocytosis and is involved in the trafficking of low density lipoprotein to the prelysosomal compartment. *J.Biol.Chem.* 2000 Oct 27;275(43):33806-33813.
- (46) Rentero C, Evans R, Wood P, Tebar F, Vila de Muga S, Cubells L, et al. Inhibition of H-Ras and MAPK is compensated by PKC-dependent pathways in annexin A6 expressing cells. *Cell.Signal.* 2006 Jul;18(7):1006-1016.
- (47) Schagger H, von Jagow G. Tricine-sodium dodecyl sulfate-polyacrylamide gel electrophoresis for the separation of proteins in the range from 1 to 100 kDa. *Anal.Biochem.* 1987 Nov 1;166(2):368-379.
- (48) Burnette WN. "Western blotting": electrophoretic transfer of proteins from sodium dodecyl sulfate--polyacrylamide gels to unmodified nitrocellulose and radiographic detection with antibody and radioiodinated protein A. *Anal.Biochem.* 1981 Apr;112(2):195-203.
- (49) Candiano G, Bruschi M, Musante L, Santucci L, Ghiggeri GM, Carnemolla B, et al. Blue silver: a very sensitive colloidal Coomassie G-250 staining for proteome analysis. *Electrophoresis* 2004 May;25(9):1327-1333.
- (50) Marshall J, Jankowski A, Furesz S, Kireeva I, Barker L, Dombrovsky M, et al. Human serum proteins pre-separated by electrophoresis or chromatography followed by tandem mass spectrometry. *J.Proteome Res.* 2004 May-Jun;3(3):364-382.
- (51) Guzzetta AW, Thakur RA, Mylchreest IC. A robust micro-electrospray ionization technique for high-throughput liquid chromatography/mass spectrometry proteomics using a sanded metal needle as an emitter. *Rapid Commun.Mass Spectrom.* 2002;16(21):2067-2072.

- (52) Solomon S, Xu Y, Wang B, David MD, Schubert P, Kennedy D, et al. Distinct structural features of caprin-1 mediate its interaction with G3BP-1 and its induction of phosphorylation of eukaryotic translation initiation factor 2alpha, entry to cytoplasmic stress granules, and selective interaction with a subset of mRNAs. *Mol.Cell.Biol.* 2007 Mar;27(6):2324-2342.
- (53) Kim MM, Wiederschain D, Kennedy D, Hansen E, Yuan ZM. Modulation of p53 and MDM2 activity by novel interaction with Ras-GAP binding proteins (G3BP). *Oncogene* 2007 Jun 21;26(29):4209-4215.
- (54) Kappas NC, Zeng G, Chappell JC, Kearney JB, Hazarika S, Kallianos KG, et al. The VEGF receptor Flt-1 spatially modulates Flk-1 signaling and blood vessel branching. *J.Cell Biol.* 2008 Jun 2;181(5):847-858.
- (55) Bliskovsky V, Ramsay ES, Scott J, DuBois W, Shi W, Zhang S, et al. Frap, FKBP12 rapamycin-associated protein, is a candidate gene for the plasmacytoma resistance locus Pctr2 and can act as a tumor suppressor gene. *Proc.Natl.Acad.Sci.U.S.A.* 2003 Dec 9;100(25):14982-14987.
- (56) Toyofuku T, Yoshida J, Sugimoto T, Zhang H, Kumanogoh A, Hori M, et al. FARP2 triggers signals for Sema3A-mediated axonal repulsion. *Nat.Neurosci.* 2005 Dec;8(12):1712-1719.
- (57) Kandpal RP. Rho GTPase activating proteins in cancer phenotypes. *Curr.Protein Pept.Sci.* 2006 Aug;7(4):355-365.
- (58) Scapin SM, Carneiro FR, Alves AC, Medrano FJ, Guimaraes BG, Zanchin NI. The crystal structure of the small GTPase Rab11b reveals critical differences relative to the Rab11a isoform. *J.Struct.Biol.* 2006 Jun;154(3):260-268.
- (59) Kuroda TS, Fukuda M, Ariga H, Mikoshiba K. The Slp homology domain of synaptotagmin-like proteins 1-4 and Slac2 functions as a novel Rab27A binding domain. *J.Biol.Chem.* 2002 Mar 15;277(11):9212-9218.
- (60) IHOP reference: A Gene Network for Navigating the Literature. Hoffmann, R., Valencia, A. *Nature Genetics* 36, 664 (2004) and
- iHOP - <http://www.ihop-net.org/>
- (61) Jankowski A, Zhu P, Marshall JG. Capture of an activated receptor complex from the surface of live cells by affinity receptor chromatography. *Anal Biochem.* 2008 Sep 15;380(2):235-48

APPENDIX

Figure 1. Optimizing binding conditions for NHS Actin affinity chromatography columns. 50 μ g Actin was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-Actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-Actin antibody, lane 3: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of Actin column, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: Actin column wash, lane 6: control column wash, lane 7: elution of Actin column with 500 μ l 1M NaCl, lane 8: elution of control column with 500 μ l 1M NaCl, lane 9: elution of Actin column with 500 μ l 0.2% FA, lane 10: elution of control column with 500 μ l 0.2% FA.

Figure 2. Optimizing binding conditions for NHS Actin affinity chromatography columns. 50 μ g Actin was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0, 0.1% N-octyl glucoside, 0.1% Na deoxycholate was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-Actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-Actin antibody, lane 3: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of Actin column, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: Actin column wash, lane 6: control column wash, lane 7: elution of Actin column with 500 μ l 1M NaCl, lane 8: elution of control column with 500 μ l 1M NaCl, lane 9: elution of Actin column with 500 μ l 0.2% FA, lane 10: elution of control column with 500 μ l 0.2% FA.

Figure 3. Optimizing binding conditions for NHS Actin affinity chromatography columns. 50 μ g Actin was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0, 0.5% N-octyl glucoside, 0.5% Na deoxycholate was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-Actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-Actin antibody, lane 3: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of Actin column, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: Actin column wash, lane 6: control column wash, lane 7: elution of Actin column with 500 μ l 1M NaCl, lane 8: elution of control column with 500 μ l 1M NaCl, lane 9: elution of Actin column with 500 μ l 0.2% FA, lane 10: elution of control column with 500 μ l 0.2% FA.

Figure 4. Optimizing binding conditions for NHS Actin affinity chromatography columns. 50 μ g Actin was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0, 1% N-octyl glucoside, 1% Na deoxycholate was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-Actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-Actin antibody, lane 3: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of Actin column, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: Actin column wash, lane 6: control column wash, lane 7: elution of Actin column with 500 μ l 1M NaCl, lane 8: elution of control column with 500 μ l 1M NaCl, lane 9: elution of Actin column with 500 μ l 0.2% FA, lane 10: elution of control column with 500 μ l 0.2% FA.

Figure 5. Optimizing background binding NHS affinity chromatography. 25 μ l NHS resin was washed 5 times with 100 μ l of the appropriate binding buffer and incubated with 50 μ l RAW cell lysate in 1 ml binding buffer for 1 hour. Elutions were run on a 9% gel and stained with Blue Silver Stain to determine the non-specific binding of NHS beads. Lane 1: Molecular weight marker, lane 2: crude extract of RAW macrophages, lane 3: 20 mM Tris pH 8.0 was used as binding buffer, lane 4: 20 mM Tris, 0.1% N-octyl glucoside pH 8.0 was used as binding buffer, lane 5: 20 mM Tris, 0.5% N-octyl glucoside pH 8.0 was used as binding buffer, lane 6: 20 mM Tris, 1% N-octyl glucoside pH 8.0 was used as binding buffer, lane 7: 20 mM Tris, 0.1% Na-deoxycholate pH 8.0 was used as binding buffer, lane 8: 20 mM Tris, 0.5% Na-deoxycholate pH 8.0 was used as binding buffer, lane 9: 20 mM Tris, 1% Na-deoxycholate pH 8.0 was used as binding buffer, lane 10: 20 mM Tris, 0.1% N-octyl glucoside, 0.1% Na-deoxycholate pH 8.0 was used as binding buffer, lane 11: 20 mM Tris, 0.5% N-octyl glucoside, 0.5% Na-deoxycholate pH 8.0 was used as binding buffer, lane 12: 20 mM Tris, 1% N-octyl glucoside, 1% Na-deoxycholate pH 8.0 was used as binding buffer, lane 13: 20 mM Tris, 40mM NaCl pH 8.0 was used as binding buffer.

Figure 6. Optimizing elution conditions of a NHS-anti-Actin affinity column. 25 µl NHS resin was washed 5 times with 100 µl 20 mM Tris pH 8.0 and incubated with 50 µl RAW cell lysate in 1 ml binding buffer for 1 hour. Actin was eluted off the column in different fractions with anti-Actin, 1M NaCl and FA. Fractions were run on a 9% gel and the gel was stained with Blue Silver Stain. Lane 1: Molecular weight marker, lane 2: crude extract of RAW macrophages, lane 3: anti-Actin antibody, lane 4: elution with anti-Actin, lane 5: elution 1 with 100 µl 1M NaCl, lane 6: elution 2 with 100 µl 1M NaCl, lane 7: elution 3 with 100 µl 1M NaCl, lane 8: elution 4 with 100 µl 1M NaCl, lane 9: elution 5 with 100 µl 1M NaCl, lane 10: elution control column (beads alone) with 500 µl 1M NaCl, lane 11: elution with 500 µl 0.2% FA, lane 12: elution control column (beads alone) with 500 µl 0.2% FA.

Figure 7. Optimizing binding and elution conditions of a NHS-anti-Actin affinity column versus a control column. 25 μ l NHS resin was washed 5 times with 100 μ l of the appropriate binding buffer and incubated with 50 μ l RAW cell lysate in 1 ml binding buffer for 1 hour. All fractions were collected and run on a 9% gel. The gel was stained with Silver nitrate. Lane 1: Molecular weight marker, lane 2: crude extract of RAW macrophages, lane 3: anti-Actin antibody, lane 4: Flow trough of 50 μ l RAW cell lysate in 1 ml binding buffer of anti-Actin column, lane 5: Flow trough of 50 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 6: anti-Actin column wash, lane 7: control column wash, lane 8: elution of anti-Actin column with 500 μ l 1M NaCl, lane 9: elution of control column with 500 μ l 1M NaCl, lane 10: elution of anti-Actin column with 500 μ l 0.2% FA, elution of control column with 500 μ l 0.2% FA.

Figure 8. NHS-anti-HS1 affinity chromatography column. 50 μ g anti-HS1 was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-Actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-HS1 antibody, lane 3: anti-Actin antibody, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of anti-HS1 column, lane 5: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 6: anti-HS1 column wash, lane 7: control column wash, lane 8: elution of anti-HS1 column with anti-HS1 antibody, lane 9: elution of anti-HS1 column with anti-Actin antibody, lane 10: elution of anti-HS1 column with 500 μ l 1 M NaCl, lane 11: elution of control column with 500 μ l 1 M NaCl.

Figure 9. NHS-anti-HS1 affinity chromatography column. 50 μ g anti-HS1 was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-HS1. Lane 1: crude extract of RAW macrophages, lane 2: anti-HS1 antibody, lane 3: anti-Actin antibody, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of anti-HS1 column, lane 5: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 6: anti-HS1 column wash, lane 7: control column wash, lane 8: elution of anti-HS1 column with anti-HS1 antibody, lane 9: elution of anti-HS1 column with anti-Actin antibody, lane 10: elution of anti-HS1 column with 500 μ l 1 M NaCl, lane 11: elution of control column with 500 μ l 1 M NaCl.

Figure 10. NHS-Actin affinity chromatography column. 50 μ g Actin was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-Actin antibody, lane 3: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of Actin column, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: Actin column wash, lane 6: control column wash, lane 7: elution of Actin column with 500 μ l 1 M NaCl, lane 8: elution of control column with 500 μ l 1 M NaCl, lane 9: elution of Actin column with 500 μ l 0.2% FA, lane 10: elution of control column with 500 μ l 0.2% FA.

Figure 11. NHS-anti-Actin affinity chromatography column. 50 µg anti-Actin was bound to 100 µl NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-Actin antibody, lane 3: Flow trough of 100 µl RAW cell lysate in 1 ml binding buffer of Actin column, lane 4: Flow trough of 100 µl RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: Actin column wash, lane 6: control column wash, lane 7: elution of Actin column with 500 µl 1 M NaCl, lane 8: elution of control column with 500 µl 1 M NaCl, lane 9: elution of Actin column with 500 µl 0.2% FA, lane 10: elution of control column with 500 µl 0.2% FA.

Figure 12. NHS-anti-HS1 affinity chromatography column. 50 μ g anti-HS1 was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-HS1 antibody, lane 3: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of anti-HS1 column, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: anti-HS1 column wash, lane 6: control column wash, lane 7: elution of anti-HS1 column with 500 μ l 1 M NaCl, lane 8: elution of control column with 500 μ l 1 M NaCl, lane 9: elution of anti-HS1 column with 500 μ l 0.2% FA, lane 10: elution of control column with 500 μ l 0.2% FA.

Figure 13. NHS-anti-AnXA1 affinity chromatography column. 50 μ g anti-AnXA1 was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-AnXA1 antibody, lane 3: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of anti-AnXA1 column, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: anti-AnXA1 column wash, lane 6: control column wash, lane 7: elution of anti-AnXA1 column with 500 μ l 1 M NaCl, lane 8: elution of control column with 500 μ l 1 M NaCl, lane 9: elution of anti-AnXA1 column with 500 μ l 0.2% FA, lane 10: elution of control column with 500 μ l 0.2% FA.

Figure 14. NHS-anti-AnXA2 affinity chromatography column. 50 µg anti-AnXA2 was bound to 100 µl NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-AnXA5 antibody, lane 3: Flow trough of 100 µl RAW cell lysate in 1 ml binding buffer of anti-AnXA5 column, lane 4: Flow trough of 100 µl RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: anti-AnXA5 column wash, lane 6: control column wash, lane 7: elution of anti-AnXA5 column with 500 µl 1 M NaCl, lane 8: elution of control column with 500 µl 1 M NaCl, lane 9: elution of anti-AnXA5 column with 500 µl 0.2% FA, lane 10: elution of control column with 500 µl 0.2% FA.

Figure 15. NHS-anti-AnXA5 affinity chromatography column. 50 μ g anti-AnXA5 was bound to 100 μ l NHS resin, 20 mM Tris pH 8.0 was used as binding buffer. Fractions were collected and run on a 9% gel and transferred to a PVDF membrane for Western blotting. The blot was probed with anti-actin. Lane 1: crude extract of RAW macrophages, lane 2: anti-AnXA5 antibody, lane 3: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of anti-AnXA5 column, lane 4: Flow trough of 100 μ l RAW cell lysate in 1 ml binding buffer of control column (beads alone), lane 5: anti-AnXA5 column wash, lane 6: control column wash, lane 7: elution of anti-AnXA5 column with 500 μ l 1 M NaCl, lane 8: elution of control column with 500 μ l 1 M NaCl, lane 9: elution of anti-AnXA5 column with 500 μ l 0.2% FA, lane 10: elution of control column with 500 μ l 0.2% FA.

Figure 16

Figure 16 continued

WNLLDITLLHSGGLIPRILLKSSK

similar to KIAA0825 protein actin
Accession 38 075 392

IWHHTFYNELR

similar to beta actin
Accession 38 086 870

KDLYANTVLSGGTTMYPGLADR

actin-like
Accession 8 850 209

QEYDEAGSIVHR

alpha actin precursor, alpha skeletal muscle actin
Accession 4 501 881

YPIEHGITTWDDMEK

B25819 actin, fetal skeletal/adult cardiac muscle-mouse
Accession 90 263

LDNPVIFDNGSLCK

actin-related protein T1
Accession 13 386 318

WSPLPPMGR

IPP_MOUSE Actin binding protein
IPP (MIPP protein)
Accession 13 432 168

AVFPSIVGRPR

S53793 actin-mouse (fragments)
Accession 1 363 149

SPWSNKYDPPLDGAMPSAR

CAPB_MOUSE F-actin capping protein beta subunit (CapZ beta)
Accession 1 345 668

AGFAGNDAPR

similar to actin, gamma, cytoplasmic

MQEITHAPPERK

similar to actin, gamma, cytoplasmic
Accession 38 090 438

RGILTLK

similar to mutant beta-actin
Accession 38 086 842

Figure 16 continued

Figure 16 continued

Figure 16 continued

Figure 16 continued

Figure 16 continued

Figure 16 continued

Figure 16. Peptides detected in captured Fc-receptor complexes by LC-MS/MS. Fc-receptor complexes were captured using the LARC method and analysed by LC-MS/MS. Alpha, beta, and gamma actin and many related actin isoforms were observed in the phagosome as well as HS1 and AnXA1, AnXA2, AnXA4, AnXA5, AnXA6 and ras-GTPase-activating protein SH3-domain binding protein, FMS-like tyrosine kinase 1, FERM, RhoGEF and pleckstrin domain protein 2, RhoGTPase-activating protein, RAB25 and FKBP-rapamycin.

Table 1. Peptides detected in the elutions with NaCl and FA of NHS affinity columns by LC-MS/MS. NHS affinity columns with the protein actin or antibodies against actin, HS1, AnXA1, AnXA2, AnXA4 or AnxA5 affixed to the beads were incubated with RAW lysates. Proteins that bound to the affinity columns were eluted from the column with NaCl followed by elution with FA. Mass spectrometry analysis of the elutions resulted in a large variety of different peptides detected by LC-MS/MS.

Column elution	Reference Scan(s)	P (pro)	Sf	Score	MW	Accession	Peptide (Hits)
Actin ENaCl		P (pep)	Sf	XC	Sp	RSp	Ions
	2 gj 6680924 ref NP_031713.1	5.02E-12	3.14	34.26	18559.4	6680924	4(3 0 0 1 0)
	5 gj 31712036 ref NP_853613.1	1.01E-11	0.97	10.25	16832.2	31712036	1(1 0 0 0 0)
	8 gj 7305027 ref NP_038537.1	1.81E-10	2.38	24.19	47296.3	7305027	3(2 0 0 1 0)
	9 gj 7077897 ref NP_032854.2	4.50E-10	4.12	54.23	44550.2	7077897	6(5 0 0 1 0)
	15 gj 6753492 ref NP_034028.1	5.19E-09	1.34	24.21	50988.9	6753492	3(2 0 0 1 0)
	18 gj 41350312 ref NP_038636.2	1.99E-08	2.03	30.24	23383.7	41350312	3(3 0 0 0 0)
	23 gj 114326446 ref NP_071855.2	4.48E-08	3.08	44.24	226389.7	114326446	6(3 0 1 2 0)
	25 gj 31982186 ref NP_032643.2	7.16E-08	1.36	34.24	35611.2	31982186	5(3 1 1 0 0)
	28 gj 7305075 ref NP_038744.1	1.64E-07	0.95	10.21	51828.4	7305075	1(1 0 0 0 0)
	29 gj 13385408 ref NP_080195.1	1.93E-07	0.98	10.24	20252.3	13385408	1(1 0 0 0 0)
	30 gj 124517663 ref NP_034860.2	2.05E-07	0.94	10.16	38734.0	124517663	1(1 0 0 0 0)
	31 gj 94378264 ref XP_983381.1	2.55E-07	1.46	20.22	8203.8	94378264	2(2 0 0 0 0)
	32 gj 52353955 ref NP_058662.2	2.81E-07	1.89	30.19	56585.3	52353955	3(3 0 0 0 0)
	34 gj 70794816 ref NP_001020559.1	4.53E-07	1.66	26.16	47140.5	70794816	3(2 0 1 0 0)
	36 gj 7106439 ref NP_035785.1	5.58E-07	1.15	28.22	49670.5	7106439	3(2 1 0 0 0)
	37 gj 8393544 ref NP_058580.1	6.62E-07	1.53	20.16	34394.5	8393544	2(2 0 0 0 0)
	39 gj 112293264 ref NP_031978.2	8.17E-07	4.79	70.18	56678.0	112293264	7(7 0 0 0 0)
	41 gj 14927453 ref NP_001473875.1	1.04E-06	0.93	10.16	87620.5	149274531	1(1 0 0 0 0)
	43 gj 37674277 ref NP_932758.1	1.23E-06	1.80	26.17	39651.7	37674277	3(2 0 1 0 0)
	45 gj 94388148 ref XP_912877.2	1.38E-06	0.92	10.18	17276.4	94388148	1(1 0 0 0 0)
	46 gj 114326546 ref NP_075907.2	1.40E-06	0.81	20.11	28831.8	114326546	2(2 0 0 0 0)
	47 gj 116256512 ref NP_001070733.1	1.54E-06	0.90	10.14	38353.9	116256512	1(1 0 0 0 0)
	48 gj 13385598 ref NP_080371.1	1.58E-06	0.94	10.15	13916.2	13385598	1(1 0 0 0 0)
	49 gj 1380669 ref NP_058655.2	2.68E-06	0.76	20.13	28885.6	31980669	2(2 0 0 0 0)
	50 gj 149233662 ref XP_001473770.1	2.75E-06	0.90	10.18	17579.2	149233662	1(1 0 0 0 0)
	52 gj 149267407 ref XP_001480522.1	3.04E-06	0.78	10.15	9820.6	149267407	1(1 0 0 0 0)
	53 gj 83004436 ref XP_894928.1	3.43E-06	1.69	30.17	22084.6	83004436	3(3 0 0 0 0)
	54 gj 149256684 ref NP_001481125.1	4.37E-06	0.52	10.10	12517.2	149256684	1(1 0 0 0 0)
	55 gj 13384620 ref NP_079555.1	4.63E-06	1.07	20.16	50975.9	13384620	2(2 0 0 0 0)
	56 gj 30061401 ref NP_835734.1	5.48E-06	1.42	20.14	20246.6	30061401	2(2 0 0 0 0)
	58 gj 82898939 ref XP_921877.1	8.24E-06	0.14	20.09	65429.2	82898939	2(2 0 0 0 0)
	59 gj 7106331 ref NP_034566.1	9.11E-06	0.84	10.18	15142.5	7106331	1(1 0 0 0 0)
	60 gj 133778949 ref NP_001003911.2	9.70E-06	0.09	12.09	177710.3	133778949	2(0 0 2 0 0)
	62 gj 58037267 ref NP_082235.1	1.33E-05	0.97	10.25	48688.8	58037267	1(1 0 0 0 0)
	63 gj 149255974 ref XP_001475303.1	1.36E-05	1.23	20.14	13757.1	149255974	2(2 0 0 0 0)
	64 gj 3468857 ref NP_032274.1	1.39E-05	0.60	16.12	13776.8	3468857	2(1 0 1 0 0)
	65 gj 149261626 ref XP_985520.2	2.04E-05	0.61	10.13	17639.4	149261626	1(1 0 0 0 0)
	66 gj 9678471 ref NP_033475.1	2.06E-05	2.01	40.16	49959.2	9678471	4(4 0 0 0 0)
	67 gj 19111158 ref NP_579927.1	2.33E-05	0.31	10.10	19281.1	19111158	1(1 0 0 0 0)
	68 gj 7657357 ref NP_056596.1	2.91E-05	0.64	10.13	45344.8	7657357	1(1 0 0 0 0)
	69 gj 6754976 ref NP_035164.1	2.93E-05	0.64	18.13	22176.3	6754976	2(1 1 0 0 0)
	70 gj 149270876 ref XP_001473955.1	2.93E-05	0.96	12.16	32837.8	149270876	2(1 0 0 0 1)
	71 gj 94385999 ref XP_486188.4	3.28E-05	0.54	10.10	31404.0	94385999	1(1 0 0 0 0)
	72 gj 126723461 ref NP_033970.3	3.61E-05	0.89	10.14	59555.1	126723461	1(1 0 0 0 0)
	73 gj 149261616 ref XP_001476808.1	4.01E-05	0.92	10.16	18495.2	149261616	1(1 0 0 0 0)
	75 gj 6680067 ref NP_032181.1	5.98E-05	0.82	18.17	62767.5	6680067	2(1 1 0 0 0)

Table 1 continued

	77	gi 6677813 ref NP_033124.1 ribosomal protein S8 [Mus musculus]	6.20E-05	0.93	10.16	24205.0	6677813	1 (1 0 0 0 0)
	78	gi 6753320 ref NP_033966.1 chaperonin subunit 3 (gamma) [Mus musculus]	6.71E-05	0.65	10.16	80629.7	6753320	1 (1 0 0 0 0)
	79	gi 110625979 ref NP_080283.3 eukaryotic translation elongation factor 1 gamma [Mus musculus]	6.97E-05	2.71	44.19	50090.4	110625979	5 (4 0 0 1 0)
	81	gi 6678439 ref NP_033456.1 protease, serine, 2 [Mus musculus]	9.19E-05	0.52	10.12	26203.4	6678439	1 (1 0 0 0 0)
	82	gi 6679078 ref NP_032731.1 nucleoside-diphosphate kinase 2 [Mus musculus]	9.77E-05	0.76	10.15	17363.0	6679078	1 (1 0 0 0 0)
	83	gi 6753324 ref NP_033968.1 chaperonin subunit 6a (zeta) [Mus musculus]	1.01E-04	0.79	10.13	58004.0	6753324	1 (1 0 0 0 0)
	84	gi 51772073 ref XP_486866.1 PREDICTED: hypothetical protein [Mus musculus]	1.04E-04	0.76	10.14	40984.6	51772073	1 (1 0 0 0 0)
	85	gi 9400775 ref NP_033061.3 recombining binding protein suppressor of hairless isoform 1 [Mus musculus]	1.08E-04	0.43	10.10	58537.1	9400775	1 (1 0 0 0 0)
	86	gi 6753090 ref NP_033803.1 annexin A5 [Mus musculus]	1.12E-04	1.57	26.14	35752.2	6753090	3 (2 0 1 0 0)
	87	gi 77404302 ref NP_062750.2 staphylococcal nuclease domain containing 1 [Mus musculus]	1.17E-04	2.82	46.16	102087.5	77404302	5 (4 0 1 0 0)
	88	gi 149251893 ref XP_001481376.1 PREDICTED: RIKEN cDNA 492501L14 gene [Mus musculus]	1.28E-04	0.83	20.13	185392.8	149251893	4 (0 2 0 0 2)
	89	gi 31542131 ref NP_075699.2 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Mus musculus]	1.34E-04	0.82	10.18	29636.3	31542131	1 (1 0 0 0 0)
	90	gi 94410198 ref NP_099357.1 PREDICTED: hypothetical protein [Mus musculus]	1.44E-04	1.27	20.13	16224.6	94410198	2 (2 0 0 0 0)
	92	gi 124485712 ref NP_077243.2 ribosome binding protein 1 isoform a [Mus musculus]	1.59E-04	1.03	14.14	153394.0	124485712	2 (1 0 0 1 0)
	93	gi 124489580 ref NP_032426.2 integrin alpha L [Mus musculus]	1.62E-04	0.21	22.10	129085.7	124489580	4 (1 1 0 0 2)
	94	gi 22122497 ref NP_066132.1 glycolipid transfer protein domain containing 2 [Mus musculus]	1.64E-04	0.26	8.10	34452.7	22122497	2 (0 0 1 0 1)
	95	gi 27370369 ref NP_768487.1 poly (ADP-ribose) polymerase family, member 12 [Mus musculus]	1.73E-04	0.01	8.06	79900.3	27370369	1 (0 1 0 1 0)
	96	gi 139949022 ref NP_001077279.1 hypothetical protein LOC72446 [Mus musculus]	1.87E-04	0.09	10.09	40981.7	139949022	1 (1 0 0 0 0)
	97	gi 30425250 ref NP_780706.1 hypothetical protein LOC238980 [Mus musculus]	1.90E-04	1.48	26.18	42004.0	30425250	3 (2 0 1 0 0)
	98	gi 94375800 ref XP_098987.1 PREDICTED: similar to nucleoside diphosphate kinase B [Mus musculus]	1.95E-04	0.86	10.14	20502.7	94375800	2 (1 1 0 0 0)
	99	gi 146259714 ref NP_001460396.1 PREDICTED: hypothetical protein LOC73673 isoform 2 [Mus musculus]	2.10E-04	0.83	10.15	28428.9	146259714	1 (1 0 0 0 0)
	100	gi 21450628 ref NP_059207.1 eukaryotic translation initiation factor 4A1 [Mus musculus]	2.31E-04	1.75	22.14	46153.7	21450628	3 (2 0 0 0 1)
	101	gi 159172039 ref NP_254279.1 chloride intracellular channel 1 [Mus musculus]	2.34E-04	0.90	20.15	27012.6	159172039	3 (1 1 0 0 1)
	102	gi 13399310 ref NP_080239.1 ribosomal protein S10 [Mus musculus]	2.42E-04	0.53	10.14	18915.6	13399310	1 (1 0 0 0 0)
	103	gi 82930015 ref NP_496217.2 PREDICTED: similar to nuclear protein-NHP2-like protein [Mus musculus]	2.43E-04	0.89	10.15	14173.5	82930015	1 (1 0 0 0 0)
	104	gi 149249349 ref XP_001471896.1 PREDICTED: hypothetical protein [Mus musculus]	2.48E-04	0.24	10.11	63949.9	149249349	1 (1 0 0 0 0)
	106	gi 6753069 ref NP_033817.1 apurinic/apyrimidinic endonuclease 1 [Mus musculus]	2.64E-04	1.08	26.19	35490.2	6753069	3 (2 0 1 0 0)
	107	gi 28077005 ref NP_092361.1 transmembrane protein 48 [Mus musculus]	2.69E-04	0.32	8.11	75409.0	28077005	2 (0 0 0 2 0)
	108	gi 41054990 ref NP_055761.1 hypothetical protein LOC212377 [Mus musculus]	3.02E-04	0.67	12.11	109241.6	41054990	2 (1 0 0 0 1)
	109	gi 239431918 ref NP_075693.1 Nice-4 protein homolog isoform 2 [Mus musculus]	4.00E-04	0.72	24.12	112450.6	239431918	4 (0 0 0 0 2)
	110	gi 34281810 ref NP_034358.2 FMS-like tyrosine kinase 1 [Mus musculus]	4.53E-04	0.03	10.09	149644.9	34281810	1 (1 0 0 0 0)
	111	gi 14923522 ref XP_282560.6 PREDICTED: serine (or cysteine) proteinase inhibitor, clade A, member 3A isoform 1 [Mus musculus]	4.63E-04	0.04	14.06	47902.8	149235222	2 (0 1 1 0 0)
	112	gi 149231960 ref NP_020570.2 chondroitin sulfate proteoglycan 4 [Mus musculus]	4.80E-04	0.20	20.10	252304.7	149231960	2 (2 0 0 0 0)
	113	gi 149269767 ref NP_033562.1 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon [Mus musculus]	5.01E-04	0.60	20.12	29188.7	149269767	2 (2 0 0 0 0)
	114	gi 149252715 ref NP_020617.3 PREDICTED: similar to hCG30306, isoform 5 [Mus musculus]	5.01E-04	1.17	22.18	303993.4	149252715	3 (1 0 2 0 0)
	115	gi 62526049 ref NP_00104066.1 zinc finger protein 386 (Krueppel-like) isoform a [Mus musculus]	5.04E-04	0.24	12.10	72494.8	62526049	3 (0 1 0 0 2)
	119	gi 6753020 ref NP_033776.1 autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dys) [Mus musculus]	5.81E-04	0.07	8.06	59042.0	6753020	1 (0 1 0 0 0)
	120	gi 27734060 ref NP_775545.1 ubiquitin carboxyl-terminal hydrolase CYLD [Mus musculus]	5.90E-04	0.03	8.05	106584.8	27734060	2 (0 0 1 0 1)
	121	gi 13980464 ref NP_058054.2 ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	6.12E-04	0.54	10.13	56300.1	13980464	1 (1 0 0 0 0)
	122	gi 149269767 ref XP_001478231.1 PREDICTED: hypothetical protein [Mus musculus]	6.52E-04	0.05	16.06	74159.6	149269767	2 (2 0 0 0 0)
	123	gi 11162657 ref NP_001036115.1 DCN1, defective in cutin neddylation 1, domain containing 2 isoform d [Mus musculus]	6.83E-04	0.69	10.19	22868.8	11162657	1 (1 0 0 0 0)
	124	gi 8300453 ref NP_358238.3 PREDICTED: similar to Hmgb1 protein [Mus musculus]	6.83E-04	0.43	8.12	21307.8	8300453	1 (1 0 0 0 0)
	126	gi 26896569 ref NP_758475.1 solute carrier family 6 (neurotransmitter transporter), member 17 [Mus musculus]	7.19E-04	0.18	8.11	80756.6	26896569	1 (1 0 0 0 0)
	127	gi 94381279 ref NP_097159.1 PREDICTED: ubiquitin specific peptidase 31 [Mus musculus]	7.24E-04	0.57	10.11	148553.5	94381279	1 (1 0 0 0 0)
	128	gi 15600303 ref NP_077745.2 tropomyosin 1, alpha [Mus musculus]	8.04E-04	0.52	18.11	32708.5	15600303	2 (1 0 0 0 0)
	129	gi 157841168 ref NP_033962.2 cyclin K [Mus musculus]	8.49E-04	0.23	18.10	64349.5	157841168	3 (0 0 3 0 0)
	130	gi 162461907 ref NP_034811.2 heat shock protein 9 [Mus musculus]	8.57E-04	1.29	18.17	73460.8	162461907	2 (1 1 0 0 0)
	131	gi 149234329 ref XP_001480303.1 PREDICTED: similar to Zinc finger, BED domain containing 4 [Mus musculus]	8.65E-04	0.12	12.09	13939.4	149234329	3 (0 0 1 1 1)
	132	gi 124487373 ref NP_089954.4 biliverdin reductase A [Mus musculus]	8.92E-04	0.21	10.11	33524.3	124487373	1 (1 0 0 0 0)
	133	gi 40549397 ref NP_112148.2 ankryin repeat domain protein 17 isoform a [Mus musculus]	9.07E-04	0.78	32.12	274209.9	40549397	5 (2 0 1 1 0)
	1	gi 6671509 ref NP_031419.1 actin, beta, cytoplasmic [Mus musculus]	9.77E-04	1.12	48.23	41736.5	6671509	6 (3 1 1 1 0)
Actin EFA	2	gi 6680824 ref NP_031713.1 cofilin 1, non-muscle [Mus musculus]	3.63E-11	2.77	30.25	18559.4	6680824	3 (3 0 0 0 0)
	3	gi 70778970 ref NP_032854.2 phosphoglycerate kinase 1 [Mus musculus]	2.42E-10	0.95	10.19	44550.2	70778970	1 (1 0 0 0 0)
	4	gi 67558639 ref NP_036761.1 tumor rejection antigen gp66 [Mus musculus]	2.00E-08	0.81	10.14	92475.1	67558639	1 (1 0 0 0 0)
	5	gi 33563240 ref NP_033736.1 actin, alpha 1, skeletal muscle [Mus musculus]	2.22E-07	3.64	50.20	42060.8	33563240	5 (5 0 0 0 0)
	6	gi 7242197 ref NP_036315.1 proteasome (prosome, macropain) subunit, beta type 1 [Mus musculus]	7.85E-07	0.80	10.13	26372.0	7242197	1 (1 0 0 0 0)
	8	gi 149249469 ref XP_001477320.1 PREDICTED: hypothetical protein [Mus musculus]	1.79E-06	0.94	10.23	31315.9	149249466	1 (1 0 0 0 0)
	9	gi 6671539 ref NP_031464.1 aktolase 1, A isoform [Mus musculus]	2.25E-06	0.39	16.10	39355.7	6671539	2 (1 0 1 0 0)
	10	gi 13980945 ref NP_081628.2 golgi reassembly stacking protein 2 [Mus musculus]	4.57E-06	0.05	10.07	47054.1	13980945	1 (1 0 0 0 0)
	12	gi 280332329 ref NP_034236.2 eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	9.51E-06	2.78	30.16	50113.5	280332329	3 (3 0 0 0 0)
	13	gi 124487183 ref NP_001074638.1 hypothetical protein LOC104816 [Mus musculus]	1.46E-05	0.07	8.08	60594.3	124487183	1 (1 0 0 0 0)
	15	gi 124301203 ref NP_789004.2 dedicator of cytokinesis 6 [Mus musculus]	3.37E-05	0.26	22.11	235652.3	124301208	3 (0 2 1 0 0)
	18	gi 52421788 ref NP_00103655.1 RAB11 family interacting protein 5 (class I) isoform 1 [Mus musculus]	6.12E-05	0.08	8.12	139554.9	52421788	1 (1 0 0 0 0)
	19	gi 149269607 ref NP_001472447.1 PREDICTED: similar to ribosomal protein L35 [Mus musculus]	7.31E-05	0.71	10.12	14585.5	149269607	1 (1 0 0 0 0)
	20	gi 22122485 ref NP_066129.1 gamma-aminobutyrate acid (GABA-A) receptor, pi [Mus musculus]	7.95E-05	0.12	10.10	50435.7	22122485	1 (1 0 0 0 0)
	21	gi 84393045 ref NP_138107.7 PREDICTED: hypothetical protein [Mus musculus]	9.13E-05	0.03	8.09	52333.3	84393045	1 (1 0 0 0 0)
	22	gi 82906666 ref NP_012823.1 PREDICTED: similar to longevity assurance 3-like protein [Mus musculus]	1.36E-04	0.04	8.09	50031.8	82906666	1 (1 0 0 0 0)
	23	gi 30425068 ref NP_780576.1 stonin 2 [Mus musculus]	2.05E-04	0.06	6.08	99510.4	30425068	1 (1 0 0 0 0)
	24	gi 51062277 ref NP_032785.1 protocadherin alpha 2 [Mus musculus]	2.19E-04	0.16	6.08	102286.6	51062277	2 (0 0 1 0 1)
	25	gi 13430980 ref NP_056802.1 histone cluster 1, H1e [Mus musculus]	3.33E-04	0.82	18.11	21977.1	13430980	2 (1 1 0 0 0)
	26	gi 110227377 ref NP_001035999.1 gelsolin-like capping protein [Mus musculus]	3.37E-04	0.24	18.10	38768.6	110227377	3 (1 0 0 0 2)
	27	gi 6680229 ref NP_032278.1 high mobility group box 2 [Mus musculus]	3.99E-04	0.27	10.09	24151.8	6680229	1 (1 0 0 0 0)
	28	gi 149249093 ref XP_016226.3 PREDICTED: similar to Ankr26 protein [Mus musculus]	4.46E-04	0.12	8.10	64351.3	149249098	1 (1 0 0 0 0)
	29	gi 149241501 ref XP_001480767.1 PREDICTED: similar to interferon-inducible protein 203 isoform 1 [Mus musculus]	4.55E-04	0.23	26.08	95137.2	149241501	3 (2 0 1 0 0)
	30	gi 82956894 ref NP_036227.1 PREDICTED: hypothetical protein isoform 4 [Mus musculus]	5.36E-04	0.95	12.15	29960.2	82956899	2 (1 0 0 0 1)
	31	gi 18026804 ref NP_031982.2 nucleolar protein family 6 [Mus musculus]	5.37E-04	0.06	8.07	129227.1	18026804	1 (0 0 0 0 0)
	32	gi 158749579 ref NP_001103632.1 cell division cycle associated 2 [Mus musculus]	5.59E-04	0.20	4.09	106365.6	158749576	2 (0 0 0 0 2)
	33	gi 22122743 ref NP_066309.1 acyl-CoA synthetase medium-chain family member 2 [Mus musculus]	5.59E-04	0.06	12.07	64289.8	22122743	2 (0 1 0 1 0)
	35	gi 82930222 ref NP_019443.2 PREDICTED: similar to mKIAA0734 protein [Mus musculus]	7.83E-04	0.04	10.10	129084.7	82930222	2 (0 1 0 0 1)
	36	gi 84794617 ref NP_001028399.1 solute carrier family 5 (sodium/glucose cotransporter), member 10 [Mus musculus]	7.99E-04	0.07	8.07	64705.9	84794617	1 (1 0 0 0 0)
	37	gi 124486863 ref NP_001074753.1 hypothetical LOC20779 [Mus musculus]	8.62E-04	0.08	14.09	8240.1	124486863	2 (1 1 0 0 0)
	38	gi 94662727 ref NP_001033788.1 fructosamine 3-kinase isoform b [Mus musculus]	8.64E-04	0.31	10.10	22887.0	94662727	1 (1 0 0 0 0)
	39	gi 66802439 ref NP_032290.1 homeobox A13 [Mus musculus]	9.59E-04	0.04	16.07	38565.2	6680245	2 (1 0 1 0 0)
	40	gi 98319509 ref NP_001034644.1 cytochrome P450, family 2, subfamily c, polypeptide 68 [Mus musculus]	9.76E-04	0.02	8.08	55969.6	98319509	1 (1 0 0 0 0)
a-actin ENaCl	1	gi 66805249 ref NP_031713.1 cofilin 1, non-muscle [Mus musculus]	1.43E-13	1.90	20.25	18559.4	6680524	2 (2 0 0 0 0)
	2	gi 33563240 ref NP_033736.1 actin, alpha 1, skeletal muscle [Mus musculus]	1.08E-10	4.88	78.19	27414.5	33563240	8 (6 1 1 1 0)
	3	gi 33563240 ref NP_033736.1 actin, alpha 1, skeletal muscle [Mus musculus]	1.22E-09	0.99	10.31	93550.6	72384374	1 (1 0 0 0 0)
	4	gi 72394374 ref NP_062426.2 DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 [Mus musculus]	3.27E-09	3.99	74.24	56878.0	112293264	8 (6 1 1 0 0)
	5	gi 112293264 ref NP_031834.1 cytochrome c, somatic [Mus musculus]	5.36E-08	0.88	10.17	11805.4	6681095	1 (1 0 0 0 0)
	19	gi 24333639 ref NP_038596.2 heat shock 70kDa protein 1-like [Mus musculus]	8.72E-06	0.87	16.13	70636.8	124339838	2 (1 0 1 0 0)
	15	gi 8353739 ref NP_050699.1 lysozyme [Mus musculus]	3.09E-07	0.96	10.25	18689.8	8393739	1 (1 0 0 0 0)
	17							

Table 1 continued

	31	g[163310765]ref[NP_033784.2] albumin [Mus musculus]	5.23E-05	0.82	10.13	68692.2	163310765	1 (1 0 0 0 0)
	32	g[110625979]ref[NP_080283.3] eukaryotic translation elongation factor 1 gamma [Mus musculus]	6.41E-05	0.85	10.18	50060.4	110625979	1 (1 0 0 0 0)
	33	g[31558917]ref[NP_765853.2] topoisomerase (DNA) II beta binding protein [Mus musculus]	1.14E-04	0.50	30.10	168958.7	31558917	4 (2 0 1 1 0)
	34	g[82892443]ref[XP_925627.1] PREDICTED: hypothetical protein LOC66625 isoform 32 [Mus musculus]	1.15E-04	0.20	14.10	93065.7	82892443	2 (0 1 0 0 0)
	35	g[31560224]ref[NP_077141.2] hypothetical protein LOC66839 [Mus musculus]	1.40E-04	0.42	8.11	55429.2	31560224	1 (0 1 0 0 0)
	37	g[123858774]ref[NP_001074175.1] BTA1 RNA polymerase II, B-TFIIID transcription factor-associated [Mus musculus]	1.48E-04	0.08	10.06	207049.6	123858774	2 (0 0 1 1 0)
	38	g[157951604]ref[NP_031624.2] CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1.61E-04	0.88	18.18	51594.3	157951604	2 (1 0 0 0 0)
	39	g[10946676]ref[NP_067328.1] solute carrier family 26, member 3 [Mus musculus]	1.75E-04	0.12	8.11	83589.1	10946676	1 (0 1 0 0 0)
	40	g[56905023]ref[NP_001008419.1] aldehyde oxidase 3-like 1 [Mus musculus]	2.07E-04	0.35	22.10	147912.0	56905023	4 (0 1 0 0 0)
	41	g[6755212]ref[NP_035318.1] proteasome (prosome, macropain) 28 subunit, alpha [Mus musculus]	2.33E-04	0.28	8.11	28672.7	6755212	2 (0 0 1 0 0)
	43	g[18087751]ref[NP_291061.1] protocadherin gamma subfamily C, 5 [Mus musculus]	2.65E-04	0.20	18.11	101690.0	18087751	2 (0 0 1 0 0)
	44	g[124487113]ref[NP_001074895.1] myosin XVI [Mus musculus]	3.82E-04	0.37	32.10	207658.9	124487113	5 (0 1 4 0 0)
	45	g[77612699]ref[NP_052280.2] thin isoform N2-B [Mus musculus]	4.25E-04	2.18	170.12	2886264.0	77612699	27 (8 4 2 10 3)
	46	g[45439330]ref[NP_034544.1] huntingtin [Mus musculus]	4.49E-04	0.38	20.09	344784.7	45439330	3 (1 0 0 0 1)
	47	g[33858474]ref[NP_031784.1] complement receptor 2 [Mus musculus]	4.55E-04	0.08	8.07	113335.6	33858474	1 (0 1 0 0 0)
	48	g[114326469]ref[NP_035558.2] Notch gene homolog 4 [Mus musculus]	4.93E-04	0.33	16.11	206700.0	114326469	4 (0 1 0 1 2)
	49	g[153945814]ref[NP_035342.3] protein tyrosine phosphatase, receptor type, E [Mus musculus]	5.00E-04	0.50	10.14	80687.1	153945814	1 (1 0 0 0 0)
	50	g[12426871]ref[NP_03584.3] zinc finger protein 51 [Mus musculus]	5.16E-04	0.05	14.09	91963.0	12426871	2 (0 1 0 0 0)
	51	g[34850068]ref[NP_090988.1] zinc finger protein 414 [Mus musculus]	5.30E-04	0.73	18.12	31987.8	34850068	2 (2 0 0 0 0)
	52	g[82905709]ref[XP_918376.1] PREDICTED: kallikrein 12 [Mus musculus]	5.30E-04	0.62	10.15	27305.3	82905709	2 (2 0 0 0 0)
	54	g[132626683]ref[NP_001010833.2] mediator of DNA damage checkpoint 1 [Mus musculus]	5.78E-04	0.34	24.11	184787.6	132626683	4 (1 0 1 2 0)
	55	g[157057150]ref[NP_001026792.2] ATP-binding cassette, sub-family A (ABC1), member 17 [Mus musculus]	5.80E-04	0.25	10.10	196017.8	157057150	1 (1 0 0 0 0)
	56	g[16042089]ref[NP_696087.3] DEAD box polypeptide 46 [Mus musculus]	5.84E-04	0.02	8.08	117348.4	16042089	1 (0 1 0 0 0)
	57	g[124468935]ref[NP_001074758.1] BAT2 domain containing 1 [Mus musculus]	6.28E-04	0.17	20.06	310888.6	124468935	2 (2 0 0 0 0)
	58	g[83716011]ref[NP_083358.2] vesicular acetylcholine transporter [Mus musculus]	6.42E-04	0.10	10.09	56612.9	83716011	1 (1 0 0 0 0)
	59	g[67783826]ref[NP_075023.2] solute carrier family 30 (zinc transporter), member 5 [Mus musculus]	6.62E-04	0.21	30.09	83772.7	67783826	4 (2 0 1 1 0)
	60	g[7242183]ref[NP_035254.1] paraoxonase 1 [Mus musculus]	7.31E-04	0.14	18.09	39530.8	7242183	3 (0 0 3 0 0)
	61	g[21312790]ref[NP_080646.1] MYST histone acetyltransferase 1 [Mus musculus]	7.61E-04	0.08	10.10	52573.6	21312790	1 (1 0 0 0 0)
	62	g[46488928]ref[NP_062387.2] estradiol 2 isoform a [Mus musculus]	7.85E-04	0.10	16.08	143641.9	46488928	2 (1 0 0 0 0)
	63	g[124487113]ref[NP_001074861.1] midasin [Mus musculus]	8.30E-04	0.82	36.13	629582.9	124487113	5 (2 0 2 1 0)
	64	g[33859640]ref[NP_035558.1] transaldolase 1 [Mus musculus]	8.47E-04	0.07	8.07	37386.7	33859640	1 (0 1 0 0 0)
	65	g[12963637]ref[NP_075809.1] TNF intracellular domain-interacting protein [Mus musculus]	8.56E-04	0.08	10.07	45996.4	12963637	2 (0 0 1 1 0)
	67	g[9790067]ref[NP_062662.1] cAMP-regulated guanine nucleotide exchange factor II [Mus musculus]	9.38E-04	0.22	12.08	113488.3	9790067	2 (1 0 0 0 0)
	68	g[13195628]ref[NP_077161.1] cleavage stimulation factor, 3' pre-RNA, subunit 1 [Mus musculus]	9.50E-04	0.09	18.09	48381.5	13195628	2 (1 0 0 0 0)
	69	g[61675698]ref[NP_080579.1] alkB, alkylase repair homolog 8 [Mus musculus]	9.64E-04	0.05	8.09	74767.1	61675698	2 (0 0 1 0 1)
a-Actin EFA	1	g[7306559]ref[NP_038725.1] transhyretin [Mus musculus]	3.33E-15	1.84	20.28	15775.8	7306559	2 (2 0 0 0 0)
	2	g[110347469]ref[NP_031402.3] pregnancy zone protein [Mus musculus]	9.62E-12	1.50	40.28	185851.0	110347469	5 (5 0 0 0 0)
	3	g[6671509]ref[NP_031419.1] actin, beta, cytoplasmic [Mus musculus]	1.10E-11	3.77	50.23	41736.5	6671509	5 (5 0 0 0 0)
	4	g[6680924]ref[NP_031713.1] cofilin 1, non-muscle [Mus musculus]	2.02E-10	2.62	30.22	18559.4	6680924	3 (3 0 0 0 0)
	5	g[31982300]ref[NP_032246.2] hemoglobin, beta adult major chain [Mus musculus]	7.05E-09	2.92	36.25	15748.0	31982300	4 (3 0 1 0 0)
	6	g[76881807]ref[NP_033270.3] serine (or cysteine) proteinase inhibitor, clade A, member 1b [Mus musculus]	9.44E-09	1.05	16.28	45974.4	76881807	3 (1 0 0 1 1)
	7	g[149264452]ref[XP_001471658.1] PREDICTED: hypothetical protein [Mus musculus]	1.73E-08	0.97	10.21	20772.2	149264452	1 (1 0 0 0 0)
	8	g[163310765]ref[NP_033784.2] albumin [Mus musculus]	3.76E-08	1.89	24.20	68692.2	163310765	3 (2 0 0 0 0)
	9	g[45301549]ref[NP_001077424.1] hemoglobin alpha, adult chain 2 [Mus musculus]	4.88E-08	2.54	30.19	15112.1	45301549	4 (3 0 0 0 0)
	10	g[6671539]ref[NP_031464.1] aldolase 1, A isoform [Mus musculus]	1.26E-07	1.03	18.16	38956.7	6671539	2 (1 0 0 0 0)
	14	g[6753912]ref[NP_034388.1] ferritin heavy chain 1 [Mus musculus]	5.32E-07	1.90	30.16	21066.5	6753912	3 (3 0 0 0 0)
	15	g[10227377]ref[NP_001035899.1] gelsolin-like capping protein [Mus musculus]	9.89E-07	1.56	30.18	38768.6	10227377	3 (3 0 0 0 0)
	16	g[110227377]ref[NP_001035899.1] gelsolin-like capping protein [Mus musculus]	3.47E-06	2.72	34.21	46672.5	110227377	4 (3 0 0 0 0)
	17	g[14874754]ref[NP_035558.2] serine (or cysteine) proteinase inhibitor, clade A, member 3K [Mus musculus]	4.81E-06	1.45	20.15	55871.1	14874754	2 (2 0 0 0 0)
	18	g[17647459]ref[NP_059652.1] hemoglobin, beta adult minor chain [Mus musculus]	2.46E-05	1.00	12.18	31291.8	17647459	2 (1 0 0 0 0)
	19	g[54267884]ref[NP_075720.2] eukaryotic translation elongation factor 1 delta isoform b [Mus musculus]	7.59E-05	0.89	10.15	23596.3	54267884	1 (1 0 0 0 0)
	20	g[153792001]ref[NP_035389.2] RAN binding protein 1 [Mus musculus]	8.01E-05	0.79	10.18	35811.7	153792001	1 (1 0 0 0 0)
	21	g[149265160]ref[XP_001478598.1] PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	9.15E-05	0.09	12.09	107584.2	149265160	2 (0 1 0 0 0)
	22	g[19527130]ref[NP_058678.1] elastin microfibril interfacer 1 [Mus musculus]	1.34E-04	3.81	62.18	189482.1	19527130	7 (6 0 0 0 1)
	23	g[126518317]ref[NP_033908.2] complement component 3 [Mus musculus]	2.45E-04	0.11	10.05	20026.0	126518317	1 (1 0 0 0 0)
	25	g[3385850]ref[NP_080624.1] integrin beta 3 binding protein [Mus musculus]	2.57E-04	0.22	26.11	193420.4	3385850	3 (1 2 0 0 0)
	27	g[33563240]ref[NP_033736.1] actin, alpha 1, skeletal muscle [Mus musculus]	3.02E-04	0.51	22.13	42050.8	33563240	3 (2 0 0 0 1)
	29	g[31981562]ref[NP_035229.2] pyruvate kinase, muscle [Mus musculus]	3.08E-04	1.07	40.16	57844.6	31981562	6 (2 2 0 0 2)
	28	g[58662377]ref[NP_080342.2] hypothetical protein LOC544678 [Mus musculus]	3.15E-04	0.22	20.09	90381.3	58662377	3 (0 2 0 0 1)
	31	g[33859580]ref[NP_034835.1] galectin 3 [Mus musculus]	3.49E-04	0.77	10.15	27414.5	33859580	1 (1 0 0 0 0)
	33	g[30425250]ref[NP_760706.1] hypothetical protein LOC238880 [Mus musculus]	3.81E-04	1.30	18.20	42004.0	30425250	2 (1 1 0 0 0)
	32	g[26077005]ref[NP_082631.1] transmembrane protein 46 [Mus musculus]	4.59E-04	0.20	12.10	75409.0	26077005	2 (0 0 0 0 0)
	34	g[148257960]ref[XP_001481361.1] PREDICTED: similar to very large inducible GTPase 1 [Mus musculus]	4.62E-04	0.12	14.10	278425.3	148257960	3 (0 0 2 0 1)
	35	g[124268623]ref[NP_001074399.1] ataxin 1-like [Mus musculus]	4.91E-04	0.08	8.07	73373.9	124268623	1 (0 1 0 0 0)
	36	g[85677482]ref[NP_766397.2] sarsin [Mus musculus]	4.91E-04	0.24	12.09	85487.8	85677482	2 (0 2 0 0 0)
	37	g[31542095]ref[NP_598008.2] transmembrane 9 superfamily protein member 4 [Mus musculus]	5.57E-04	0.10	8.11	74692.8	31542095	3 (0 0 2 0 1)
	38	g[70778749]ref[NP_444442.1] taste receptor, type 1 member 11B [Mus musculus]	5.58E-04	0.06	12.06	35085.0	70778749	2 (0 0 0 0 1)
	39	g[9505641]ref[NP_062378.1] diacylglycerol kinase, epsilon [Mus musculus]	6.17E-04	0.04	10.06	63634.2	9505641	1 (1 0 0 0 0)
	40	g[83004247]ref[XP_915124.1] PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown	6.80E-04	0.05	8.08	14211.6	83004247	1 (0 1 0 0 0)
	41	g[149270673]ref[XP_999161.2] PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	6.90E-04	0.53	8.15	39712.0	149270673	1 (0 1 0 0 0)
	42	g[40789298]ref[NP_786347.2] PTPRF interacting protein alpha 2 [Mus musculus]	6.93E-04	0.01	8.07	143245.5	40789298	1 (0 1 0 0 0)
	43	g[149249190]ref[XP_001478838.1] PREDICTED: hypothetical protein [Mus musculus]	6.99E-04	0.92	26.14	111160.2	149249190	3 (2 0 1 0 0)
	44	g[86990460]ref[NP_597565.2] kinesin family member 1B isoform b [Mus musculus]	7.49E-04	1.46	28.13	198918.2	86990460	4 (1 2 0 0 1)
	45	g[23956534]ref[NP_705787.1] quiescent G6 sulfhydryl oxidase 2 [Mus musculus]	7.71E-04	0.50	8.14	71476.5	23956534	1 (0 1 0 0 0)
	46	g[149250061]ref[XP_019828.4] PREDICTED: similar to Transcriptional repressor scratch 2 (Scratch homolog 2 zeta)	7.85E-04	0.59	30.11	68125.2	149250061	4 (1 0 0 0 1)
	47	g[31982472]ref[NP_031864.2] chaperonin subunit 7 (eta) [Mus musculus]	8.28E-04	0.09	8.08	59335.5	31982472	1 (0 1 0 0 0)
	48	g[157041258]ref[NP_081471.2] castor homolog 1, zinc finger [Mus musculus]	8.98E-04	0.06	14.06	125595.3	157041258	2 (1 0 0 0 0)
	49	g[6880457]ref[NP_032410.1] inositol polyphosphate 1-phosphatase [Mus musculus]	9.91E-04	0.20	8.12	43371.0	6880457	1 (0 1 0 0 0)
HS1 ENaC1	2	g[6880924]ref[NP_031713.1] cofilin 1, non-muscle [Mus musculus]	1.28E-10	3.56	10.27	18559.4	6880924	1 (1 0 0 0 0)
	7	g[11220236]ref[NP_031678.2] protein disulfide isomerase associated 3 [Mus musculus]	1.42E-08	0.32	60.20	58678.0	11220236	6 (6 0 0 0 0)
	8	g[31982196]ref[NP_032643.2] insulate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1.82E-08	1.07	24.24	35611.2	31982196	3 (1 0 1 1 0)
	13	g[41350312]ref[NP_038636.2] nascent polypeptide-associated complex alpha subunit isoform b [Mus musculus]	6.38E-08	1.02	12.27	23363.7	41350312	2 (0 0 0 0 1)
	14	g[6753060]ref[NP_033803.1] annexin A5 [Mus musculus]	7.97E-08	1.62	20.24	35752.2	6753060	2 (2 0 0 0 0)
	17	g[6681095]ref[NP_031834.1] cytochrome c, somatic [Mus musculus]	2.70E-07	0.89	10.15	11605.4	6681095	1 (1 0 0 0 0)
	19	g[8393739]ref[NP_050068.1] lysozyme [Mus musculus]	4.47E-07	1.18	12.23	16688.9	8393739	2 (1 0 0 0 1)
	21	g[31560030]ref[NP_07745.2] tropomyosin 1, alpha [Mus musculus]	5.41E-07	1.01	20.15	32708.5	31560030	2 (2 0 0 0 0)
	23	g[31982742]ref[NP_058056.2] MYB binding protein (P160) 1a [Mus musculus]	1.38E-06	0.94	10.19	152035.8	31982742	1 (1 0 0 0 0)
	26	g[6678359]ref[NP_033414.1] transketolase [Mus musculus]	2.75E-06	0.70	10.15	67303.1	6678359	1 (0 1 0 0 0)
	27	g[7305075]ref[NP_038744.1] ras-GTPase-activating protein SH3-domain binding protein [Mus musculus]	4.84E-06	1.18	20.18	51828.4	7305075	2 (2 0 0 0 0)
	31	g[153792337]ref[NP_035394.2] REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like [Mus musculus]	9.28E-06	0.94	24.12	350708.7	153792337	3 (1 1 1 0 0)
	34	g[30425250]ref[NP_760706.1] hypothetical protein LOC238880 [Mus musculus]	1.84E-06	0.81	16.15	42004.0	30425250	2 (0 2 0 0 0)
	36	g[82956899]ref[XP_926227.1] PREDICTED: hypothetical protein isoform 4 [Mus musculus]	2.35E-05	0.93	10.16	29980.2	82956899	1 (1 0 0 0 0)
	37	g[124338938]ref[NP_038586.2] heat shock 70kDa protein 1-like [Mus musculus]						

Table 1 continued

	52	g[37574080]ref[INP_932116.1] hypothetical protein LOC72361 [Mus musculus]	1.59E-04	0.33	10.11	62734.5	37574080	2 (0.0110)
	53	g[10194153]ref[INP_032305.2] mitogen activated protein kinase kinase kinase kinase 1 [Mus musculus]	1.89E-04	0.33	16.09	91534.3	10194153	3 (1.0011)
	54	g[16155748]ref[INP_080303.1] hypothetical protein LOC67246 [Mus musculus]	2.08E-04	0.14	4.11	169043.1	61557468	2 (0.0002)
	55	g[13994140]ref[INP_038928.1] antigen p87 (melanoma associated) identified by monoclonal antibodies 133.2 and	2.16E-04	0.07	14.10	81262.8	13994140	2 (0.1100)
	56	g[14925151]ref[INP_912140.3] PREDICTED: similar to mKIAA1450 protein [Mus musculus]	2.21E-04	0.05	10.09	125908.2	14925151	2 (0.0110)
	58	g[16753234]ref[INP_033914.1] calcium channel, voltage-dependent, alpha2/delta subunit 1 isoform e [Mus musculus]	2.42E-04	0.56	30.11	122518.6	6753234	4 (1.2010)
	59	g[15803751]ref[INP_064301.1] hypothetical protein LOC78016 [Mus musculus]	2.61E-04	0.42	18.12	128515.7	58037517	2 (1.1000)
	62	g[182894802]ref[INP_916068.1] PREDICTED: similar to mKIAA0754 protein [Mus musculus]	2.82E-04	0.16	16.06	115257.9	82894802	2 (1.1000)
	63	g[19111159]ref[INP_579927.1] zinc finger, AN1-type domain 2A [Mus musculus]	3.43E-04	0.34	8.10	19281.1	19111159	1 (0.1000)
	65	g[114205385]ref[INP_766289.3] hypothetical protein LOC229473 [Mus musculus]	3.89E-04	0.74	22.11	175770.7	114205385	5 (1.0103)
	66	g[128893223]ref[INP_796175.1] PHD finger protein 6 [Mus musculus]	3.90E-04	0.09	22.10	88918.2	28893223	3 (1.1010)
	68	g[121704022]ref[INP_663494.1] FERM, RhoGEF and pleckstrin domain protein 2 [Mus musculus]	4.15E-04	0.17	10.11	121265.8	21704022	1 (1.0000)
	69	g[19055386]ref[INP_061229.1] zinc finger protein 326 [Mus musculus]	4.83E-04	0.08	8.09	65224.8	9055386	1 (0.1000)
	70	g[182942342]ref[INP_821807.1] PREDICTED: similar to mKIAA0586 protein [Mus musculus]	4.93E-04	0.00	10.05	164902.7	82942342	1 (1.0000)
	71	g[16755589]ref[INP_035537.1] schlafen 1 [Mus musculus]	5.14E-04	0.16	16.10	37966.3	6755589	3 (0.1101)
	72	g[17305027]ref[INP_038537.1] endolase 2, gamma neuronal [Mus musculus]	5.16E-04	0.88	10.15	47296.3	7305027	2 (1.0000)
	73	g[127532956]ref[INP_080783.2] Zwilch [Mus musculus]	5.83E-04	0.04	16.08	68838.9	27532956	2 (0.2000)
	74	g[149280134]ref[INP_001473289.1] PREDICTED: hypothetical protein [Mus musculus]	6.30E-04	0.47	12.10	28222.0	149280134	2 (1.0001)
	75	g[130425202]ref[INP_780699.1] nicotinamide nucleotide adenyltransferase 2 [Mus musculus]	6.82E-04	0.14	10.11	34504.5	30425202	1 (1.0000)
	76	g[157951605]ref[INP_765988.2] DnaJ (Hsp40) homolog, subfamily C, member 8 [Mus musculus]	6.85E-04	0.42	10.11	29812.4	157951606	1 (1.0000)
	79	g[138348566]ref[INP_941024.1] H1 histone family, member X [Mus musculus]	7.80E-04	0.72	18.13	20151.0	38348566	3 (0.1110)
	79	g[145207866]ref[INP_848910.3] histidine acid phosphatase domain containing 2A [Mus musculus]	7.83E-04	0.70	24.12	159921.0	145207866	4 (1.2100)
	80	g[135803866]ref[INP_064382.2] alpha-1,3-mannosyltransferase ALG2 [Mus musculus]	8.09E-04	0.05	8.07	47370.7	31560386	1 (0.1000)
	82	g[110558631]ref[INP_796361.2] uronyl-2-sulfotransferase [Mus musculus]	8.90E-04	0.18	12.10	47729.7	110558631	2 (1.0001)
	83	g[15803335]ref[INP_796314.2] synaptotagmin isoform A [Mus musculus]	9.48E-04	0.14	28.09	98248.6	15803335	4 (0.3010)
	84	g[124496743]ref[INP_001074800.1] hypothetical protein LOC71007 [Mus musculus]	9.49E-04	0.36	16.10	71520.6	124496743	2 (1.0000)
	4	g[6880924]ref[INP_031713.1] cofilin 1, non-muscle [Mus musculus]	2.31E-09	0.98	10.34	18559.4	6880924	1 (1.0000)
	6	g[13981562]ref[INP_035229.2] pyruvate kinase, muscle [Mus musculus]	1.04E-08	0.43	18.11	57444.6	31981562	2 (1.1000)
	6	g[18671508]ref[INP_031419.1] actin, beta, cytoplasmic [Mus musculus]	1.95E-08	0.20	42.21	41736.5	6671508	5 (4.0001)
	9	g[14243778]ref[INP_808385.1] hypothetical protein 4732458N10 [Mus musculus]	2.17E-06	0.62	10.17	31291.8	54287684	1 (1.0000)
	11	g[12624417]ref[INP_808385.1] hypothetical protein 4732458N10 [Mus musculus]	1.19E-05	0.82	8.16	58268.0	29244176	1 (1.0000)
	12	g[121313505]ref[INP_084475.1] zinc finger protein 623 [Mus musculus]	1.77E-05	0.12	10.09	57142.1	21313506	1 (1.0000)
	14	g[13386014]ref[INP_080783.1] hypothetical protein LOC68032 [Mus musculus]	3.84E-05	0.23	14.11	20116.5	13386014	3 (2.0001)
	15	g[149233825]ref[INP_001002308.2] PREDICTED: ATP-binding cassette, sub-family A (ABC1), member 12 isoform	7.34E-05	0.03	14.10	292272.1	149233825	2 (1.0001)
	16	g[17304963]ref[INP_035813.1] chloride intracellular channel 4 (mitochondrial) [Mus musculus]	7.73E-05	0.06	10.08	28728.9	3704963	1 (1.0000)
	17	g[141350312]ref[INP_035636.2] nascent polypeptide-associated complex alpha subunit isoform b [Mus musculus]	8.65E-05	0.91	10.17	23383.7	41350312	1 (1.0000)
	20	g[127734089]ref[INP_755622.1] transmembrane protein 28 [Mus musculus]	1.84E-04	0.25	14.09	52738.8	27734086	2 (0.1010)
	21	g[131980835]ref[INP_055895.2] RAB25, member RAS oncogene family [Mus musculus]	1.68E-04	0.20	10.10	23472.4	31980835	1 (1.0000)
	22	g[149697031]ref[INP_001033789.1] tropomodulin 2 [Mus musculus]	2.31E-04	0.03	10.07	39510.5	8497031	1 (1.0000)
	23	g[157428671]ref[INP_00108722.1] transmembrane channel-like 5 isoform a [Mus musculus]	2.54E-04	0.33	18.13	111089.3	157428671	3 (0.1110)
	24	g[140254525]ref[INP_071709.2] tropomyosin 3, gamma [Mus musculus]	2.89E-04	0.81	10.13	33148.2	40254525	1 (1.0000)
	25	g[177404229]ref[INP_080963.1] epsin [Mus musculus]	2.99E-04	0.06	4.06	46390.5	77404229	2 (0.0002)
	26	g[149267109]ref[INP_001478961.1] PREDICTED: similar to Bridging integrator 2 [Mus musculus]	3.50E-04	0.22	10.12	59895.2	149267109	1 (1.0000)
	27	g[121704042]ref[INP_663504.1] cleavage stimulation factor subunit 3 isoform 1 [Mus musculus]	3.72E-04	0.11	12.07	82876.1	21704042	2 (0.1010)
	28	g[132401429]ref[INP_660253.2] UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase-like 3 [Mus musculus]	4.20E-04	0.19	18.10	67690.6	32401429	2 (1.0000)
	29	g[126032329]ref[INP_034236.2] eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	5.30E-04	0.86	22.09	50113.5	126032329	3 (2.0001)
	30	g[124487379]ref[INP_001074570.1] hypothetical protein LOC71101 [Mus musculus]	5.48E-04	0.02	8.09	81758.9	124487379	1 (1.0000)
	31	g[124487149]ref[INP_001074871.1] WD repeat domain 70 [Mus musculus]	5.74E-04	0.12	14.08	73060.4	124487149	2 (1.0001)
	32	g[16750408]ref[INP_034466.1] endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 [Mus musculus]	8.21E-04	0.19	10.10	41178.1	6754048	1 (1.0000)
	33	g[16766038]ref[INP_035816.1] vomeronasal 2, receptor 88 [Mus musculus]	9.77E-04	0.36	10.10	98178.7	16766038	1 (1.0000)
	1	g[131712036]ref[INP_853613.1] eukaryotic translation initiation factor 5A [Mus musculus]	1.00E-30	1.95	20.30	18832.2	31712036	2 (2.0000)
	2	g[157851599]ref[INP_039391.4] carbonic anhydrase 2 [Mus musculus]	2.38E-11	0.87	10.23	29032.3	157851599	1 (1.0000)
	3	g[157851604]ref[INP_031624.2] CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1.57E-10	1.36	26.25	51564.5	157851604	3 (2.0100)
	5	g[117606335]ref[INP_035470.3] serine (or cysteine) proteinase inhibitor, clade F, member 1 [Mus musculus]	8.48E-09	0.92	10.22	46233.7	117606335	1 (1.0000)
	6	g[16880067]ref[INP_032181.1] glucose phosphate isomerase 1 [Mus musculus]	1.08E-08	0.98	10.24	62767.5	6880067	1 (1.0000)
	7	g[157851609]ref[INP_765988.2] DnaJ (Hsp40) homolog, subfamily C, member 8 [Mus musculus]	1.89E-08	0.96	10.27	28912.4	157851606	1 (1.0000)
	9	g[121426823]ref[INP_085112.1] histone cluster 1, H1a [Mus musculus]	4.89E-08	0.87	14.28	21785.0	121426823	2 (1.0010)
	12	g[131982724]ref[INP_058056.2] MYB binding protein (P160) 1a [Mus musculus]	9.67E-07	1.00	16.18	152035.8	31982724	3 (1.0111)
	13	g[16753096]ref[INP_033817.1] apurinic/apyrimidinic endonuclease 1 [Mus musculus]	2.35E-08	1.18	20.18	35490.2	6753096	2 (2.0000)
	15	g[131982189]ref[INP_032643.2] malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	3.52E-08	1.30	20.25	35611.2	31982189	2 (2.0000)
	16	g[112293264]ref[INP_031878.2] protein disulfide isomerase associated 3 [Mus musculus]	6.95E-06	1.90	38.18	58678.0	112293264	4 (3.1000)
	18	g[133239214]ref[INP_666717.1] olfactory receptor 945 [Mus musculus]	1.20E-05	0.04	8.09	35861.1	33239214	1 (1.0000)
	22	g[134808712]ref[INP_035203.2] perlemin 1 [Mus musculus]	3.05E-05	0.51	10.14	62094.7	34808712	1 (1.0000)
	24	g[16880924]ref[INP_031713.1] cofilin 1, non-muscle [Mus musculus]	3.15E-05	1.37	20.21	18559.4	6880924	2 (2.0000)
	26	g[149385999]ref[INP_486188.4] PREDICTED: similar to Nucleophosmin 1 isoform 1 [Mus musculus]	3.45E-05	0.98	10.21	31404.0	94385999	1 (1.0000)
	29	g[149233825]ref[INP_001473161.1] PREDICTED: similar to ciliary dynein heavy chain 7 [Mus musculus]	4.01E-05	0.49	24.10	462264.0	149233825	4 (0.2020)
	29	g[149258880]ref[INP_001477748.1] PREDICTED: similar to ribosomal protein L22 [Mus musculus]	4.14E-05	0.80	10.10	14758.8	149258880	2 (1.0000)
	35	g[182930015]ref[INP_486217.2] PREDICTED: similar to nuclear protein-NHP2-like protein [Mus musculus]	6.89E-05	0.90	14.16	14173.5	82930015	2 (1.0010)
	36	g[131542017]ref[INP_848756.2] inositol polyphosphate-5-phosphatase F [Mus musculus]	9.25E-05	0.17	14.11	127607.6	31542017	2 (1.0010)
	37	g[16880868]ref[INP_031657.1] cyclin D1 [Mus musculus]	1.05E-04	0.08	8.09	33426.6	6880868	1 (1.0000)
	38	g[16878439]ref[INP_033456.1] protease, serine, 2 [Mus musculus]	1.07E-04	0.58	12.10	26203.4	6878439	2 (1.0001)
	41	g[182917230]ref[INP_928154.1] PREDICTED: hypothetical protein [Mus musculus]	1.34E-04	0.85	10.16	12418.3	82917230	1 (1.0000)
	45	g[17677895]ref[INP_598452.2] poly-U binding splicing factor 60 isoform b [Mus musculus]	1.89E-04	0.93	4.15	58544.6	7677895	2 (0.0002)
	46	g[153791474]ref[INP_473394.3] G protein-coupled receptor 98 [Mus musculus]	1.97E-04	0.69	54.11	887610.3	153791474	9 (2.2122)
	47	g[149256684]ref[INP_001481125.1] PREDICTED: similar to macrophage migration inhibitory factor isoform 1 [Mus musculus]	2.01E-04	0.21	10.09	12517.2	149256684	1 (1.0000)
	48	g[131324532]ref[INP_083821.1] hypothetical protein LOC328092 [Mus musculus]	2.40E-04	0.78	18.15	18235.7	31324532	2 (1.1000)
	49	g[150726896]ref[INP_001002842.1] PML-RARA regulated adaptor molecule 1 [Mus musculus]	2.62E-04	0.01	8.07	75491.8	50726896	1 (1.0000)
	50	g[186262151]ref[INP_033836.2] Rho GTPase activating protein 5 [Mus musculus]	2.99E-04	0.39	20.11	172470.2	86262151	3 (1.0110)
	51	g[125660464]ref[INP_001009947.2] dedicator of cytokinesis 11 [Mus musculus]	3.40E-04	0.13	8.09	237768.6	125660464	1 (1.0000)
	52	g[131541822]ref[INP_081188.2] WD repeat domain 40A [Mus musculus]	3.75E-04	0.08	10.07	50458.9	31541822	1 (1.0000)
	53	g[186662408]ref[INP_031786.2] carnitine acetyltransferase [Mus musculus]	3.77E-04	0.12	8.09	70839.3	86662408	1 (1.0000)
	54	g[129789329]ref[INP_598578.1] zinc finger protein 451 [Mus musculus]	4.11E-04	0.58	10.16	120069.2	29789329	1 (1.0000)
	55	g[127370290]ref[INP_768441.1] cadherin 7, type 2 [Mus musculus]	4.20E-04	0.12	18.06	87200.9	27370290	2 (1.1000)
	56	g[121312780]ref[INP_080646.1] MYST histone acetyltransferase 1 [Mus musculus]	4.34E-04	0.07	10.09	52573.6	21312780	1 (1.0000)
	57	g[146149270]ref[INP_001078890.1] test						

Table 1 continued

13	g[34147232]ref[NP_890002.1] potassium channel, subfamily V, member 2 [Mus musculus]	1.98E-05	0.11	12.08	64461.1	34147232	2 (0 10 10)
16	g[29244176]ref[NP_808385.1] hypothetical protein 4732456N10 [Mus musculus]	2.77E-05	1.10	22.15	58266.0	29244176	3 (1 10 10)
18	g[51772073]ref[XP_486986.1] PREDICTED: hypothetical protein [Mus musculus]	6.64E-05	0.23	10.10	40984.6	51772073	1 (1 00 00)
19	g[40789298]ref[NP_796347.2] PTPRF interacting protein alpha 2 [Mus musculus]	5.43E-05	0.08	20.10	143245.5	40789298	3 (1 10 11)
20	g[110625972]ref[NP_766294.2] hypothetical protein LOC231014 [Mus musculus]	5.55E-05	0.07	10.08	113658.9	110625972	1 (1 00 00)
21	g[13430690]ref[NP_056602.1] histone cluster 1, H1e [Mus musculus]	5.69E-05	0.86	10.15	21977.1	13430690	1 (1 00 00)
22	g[6678318]ref[NP_033394.1] transforming growth factor, beta 3 [Mus musculus]	9.28E-05	0.34	28.11	46884.4	6678318	3 (2 10 00)
23	g[23346495]ref[NP_694721.1] solute carrier family 16, member 11 [Mus musculus]	1.03E-04	0.23	20.09	29030.3	23346495	2 (2 00 00)
24	g[40254190]ref[NP_668194.2] hypothetical protein LOC225004 [Mus musculus]	2.15E-04	0.54	10.12	139296.7	40254190	1 (1 00 00)
25	g[148233660]ref[XP_001473646.1] PREDICTED: similar to Potassium voltage-gated channel subfamily B membe	2.25E-04	0.33	18.09	102349.3	148233660	3 (0 10 10)
26	g[118964712]ref[NP_084450.2] multiple C2 domains, transmembrane 1 [Mus musculus]	2.89E-04	0.10	10.08	80593.3	118964712	1 (1 00 00)
28	g[96196318]ref[NP_031656.2] cyclin B2 [Mus musculus]	3.88E-04	0.11	26.08	45382.5	96196318	3 (2 00 00)
29	g[84875537]ref[NP_035010.3] nucleolin [Mus musculus]	3.90E-04	0.82	10.15	76722.7	84875537	1 (1 00 00)
30	g[162138926]ref[NP_031794.3] C-reactive protein, pentraxin-related [Mus musculus]	3.98E-04	0.70	10.12	25359.8	162138926	1 (1 00 00)
31	g[134031978]ref[NP_052509.2] leucine-rich PPR motif-containing protein [Mus musculus]	4.18E-04	0.11	10.10	156613.3	134031978	1 (1 00 00)
32	g[160358787]ref[NP_031430.2] a disintegrin and metalloprotease domain 9 precursor [Mus musculus]	4.31E-04	0.19	18.08	92079.0	160358787	3 (0 11 10)
33	g[149267887]ref[XP_922530.2] PREDICTED: similar to MSP23 isoform 1 [Mus musculus]	6.22E-04	0.85	18.15	33775.4	149267887	2 (1 10 00)
34	g[7948989]ref[NP_058044.1] peroxiredoxin 4 [Mus musculus]	6.22E-04	0.83	12.15	31052.3	7948989	2 (2 00 01)
35	g[133507240]ref[NP_082595.1] zinc finger protein 518 [Mus musculus]	6.83E-04	0.79	16.12	165602.5	133507240	2 (2 01 00)
36	g[20682847]ref[NP_631689.1] calcium response factor [Mus musculus]	7.75E-04	0.80	10.18	76396.2	20682847	1 (1 00 00)
37	g[21312790]ref[NP_080646.1] MYST histone acetyltransferase 1 [Mus musculus]	8.14E-04	0.16	10.11	52573.6	21312790	1 (1 00 00)
38	g[9678946]ref[NP_032660.1] microtubule-associated protein 1 B [Mus musculus]	9.32E-04	0.05	18.06	270407.9	9678946	3 (0 03 00)
39	g[37537522]ref[NP_658097.2] epiplakin 1 [Mus musculus]	9.63E-04	0.71	10.12	724671.4	37537522	3 (0 01 02)
1	g[157951604]ref[NP_031624.2] CAP, adenylate cyclase-associated protein 1 [Mus musculus]	4.81E-13	3.46	60.25	51564.5	157951604	6 (6 00 00)
2	g[21246823]ref[NP_085112.1] histone cluster 1, H1a [Mus musculus]	2.00E-12	0.98	10.30	21785.0	21246823	1 (1 00 00)
3	g[31712036]ref[NP_853613.1] eukaryotic translation initiation factor 5A [Mus musculus]	2.05E-12	1.95	20.31	16832.2	31712036	2 (2 00 00)
5	g[157951605]ref[NP_765988.2] DnaJ (Hsp40) homolog, subfamily C, member 5 [Mus musculus]	1.78E-10	1.31	28.27	29812.4	157951605	3 (2 10 00)
6	g[94380203]ref[XP_001003154.1] PREDICTED: similar to Glucose phosphate isomerase 1 isoform 2 [Mus muscu	2.00E-10	2.80	32.24	37943.3	94380203	4 (3 00 01)
7	g[15808983]ref[NP_291039.1] eukaryotic translation initiation factor 4H [Mus musculus]	6.71E-09	0.93	10.22	27340.8	15808983	1 (1 00 00)
10	g[11760333]ref[NP_035470.3] serine (or cysteine) proteinase inhibitor, clade F, member 1 [Mus musculus]	3.43E-08	0.56	10.11	46233.7	11760333	1 (1 00 00)
11	g[6680309]ref[NP_032329.1] heat shock protein 1 (chaperonin 10) [Mus musculus]	4.25E-08	0.97	10.22	10962.6	6680309	1 (1 00 00)
13	g[66800067]ref[NP_032181.1] glucose phosphate isomerase 1 [Mus musculus]	9.48E-08	1.04	16.23	62767.5	66800067	2 (2 01 00)
14	g[11232634]ref[NP_031978.2] protein disulfide isomerase associated 3 [Mus musculus]	1.71E-07	0.81	10.15	56978.0	11232634	1 (1 00 00)
15	g[6680924]ref[NP_031713.1] cofilin 1, non-muscle [Mus musculus]	1.85E-07	1.84	20.19	18599.4	6680924	2 (2 00 00)
19	g[11464971]ref[NP_062422.1] plectstrin [Mus musculus]	1.77E-06	0.13	10.09	39900.4	11464971	1 (1 00 00)
20	g[7305061]ref[NP_038930.1] FK506 binding protein 3 [Mus musculus]	2.38E-06	1.01	18.22	25147.6	7305061	2 (1 10 00)
21	g[6753099]ref[NP_033817.1] apurinic/apyrimidinic endonuclease 1 [Mus musculus]	2.44E-06	1.95	30.21	35490.2	6753099	3 (3 00 00)
22	g[31982724]ref[NP_068056.2] MYB binding protein (P160) 1a [Mus musculus]	2.97E-06	1.09	28.21	152035.8	31982724	3 (2 01 00)
23	g[6756041]ref[NP_038870.1] tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta pol	3.72E-06	0.88	10.17	27771.0	6756041	1 (1 00 00)
27	g[6678439]ref[NP_033456.1] protease, serine, 2 [Mus musculus]	1.59E-06	0.84	10.14	26203.4	6678439	1 (1 00 00)
31	g[116517303]ref[NP_032982.2] polypyrimidine tract binding protein 1 isoform 2 [Mus musculus]	2.08E-06	0.49	10.15	59891.5	116517303	2 (2 00 00)
32	g[21703784]ref[NP_663367.1] Sd2-associated alphanogene 2 [Mus musculus]	2.40E-06	1.04	10.13	23473.5	21703784	1 (1 00 00)
33	g[82917230]ref[XP_926154.1] PREDICTED: hypothetical protein [Mus musculus]	3.74E-06	0.69	10.15	12418.3	82917230	1 (1 00 00)
35	g[40556396]ref[NP_855006.1] leucine rich repeat and sterile alpha motif containing 1 [Mus musculus]	4.98E-06	1.12	26.10	83976.0	40556396	4 (3 01 00)
36	g[94385969]ref[XP_486188.4] PREDICTED: similar to Nucleophosmin 1 isoform 1 [Mus musculus]	6.39E-06	0.95	10.20	31404.0	94385969	1 (1 00 00)
37	g[6678803]ref[NP_032045.1] FK506 binding protein 1a [Mus musculus]	6.80E-06	0.81	10.17	11922.6	6678803	1 (1 00 00)
38	g[8570167]ref[NP_001026328.1] F-box protein 33 [Mus musculus]	6.98E-06	0.00	8.06	33530.1	85701674	1 (0 10 00)
39	g[149262849]ref[XP_001480231.1] PREDICTED: hypothetical protein [Mus musculus]	7.72E-05	0.19	18.11	39304.9	149262849	2 (1 10 00)
43	g[21105865]ref[NP_631939.1] plectstrin homolog, Sec7 and coiled-coil domains, binding protein [Mus musculus]	1.35E-04	0.09	10.08	40142.7	21105865	2 (0 01 10)
46	g[85862397]ref[NP_001028536.1] protocadherin LKO [Mus musculus]	1.85E-04	0.09	10.08	142533.2	85862397	2 (0 01 10)
47	g[30425112]ref[NP_788612.1] hypothetical protein LOC109154 [Mus musculus]	1.98E-04	0.37	10.12	32293.8	30425112	1 (1 00 00)
50	g[6755100]ref[NP_035248.1] ErbB3-binding protein 1 [Mus musculus]	2.15E-04	0.78	20.14	43698.6	6755100	2 (2 00 00)
51	g[149257980]ref[XP_001476336.1] PREDICTED: hypothetical protein LOC78552 [Mus musculus]	2.92E-04	0.31	24.14	23369.5	149257980	3 (2 01 00)
52	g[85702355]ref[NP_001034268.1] bicucullin D homolog 2 isoform 1 [Mus musculus]	3.05E-04	0.16	14.08	98646.7	85702355	3 (3 00 02)
53	g[20806109]ref[NP_031441.2] poly (ADP-ribose) polymerase family, member 1 [Mus musculus]	3.20E-04	0.64	12.12	112720.6	20806109	1 (2 00 01)
54	g[14925367]ref[XP_893843.3] PREDICTED: similar to CLRN2 protein [Mus musculus]	3.27E-04	0.24	12.11	33527.7	149253671	2 (0 10 01)
55	g[31542579]ref[NP_852682.1] synaptotagmin XV isoform a [Mus musculus]	3.54E-04	0.11	8.09	47270.0	31542579	1 (0 10 00)
57	g[31543487]ref[NP_032687.2] polycystic kidney disease 2 [Mus musculus]	3.59E-04	0.07	18.00	108995.4	31543487	3 (0 11 01)
58	g[38710169]ref[NP_035841.1] ferritin-like 3 protein [Mus musculus]	3.71E-04	0.06	8.09	117167.8	38708163	2 (0 01 10)
59	g[40254337]ref[NP_848724.2] E2F transcription factor 7 [Mus musculus]	4.39E-04	0.22	16.13	99534.4	40254337	3 (0 10 02)
60	g[14925631]ref[XP_89743.2] PREDICTED: hypothetical protein LOC223825 [Mus musculus]	4.42E-04	0.51	34.11	186020.6	149256314	4 (2 11 00)
61	g[149267887]ref[XP_922530.2] PREDICTED: similar to MSP23 isoform 1 [Mus musculus]	4.54E-04	1.59	18.15	33775.4	149267887	2 (1 10 00)
62	g[7948989]ref[NP_058044.1] peroxiredoxin 4 [Mus musculus]	4.54E-04	0.87	10.15	31052.3	7948989	1 (1 00 00)
63	g[117414170]ref[NP_033257.2] son of sevenless 1 [Mus musculus]	4.70E-04	0.22	16.11	150881.8	117414170	2 (2 00 00)
64	g[14925134]ref[XP_001479436.1] PREDICTED: hypothetical protein [Mus musculus]	5.28E-04	0.32	10.11	27772.0	149251341	1 (1 00 00)
65	g[6754256]ref[NP_034612.1] 5-hydroxytryptamine (serotonin) receptor 1B [Mus musculus]	5.51E-04	0.35	10.10	43078.4	6754256	1 (1 00 00)
66	g[149263539]ref[XP_001475822.1] PREDICTED: tumor domain containing 9 [Mus musculus]	5.74E-04	0.12	10.08	138782.0	149263539	2 (0 01 10)
67	g[20688581]ref[XP_134800.1] PREDICTED: hypothetical protein LOC69809 isoform 1 [Mus musculus]	5.78E-04	0.17	10.09	25444.9	20688581	1 (1 00 00)
68	g[158110787]ref[NP_032981.2] microtubule-associated protein 7 [Mus musculus]	6.74E-04	0.13	18.08	81973.0	158110787	3 (0 11 10)
70	g[157277999]ref[NP_001098107.1] vomeronasal receptor Vmn2r22 [Mus musculus]	7.27E-04	0.39	20.13	96138.4	157277998	2 (2 00 00)
71	g[34808712]ref[NP_035203.2] perforin 1 [Mus musculus]	7.45E-04	0.39	8.12	62094.7	34808712	1 (1 00 00)
72	g[149250077]ref[XP_001480904.1] PREDICTED: zinc finger protein 690 [Mus musculus]	7.49E-04	0.06	8.09	95460.9	149250077	1 (1 00 00)
73	g[6755040]ref[NP_035002.1] profilin 1 [Mus musculus]	7.67E-04	0.93	10.21	14957.1	6755040	1 (1 00 00)
74	g[21703812]ref[NP_663381.1] protein P3 [Mus musculus]	7.95E-04	0.34	8.11	50254.6	21703812	2 (0 00 02)
75	g[9910502]ref[NP_064333.1] ubiquitin-conjugating enzyme E2L 6 [Mus musculus]	8.34E-04	0.23	10.08	17757.6	9910502	2 (0 01 10)
76	g[9898581]ref[NP_570947.2] paternally expressed 10 isoform RF1RF2 [Mus musculus]	8.58E-04	1.12	8.09	115496.4	98985814	1 (1 00 00)
1	g[157951604]ref[NP_031624.2] CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1.70E-11	2.09	36.25	51564.5	157951604	5 (3 00 11)
2	g[29244176]ref[NP_808385.1] hypothetical protein 4732456N10 [Mus musculus]	3.67E-08	1.80	26.17	58266.0	29244176	3 (2 10 00)
3	g[31981562]ref[NP_035229.2] pyruvate kinase, muscle [Mus musculus]	2.37E-06	1.60	28.16	57844.6	31981562	4 (2 01 01)
8	g[13430880]ref[NP_056602.1] histone cluster 1, H1e [Mus musculus]	1.91E-05	0.91	10.16	21977.1	13430880	1 (1 00 00)
9	g[82917230]ref[XP_926154.1] PREDICTED: hypothetical protein [Mus musculus]	2.02E-05	0.73	8.15	12418.3	82917230	1 (1 00 00)
11	g[76677885]ref[NP_598452.2] poly-U binding splicing factor 50 isoform b [Mus musculus]	2.84E-05	1.08	22.16	58544.6	76677885	3 (1 10 10)
12	g[31981690]ref[NP_112442.2] heat shock protein 8 [Mus musculus]	3.14E-05	0.13	10.11	70870.6	31981690	1 (1 00 00)
13	g[6671509]ref[NP_031419.1] actin, beta, cytoplasmic [Mus musculus]	4.28E-05	0.45	10.12	41735.5	6671509	1 (1 00 00)
14	g[3318692]ref[NP_808332.2] plasticity related gene 1 [Mus musculus]	5.47E-05	0.03	4.07	83361.8	33186921	2 (0 00 02)
15	g[117647243]ref[NP_038934.2] a disintegrin-like and metalloprotease (repolyrin type) with thrombospondin type	9.94E-05	0.03	18.00	96822.5	117647243	2 (1 10 00)
16	g[58901478]ref[NP_00101860.1] olfactory receptor 1222 [Mus musculus]	1.03E-04	0.05	10.18	35222.8	58901478	1 (1 00 00)
17	g[6678439]ref[NP_031958.1] endoglin [Mus musculus]	1.11E-04	0.23	16.10	70034.4	6678439	2 (0 20 00)
18	g[4247609]ref[NP_766536.2] mannoside acetylglucosaminyltransferase 5, isoenzyme B [Mus musculus]	1.22E-04	0.54	18.11	89472.5	4247609	2 (1 10 00)
19	g[9440801]ref[XP_990685.1] PREDICTED: similar to valosin isoform 1 [Mus musculus]	1.28E-04	0.64	10.12	88850.7	94408011	1 (1 00 00)
20	g[33942081]ref[NP_898838.1] tubulin tyrosine ligase-like family, member 12 [Mus musculus]	2.18E-04	0.40	10.09	74038.8	33942081	1 (1 00 00)
23	g[31560462]ref[NP_058077.2] syntaxin 7 [Mus musculus]	2.29E-04	0.04	4.08	29736.3	31560462	2 (0 00 02)
24	g[106827652]ref[NP_034018.2] complement component factor H [Mus musculus]	2.98E-04	0.22	18.10	141270.4	106827652	2 (1 10 00)
25	g[124486690]ref[NP_032426.2] integrin alpha L [Mus musculus]	3.48E-04	0.22	8.09	128065.7	124486690	1 (1 00 00)
26	g[1246893]ref[NP_064418.1] histone cluster 1, H1b [Mus musculus]	3.62E-04	1.24	20.13	22576.0	21426993	2 (2 00 00)
27	g[94385769]ref[XP_001004138.1] PREDICTED: similar to serine beta lactamase-like protein LACT-1 isoform 2 [M	3.84E-04	0.05	12.09	60705.1	94385759	2 (1 00 01)
28	g[149266532]ref[XP_001475762.1] PREDICTED: similar to ribosomal protein L23a [Mus musculus]	3.86E-04	0.69	10.13			

Table 1 continued

	32	g 6678902 ref NP_032536.1 matrix metalloproteinase 2 [Mus musculus]	4.39E-04	0.75	10.14	74101.9	6578802	2 (2 000 0)
	33	g 232595314 ref NP_705774.1 membrane bound O-acetyltransferase domain containing 1 [Mus musculus]	5.40E-04	0.19	12.12	56159.7	23953614	2 (0 101 0)
	34	g 19705424 ref NP_033465.1 proteasome 26S non-ATPase subunit 3 [Mus musculus]	5.54E-04	0.55	8.11	60717.9	19705424	2 (0 101 0)
	35	g 37497112 ref NP_058088.2 RNA binding motif protein 3 [Mus musculus]	5.58E-04	0.07	8.10	16760.8	37497112	1 (0 100 0)
	36	g 34808712 ref NP_035203.2 perforin 1 [Mus musculus]	5.64E-04	0.88	10.13	62094.7	34808712	1 (0 100 0)
	37	g 181333917 ref NP_001028467.2 homeodomain interacting protein kinase 4 [Mus musculus]	5.83E-04	0.03	10.07	69278.4	181333917	1 (1 000 0)
	38	g 935701740 ref NP_001028413.1 hypothetical protein LOC211206 [Mus musculus]	6.08E-04	0.18	12.14	142108.2	85701740	3 (0 100 2)
	39	g 157951655 ref NP_033785.2 advinin [Mus musculus]	6.93E-04	0.24	6.11	82031.2	157951655	2 (0 001 1)
	40	g 40353214 ref NP_954665.1 suppressor of zeste 12 homolog [Mus musculus]	7.03E-04	0.03	8.08	83025.3	40353214	1 (0 100 0)
	41	g 76574171 ref NP_035987.2 odd Oziten-m homolog 3 [Mus musculus]	7.05E-04	0.19	14.11	303063.9	76574171	3 (1 000 2)
	42	g 149256458 ref XP_194337.7 PREDICTED: multiple EGF-like-domains 8 [Mus musculus]	8.05E-04	0.34	24.10	303496.9	149256458	5 (0 112 1)
	43	g 157951641 ref NP_001074755.2 FAT tumor suppressor homolog 1 [Mus musculus]	8.07E-04	0.38	20.11	506263.8	157951641	3 (1 011 0)
	44	g 84939750 ref NP_001034204.1 zinc finger protein 306-like [Mus musculus]	8.15E-04	0.58	10.10	54088.3	84939750	1 (1 000 0)
	45	g 183944270 ref NP_001074747.2 TBC1 domain family, member 4 [Mus musculus]	8.37E-04	0.63	28.10	140330.2	183944270	3 (2 100 0)
	46	g 126032329 ref NP_034236.2 eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	8.53E-04	2.80	48.20	50113.5	126032329	5 (4 100 0)
	47	g 84875498 ref NP_067518.2 voltage-gated sodium channel type V alpha [Mus musculus]	8.57E-04	0.11	24.10	227704.3	84875498	3 (0 300 0)
	48	g 21704042 ref NP_663504.1 cleavage stimulation factor subunit 3 isoform 1 [Mus musculus]	8.92E-04	0.14	14.09	82876.1	21704042	2 (1 001 0)
	49	g 175677440 ref NP_031427.2 a disintegrin and metalloproteinase domain 5 [Mus musculus]	8.93E-04	0.15	10.11	84534.0	175677440	2 (1 001 0)
	1	g 31712036 ref NP_853613.1 eukaryotic translation initiation factor 5A [Mus musculus]	3.33E-16	1.94	20.28	16832.2	31712036	2 (2 000 0)
	2	g 42415475 ref NP_035162.1 prolly 4-hydroxyase, beta polypeptide [Mus musculus]	7.33E-13	0.96	10.24	57058.0	42415475	1 (1 000 0)
AnXA4 ENaCl	7	g 47894399 ref NP_00101491.1 tropomyosin 4 [Mus musculus]	6.05E-09	2.67	28.17	28467.8	47894399	3 (2 100 0)
	8	g 6830087 ref NP_032181.1 glucose phosphate isomerase 1 [Mus musculus]	3.93E-09	0.56	18.19	62767.5	6830087	2 (1 100 0)
	10	g 34380223 ref XP_001003154.1 PREDICTED: similar to Glucose phosphate isomerase 1 isoform 2 [Mus musculus]	1.55E-07	1.66	20.21	37843.3	34380223	2 (2 000 0)
	11	g 157951604 ref NP_031624.2 CAP, adenylate cyclase-associated protein 1 [Mus musculus]	3.04E-07	2.00	38.21	51564.5	157951604	4 (3 100 0)
	17	g 157951589 ref NP_033931.4 carbonic anhydrase 2 [Mus musculus]	1.32E-05	0.92	10.19	28032.3	157951589	1 (1 000 0)
	18	g 41350312 ref NP_038636.2 nascent polypeptide-associated complex alpha subunit isoform b [Mus musculus]	1.62E-05	0.85	10.16	23383.7	41350312	1 (1 000 0)
	19	g 31962724 ref NP_058056.2 MYB binding protein (P160) 1a [Mus musculus]	1.73E-06	0.92	18.16	152035.8	31962724	2 (1 010 0)
	24	g 82917230 ref XP_928154.1 PREDICTED: hypothetical protein [Mus musculus]	4.38E-06	0.78	10.16	12418.3	82917230	1 (1 000 0)
	26	g 124358949 ref NP_808448.2 dedicator of cytokinesis 5 [Mus musculus]	7.68E-05	0.33	26.09	214428.5	124358949	4 (1 102 0)
	28	g 124339839 ref NP_038586.2 heat shock 70kDa protein 1-like [Mus musculus]	1.98E-05	0.68	12.12	70638.8	124339839	3 (0 100 2)
	31	g 34808712 ref NP_035203.2 perforin 1 [Mus musculus]	4.16E-05	0.62	10.14	62094.7	34808712	1 (1 000 0)
	33	g 6753089 ref NP_033817.1 apurinic/apyrimidinic endonuclease 1 [Mus musculus]	5.58E-05	0.89	10.18	35480.2	6753089	1 (1 000 0)
	39	g 124497249 ref NP_001074886.1 chromodomain helicase DNA binding protein 7 [Mus musculus]	6.09E-05	0.02	10.05	51198.7	124497249	1 (1 000 0)
	40	g 76677893 ref NP_598453.2 poly-U binding splicing factor 80 isoform b [Mus musculus]	1.00E-04	1.00	20.23	334055.5	124497249	3 (0 201 0)
	42	g 82930015 ref XP_486217.2 PREDICTED: similar to nuclear protein-NHP2-like protein [Mus musculus]	1.31E-04	0.99	8.15	58544.6	76677893	2 (0 002 0)
	43	g 153945822 ref NP_033038.2 RAD50 homolog [Mus musculus]	2.08E-04	0.86	10.15	14173.5	82930015	1 (1 000 0)
	44	g 153945822 ref NP_033038.2 RAD50 homolog [Mus musculus]	2.25E-04	0.10	10.10	153545.6	153945822	2 (0 100 1)
	47	g 86262161 ref NP_796294.2 phosphoinositide-3-kinase, regulatory subunit 5, p101 [Mus musculus]	2.53E-04	0.03	10.08	96933.1	86262161	2 (0 011 0)
	48	g 67893339 ref NP_032049.1 forkhead box B2 [Mus musculus]	2.71E-04	0.41	18.13	45170.0	67893339	2 (1 100 0)
	49	g 84385999 ref XP_486188.4 PREDICTED: similar to Nucleophosmin 1 isoform 1 [Mus musculus]	3.22E-04	0.01	12.19	31404.0	84385999	2 (1 000 1)
	47	g 53791438 ref NP_660258.2 Aistrom syndrome 1 [Mus musculus]	3.35E-04	0.57	24.10	280212.1	53791438	5 (1 011 2)
	48	g 6790197 ref NP_062773.1 Rhesus blood group-associated C glycoprotein [Mus musculus]	4.31E-04	0.03	18.08	54947.5	6790197	2 (1 100 0)
	49	g 118964694 ref NP_031688.2 cadherin 15 [Mus musculus]	4.33E-04	0.06	10.07	85643.1	118964694	2 (0 100 1)
	50	g 33239431 ref NP_776292.1 RCC1-like [Mus musculus]	4.48E-04	0.60	12.13	55983.0	33239431	2 (1 000 1)
	51	g 31542192 ref NP_658190.2 microtubule-associated protein 7 domain containing 1 [Mus musculus]	5.11E-04	1.00	10.11	93341.4	31542192	1 (1 000 0)
	52	g 6755040 ref NP_035202.1 profilin 1 [Mus musculus]	5.23E-04	1.03	18.19	14957.1	6755040	2 (1 100 0)
	53	g 149256048 ref XP_001475846.1 PREDICTED: similar to LAIR Hlog [Mus musculus]	5.77E-04	0.08	10.09	19857.5	149256048	1 (1 000 0)
	54	g 121247243 ref NP_001073400.1 hypothetical protein LOC384814 [Mus musculus]	6.10E-04	0.11	10.07	80579.0	121247243	3 (0 101 1)
	55	g 46048259 ref NP_084444.2 RIKEN cDNA 4921505C17 [Mus musculus]	6.11E-04	0.08	10.09	191567.8	46048259	2 (0 011 0)
	56	g 20208103 ref NP_031441.2 poly (ADP-ribose) polymerase family, member 1 [Mus musculus]	6.41E-04	0.55	10.12	112720.8	20208103	1 (1 000 0)
	57	g 149255911 ref XP_001477495.1 PREDICTED: similar to putative pheromone receptor [Mus musculus]	7.13E-04	0.01	10.03	84630.6	149255911	1 (1 000 0)
	59	g 221299593 ref NP_667194.1 olfactory receptor 1259 [Mus musculus]	7.20E-04	0.18	12.10	34895.5	22129959	2 (0 101 0)
	60	g 10181180 ref NP_065650.1 zinc finger protein 297 [Mus musculus]	7.29E-04	0.09	20.09	66028.2	10181180	6 (2 031 0)
	61	g 6880423 ref NP_032391.1 interleukin 18 receptor 1 [Mus musculus]	7.30E-04	0.27	20.09	81800.4	6880423	2 (2 000 0)
	62	g 34328045 ref NP_031761.1 procollagen, type IV, alpha 4 [Mus musculus]	7.43E-04	0.23	20.10	164085.5	34328045	2 (2 000 0)
	65	g 40786539 ref NP_954551.1 zona pellucida binding protein 2 isoform 2 [Mus musculus]	8.83E-04	0.14	8.10	26450.8	40786539	1 (0 100 0)
	67	g 145045239 ref NP_062679.2 RanBP-type and C3HC4-type zinc finger containing 1 [Mus musculus]	8.19E-04	0.35	22.11	57534.3	145045239	3 (1 101 0)
	68	g 96792033 ref NP_032803.1 phenylalanine hydroxylase [Mus musculus]	8.95E-04	0.05	8.07	51928.6	96792033	1 (0 100 0)
	69	g 82801053 ref XP_820730.1 PREDICTED: similar to REX1, RNA exonuclease 1 homolog (S. cerevisiae) [Mus musculus]	8.95E-04	0.10	14.09	69035.3	82801053	2 (0 110 0)
	70	g 6679159 ref NP_032774.1 dual specificity phosphatase 8 [Mus musculus]	8.95E-04	0.06	8.09	89947.2	6679159	2 (0 011 0)
	71	g 29135339 ref NP_186155.2 polycystic kidney and hepatic disease 1-like 1 [Mus musculus]	8.99E-04	0.54	48.17	464728.7	29135339	7 (3 110 2)
	1	g 112181167 ref NP_031599.2 complement component 1, q subcomponent binding protein [Mus musculus]	7.33E-14	0.88	10.21	31024.7	112181167	1 (1 000 0)
	2	g 6830924 ref NP_031713.1 collagen 1, non-muscle [Mus musculus]	1.12E-09	1.68	20.21	19599.4	6830924	2 (2 000 0)
	3	g 31981562 ref NP_035228.2 pyruvate kinase, muscle [Mus musculus]	2.01E-09	3.31	42.19	57844.8	31981562	5 (4 000 1)
	5	g 148258641 ref XP_001478027.1 PREDICTED: similar to Phosphoserine aminotransferase 1 isoform 1 [Mus musculus]	8.76E-09	0.91	10.16	40531.4	148258641	1 (1 000 0)
	9	g 28244176 ref NP_808385.1 hypothetical protein 4732456N10 [Mus musculus]	5.44E-08	2.73	30.17	55266.0	28244176	4 (2 100 1)
	10	g 148274047 ref XP_863988.2 PREDICTED: similar to pol protein [Mus musculus]	1.02E-05	0.04	10.07	24400.9	148274047	1 (1 000 0)
	12	g 82917230 ref XP_928154.1 PREDICTED: hypothetical protein [Mus musculus]	1.67E-05	0.46	8.11	12418.3	82917230	1 (1 000 0)
	13	g 6871509 ref NP_031419.1 actin, beta, cytoplasmic [Mus musculus]	2.23E-05	1.48	30.19	41736.5	6871509	3 (3 000 0)
	14	g 13195628 ref NP_077161.1 cleavage stimulation factor, 3' pre-RNA, subunit 1 [Mus musculus]	4.11E-05	0.03	10.07	43831.5	13195628	1 (1 000 0)
	15	g 21704162 ref NP_663563.1 kinesin family member 22 [Mus musculus]	5.79E-05	0.10	10.08	73189.4	21704162	1 (1 000 0)
	16	g 15743554 ref NP_277059.1 sprouty-related protein 1 with EVH-1 domain [Mus musculus]	1.49E-04	0.37	14.12	50663.9	15743554	2 (1 000 0)
	17	g 151921287 ref NP_001004141.1 cytochrome P450, family 2, subfamily j, polypeptide 11 [Mus musculus]	1.75E-04	0.26	10.12	57490.3	151921287	1 (1 000 0)
	21	g 6754900 ref NP_035981.1 5' nucleotidase, ecto [Mus musculus]	1.88E-04	0.05	14.08	63864.0	6754900	2 (1 000 0)
	22	g 84385999 ref XP_486188.4 PREDICTED: similar to Nucleophosmin 1 isoform 1 [Mus musculus]	1.97E-04	0.78	10.13	31404.0	84385999	1 (1 000 0)
	23	g 47078289 ref NP_035406.3 ring finger protein 12 [Mus musculus]	2.08E-04	0.61	10.14	86375.5	47078289	1 (1 000 0)
	24	g 149265559 ref XP_001478902.1 PREDICTED: similar to PES1 protein [Mus musculus]	2.08E-04	0.17	18.07	64781.3	149265559	3 (1 011 0)
	26	g 42475692 ref NP_780358.2 hypothetical protein LOC69551 [Mus musculus]	2.30E-04	0.25	10.09	35302.2	42475692	1 (1 000 0)
	27	g 149260369 ref XP_001474560.1 PREDICTED: similar to Zfp187 protein [Mus musculus]	2.45E-04	0.19	8.09	81351.2	149260369	2 (0 002 0)
	28	g 126032329 ref NP_034236.2 eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2.64E-04	2.83	48.20	50113.5	126032329	5 (4 010 0)
	29	g 14845510 ref NP_569721.1 RecQ protein-like 5 [Mus musculus]	3.00E-04	0.40	12.09	108244.9	14845510	3 (0 100 2)
	30	g 28244494 ref NP_808548.1 hypothetical protein LOC330228 [Mus musculus]	3.28E-04	0.28	18.07	27894.9	28244494	2 (1 100 0)
	31	g 31541815 ref NP_076226.2 L-specific multifunctional beta-oxidation protein [Mus musculus]	3.94E-04	0.01	8.05	78301.0	31541815	1 (0 100 0)
	32	g 84000050 ref NP_786320.2 G protein-coupled receptor 149 [Mus musculus]	4.17E-04	0.07	14.06	60519.1	84000050	2 (0 110 0)
	33	g 148271040 ref XP_001481302.1 PREDICTED: hypothetical protein [Mus musculus]	4.58E-04	0.08	10.07	20232.8	148271040	1 (1 000 0)
	34	g 8055314 ref NP_051265.1 nucleoporin 210 [Mus musculus]	4.60E-04	0.28	22.10	204137.2	8055314	3 (1 101 0)
	35	g 124486789 ref NP_001074760.1 PDSS, regulator of cohesion maintenance, homolog A [Mus musculus]	4.83E-04	0.29	10.13	150221.1	124486789	1 (1 000 0)
	36	g 30425250 ref NP_780706.1 hypothetical protein LOC238980 [Mus musculus]	4.70E-04	0.59	8.16	42004.0	30425250	1 (0 100 0)
	37	g 157951604 ref NP_031624.2 CAP, adenylate cyclase-associated protein 1 [Mus musculus]	4.93E-04	0.48	12.12	51564.5	157951604	2 (1 000 1)
	38	g 29789329 ref NP_598578.1 zinc finger protein 451 [Mus musculus]	5.29E-04	0.88	18.18	120099.2	29789329	2 (1 100 0)
	39	g 48227553 ref NP_667135.1 olfactory receptor 476 [Mus musculus]	5.37E-04	0.02	10.09	34192.4	48227553	1 (1 000 0)
	40	g 149259278 ref XP_921768.2 PREDICTED: similar to Phlpp protein isoform 3 [Mus musculus]	5.47E-04	0.13	24.09	288733.5	910228	3 (0 300 0)
	41	g 149259278 ref XP_921768.2 PREDICTED: similar to Phlpp protein isoform 3 [Mus musculus]	5.60E-04	0.31	14.08	147717.2	149259278	2 (1 100 0)
	42	g 8440						

Table 1 continued

AnXAS ENaCl	49	g[139948022]refNP_001077278.1	hypothetical protein LOC72446 [Mus musculus]	7.72E-04	0.36	4.10	40981.7	139949022	2 (0.0002)
	50	g[14235747]refNP_856747.1	hypothetical protein LOC390967 [Mus musculus]	7.98E-04	0.77	20.15	28561.9	41235747	2 (0.0000)
	51	g[134031978]refNP_082508.2	leucine-rich FPR motif-containing protein [Mus musculus]	8.25E-04	0.23	26.10	156613.3	134031978	3 (0.0100)
	52	g[58037343]refNP_053011.1	tetratricopeptide repeat domain 21A [Mus musculus]	8.88E-04	0.18	10.11	148633.5	58037343	2 (0.0110)
	53	g[22128741]refNP_867323.1	olfactory receptor 559 [Mus musculus]	9.02E-04	0.44	14.10	354162	22128741	2 (0.0101)
	54	g[96355469]refNP_038959.3	proline-serine-threonine phosphatase-interacting protein 2 [Mus musculus]	9.21E-04	0.06	8.08	39947.9	96355469	1 (0.1000)
	55	g[3155993]refNP_558434.2	tor1a family, member B [Mus musculus]	9.71E-04	0.10	12.09	37817.3	31559990	2 (0.0001)
	56	g[11395591]refNP_001038994.1	microchidia 3 [Mus musculus]	9.92E-04	0.09	8.09	106495.9	113955911	1 (0.1000)
	57	g[11712036]refNP_853613.1	eukaryotic translation initiation factor 5A [Mus musculus]	5.45E-12	2.89	30.28	16832.2	31712036	3 (0.0000)
	58	g[9438023]refNP_00103154.1	PREDICTED: similar to Glucose phosphate isomerase 1 isoform 2 [Mus muscu]	4.11E-10	1.71	20.23	37843.3	94380203	2 (0.0000)
	59	g[680824]refNP_031713.1	collin 1, non-muscle [Mus musculus]	1.44E-08	3.60	40.25	18559.4	6808024	4 (0.0000)
	60	g[31982196]refNP_032643.2	malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1.53E-08	0.98	10.27	35611.2	31982186	1 (0.0000)
	61	g[6810659]refNP_031634.1	cytochrome c, somatic [Mus musculus]	6.21E-08	0.93	10.15	11605.4	681065	1 (0.0000)
	62	g[6756941]refNP_035670.1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta pol	6.49E-08	0.87	10.24	27771.0	6756941	1 (0.0000)
	63	g[112293264]refNP_031978.2	protein disulfide isomerase associated 3 [Mus musculus]	2.19E-07	1.34	20.23	59678.0	112293264	2 (0.0000)
	64	g[124339838]refNP_038586.2	heat shock 70kDa protein 1-like [Mus musculus]	5.51E-07	0.85	10.14	70636.8	124339838	1 (0.0000)
	65	g[31982724]refNP_058056.2	MYB binding protein (P160) 1a [Mus musculus]	6.92E-07	1.11	22.18	152035.8	31982724	4 (0.0111)
	66	g[6755040]refNP_035202.1	profilin 1 [Mus musculus]	1.22E-06	1.57	24.19	14957.1	6755040	3 (0.0001)
	67	g[3065061]refNP_038930.1	FK506 binding protein 3 [Mus musculus]	1.66E-06	0.87	10.15	25147.6	3065061	1 (0.0000)
	68	g[113722131]refNP_032150.2	senatatin 3 [Mus musculus]	2.43E-06	0.20	12.11	287586.7	113722131	2 (0.1010)
	69	g[157951609]refNP_765988.2	DnaJ (Hsp40) homolog, subfamily C, member 8 [Mus musculus]	2.58E-06	0.82	10.19	28912.4	157951606	1 (0.0000)
70	g[157951599]refNP_033931.4	carbonic anhydrase 2 [Mus musculus]	8.64E-06	0.87	10.16	20302.3	157951596	1 (0.0000)	
AnXAS EFA	71	g[94385699]refNP_486189.4	PREDICTED: similar to Nucleophosmin 1 isoform 1 [Mus musculus]	1.61E-05	0.49	38.20	31400.4	94385699	4 (0.3100)
	72	g[14925735]refNP_001478931.1	PREDICTED: olfactory receptor 694 [Mus musculus]	3.62E-05	0.36	10.02	38271.3	14925735	1 (0.0000)
	73	g[67553644]refNP_035424.1	RNA polymerase II transcriptional coactivator [Mus musculus]	3.91E-05	0.87	10.14	14427.4	6755364	1 (0.0000)
	74	g[124487380]refNP_038658.2	polyclonin 1 [Mus musculus]	5.63E-05	0.86	58.12	466573.3	124487380	8 (0.3130)
	75	g[6753069]refNP_033817.1	apurinic/apyrimidinic endonuclease 1 [Mus musculus]	8.78E-05	0.93	10.19	35490.2	6753069	1 (0.0000)
	76	g[149267887]refNP_922530.2	PREDICTED: similar to MSP23 isoform 1 [Mus musculus]	1.18E-04	0.80	10.12	33775.4	149267887	1 (0.0000)
	77	g[7035383]refNP_038812.1	phosphatidylinositol glycan anchor biosynthesis, class N [Mus musculus]	1.21E-04	0.36	18.10	105076.3	7035383	2 (1.1000)
	78	g[11760531]refNP_078362.2	centrosomal protein 70 [Mus musculus]	1.28E-04	0.43	14.12	71064.1	117605316	2 (0.1100)
	79	g[34587876]refNP_919238.1	T-box 20 isoform 1 [Mus musculus]	1.34E-04	0.10	20.08	49065.4	34587876	2 (0.0000)
	80	g[116347527]refNP_064223.2	PR domain containing 8 [Mus musculus]	1.39E-04	0.68	22.12	71728.7	116347527	4 (2.0101)
	81	g[27229050]refNP_090532.1	gonad specific ankyrin repeat protein isoform 1 [Mus musculus]	1.97E-04	0.32	12.13	39228.7	27229050	2 (0.0200)
	82	g[21311877]refNP_083037.1	poly(A)-specific ribonuclease (deadenylation nuclease) [Mus musculus]	2.18E-04	0.26	12.09	71588.9	21311877	2 (0.0200)
	83	g[124487341]refNP_808276.2	hypothetical protein LOC70354 [Mus musculus]	2.22E-04	0.18	16.10	119748.2	124487341	3 (0.0011)
	84	g[148228285]refNP_671511.2	T-cell activation GTPase activating protein 1 [Mus musculus]	2.27E-04	0.43	8.11	55746.6	148228285	1 (0.1000)
	85	g[126050572]refNP_001028547.2	hypothetical protein LOC319277 [Mus musculus]	2.99E-04	0.58	16.09	136389.0	126050572	2 (0.1000)
	86	g[26077005]refNP_082631.1	transmembrane protein 48 [Mus musculus]	3.55E-04	0.19	8.11	75408.0	26077005	1 (0.1000)
	87	g[31982823]refNP_033355.2	zinc finger protein 354A [Mus musculus]	3.73E-04	0.02	8.05	58662.2	31982823	1 (0.1000)
	88	g[133863022]refNP_780606.3	Sp110 nuclear body protein [Mus musculus]	4.63E-04	0.16	8.08	50140.2	133863022	2 (0.0101)
	89	g[34808712]refNP_035203.2	perforin 1 [Mus musculus]	5.47E-04	0.61	12.20	62094.7	34808712	2 (0.0001)
	90	g[6767816]refNP_032538.1	low density lipoprotein receptor-related protein 5 [Mus musculus]	5.53E-04	0.38	18.11	178965.3	6767816	3 (0.1010)
	Control EHaCl	91	g[30142693]refNP_838975.1	transmembrane epididymal protein 1 [Mus musculus]	5.76E-04	0.03	8.08	34794.1	30142695
92		g[31982322]refNP_032174.2	glycoprotein 5 (platelet) [Mus musculus]	6.31E-04	0.07	14.09	63381.5	31982322	2 (0.0101)
93		g[14504623]refNP_062678.2	RanBP-type and C/EBP-type zinc finger containing 1 [Mus musculus]	7.11E-04	0.24	12.09	57534.3	145046239	2 (0.0001)
94		g[17978260]refNP_536718.1	SAC (structural maintenance of chromosomes 1)-like 2 [Mus musculus]	7.30E-04	0.65	12.10	144512.3	17978260	4 (1.1002)
95		g[52350563]refNP_001047651.1	G protein-coupled receptor 158 [Mus musculus]	7.54E-04	0.03	8.11	134425.2	52350563	1 (0.1000)
96		g[50345972]refNP_032818.2	forkhead box C1 [Mus musculus]	7.69E-04	0.05	18.08	59939.6	50345972	2 (1.1000)
97		g[29244242]refNP_808420.1	essential mitotic endonuclease 1 homolog 1 [Mus musculus]	7.88E-04	0.39	12.10	34980.3	29244242	2 (0.0001)
98		g[148262292]refNP_001476968.1	PREDICTED: similar to Nucleoside diphosphate kinase A (NDK A) (NDP kinase)	9.09E-04	0.82	10.12	172807.7	148262292	1 (0.0000)
99		g[91585569]refNP_570614.2	sorting nexin associated golgi protein 1 [Mus musculus]	9.16E-04	0.41	10.12	67789.7	91585569	1 (0.0000)
100		g[65070233]refNP_062382.1	Rab geranyltransferase, a subunit [Mus musculus]	9.41E-04	0.23	10.09	494989.2	6507023	1 (0.0000)
101		g[83004553]refNP_358238.3	PREDICTED: similar to Hmgbl protein [Mus musculus]	9.68E-04	0.28	8.10	21307.8	83004553	1 (0.1000)
102		g[671509]refNP_031419.1	actin, beta, cytoplasmic [Mus musculus]	7.14E-08	2.10	30.20	41736.5	671509	3 (0.0000)
103		g[31981562]refNP_035229.2	pyruvate kinase, muscle [Mus musculus]	4.39E-08	2.55	38.24	57844.6	31981562	4 (0.3100)
104		g[15258941]refNP_001478027.1	PREDICTED: similar to Phosphoserine aminotransferase 1 isoform 1 [Mus mt]	3.46E-07	1.29	10.08	40531.4	15258941	1 (0.0000)
105		g[42734467]refNP_063574.2	transmembrane protein 34 [Mus musculus]	7.09E-06	0.20	18.10	71153.6	42734467	3 (0.1010)
106		g[29244176]refNP_808385.1	hypothetical protein 4732459N10 [Mus musculus]	8.49E-06	1.18	26.16	52880.0	29244176	3 (1.2000)
107		g[26266967]refNP_444319.2	NMDA receptor-regulated gene 1 [Mus musculus]	1.09E-05	0.27	24.09	101086.5	26266967	3 (1.1100)
108		g[16213882]refNP_031794.3	C-reactive protein, pentraxin-related [Mus musculus]	1.61E-05	0.62	10.11	25358.8	162138826	3 (1.1000)
109		g[16981203]refNP_031894.1	dystrophin, muscular dystrophy [Mus musculus]	4.49E-05	0.42	20.10	45588.7	16981203	3 (0.0101)
110		g[22128781]refNP_857305.1	olfactory receptor 605 [Mus musculus]	5.93E-05	0.14	20.09	36040.2	22128781	2 (0.0000)
111		g[124339838]refNP_038586.2	heat shock 70kDa protein 1-like [Mus musculus]	7.62E-05	0.04	12.08	70636.8	124339838	2 (0.1010)
112		g[92956179]refNP_914504.1	PREDICTED: hypothetical protein LOC698439 [Mus musculus]	1.05E-04	0.01	8.05	112773.2	92956179	1 (0.0000)
113		g[29244176]refNP_808385.1	PREDICTED: hypothetical protein LOC698439 [Mus musculus]	1.17E-04	0.41	10.11	15381.8	29244176	1 (0.0000)
114		g[29244176]refNP_808385.1	PREDICTED: hypothetical protein LOC698439 [Mus musculus]	1.42E-04	0.53	10.15	67830.1	678359	1 (0.0000)
115		g[6767816]refNP_032538.1	low density lipoprotein receptor-related protein 5 [Mus musculus]	1.52E-04	0.12	10.08	15401.1	6767816	1 (0.0000)
116		g[31985579]refNP_080558.1	proline-rich nuclear receptor coactivator 2 [Mus musculus]	1.60E-04	0.06	10.07	73427.5	2541235	1 (0.0000)
117		g[251415871]refNP_036138.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked [Mus musculus]	1.60E-04	0.06	10.08	150703.5	114158711	3 (0.0002)
118		g[11415871]refNP_001041069.1	tetratricopeptide repeat domain 21B [Mus musculus]	2.71E-04	0.27	8.10	35227.8	16716543	2 (0.0101)
119		g[167185439]refNP_444460.1	vonersasal 1 receptor, B9 [Mus musculus]	3.30E-04	0.10	14.09	38595.9	14927476	2 (0.0001)
120		g[14927476]refNP_488431.4	PREDICTED: similar to bryophyllin-like 4 [Mus musculus]	3.48E-04	0.59	12.11	99661.8	154240724	2 (0.0001)
121		g[154240724]refNP_508786.2	ectonucleotide pyrophosphatase/phosphodiesterase 3 [Mus musculus]	4.91E-04	0.20	8.09	58102.2	149283234	1 (0.1000)
122		g[14925362]refNP_001477260.1	PREDICTED: similar to zinc finger protein 759 [Mus musculus]	4.98E-04	0.03	10.07	106862	149253621	1 (0.0000)
123		g[13386169]refNP_080612.1	tetratricopeptide repeat domain 35 [Mus musculus]	5.14E-04	0.01	10.06	34934.5	13386169	1 (0.0000)
124		g[149265160]refNP_001478568.1	P						

Table 1 continued

15	gi 30061369 ref NP_835584.1 histone cluster 2, H2aa2 [Mus musculus]	2.41E-08	5.51	60.24	14095.4	30061369	6 (6 0 0 0 0)
16	gi 33859482 ref NP_031331.1 eukaryotic translation elongation factor 2 [Mus musculus]	8.88E-08	0.96	10.26	95313.5	33859482	1 (1 0 0 0 0)
17	gi 20809532 ref NP_035863.1 cold shock domain protein A short isoform [Mus musculus]	1.80E-07	0.96	12.21	30764.6	20809532	2 (2 0 0 0 1)
18	gi 31891722 ref NP_071705.2 heat shock protein 5 [Mus musculus]	1.96E-07	1.29	26.20	74242.5	31891722	4 (3 0 0 1 0)
19	gi 6755863 ref NP_035781.1 tumor rejection antigen gp95 [Mus musculus]	2.36E-07	0.96	10.20	82475.1	6755863	1 (1 0 0 0 0)
20	gi 51092233 ref NP_01003667.1 keratin 77 [Mus musculus]	3.59E-07	4.77	60.27	61353.3	51092233	6 (6 0 0 0 0)
21	gi 13385998 ref NP_080784.1 TNF receptor-associated protein 1 [Mus musculus]	6.57E-07	0.98	12.21	80208.5	13385998	3 (2 0 0 0 1)
22	gi 29243842 ref NP_080254.1 eukaryotic translation initiation factor 5A2 [Mus musculus]	1.19E-06	0.97	10.19	16793.1	29243842	1 (1 0 0 0 0)
23	gi 149259699 ref XP_001473715.1 PREDICTED: similar to Hmgb1 protein [Mus musculus]	1.43E-06	1.22	20.19	20199.2	149259699	2 (2 0 0 0 0)
24	gi 51092301 ref NP_01003670.1 type II keratin K614 [Mus musculus]	1.98E-06	2.18	34.17	60227.7	51092301	4 (2 1 1 0 0)
25	gi 86198323 ref NP_057869.2 high mobility group AT-hook 1 [Mus musculus]	3.08E-06	0.38	20.13	11613.9	86198323	2 (2 0 0 0 0)
26	gi 82950147 ref XP_0321314.2 PREDICTED: desmoplakin isoform 1 [Mus musculus]	3.74E-06	1.15	42.18	33208.9	82950147	6 (2 2 0 1 1)
27	gi 21313439 ref NP_079854.1 exocyst complex component 2 [Mus musculus]	3.94E-06	0.19	18.09	103558.6	21313439	2 (1 1 0 0 0)
28	gi 7077891 ref NP_034963.2 moesin [Mus musculus]	4.03E-06	1.58	26.14	67766.5	7077891	3 (2 0 1 0 0)
29	gi 11298353 ref NP_034790.2 keratin complex 1, acidic, gene 10 [Mus musculus]	5.20E-06	4.95	74.21	57040.7	11298353	11 (6 0 2 1 2)
30	gi 20911031 ref NP_081287.1 keratin 5 [Mus musculus]	5.48E-06	2.54	30.20	51766.3	20911031	3 (3 0 0 0 0)
31	gi 29244176 ref NP_080385.1 hypothetical protein LOC434632 [Mus musculus]	5.48E-06	1.87	28.15	58266.0	29244176	4 (0 2 2 0 0)
32	gi 31981693 ref NP_112442.2 heat shock protein 8 [Mus musculus]	7.92E-06	3.31	56.21	70870.6	31981693	6 (5 0 1 0 0)
33	gi 56960637 ref NP_01008551.1 hypothetical protein LOC434632 [Mus musculus]	1.10E-05	2.07	34.18	33335.5	56960637	4 (3 0 0 1 0)
34	gi 15379272 ref NP_001093249.1 pyruvate kinase liver and red blood cell isoform 2 [Mus musculus]	1.24E-05	1.15	22.15	58820.3	15379272	3 (2 0 0 0 1)
35	gi 11305059 ref NP_035862.2 nuclease sensitive element binding protein 1 [Mus musculus]	1.31E-05	0.74	10.14	35729.6	11305059	1 (1 0 0 0 0)
36	gi 17174133 ref NP_032579.2 peptidylprolyl isomerase B [Mus musculus]	1.60E-05	2.08	28.19	23713.3	17174133	3 (2 1 0 0 0)
37	gi 26032329 ref NP_034236.2 eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1.74E-05	2.82	50.16	50113.5	26032329	5 (5 0 0 0 0)
38	gi 110227377 ref NP_01035999.1 gelatin-like capping protein [Mus musculus]	2.42E-05	0.89	10.17	38768.6	110227377	1 (1 0 0 0 0)
39	gi 84395014 ref NP_01001311.1 PREDICTED: heterogeneous nuclear ribonucleoprotein A0 [Mus musculus]	2.52E-05	0.36	10.11	30530.1	84395014	1 (1 0 0 0 0)
40	gi 17978269 ref NP_036894.1 helicase (DNA) B [Mus musculus]	2.63E-05	0.48	10.10	42148.4	17978269	3 (0 0 1 0 2)
41	gi 6971539 ref NP_031464.1 aldolase 1, A isoform [Mus musculus]	2.73E-05	0.55	28.12	39355.7	6971539	4 (1 1 1 0 0)
42	gi 113931159 ref NP_081457.1 protein (peptidyl-prolyl isomerase) NIMA-interacting, 4 (parvulin) [Mus musculus]	2.78E-05	0.78	10.13	13814.9	113931159	1 (1 0 0 0 0)
43	gi 112807207 ref NP_034507.2 histone cluster 1, H11 [Mus musculus]	3.27E-05	0.93	18.15	21999.3	112807207	2 (1 1 0 0 0)
44	gi 84372553 ref NP_079405.1 PREDICTED: similar to fusion protein: ubiquitin (bases 43_513); ribosomal protein	5.26E-05	0.80	10.17	13337.7	84372553	1 (1 0 0 0 0)
45	gi 83921618 ref NP_033536.2 vlin 2 [Mus musculus]	6.12E-05	1.72	24.14	69406.3	83921618	3 (2 0 0 1 0)
46	gi 5690223 ref NP_032276.1 high mobility group box 2 [Mus musculus]	6.40E-05	1.84	23.15	24181.8	5690223	2 (2 0 0 0 0)
47	gi 31543553 ref NP_042129.2 U box domain containing 5 [Mus musculus]	7.27E-05	0.51	10.13	58731.8	31543553	1 (1 0 0 0 0)
48	gi 40556993 ref NP_032028.2 heat shock protein 1, beta [Mus musculus]	8.06E-05	1.26	22.17	83290.7	40556993	3 (2 0 0 0 1)
49	gi 162138029 ref NP_031794.3 C-reactive protein, pentraxin-related [Mus musculus]	8.72E-05	0.48	10.11	25359.6	162138029	1 (1 0 0 0 0)
50	gi 13430900 ref NP_056802.1 histone cluster 1, H1e [Mus musculus]	9.63E-05	2.63	40.16	21977.1	13430900	4 (4 0 0 0 0)
51	gi 30022023 ref NP_014836.1 PREDICTED: hypothetical protein [Mus musculus]	9.89E-05	0.74	16.13	15956.9	30022023	2 (2 0 0 0 0)
52	gi 62241030 ref NP_083061.2 dedicator of cytokinesis 8 [Mus musculus]	1.05E-04	0.05	18.07	238975.8	62241030	2 (1 0 1 0 0)
53	gi 7304933 ref NP_038511.1 butyrophilin, subfamily 1, member A1 [Mus musculus]	1.14E-04	0.20	10.11	54006.4	7304933	1 (1 0 0 0 0)
54	gi 15091026 ref NP_033487.2 ubiquitin protein ligase E3 component n-recognin 1 [Mus musculus]	1.18E-04	0.13	14.11	200237.7	15091026	3 (0 1 0 1 1)
55	gi 13385429 ref NP_080210.1 RIO kinase 2 [Mus musculus]	1.21E-04	0.18	10.09	62490.1	13385429	1 (1 0 0 0 0)
56	gi 50398960 ref NP_113580.2 debranching enzyme homolog 1 [Mus musculus]	1.30E-04	0.47	16.11	62289.0	50398960	2 (1 0 1 0 0)
57	gi 8945257 ref NP_056601.1 histone cluster 1, H1c [Mus musculus]	1.37E-04	0.80	10.13	21265.5	8945257	1 (1 0 0 0 0)
58	gi 21389311 ref NP_034623.1 intercellular adhesion molecule [Mus musculus]	1.44E-04	0.35	22.12	58843.9	21389311	3 (1 1 0 1 0)
59	gi 40254525 ref NP_071709.2 tropomyosin 3, gamma [Mus musculus]	1.47E-04	1.09	20.13	33148.2	40254525	2 (2 0 0 0 0)
60	gi 31882178 ref NP_032644.2 malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1.50E-04	0.68	10.12	34667.9	31882178	1 (1 0 0 0 0)
61	gi 153791358 ref NP_112456.2 splicing factor 3b, subunit 1 [Mus musculus]	1.65E-04	0.03	14.07	145828.1	153791358	2 (1 0 0 1 0)
62	gi 84662721 ref NP_001033784.1 jumoni domain containing 1A isoform 2 [Mus musculus]	1.66E-04	0.08	8.09	34780.5	84662721	2 (0 0 1 0 1)
63	gi 31880723 ref NP_038918.2 F-box and WD-40 domain protein 2 [Mus musculus]	1.66E-04	0.08	8.10	51483.8	31880723	1 (1 0 0 0 0)
64	gi 14823833 ref NP_062357.3 RNA and export factor binding protein 2 [Mus musculus]	1.68E-04	0.63	10.12	23765.3	14823833	1 (1 0 0 0 0)
65	gi 11185905 ref NP_031580.2 ecotropic viral integration site 5 [Mus musculus]	1.87E-04	1.18	18.07	92900.3	11185905	2 (1 1 0 0 0)
66	gi 162287042 ref NP_00104923.1 angiotensin I converting enzyme (peptidyl-dipeptidase A) 3 [Mus musculus]	2.12E-04	0.29	34.10	87185.5	162287042	4 (2 1 1 0 0)
67	gi 47059476 ref NP_070576.2 zinc finger, CCHC domain containing 6 [Mus musculus]	2.15E-04	0.59	16.10	167168.9	47059476	2 (2 0 0 0 0)
68	gi 86198333 ref NP_001034442.1 nuclear and cold-body phosphoprotein 1 isoform D [Mus musculus]	2.35E-04	0.86	10.11	73555.1	86198333	3 (0 0 1 0 2)
69	gi 149251403 ref XP_143529.6 PREDICTED: similar to FLJ44891 protein [Mus musculus]	2.44E-04	1.18	12.11	74828.8	149251403	2 (1 0 0 0 1)
70	gi 149249469 ref XP_001477320.1 PREDICTED: hypothetical protein [Mus musculus]	2.73E-04	0.85	10.15	31315.9	149249469	1 (1 0 0 0 0)
71	gi 21291917 ref NP_067042.1 olfactory receptor 133 [Mus musculus]	2.83E-04	0.28	16.10	34988.8	21291917	2 (1 0 1 0 0)
72	gi 162951865 ref NP_033724.2 v-abl Abelson murine leukemia oncogene 1 isoform b [Mus musculus]	2.85E-04	0.10	14.09	122671.9	162951865	3 (1 0 0 0 2)
73	gi 47271413 ref NP_032777.2 slingshot homolog 1 [Mus musculus]	3.50E-04	0.42	18.12	115296.1	47271413	2 (1 1 0 0 0)
74	gi 14509094 ref NP_097648.2 keratin 42 [Mus musculus]	3.87E-04	2.97	44.16	50132.8	14509094	5 (3 1 1 0 0)
75	gi 149253262 ref XP_005435.5 PREDICTED: hypothetical protein [Mus musculus]	4.07E-04	0.05	10.10	54378.3	149253262	1 (1 0 0 0 0)
76	gi 126628634 ref NP_064329.2 microtubule associated serine/threonine kinase 1 [Mus musculus]	4.40E-04	0.65	34.12	70865.6	126628634	5 (2 1 0 1 1)
77	gi 84703203 ref NP_00102956.1 far upstream element (FUSE) binding protein 3 [Mus musculus]	4.42E-04	0.39	16.11	61900.5	84703203	2 (1 0 1 0 0)
78	gi 149250813 ref XP_001478733.1 PREDICTED: hypothetical protein LOC89642 [Mus musculus]	4.44E-04	0.05	10.09	32443.2	149250813	2 (0 0 1 1 0)
79	gi 149250499 ref NP_001477837.1 PREDICTED: similar to experimental autoimmune prostatitis antigen 1 [Mus musculus]	4.59E-04	0.01	8.05	87470.1	149250499	1 (0 1 0 0 0)
80	gi 149250499 ref NP_001477837.1 PREDICTED: similar to experimental autoimmune prostatitis antigen 1 [Mus musculus]	5.04E-04	0.03	10.09	64900.2	149250499	1 (1 0 0 0 0)
81	gi 149250499 ref NP_001477837.1 PREDICTED: similar to experimental autoimmune prostatitis antigen 1 [Mus musculus]	5.05E-04	2.03	34.15	48161.6	149250499	5 (1 2 1 0 1)
82	gi 149250499 ref NP_001477837.1 PREDICTED: similar to experimental autoimmune prostatitis antigen 1 [Mus musculus]	5.14E-04	0.35	14.11	16444.6	149250499	2 (0 1 0 0 0)
83	gi 16716569 ref NP_044473.1 protease, serine, 1 [Mus musculus]	5.32E-04	0.31	8.10	26134.5	16716569	1 (1 0 0 0 0)
84	gi 21312532 ref NP_082328.1 transmembrane protein 38B [Mus musculus]	6.09E-04	0.90	20.15	32639.8	21312532	2 (2 0 0 0 0)
85	gi 22164779 ref NP_066175.1 keratin 6L [Mus musculus]	6.14E-04	1.08	26.20	57551.9	22164779	3 (1 2 0 0 0)
86	gi 149256649 ref NP_011841.3 PREDICTED: similar to BAF57 [Mus musculus]	6.15E-04	0.18	8.10	28672.6	149256649	1 (0 1 0 0 0)
87	gi 149251349 ref XP_00147755.1 PREDICTED: similar to mKIAA0184 protein [Mus musculus]	6.50E-04	0.22	18.09	147909.2	149251349	3 (0 0 3 0 0)
88	gi 21583909 ref NP_058788.2 Ppar binding protein isoform 2 [Mus musculus]	6.62E-04	0.89	23.11	61565.9	21583909	4 (2 0 0 2 0)
89	gi 40538839 ref NP_035166.2 hypothetical protein LOC89497 [Mus musculus]	6.66E-04	0.24	20.11	94210.2	40538839	3 (1 0 1 1 0)
90	gi 681090 ref NP_031836.1 cytochrome P450, family 19, subfamily a, polypeptide 1 [Mus musculus]	6.69E-04	0.09	10.09	58014.9	681090	1 (1 0 0 0 0)
91	gi 33563305 ref NP_0796317.1 nucleotide-binding oligomerization domain containing 1 [Mus musculus]	6.82E-04	0.57	16.13	107738.2	33563305	2 (2 0 0 0 0)
92	gi 82897081 ref NP_015830.1 PREDICTED: similar to YTH domain containing 2 [Mus musculus]	6.91E-04	0.13	20.08	61080.5	82897081	3 (1 1 0 0 1)
93	gi 113930737 ref NP_033021.2 peroxin 5 isoform 1 [Mus musculus]	7.07E-04	0.17	16.10	70755.1	113930737	2 (1 0 1 0 0)
94	gi 7305143 ref NP_038648.1 hexokinase 2 [Mus musculus]	7.21E-04	0.09	14.11	102534.6	7305143	3 (0 1 0 1 1)
95	gi 20270043 ref NP_061289.2 adaptor-related protein complex 3, mu 1 subunit [Mus musculus]	7.50E-04	0.16	10.07	49922.8	20270043	1 (1 0 0 0 0)
96	gi 13122609 ref NP_076013.1 TCF3 (E2A) fusion partner [Mus musculus]	8.12E-04	0.39	10.13	28012.8	13122609	1 (1 0 0 0 0)
97	gi 23956059 ref NP_034772.1 kallikrein 1-related peptidase b21 [Mus musculus]	8.35E-04	0.67	10.12	28689.8	23956059	1 (1 0 0 0 0)
98	gi 149254113 ref XP_082145.2 PREDICTED: HFM1 protein [Mus musculus]	8.74E-04	0.25	12.11	161377.1	149254113	2 (1 0 0 0 1)
99	gi 675372 ref NP_036182.1 ribosomal protein S3 [Mus musculus]	9.05E-04	1.41	30.14	26674.1	675372	3 (3 0 0 0 0)
100	gi 87042277 ref NP_035080.2 numb-like [Mus musculus]	9.18E-04	0.01	10.07	64130.1	87042277	1 (1 0 0 0 0)
101	gi 214268833 ref NP_064418.1 histone cluster 1, H1b [Mus musculus]	9.22E-04	0.56	10.11	22576.0	21426883	1 (1 0 0 0 0)
102	gi 31556989 ref NP_053105.2 TBC1 domain family, member 10b [Mus musculus]	9.24E-04	0.26	12.10	91988.4	31556989	2 (0 1 0 1 0)
103	gi 85701589 ref NP_001032723.1 placenta-specific 1-like [Mus musculus]	9.24E-04	0.47	18.14	19222.9	85701589	2 (1 1 0 0 0)
104	gi 36796741 ref NP_082305.1 dynamin binding protein [Mus musculus]	9.43E-04	0.08	8.08	177217.1	36796741	2 (0 0 0 2 0)
105	gi 21312339 ref NP_081403.1 hypothetical protein LOC89590 [Mus musculus]	9.57E-04	0.01	10.09	24148.1	21312339	1 (1 0 0 0 0)
106	gi 124487259 ref NP_001074891.1 hypothetical protein LOC85575 [Mus musculus]	9.87E-04	0.13	16.09	327450.5	124487259	5 (0 0 1 1 3)
1	gi 30061369 ref NP_835584.1 histone cluster 2, H2aa2 [Mus musculus]	1.48E-10	1.02	26.21	14095.4	30061369	3 (1 2 0 0 0)
2	gi 8945257 ref NP_056601.1 histone cluster 1, H1c [Mus musculus]	5.88E-07	1.39	20.15	21265.5	8945257	2 (2 0 0 0 0)
3	gi 213611209 ref NP_291074.1 histone cluster 2, H4 [Mus musculus]	2.35E-08	1.08	16.17	11367.3	213611209	2 (1 0 1 0 0)
4	gi 23368						

Table 1 continued

9	g 63003923 ref NP_081216.1 hypothetical protein LOC69101 [Mus musculus]	3.06E-04	0.30	10.09	33093.4	63003923	1 (1 0 0 0)
10	g 11022737 ref NP_001035999.1 gelsolin-like capping protein [Mus musculus]	3.70E-04	1.00	20.14	38788.6	11022737	2 (2 0 0 0)
11	g 126116587 ref NP_084542.2 inositol polyphosphate-4-phosphatase, type I isoform 1 [Mus musculus]	4.67E-04	0.58	10.16	105573.0	126116587	1 (1 0 0 0)
12	g 39930549 ref NP_019324.1 tripartite motif-containing 45 [Mus musculus]	5.27E-04	0.01	4.07	64185.0	39930549	2 (0 0 0 2)
13	g 149258982 ref XP_001475535.1 PREDICTED: hypothetical protein [Mus musculus]	6.48E-04	0.15	10.11	27800.7	149258982	1 (1 0 0 0)
14	g 6677973 ref NP_033211.1 Scf/Tal1 interrupting locus [Mus musculus]	6.81E-04	0.06	12.10	138756.6	6677973	2 (1 0 0 1)
15	g 21312236 ref NP_082582.1 HSPA12B [Mus musculus]	6.91E-04	0.27	14.11	76118.9	21312236	2 (1 0 0 1)
16	g 67162474 ref NP_001034577.1 receptor-interacting factor 1 isoform 1 [Mus musculus]	7.13E-04	0.20	10.10	82997.0	67162474	1 (1 0 0 0)
17	g 66782777 ref NP_033373.1 lectrin alpha [Mus musculus]	9.18E-04	0.01	8.06	239533.6	66782777	1 (0 1 0 0)
18	g 21687186 ref NP_073453.1 voltage-dependent calcium channel gamma-8 subunit [Mus musculus]	9.41E-04	0.01	16.07	43452.7	21687186	2 (0 2 0 0)
19	g 149256340 ref XP_001479253.1 PREDICTED: similar to pheromone receptor V3R8 [Mus musculus]	9.50E-04	0.04	8.08	14658.5	149256340	1 (0 1 0 0)
20	g 12746428 ref NP_075540.1 twisted gastrulation homolog 1 [Mus musculus]	9.83E-04	0.07	18.08	24800.6	12746428	2 (1 1 0 0)

Table 2. Peptides detected in captured Fc-receptor complexes by LC-MS/MS. Fc-receptor complexes were captured using the LARC method and analysed by LC-MS/MS. Alpha, beta, and gamma actin and many related actin isoforms were observed in the phagosome as well as HS1 and AnXA1, AnXA2, AnXA4, AnXA5, AnXA6 and ras-GTPase-activating protein SH3-domain binding protein, FMS-like tyrosine kinase 1, FERM, RhoGEF and pleckstrin domain protein 2, RhoGTPase-activating protein, RAB25 and FKBP-rapamycin.

Reference	Sequence	MH+	Charge	Score	Score XC	Delta CN	Sp	Peptides/ions
put. beta-actin (aa 27-375) [Mus musculus]					3828521.85	49868.0		11
rawextr_150beadig2_Mar04_18	-EITALAPSTMK-	1162.38	2	3419.61	1.76	0.3	765	7/10
rawextr_150beadig2_Mar04_26	-EITALAPSTMK-	1162.38	2	3925.98	2.13	0.4	552	7/10
rawextr_150beadig2_Mar04_192-194	-VAPEEHPVLLTEAPLNPK-	1955.24	3	5701.13	2.70	0.4	473	21/68
rawextr_150beadig2_Mar04_198-200	-VAPEEHPVLLTEAPLNPK-	1955.24	2	13577.45	3.58	0.5	762	21/34
rawextr_actinbeadig_Mar04_256	-HQGVIVMGQK-	1172.41	2	7802.74	2.82	0.4	876	4/5
rawextr_450beadig_Mar04_606	-HQGVIVMGQK-	1172.41	3	5925.77	2.80	0.3	938	11/20
rawextr_450beadig_Mar04_612	-HQGVIVMGQK-	1172.41	2	9645.53	2.97	0.4	1379	9/10
rawextr_150beadig_Mar04_622	-HQGVIVMGQK-	1172.41	2	4155.99	1.92	0.4	622	7/10
rawextr_300beadig_Mar04_652	-HQGVIVMGQK-	1172.41	2	8608.51	2.73	0.5	922	4/5
rawextr_150bead_Mar04_653-655	-OEYDESGPSVHR-	1517.58	3	1918.71	2.17	0.2	338	5/16
rawextr_chfibeat_Mar04_658	-IIAPFERK-	924.12	2	2493.98	1.77	0.3	487	7/9
rawextr_150beadig2_Mar04_704	-TTGVIMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3	1153.20	3.93	0.5	1032	15/16
rawextr_150beadig2_Mar04_710-712	-SYELPDGQVITIGNER-	1791.94	2	18797.72	4.68	0.5	1651	11/15
rawextr_450bead_Mar04_788	-DLTDYLMK-	999.16	1	11098.57	1.40	0.1	611	5/7
rawextr_700bead_Mar04_777-779	-GYSFTTTAER-	1133.19	2	3871.18	1.89	0.4	523	2/3
rawextr_200beadig_Mar04_787-789	-VAPEEHPVLLTEAPLNPK-	1955.24	3	9059.12	3.25	0.4	1064	27/68
rawextr_actinbeadig_Mar04_805	-EITALAPSTMK-	1162.38	2	2371.31	2.07	0.3	434	3/5
rawextr_450beadig_Mar04_808-810	-EITALAPSTMK-	1162.38	2	2475.46	2.41	0.4	589	3/5
rawextr_actinbeadig_Mar04_813	-GYSFTTTAER-	1133.19	2	4057.55	2.35	0.3	418	5/17
FPbeads150_Dec19_815	-EITALAPSTMK-	1162.38	2	2329.20	2.33	0.2	606	7/10
rawextr_300bead_Mar04_818	-EITALAPSTMK-	1162.38	2	1201.43	1.62	0.2	269	1/2
rawextr_500beadig_Mar04_842	-EITALAPSTMK-	1162.38	2	1539.63	1.52	0.2	725	13/20
rawextr_800bead_Mar04_884-886	-EITALAPSTMK-	1162.38	2	3033.27	1.89	0.4	378	11/20
rawextr_350bead_Mar04_896	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3422.19	2.26	0.4	358	19/68
rawextr_400beadig_Mar04_896-898	-EITALAPSTMK-	1162.38	2	3977.42	1.83	0.4	735	13/20
rawextr_250beadig2_Mar04_908-910	-GYSFTTTAER-	1133.19	2	2970.13	2.41	0.4	505	7/9
rawextr_450beadig_Mar04_928-928	-EITALAPSTMK-	1133.19	2	7846.29	2.59	0.4	1078	5/6
rawextr_250beadig_Mar04_930-932	-EITALAPSTMK-	1162.38	2	2978.87	1.96	0.3	522	13/20
rawextr_200beadig_Mar04_943-945	-EITALAPSTMK-	1162.38	2	2407.30	2.43	0.4	459	3/5
rawextr_900bead_Mar04_962	-VAPEEHPVLLTEAPLNPK-	1955.24	3	12096.82	3.89	0.5	810	6/17
rawextr_300bead_Mar04_962	-VAPEEHPVLLTEAPLNPK-	1955.24	3	1167.35	1.70	0.2	420	5/17
rawextr_1000_beadig_Mar04_967-969	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3705.56	2.05	0.3	523	21/68
rawextr_250bead_Mar04_976	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3604.76	3.07	0.4	492	5/17
rawextr_500beadig_Mar04_984	-EITALAPSTMK-	1162.38	2	3975.86	1.81	0.4	769	3/4
rawextr_800beadig_Mar04_1014	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3173.93	2.04	0.2	364	16/68
rawextr_800beadig_Mar04_1028	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3225.20	2.24	0.2	519	21/68
rawextr_60MeOHbead_Mar04_1028	-VAPEEHPVLLTEAPLNPK-	1955.24	3	5019.44	2.42	0.4	773	6/17
rawextr_actinbead_Mar04_1032	-EITALAPSTMK-	1162.38	2	2047.44	2.03	0.2	535	13/20
rawextr_400beadig_Mar04_1034-1036	-EITALAPSTMK-	1162.38	2	2486.24	2.21	0.4	576	3/5
rawextr_700beadig_Mar04_1042-1044	-EITALAPSTMK-	1162.38	2	2698.24	1.84	0.4	505	3/5
rawextr_450bead_Mar04_1048	-VAPEEHPVLLTEAPLNPK-	1955.24	3	8552.32	3.93	0.4	733	13/34
rawextr_350beadig2_Mar04_1050	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3424.25	2.54	0.3	484	11/34
rawextr_250beadig2_Mar04_1054	-EITALAPSTMK-	1162.38	2	3718.97	2.05	0.4	434	11/20
rawextr_300beadig_Mar04_1058	-EITALAPSTMK-	1162.38	2	2121.47	1.95	0.3	459	3/5
rawextr_350bead_Mar04_1058	-EITALAPSTMK-	1162.38	2	2264.86	1.66	0.4	331	1/2
rawextr_300beadig_Mar04_1062	-VAPEEHPVLLTEAPLNPK-	1955.24	3	5954.79	2.59	0.4	775	13/34
rawextr_700beadig_Mar04_1072	-EITALAPSTMK-	1162.38	2	2718.21	1.97	0.4	492	11/20
rawextr_450beadig_Mar04_1092	-VAPEEHPVLLTEAPLNPK-	1955.24	3	4291.92	2.01	0.4	240	6/17
rawextr_450beadig_Mar04_1096	-VAPEEHPVLLTEAPLNPK-	1955.24	3	13988.84	3.78	0.5	984	25/68
rawextr_250beadig_Mar04_1096	-VAPEEHPVLLTEAPLNPK-	1955.24	3	8120.44	3.12	0.4	1018	15/34
rawextr_450beadig_Mar04_1100	-VAPEEHPVLLTEAPLNPK-	1955.24	3	5705.82	2.74	0.4	668	6/17
rawextr_250beadig_Mar04_1102	-VAPEEHPVLLTEAPLNPK-	1955.24	2	10137.31	3.25	0.5	826	10/17
rawextr_700bead_Mar04_1105	-VAPEEHPVLLTEAPLNPK-	1955.24	3	8128.29	3.07	0.3	772	25/68
rawextr_450beadig_Mar04_1124	-SYELPDGQVITIGNER-	1791.94	2	1958.47	3.85	0.4	928	19/30
rawextr_400beadig_Mar04_1182	-VAPEEHPVLLTEAPLNPK-	1955.24	2	1142.13	1.43	0.2	339	13/34
rawextr_actinbead_Mar04_1185-1188	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3099.18	1.93	0.3	654	21/68
rawextr_400beadig_Mar04_1198	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3672.54	2.46	0.5	579	11/34
rawextr_250beadig2_Mar04_1222-1224	-VAPEEHPVLLTEAPLNPK-	1955.24	2	16809.52	3.86	0.6	785	10/17
rawextr_800bead_Mar04_1232	-VAPEEHPVLLTEAPLNPK-	1955.24	3	10031.07	3.70	0.4	949	13/34
rawextr_300beadig_Mar04_1240	-SYELPDGQVITIGNER-	1791.94	2	9531.77	3.51	0.4	1032	2/3
rawextr_300beadig_Mar04_1246	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3033.78	2.56	0.2	568	23/68
rawextr_300beadig_Mar04_1252	-VAPEEHPVLLTEAPLNPK-	1955.24	3	3807.68	2.57	0.3	556	23/68
FPbeads200_Dec19_1299	-VAPEEHPVLLTEAPLNPK-	1955.24	2	21540.27	4.14	0.5	785	10/17
rawextr_500beadig_Mar04_1306	-SYELPDGQVITIGNER-	1791.94	2	8475.07	2.83	0.4	1161	2/3
FPbeads200_Dec19_1309	-SYELPDGQVITIGNER-	1791.94	2	11757.92	3.37	0.5	1046	16/30
rawextr_500beadig_Mar04_1316	-SYELPDGQVITIGNER-	1791.94	2	12155.13	3.25	0.5	1340	2/3
rawextr_900bead_Mar04_1318-1320	-SYELPDGQVITIGNER-	1791.94	2	13923.97	3.63	0.5	1309	23/30
rawextr_400bead_Mar04_1325	-SYELPDGQVITIGNER-	1791.94	2	14420.65	4.45	0.4	1378	23/30
rawextr_500beadig_Mar04_1332	-SYELPDGQVITIGNER-	1791.94	2	12168.94	3.63	0.5	1194	7/10
FPbeads150_Dec19_1335-1337	-SYELPDGQVITIGNER-	1791.94	2	4837.05	2.83	0.3	702	17/30
rawextr_200beadig_Mar04_1339	-SYELPDGQVITIGNER-	1791.94	2	16334.32	4.04	0.6	1441	7/10
rawextr_200beadig_Mar04_1343	-SYELPDGQVITIGNER-	1791.94	2	11910.14	3.61	0.4	1297	23/30
rawextr_450beadig_Mar04_1348	-SYELPDGQVITIGNER-	1791.94	2	14803.93	3.99	0.5	1540	23/30
rawextr_900beadig_Mar04_1358	-KDLVANTVLSGGTTMYGIADR-	2344.63	3	3525.12	2.19	0.3	486	1/4
rawextr_800beadig_Mar04_1366	-SYELPDGQVITIGNER-	1791.94	2	10114.32	3.58	0.4	1059	2/3
rawextr_actinbeadig_Mar04_1367-1369	-SYELPDGQVITIGNER-	1791.94	2	3671.83	3.22	0.5	537	1/2
rawextr_700beadig_Mar04_1376-1378	-SYELPDGQVITIGNER-	1791.94	2	21555.05	4.02	0.5	1252	7/10
rawextr_150bead_Mar04_1385-1387	-SYELPDGQVITIGNER-	1791.94	2	12927.54	3.91	0.5	1129	19/30
rawextr_200beadig_Mar04_1389	-SYELPDGQVITIGNER-	1791.94	2	19780.11	4.65	0.5	1380	11/15
rawextr_200beadig_Mar04_1397	-TTGVIMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3	5390.55	2.23	0.4	772	27/116
rawextr_450bead_Mar04_1416	-TTGVIMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3	1624.70	3.39	0.5	1080	33/116
rawextr_actinbeadig_Mar04_1419	-SYELPDGQVITIGNER-	1791.94	2	12775.88	3.26	0.5	1103	2/3
FPbeads150_Dec19_1416	-SYELPDGQVITIGNER-	1791.94	2	11153.20	3.93	0.5	818	31/116
rawextr_actinbeadig_Mar04_1423	-DLTDYLMK-	999.16	2	733.18	1.33	0.2	163	4/7
rawextr_150bead_Mar04_1437-1439	-TTGVIMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3	12109.80	3.29	0.5	1043	31/116
rawextr_350bead_Mar04_1456-1458	-TTGVIMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3	36866.00	5.03	0.6	1421	9/29
rawextr_450beadig_Mar04_1480	-SYELPDGQVITIGNER-	1791.94	2	15454.13	4.35	0.5	978	2/3
rawextr_450beadig_Mar04_1486	-SYELPDGQVITIGNER-	1791.94	2	11778.07	3.93	0.4	1230	2/3
rawextr_250beadig_Mar04_1502-1504	-SYELPDGQVITIGNER-	1791.94	2	17622.73	4.80	0.5	1123	7/10
rawextr_250bead_Mar04_1514	-SYELPDGQVITIGNER-	1791.94	2	15382.22	4.12	0.5	1363	11/15
rawextr_500bead_Mar04_1518	-SYELPDGQVITIGNER-	1791.94	2	24147.85	2.55	0.3	601	8/15
rawextr_500bead_Mar04_1532	-SYELPDGQVITIGNER-	1791.94	2	9219.89	2.98	0.5	1035	2/3
rawextr_500bead_Mar04_1536	-SYELPDGQVITIGNER-	1791.94	2	27786.66	2.78	0.4	824	3/5
rawextr_chfibeat_Mar04_1540	-SYELPDGQVITIGNER-	1791.94	2	11102.18	3.20	0.5	733	17/30
rawextr_600bead_Mar04_1542	-SYELPDGQVITIGNER-	1791.94	2	2413.25	1.95	0.3	450	13/30
	-SYELPDGQVITIGNER-	1791.94	2	13756.89	4.00	0.5	1288	2/3

Table 2 continued

rawextr_400beadig_Mar 04,1552-1554	-SYELPDGGQVITIGNER-	1791.94	2 11989.55	3.37	0.5	1313	11/15
rawextr_600bead_Mar 04, 1558	-SYELPDGGQVITIGNER-	1791.94	2 12845.91	3.05	0.5	995	2/3
FPbeads250_Dec19,1572-1574	-VAPEEHPVLLTEAPLNPK-	1955.24	3 3054.02	2.43	0.3	535	5/17
rawextr_250beadig_Mar 04,1586-1588	-DLTDYLMK-	699.16	1 1502.22	1.90	0.1	625	5/7
rawextr_actinbead_Mar 04,1592-1594	-SYELPDGGQVITIGNER-	1791.94	2 14201.01	4.02	0.5	1204	11/15
rawextr_400beadig_Mar 04,1598-1600	-TTGVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 17821.41	3.76	0.6	1189	17/58
rawextr_250beadig2_Mar 04,1622-1624	-SYELPDGGQVITIGNER-	1791.94	2 15216.37	3.00	0.5	1313	11/15
rawextr_300beadig_Mar 4, 1636	-SYELPDGGQVITIGNER-	1791.94	2 6275.25	3.28	0.4	1016	19/30
rawextr_300beadig_Mar 4, 1640	-SYELPDGGQVITIGNER-	1791.94	2 6734.89	2.98	0.4	543	7/15
rawextr_200bead_Mar 04,1665-1668	-SYELPDGGQVITIGNER-	1791.94	2 16828.59	4.43	0.5	1524	11/15
FPbeads300_Dec19,2254-2266	-SYELPDGGQVITIGNER-	1791.94	2 7607.21	2.87	0.4	1209	10/30
rawuicrfp_60MeOHphagig_Mar 04, 632	-HQQVMVGMGQKDSYVGDEAQSRR-	2509.78	3 17908.46	4.41	0.8	894	31/68
rawuicrfp_60MeOHphagig_Mar 04, 678	-GYSFTTTAER-	1133.19	2 7099.16	2.07	0.5	1169	5/6
rawuicrfp_actinphagig_Mar 04, 712	-QEYDESGPSIVHR-	1517.58	3 1180.56	1.86	0.1	524	17/48
rawuicrfp_chilphagig_Mar 04, 755	-IIAPPER-	785.95	2 758.73	1.53	0.2	254	2/3
rawuicrfp_60MeOHphagig_Mar 04, 790-792	-EITALAPSTMK-	1162.38	2 2091.52	2.34	0.2	595	13/20
rawuicrfp_60MeOHphagig_Mar 04, 830	-EITALAPSTMKIK-	1403.71	2 2419.22	2.76	0.2	479	5/8
rawuicrfp_60MeOHphagig_Mar 04, 930	-VAPEEHPVLLTEAPLNPK-	1955.24	3 5577.58	3.24	0.3	591	23/68
rawuicrfp_chilphagig_Mar 04, 950	-VAPEEHPVLLTEAPLNPK-	1955.24	2 19018.02	4.55	0.6	795	10/17
phagr avFauc60MeOH_Dec23, 968	-GYSFTTTAER-	1133.19	2 8407.18	2.28	0.5	1319	8/9
rawuicrfp_300phagig_Mar 04,959-971	-DSYVGDEAQSRR-	1109.21	2 521.80	1.02	0.2	718	7/20
rawuicrfp_300phagig_Mar 04, 1022	-VAPEEHPVLLTEAPLNPK-	1955.24	3 6978.39	3.35	0.4	652	6/17
rawuicrfp_800phagig_Mar 04, 1026	-VAPEEHPVLLTEAPLNPK-	1955.24	3 6559.72	3.11	0.4	800	13/34
rawuicrfp_800phagig_Mar 04, 1034	-VAPEEHPVLLTEAPLNPK-	1955.24	3 8024.20	3.18	0.4	738	27/68
rawuicrfp_800phagig_Mar 04, 1034	-VAPEEHPVLLTEAPLNPK-	1955.24	3 7670.52	2.90	0.3	559	21/68
rawuicrfp_chilphagig_Mar 04, 1040	-VAPEEHPVLLTEAPLNPK-	1955.24	3 2189.81	1.98	0.2	771	23/68
rawuicrfp_150phagig_Mar 04, 1072-1074	-EITALAPSTMK-	1162.38	2 2526.71	2.30	0.2	508	13/20
rawuicrfp_450phagig_Mar 04, 1126	-VAPEEHPVLLTEAPLNPK-	1955.24	3 1465.56	2.40	0.1	598	11/34
rawuicrfp_450phagig_Mar 04, 1152	-VAPEEHPVLLTEAPLNPK-	1955.24	3 9532.12	3.02	0.5	795	13/34
rawuicrfp_450phagig_Mar 04, 1180	-VAPEEHPVLLTEAPLNPK-	1955.24	3 1727.65	2.01	0.2	461	5/17
rawuicrfp_700phagig_Mar 04,1161-1163	-VAPEEHPVLLTEAPLNPK-	1955.24	3 6278.01	2.94	0.4	759	23/68
rawuicrfp_400phagig_Mar 04, 1152	-VAPEEHPVLLTEAPLNPK-	1955.24	3 4655.73	2.09	0.3	559	21/68
rawuicrfp_400phagig_Mar 04, 1168	-VAPEEHPVLLTEAPLNPK-	1955.24	3 5755.60	2.74	0.4	589	6/17
rawuicrfp_300phagig_Mar 04, 1175	-KDLVANTVLSGTTTMYPIADIR-	2344.63	3 336.12	1.60	0.1	184	4/21
rawuicrfp_chilphagig_Mar 04, 1238-1240	-VAPEEHPVLLTEAPLNPK-	1955.24	3 2703.38	2.08	0.3	661	11/34
rawuicrfp_chilphagig_Mar 04, 1242	-VAPEEHPVLLTEAPLNPK-	1955.24	2 6986.42	3.05	0.5	421	1/2
rawuicrfp_60MeOHphagig_Mar 04, 1242-1244	-SYELPDGGQVITIGNER-	1791.94	2 15411.93	4.17	0.5	1498	4/5
rawuicrfp_1000phagig_Mar 04, 1269	-VAPEEHPVLLTEAPLNPK-	1955.24	3 8274.72	2.65	0.5	970	25/68
rawuicrfp_60MeOHphagig_Mar 04, 1282	-TTGVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 10059.69	3.67	0.4	1371	7/10
rawuicrfp_300phagig_Mar 04, 1301-1303	-SYELPDGGQVITIGNER-	1791.94	2 11368.93	3.73	0.4	1474	11/15
rawuicrfp_actinphagig_Mar 04, 1340	-SYELPDGGQVITIGNER-	1791.94	2 13790.81	3.42	0.5	1199	2/3
rawuicrfp_800phagig_Mar 04, 1360	-SYELPDGGQVITIGNER-	1791.94	2 15840.58	3.73	0.6	1400	19/30
rawuicrfp_150phagig_Mar 04,1450-1452	-SYELPDGGQVITIGNER-	1791.94	2 7783.89	3.12	0.4	907	3/5
rawuicrfp_800phagig_Mar 04, 1472	-SYELPDGGQVITIGNER-	1791.94	2 9251.96	3.86	0.4	767	17/30
rawuicrfp_700phagig_Mar 04, 1492	-SYELPDGGQVITIGNER-	1791.94	2 9130.78	3.57	0.4	1223	2/3
rawuicrfp_400phagig_Mar 04,1492-1501	-SYELPDGGQVITIGNER-	1791.94	2 18198.39	4.55	0.5	1489	4/5
rawuicrfp_250phagig_Mar 04, 1500	-SYELPDGGQVITIGNER-	1791.94	2 11832.00	3.21	0.5	1333	7/10
rawuicrfp_250phagig_Mar 04, 1506	-SYELPDGGQVITIGNER-	1791.94	2 8016.45	3.89	0.3	961	2/3
rawuicrfp_chilphagig_Mar 04, 1504-1506	-SYELPDGGQVITIGNER-	1791.94	2 15130.52	4.32	0.5	1386	11/15
rawuicrfp_60MeOHphagig_Mar 04, 1504-1506	-TTGVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 2659.61	1.93	0.3	484	25/116
rawuicrfp_1000phagig_Mar 04, 1506	-HQQVMVGMGQK-	1172.41	2 7344.58	2.33	0.4	847	4/5
rawuicrfp_1000phagig_Mar 04, 1506	-HQQVMVGMGQK-	1172.41	3 4546.39	2.60	0.3	874	1/2
rawuicrfp_1000phagig_Mar 04, 1506	-HQQVMVGMGQK-	1172.41	3 6121.27	2.95	0.3	1690	3/5
rawuicrfp_1000phagig_Mar 04, 1506	-HQQVMVGMGQK-	1172.41	2 7873.38	3.01	0.4	905	4/5
rawuicrfp_1000phagig_Mar 04, 1506	-HQQVMVGMGQK-	1172.41	2 7463.30	2.71	0.4	844	4/5
rawuicrfp_1000phagig_Mar 04, 1506	-HQQVMVGMGQK-	1172.41	2 7814.16	2.89	0.4	1075	9/10
rawuicrfp_1000phagig_Mar 04, 1506	-IIAPPER-	795.95	2 308.57	1.24	0.1	163	1/2
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 5695.12	2.62	0.3	1074	17/48
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 5427.81	2.45	0.4	883	5/12
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 3299.98	2.70	0.2	615	17/48
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 3120.04	2.00	0.3	914	7/16
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 6308.99	1.94	0.5	709	2/3
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 3537.31	2.08	0.3	797	19/48
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 1593.95	2.36	0.1	642	17/48
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 4819.01	2.16	0.4	921	7/16
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 6520.87	2.79	0.5	745	19/48
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 8172.44	2.08	0.5	978	7/6
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 12327.80	2.56	0.6	1279	8/9
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 5897.14	1.92	0.5	868	13/18
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	2 5241.18	2.07	0.5	477	13/24
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 10322.84	2.78	0.5	1255	8/9
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 2755.25	2.05	0.3	716	3/8
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	2 5184.19	2.35	0.4	964	13/24
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 7083.98	2.61	0.4	329	11/24
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 6531.03	2.65	0.4	866	5/12
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 11370.99	2.84	0.5	1046	5/6
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 6406.74	2.37	0.4	968	7/16
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 10866.18	2.37	0.6	1020	7/9
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 7507.19	2.27	0.5	1285	5/6
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 11040.95	2.69	0.6	901	5/6
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 7554.47	2.54	0.4	1351	1/2
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 4677.58	2.19	0.4	884	7/16
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 13680.23	2.90	0.6	1590	8/9
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 11511.73	2.74	0.6	1029	5/6
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 5285.63	2.49	0.4	814	19/48
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 4183.99	2.57	0.3	772	16/48
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 10465.70	2.69	0.5	1388	8/9
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 10955.90	2.72	0.5	1135	5/6
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	2 1498.44	1.32	0.3	324	11/24
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 6875.02	2.94	0.3	1238	23/48
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 6740.84	2.91	0.4	747	7/12
rawuicrfp_1000phagig_Mar 04, 1506	-QEYDESGPSIVHR-	1517.58	3 3711.63	2.41	0.3	915	19/48
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 8037.01	2.15	0.5	1009	7/8
rawuicrfp_1000phagig_Mar 04, 1506	-GYSFTTTAER-	1133.19	2 9698.72	2.82	0.5	1019	5/6
rawuicrfp_1000phagig_Mar 04, 1506	-EITALAPSTMK-	1162.38	2 4009.55	2.21	0.4	439	11/20
rawuicrfp_1000phagig_Mar 04, 1506	-EITALAPSTMK-	1162.38	2 4307.93	2.13	0.4	558	13/20
rawuicrfp_1000phagig_Mar 04, 1506	-EITALAPSTMK-	1162.38	2 4625.42	2.03	0.4	618	7/10
rawuicrfp_1000phagig_Mar 04, 1506	-EITALAPSTMK-	1162.38	2 5427.38	2.41	0.4	540	13/20
rawuicrfp_1000phagig_Mar 04, 1506	-EITALAPSTMK-	1162.38	2 4610.04	2.78	0.4	364	3/5

Table 2 continued

jmfag5miniggl50mmnaci, 746	-ETALAPSTMK-	1162.38	2 4699.93	2.40	0.4	514	3/5
jmfag5miniggl50mmnaci, 750	-ETALAPSTMK-	1162.38	2 9609.30	2.32	0.3	366	1/2
jmfag5miniggl50mmnaci, 762	-HQGVVMGGMQK-	1172.41	2 4275.03	2.04	0.4	508	7/10
jmfag5miniggl50mmnaci, 766	-HQGVVMGGMQK-	1172.41	2 4855.74	2.09	0.4	920	4/5
jmfag1mnacl2.5miniggl, 782-784	-ETALAPSTMK-	1162.38	2 5160.34	2.13	0.4	785	4/5
JMMAGT ube1B 16E3, 790-792	-ETALAPSTMK-	1162.38	2 3010.50	2.06	0.3	444	3/5
jmfag1mnacl7.5miniggl, 798	-ETALAPSTMK-	1162.38	2 3100.35	1.75	0.4	349	1/2
jmfag5miniggl250mmnaci, 798-800	-HQGVVMGGMQK-	1172.41	2 6421.20	2.88	0.4	1043	4/5
jmfag1mnacl7.5miniggl, 802	-ETALAPSTMK-	1162.38	2 6625.41	2.47	0.4	699	7/10
jmfag5minigglbead, 803	-VAPEEHPVLLTEAPLNPK-	1955.24	3 5386.28	2.40	0.4	420	11/34
jmfag5minigglbead, 805-807	-VAPEEHPVLLTEAPLNPK-	1955.24	2 18121.68	4.80	0.5	927	21/34
jmfag5minigglbead, 030528200105, 809-811	-ETALAPSTMK-	1162.38	2 5006.87	2.53	0.4	442	3/5
jmfag5miniggl400mmnaci, 828-830	-ETALAPSTMK-	1162.38	2 2878.94	2.09	0.3	545	13/20
jmfag5miniggl1000mmnaci, 864-866	-ETALAPSTMK-	1162.38	2 5069.05	2.24	0.4	733	3/4
jmfag5miniggl200mmnaci, 872-874	-ETALAPSTMK-	1162.38	2 5448.36	2.43	0.4	352	11/20
jmfag5mincon500mmnaci, 876-878	-HQGVVMGGMQK-	1172.41	2 5708.44	2.54	0.5	875	4/5
jmfag5miniggl450mmnaci, 030527025134, 878-880	-HQGVVMGGMQK-	1172.41	2 10169.85	2.98	0.5	778	17/20
jmfag5miniggl350mmnaci, 881-883	-VAPEEHPVLLTEAPLNPK-	1955.24	3 6876.65	2.91	0.4	748	6/17
jmfag5miniggl350mmnaci, 893	-VAPEEHPVLLTEAPLNPK-	1955.24	2 14803.45	3.27	0.6	752	10/17
jmfag5miniggl300mmnaci, 884-886	-HQGVVMGGMQK-	1172.41	2 6251.60	2.46	0.4	691	3/4
jmfag5miniggl500mmnaci, 900-902	-QEYDESGPSIVHR-	1517.58	3 1892.10	2.26	0.2	566	3/8
jmfag5miniggl600mmnaci, 904-906	-VAPEEHPVLLTEAPLNPK-	1955.24	3 584.69	1.68	0.0	329	9/34
jmfag5miniggl600mmnaci, 906-910	-VAPEEHPVLLTEAPLNPK-	1955.24	2 18926.07	4.41	0.6	1105	11/17
JMFAGNACL10_2B21E3, 914	-VAPEEHPVLLTEAPLNPK-	1955.24	3 4839.61	2.55	0.4	437	21/68
jmfag1mnacl5miniggl, 918-920	-ETALAPSTMK-	1162.38	2 6840.34	2.36	0.5	618	7/10
jmfag1mnacl5mincon, 926-928	-VAPEEHPVLLTEAPLNPK-	1955.24	3 9859.87	3.42	0.4	920	27/68
jmfag1mnacl5mincon, 940-942	-ETALAPSTMK-	1162.38	2 5451.83	2.30	0.4	605	7/10
jmfag5miniggl150mmnaci, 958	-VAPEEHPVLLTEAPLNPK-	1955.24	2 14625.46	3.33	0.6	815	16/34
jmfag5miniggl500mmnaci, 962	-GYSFTTTAER-	1133.19	2 8867.17	2.24	0.5	1309	8/9
jmfag5miniggl450mmnaci, 030527025134, 982	-JIAPPER-	795.65	2 818.31	1.36	0.2	221	7/12
JMMAGNEGB16D3, 982	-VAPEEHPVLLTEAPLNPK-	1955.24	2 14453.15	3.64	0.5	1009	11/17
jmfag1mnacl2.5miniggl, 988-990	-VAPEEHPVLLTEAPLNPK-	1955.24	2 16791.42	4.10	0.6	951	11/17
jmfag5minigglbead, 030528200105, 997	-VAPEEHPVLLTEAPLNPK-	1955.24	3 5350.31	2.63	0.4	772	19/34
jmfag1mnacl7.5miniggl, 998-1000	-VAPEEHPVLLTEAPLNPK-	1955.24	3 8075.36	3.17	0.4	636	25/68
JMMAGT ube1B 16E3, 1000-1002	-VAPEEHPVLLTEAPLNPK-	1955.24	2 20048.28	4.46	0.6	998	11/17
jmfag1mnacl7.5miniggl, 1004	-VAPEEHPVLLTEAPLNPK-	1955.24	2 9769.82	3.83	0.4	752	10/17
JMMAGT ube1B 16E3, 1006-1010	-VAPEEHPVLLTEAPLNPK-	1955.24	2 13067.18	3.99	0.5	945	7/17
jmfag5minigglbead, 1009	-KOLYANTVLSGGTMYPGIADR-	2344.63	3 6610.63	2.77	0.4	445	23/84
jmfag5minigglbead, 030528200105, 1017	-VAPEEHPVLLTEAPLNPK-	1955.24	2 9718.16	2.96	0.5	602	9/17
jmfag5miniggl250mmnaci, 1020	-GYSFTTTAER-	1133.19	2 14965.62	2.98	0.6	1530	8/9
jmfag5miniggl450mmnaci, 1044-1046	-VAPEEHPVLLTEAPLNPK-	1955.24	2 15441.35	4.50	0.5	730	19/34
jmfag5miniggl150mmnaci, 1066	-VAPEEHPVLLTEAPLNPK-	1955.24	3 728.27	1.38	0.4	527	19/68
jmfag5miniggl1000mmnaci, 1086-1088	-VAPEEHPVLLTEAPLNPK-	1955.24	3 2130.00	1.77	0.3	426	5/17
jmfag5miniggl200mmnaci, 1092-1094	-VAPEEHPVLLTEAPLNPK-	1955.24	3 9124.01	3.24	0.4	874	13/34
jmfag5miniggl1000mmnaci, 1100	-VAPEEHPVLLTEAPLNPK-	1955.24	2 16130.06	4.35	0.5	817	10/17
jmfag5miniggl200mmnaci, 1100-1102	-VAPEEHPVLLTEAPLNPK-	1955.24	2 19265.36	4.72	0.5	1130	11/17
jmfag5miniggl350mmnaci, 1103	-KOLYANTVLSGGTMYPGIADR-	2344.63	3 539.76	1.87	0.0	287	3/14
jmfag5miniggl500mmnaci, 1104-1106	-ETALAPSTMK-	1162.38	2 6673.47	2.35	0.5	448	3/5
JMFAGNACL10_1B21E3, 1110-1112	-VAPEEHPVLLTEAPLNPK-	1955.24	3 2969.79	2.88	0.2	634	23/68
jmfag5miniggl450mmnaci, 030527025134, 1116-1118	-QEYDESGPSIVHR-	1517.58	3 1275.44	2.64	0.4	1157	7/16
jmfag5miniggl300mmnaci, 1130-1132	-QEYDESGPSIVHR-	1517.58	3 7566.14	2.82	0.4	985	7/16
jmfag5minigglbead, 1137	-SYELPDGQVITIGNER-	1791.94	2 8188.81	3.22	0.4	893	16/30
jmfag5minigglbead, 1141	-SYELPDGQVITIGNER-	1791.94	2 16068.67	4.40	0.5	1423	11/15
jmfag5mincon500mmnaci, 1144	-QEYDESGPSIVHR-	1517.58	3 1245.46	1.65	0.1	538	17/48
jmfag1mnacl5miniggl, 1143-1150	-VAPEEHPVLLTEAPLNPK-	1955.24	3 11140.69	3.46	0.5	630	23/68
jmfag5mincon500mmnaci, 1152	-QEYDESGPSIVHR-	1517.58	3 2171.07	2.06	0.2	471	17/48
jmfag5miniggl450mmnaci, 030527025134, 1154	-GYSFTTTAER-	1133.19	2 10806.15	2.51	0.6	1170	5/6
jmfag1mnacl5miniggl, 1156	-VAPEEHPVLLTEAPLNPK-	1955.24	2 19538.21	3.65	0.6	828	10/17
jmfag5miniggl450mmnaci, 030527025134, 1158	-GYSFTTTAER-	1133.19	2 14403.68	2.59	0.7	1103	5/6
jmfag1mnacl5miniggl, 1160	-VAPEEHPVLLTEAPLNPK-	1955.24	2 7627.04	3.97	0.3	713	10/17
jmfag5miniggl250mmnaci, 1180-1182	-ETALAPSTMK-	1162.38	2 6354.44	2.49	0.5	488	3/5
jmfag5miniggl300mmnaci, 1176	-GYSFTTTAER-	1133.19	2 5583.33	2.26	0.5	972	13/19
jmfag1mnacl5mincon, 1178-1180	-VAPEEHPVLLTEAPLNPK-	1955.24	3 2498.82	2.36	0.3	422	19/68
jmfag5miniggl300mmnaci, 1182	-GYSFTTTAER-	1133.19	2 4806.88	1.74	0.5	703	2/3
jmfag1mnacl5mincon, 1184	-VAPEEHPVLLTEAPLNPK-	1955.24	2 11051.30	3.21	0.5	786	21/34
jmfag5mincon500mmnaci, 1184-1186	-GYSFTTTAER-	1133.19	2 9243.76	2.60	0.5	1450	8/9
jmfag1mnacl5mincon, 1188	-VAPEEHPVLLTEAPLNPK-	1955.24	2 16298.52	4.44	0.5	882	21/34
jmfag1mnacl2.5miniggl, 1204-1206	-KOLYANTVLSGGTMYPGIADR-	2344.63	3 6303.52	3.19	0.4	470	2/7
jmfag5minigglbead, 030528200105, 1209-1211	-KOLYANTVLSGGTMYPGIADR-	2344.63	3 5984.02	2.69	0.4	478	5/21
JMMAGT ube1B 16E3, 1228-1230	-KOLYANTVLSGGTMYPGIADR-	2344.63	3 14322.25	3.86	0.5	910	9/28
jmfag5minigglbead, 1229	-TTGVMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3 25921.37	5.88	0.5	1454	9/29
jmfag5minigglbead, 1233	-TTGVMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3 16388.67	4.27	0.5	1279	35/116
jmfag5miniggl350mmnaci, 1233-1235	-SYELPDGQVITIGNER-	1791.94	2 16522.50	4.05	0.5	1627	11/15
JMMAGT ube1B 16E3, 1238-1240	-KOLYANTVLSGGTMYPGIADR-	2344.63	2 37138.96	5.37	0.7	2347	9/14
jmfag5miniggl350mmnaci, 1241	-SYELPDGQVITIGNER-	1791.94	2 14014.35	4.52	0.4	1306	11/15
jmfag5miniggl600mmnaci, 1258-1260	-SYELPDGQVITIGNER-	1791.94	2 14741.63	4.18	0.5	1242	2/3
jmfag1mnacl5miniggl, 1268-1300	-SYELPDGQVITIGNER-	1791.94	2 9514.51	3.42	0.4	1205	11/15
jmfag5miniggl500mmnaci, 1300-1302	-VAPEEHPVLLTEAPLNPK-	1955.24	3 6227.85	3.09	0.4	740	25/68
jmfag5miniggl350mmnaci, 1309	-DLTDYLMK-	999.16	2 1103.24	1.46	0.2	239	9/14
jmfag5miniggl500mmnaci, 1312	-VAPEEHPVLLTEAPLNPK-	1955.24	2 17925.21	3.82	0.8	1134	11/17
jmfag5miniggl350mmnaci, 1315	-DLTDYLMK-	999.16	2 1641.77	1.52	0.3	425	6/7
jmfag5miniggl150mmnaci, 1328-1330	-VAPEEHPVLLTEAPLNPK-	1955.24	2 11223.00	3.79	0.5	699	19/34
jmfag5miniggl600mmnaci, 1332	-SYELPDGQVITIGNER-	1791.94	2 13753.61	3.97	0.5	1205	11/15
jmfag5miniggl350mmnaci, 1335-1337	-DLTDYLMK-	999.16	2 3595.89	2.54	0.3	368	11/14
jmfag5miniggl600mmnaci, 1336	-TTGVMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3 8234.49	3.32	0.4	831	15/68
jmfag5minigglbead, 030528200105, 1337	-DLTDYLMK-	999.16	2 3639.06	2.09	0.4	361	11/14
jmfag5minigglbead, 030528200105, 1341	-SYELPDGQVITIGNER-	1791.94	2 13908.87	3.56	0.5	1216	7/10
jmfag1mnacl2.5miniggl, 1342-1344	-SYELPDGQVITIGNER-	1791.94	2 9846.26	3.62	0.4	1029	19/30
jmfag5miniggl250mmnaci, 030527025134, 1342-1344	-SYELPDGQVITIGNER-	1791.94	2 16697.46	4.29	0.5	1802	23/30
jmfag5miniggl300mmnaci, 1344-1346	-ETALAPSTMK-	1162.38	2 5890.90	2.33	0.5	466	13/20
JMMAGNEGB16D3, 1348	-ETALAPSTMK-	1162.38	2 3612.61	2.20	0.4	491	13/20
JMMAGNEGB16D3, 1352	-SYELPDGQVITIGNER-	1791.94	2 8809.57	3.38	0.4	1084	7/10
jmfag5miniggl600mmnaci, 1358	-SYELPDGQVITIGNER-	1791.94	2 9959.46	3.34	0.5	751	3/5
jmfag1mnacl7.5miniggl, 1368	-TTGVMDSGDGVHTVPIYEGYALPHAILR-	3185.60	3 8058.39	3.08	0.4	1172	8/29
jmfag1mnacl7.5miniggl, 1372	-SYELPDGQVITIGNER-	1791.94	2 10625.61	4.09	0.4	1399	23/30
jmfag1mnacl5miniggl, 1374	-SYELPDGQVITIGNER-	1791.94	2 7637.53	2.89	0.4	812	3/5
jmfag5miniggl250mmnaci, 1374-1376	-DLTDYLMK-	999.16	2 1291.46	1.80	0.2	429	11/14
JMMAGT ube1B 16E3, 1374-1376	-VAPEEHPVLLTEAPLNPK-	1955.24	2 13511.69	4.21	0.5	968	9/17
jmfag5mincon500mmnaci, 1380-1382	-SYELPDGQVITIGNER-	1791.94	2 15881.82	4.32	0.5	1402	4/5
	-ETALAPSTMK-	1162.38	2 7883.43	2.70	0.5	471	3/5

Table 2 continued

jmag5mincon500mmnaci, 1388	-EITALAPSTMK-	1162.38	2 1555.60	2.05	0.2 348	11/20
JMMAGTube1B16E3, 1388	-SYELPDGQVITIGNER-	1791.94	1 186.74	1.26	0.1 84	3/10
jmfag5minig9400mmnaci, 1392	-SYELPDGQVITIGNER-	1791.94	2 1139.69	3.79	0.4 1213	11/15
jmfag5minig9400mmnaci, 1396	-SYELPDGQVITIGNER-	1791.94	2 15766.86	3.81	0.5 2023	9/6
jmfag5minig9400mmnaci, 1410	-DLTDYLMK-	999.16	2 2047.29	1.79	0.3 314	11/14
jmfag1mnacl5minig, 1412	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 11560.12	3.67	0.5 851	15/8
jmfag1mnacl5minig, 1418	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 19317.74	4.55	0.5 2066	39/16
jmfag1mnacl5minig, 1418-1420	-KDLVANTVLSGGTTMYPGIADR-	2344.63	3 4855.45	2.76	0.4 501	23/64
jmfag1mnacl2.5minig, 1420	-DLTDYLMK-	999.16	2 2699.40	2.20	0.3 398	11/14
JMMAGNEGB16D3, 1420-1422	-DLTDYLMK-	999.16	1 1351.67	1.50	0.1 766	5/7
JMMAGNEGB16D3, 1428	-DLTDYLMK-	999.16	2 3809.43	2.39	0.3 393	11/14
jmfag1mnacl2.5minig, 1428	-DLTDYLMK-	999.16	2 2008.86	1.84	0.2 501	3/718
jmfag5minig9400mmnaci, 1428	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 24360.79	5.54	0.5 1691	3/718
jmfag5minig9400mmnaci, 1450	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 6446.21	3.19	0.4 1075	8/29
jmfag1mnacl7.5minig, 1452	-SYELPDGQVITIGNER-	1791.94	2 13004.29	4.10	0.4 1388	23/30
jmfag1mnacl2.5minig, 1454	-DLTDYLMK-	999.16	2 1815.03	1.81	0.2 481	6/7
jmfag5minig9400mmnaci, 1454	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 15771.62	4.14	0.5 1015	1/4
JMMAGTube1B16E3, 1454-1456	-SYELPDGQVITIGNER-	1791.94	2 11992.73	3.86	0.4 1161	2/3
jmfag1mnacl2.5minig, 1458	-DLTDYLMK-	999.16	2 3610.92	2.22	0.3 467	8/7
jmfag5minig9400mmnaci, 1458	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 6226.66	2.70	0.4 944	31/118
jmfag5minig9400mmnaci, 1460	-DLTDYLMK-	999.16	2 2512.52	1.90	0.3 400	11/14
jmfag5minig9400mmnaci, 1462	-SYELPDGQVITIGNER-	1791.94	1 1565.08	1.96	0.2 976	2/5
jmfag5minig9400mmnaci, 1464-1466	-DLTDYLMK-	999.16	2 3376.52	2.25	0.3 408	11/14
jmfag5minig9400mmnaci, 1478-1480	-DLTDYLMK-	999.16	1 4715.62	2.68	0.3 776	5/7
JMMAGTube1B16E3, 1480-1482	-SYELPDGQVITIGNER-	1791.94	2 16111.10	4.17	0.5 1533	11/15
jmfag1mnacl7.5minig, 1484-1486	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 15897.46	4.20	0.6 598	1/4
JMMAGTube1B16E3, 1486	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 6164.07	2.55	0.4 907	1/4
JMMAGTube1B16E3, 1492	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	2 657.83	1.36	0.2 158	7/29
jmfag5minig9400mmnaci, 1498-1500	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	2 14028.15	3.48	0.8 387	21/58
jmfag5minig9400mmnaci, 1526	-DLTDYLMK-	3185.60	3 3152.29	3.94	0.3 978	31/118
jmfag1mnacl5minig, 1528-1529	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	999.16	2 1239.25	1.74	0.2 484	6/7
jmfag5minig9400mmnaci, 1530	-SYELPDGQVITIGNER-	1791.94	2 13485.08	3.70	0.5 1540	11/15
jmfag5minig9400mmnaci, 1548-1550	-DLTDYLMK-	999.16	2 667.83	1.74	0.1 209	4/7
jmfag1mnacl5mincon, 1558-1560	-DLTDYLMK-	999.16	2 3686.65	2.16	0.4 475	6/7
jmfag1mnacl5mincon, 1574	-SYELPDGQVITIGNER-	1791.94	2 13124.34	4.11	0.4 1421	2/3
jmfag5minig9400mmnaci, 1574-1576	-SYELPDGQVITIGNER-	1791.94	1 3168.18	1.70	0.4 161	2/5
jmfag5minig9400mmnaci, 1580	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 8125.64	3.08	0.4 694	7/29
jmfag1mnacl5mincon, 1580	-VAPEEHPVLLTEAPLNPK-	1955.24	2 10930.59	2.83	0.6 593	1/2
jmfag5minig9400mmnaci, 1588	-SYELPDGQVITIGNER-	1791.94	2 8322.33	3.07	0.4 698	17/30
jmfag1mnacl5minig, 1596	-VAPEEHPVLLTEAPLNPK-	1955.24	2 7927.36	2.72	0.5 844	10/17
jmfag5minig9400mmnaci, 2060-2062	-DLTDYLMK-	999.16	2 1214.55	2.12	0.0 560	6/7
jmfag5minig9400mmnaci, 2076	-SYELPDGQVITIGNER-	1791.94	2 20205.50	4.50	0.5 1478	23/30
jmfag5minig9400mmnaci, 2136-2138	-SYELPDGQVITIGNER-	1791.94	3 1555.40	1.84	0.0 833	23/60
jmfag5minig9400mmnaci, 2136-2138	-DLTDYLMK-	999.16	2 3401.84	2.21	0.4 289	5/7
jmfag5minig9400mmnaci, 2144	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 8613.59	3.39	0.4 589	7/29
jmfag5minig9400mmnaci, 2146	-DLTDYLMK-	999.16	1 856.42	1.40	0.1 535	5/7
jmfag5minig9400mmnaci, 2148	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 10263.38	3.09	0.4 1688	19/58
jmag5mincon500mmnaci, 2160-2162	-DLTDYLMK-	999.16	2 881.04	1.58	0.2 272	9/14
jmag5mincon500mmnaci, 2166	-DLTDYLMK-	999.16	2 3024.23	2.31	0.3 371	11/14
jmag5mincon500mmnaci, 2172	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 21172.58	4.32	0.6 1705	37/116
jmfag5minig9400mmnaci, 2174	-DLTDYLMK-	999.16	1 838.55	1.33	0.1 551	9/14
jmfag5minig9400mmnaci, 2178	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 15454.15	3.53	0.5 1820	35/116
jmag5mincon500mmnaci, 2178	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 4764.54	2.82	0.3 853	31/116
jmfag1mnacl7.5minig, 2514	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 9497.38	2.94	0.5 936	31/116
jmfag5minig9400mmnaci, 984-986	-CDVDRKDLVANTVLSGGTTMYPGIADR-	3046.43	2 225.49	1.03	0.1 98	5/27
JMMAGNEGB16D3, 974-976	-QEVDESGPSVHR-	1517.58	3 6742.33	2.99	0.3 1106	11/24
JMMAGNEGB16D3, 978	-VAPEEHPVLLTEAPLNPK-	1955.24	3 2564.74	2.48	0.3 291	19/68
jmfag1mnacl2.5minig, 978-980	-VAPEEHPVLLTEAPLNPK-	1955.24	2 15316.70	3.63	0.6 974	10/17
jmfag1mnacl7.5minig, 1456	-VAPEEHPVLLTEAPLNPK-	1955.24	3 5639.91	2.53	0.4 748	25/68
jmfag1mnacl5minig, 1600	-DLTDYLMK-	999.16	2 1555.48	1.88	0.2 456	6/7
jmfag5mincon500mmnaci, 1600-1602	-DLTDYLMK-	999.16	2 3464.59	2.27	0.3 511	11/14
jmfag1mnacl5minig, 1604	-VAPEEHPVLLTEAPLNPK-	1955.24	3 4396.72	2.49	0.3 700	23/68
jmag5mincon500mmnaci, 1604	-DLTDYLMK-	999.16	1 1630.59	1.68	0.2 595	5/7
jmag5mincon500mmnaci, 1608	-VAPEEHPVLLTEAPLNPK-	1955.24	2 12434.89	3.67	0.5 869	10/17
jmfag1mnacl5minig, 1640	-VAPEEHPVLLTEAPLNPK-	1955.24	2 16755.86	4.19	0.6 748	19/34
jmfag1mnacl5mincon, 1642-1644	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 10182.43	2.97	0.5 1374	35/116
jmfag1mnacl5mincon, 1646	-DLTDYLMK-	999.16	2 3099.01	2.40	0.3 434	6/7
jmfag1mnacl5mincon, 1674	-DLTDYLMK-	999.16	1 1414.10	1.63	0.0 852	11/14
jmfag1mnacl5mincon, 1684	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 17537.05	4.78	0.5 1025	17/58
jmfag5minig9400mmnaci, 1754-1756	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	2 7416.89	2.97	0.5 326	17/58
jmfag1mnacl7.5minig, 1822-1824	-SYELPDGQVITIGNER-	1791.94	2 13151.62	3.63	0.5 1018	19/30
jmfag5minig9400mmnaci, 1850	-CPAELFQPSFLGMESCGIHETTFSIMK-	3119.61	3 602.57	1.72	0.1 304	19/108
jmfag5minig9400mmnaci, 1854	-DLTDYLMK-	999.16	2 1973.16	1.66	0.3 400	11/14
jmfag5minig9400mmnaci, 1862	-DLTDYLMK-	999.16	2 472.48	1.58	0.1 240	9/14
jmfag5minig9400mmnaci, 1862	-DLTDYLMK-	999.16	1 717.58	1.23	0.0 567	5/7
jmfag5minig9400mmnaci, 1862-1864	-SYELPDGQVITIGNER-	1791.94	2 18015.73	4.59	0.5 1469	23/30
jmfag5minig9400mmnaci, 1872	-KDLVANTVLSGGTTMYPGIADR-	2344.63	3 4642.09	2.56	0.3 755	13/42
jmfag5minig9400mmnaci, 1874	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 15532.24	3.40	0.6 1291	33/116
jmfag5minig9400mmnaci, 1878	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 2226.92	1.69	0.2 955	15/58
jmfag5minig9400mmnaci, 1886	-KDLVANTVLSGGTTMYPGIADR-	2344.63	3 6470.44	2.92	0.4 774	9/28
jmfag5minig9400mmnaci, 1910	-KDLVANTVLSGGTTMYPGIADR-	2344.63	3 15301.57	4.26	0.5 590	25/84
jmfag5minig9400mmnaci, 1918-1920	-CPAELFQPSFLGMESCGIHETTFSIMK-	3119.61	2 1598.08	1.74	0.3 146	5/27
jmfag5minig9400mmnaci, 1956-1958	-CPAELFQPSFLGMESCGIHETTFSIMK-	3119.61	2 203.49	1.54	0.0 118	1/6
jmfag5minig9400mmnaci, 1966-1968	-TTGIVMDSGDGVTHTVPIYEGYALPHAILR-	3185.60	3 15275.64	3.69	0.5 1367	17/58
jmfag5minig9400mmnaci, 1970	-DLTDYLMK-	999.16	2 1034.12	1.56	0.2 236	9/14
jmfag5minig9400mmnaci, 1976	-DLTDYLMK-	999.16	1 2844.74	1.85	0.2 523	9/14
jmfag5minig9400mmnaci, 2034	-DLTDYLMK-	999.16	1 2423.73	1.75	0.3 749	5/7
jmfag1mnacl5mincon, 2042-2044	-SYELPDGQVITIGNER-	1791.94	2 5137.61	2.56	0.4 643	8/15
jmag5mincon500mmnaci, 2048	-CPAELFQPSFLGMESCGIHETTFSIMK-	3119.61	2 1763.68	1.57	0.3 187	11/54
jmag5mincon500mmnaci, 2052	-SYELPDGQVITIGNER-	1791.94	2 7627.73	2.46	0.5 778	3/5
jmag5mincon500mmnaci, 2052	-SYELPDGQVITIGNER-	1791.94	2 11415.55	3.61	0.4 1243	2/3
jmag5mincon500mmnaci, 474	-QEVDESGPSVHR-	1517.58	3 8686.79	2.50	0.4 1154	11/24
jmagG150arwphag3007, 756	-HQGVMMVGMGQK-	1172.41	2 6368.18	2.49	0.4 927	4/5
jmagG150arwphag3007, 760	-HQGVMMVGMGQK-	1172.41	2 5806.60	2.54	0.4 739	3/4
jmagG150arwphag3007, 762	-HQGVMMVGMGQK-	1172.41	2 6134.16	2.13	0.4 1204	9/10
jmagG250arwphag3007, 772-774	-HQGVMMVGMGQK-	1172.41	2 6901.41	2.87	0.4 1065	17/20
jmagG300arwphag3007, 796	-HQGVMMVGMGQK-	1172.41	3 1926.95	2.25	0.2 418	2/5
jmagG300arwphag3007, 800-802	-HQGVMMVGMGQK-	1172.41	2 9624.49	3.03	0.5 1088	17/20
jmagG300arwphag3007, 808	-EITALAPSTMK-	1162.38	2 1719.78	1.69	0.3 245	9/20
jmagG300arwphag3007, 825-827	-VAPEEHPVLLTEAPLNPK-	1955.24	3 4555.21	3.16	0.3 584	21/68

Table 2 continued

jmlgG350nacr1rawphag3007,849-851	-HGVMMVGMGQK-	1172.41	2 9182.44	2.69	0.5	943	4/5
AJRAWActinG_June13,886-890	-HGVMMVGMGQK-	1172.41	2 10826.72	3.30	0.5	970	4/5
jmravigg5minbeadfreeezethaw,954-958	-VAPEEHPVLLTEAPLNPK-	1955.24	3 6057.56	3.14	0.4	458	5/17
jmravigg5minbeadfreeezethaw,962	-VAPEEHPVLLTEAPLNPK-	1955.24	2 12094.23	3.01	0.6	667	21/24
jmravigg5minbeadfreeezethaw,966	-VAPEEHPVLLTEAPLNPK-	1955.24	2 10890.33	3.39	0.5	717	10/17
jmlgG300rawphag3007,1004	-HGVMMVGMGQKQSYVGDQAQSK-	2352.59	3 11422.19	3.47	0.5	1047	1/3
jmlgG350nacr1rawphag3007,1015	-QEYDESGPSIVHR-	1517.58	3 4672.49	2.70	0.3	785	5/12
jmlgG350nacr1rawphag3007,1019	-QEYDESGPSIVHR-	1517.58	3 1967.03	1.97	0.2	780	10/48
jmravigg5min150mmnaci,1026-1028	-VAPEEHPVLLTEAPLNPK-	1955.24	3 8617.18	3.33	0.4	785	25/68
jmlgG350nacr1rawphag3007,1057	-HGVMMVGMGQKQSYVGDQAQSK-	2352.59	3 22694.35	4.33	0.6	1458	17/42
jmravigg5min300mmnaci,1057-1058	-SYELPDGQVITIGNER-	1791.94	2 7328.04	3.25	0.3	1086	2/3
ajrawphag1MNaCl20,1182	-IIAPPER-	795.95	2 1196.35	1.35	0.3	244	7/12
ajrawphag1MNaCl20,1188	-IIAPPER-	795.95	2 818.35	1.35	0.2	199	1/2
jmravigg5minbeadfreeezethaw,1196	-KDYANTVLSGGTTMYPGIADR-	2344.63	2 23579.68	4.49	0.6	1662	4/7
jmlgG350nacr1rawphag3007,1203	-EITALAPSTMK-	1162.38	2 3247.76	1.66	0.4	582	3/5
jmlgG350nacr1rawphag3007,1207	-EITALAPSTMK-	1162.38	2 3381.48	1.99	0.3	487	3/5
jmravigg5min150mmnaci,1244	-KDYANTVLSGGTTMYPGIADR-	2344.63	3 16734.41	4.68	0.5	893	20/84
AJRAWActinG_June13,1288-1290	-EITALAPSTMK-	1162.38	2 3457.09	2.13	0.3	454	11/20
jmravigg5minbeadfreeezethaw,1324	-SYELPDGQVITIGNER-	1791.94	2 9928.37	3.75	0.4	1255	7/10
jmravigg5minbeadfreeezethaw,1328	-SYELPDGQVITIGNER-	1791.94	2 11482.80	3.69	0.4	1234	7/10
jmravigg5minbeadfreeezethaw,1330-1332	-SYELPDGQVITIGNER-	1791.94	1 4079.88	2.13	0.4	276	1/2
jmravminigg200mmnaci,1350-1352	-VAPEEHPVLLTEAPLNPK-	1955.24	3 3817.98	2.49	0.2	972	13/34
jmravminigg200mmnaci,1390	-VAPEEHPVLLTEAPLNPK-	1955.24	2 10825.02	3.30	0.5	680	9/17
jmravminigg500mmnaci,1390-1392	-VAPEEHPVLLTEAPLNPK-	1955.24	3 1087.42	1.56	0.1	502	5/17
jmravminigg200mmnaci,1392-1394	-VAPEEHPVLLTEAPLNPK-	1955.24	2 10959.90	3.64	0.5	571	9/17
jmravigg5min150mmnaci,1370-1372	-SYELPDGQVITIGNER-	1791.94	2 16401.43	4.22	0.5	1591	23/30
jml5minigrawlowonic,1422	-EITALAPSTMK-	1162.38	2 6507.93	2.48	0.4	674	13/20
jmravigg5minbeadfreeezethaw,1426	-TTGVMDSDGQVTHTVPIYEGYALPHAILR-	3185.60	2 9676.99	3.21	0.5	299	9/29
jml5minigrawlowonic,1426	-EITALAPSTMK-	1162.38	2 1652.45	1.68	0.2	590	13/20
jmravigg5minbeadfreeezethaw,1430-1432	-TTGVMDSDGQVTHTVPIYEGYALPHAILR-	3185.60	3 20063.27	5.22	0.5	951	8/29
AJRAWActinG_June13,1470	-VAPEEHPVLLTEAPLNPK-	1955.24	3 1205.00	1.58	0.2	410	5/17
AJRAWActinG_June13,1474	-VAPEEHPVLLTEAPLNPK-	1955.24	3 937.86	1.85	0.1	502	5/17
AJRAWActinG_June13,1478	-VAPEEHPVLLTEAPLNPK-	1955.24	2 4679.38	2.82	0.3	590	9/17
jmrav5miniggg600mmnaci,1534	-VAPEEHPVLLTEAPLNPK-	1955.24	3 1238.04	1.57	0.2	244	1/4
jmrav5miniggg250mmnaci,1536-1538	-VAPEEHPVLLTEAPLNPK-	1955.24	3 3729.24	2.61	0.3	760	23/68
jmrav5minigglowonic,1609	-EIVROK-	873.03	1 388.94	1.08	0.1	288	7/12
jmrav5miniggg500mmnaci,1624	-KDYANTVLSGGTTMYPGIADR-	2344.63	3 6563.10	2.89	0.4	447	11/42
jml5minigrawlowonic,1628-1628	-VAPEEHPVLLTEAPLNPK-	1955.24	3 3819.28	2.16	0.4	525	11/34
jmrav5miniggg500mmnaci,1628	-KDYANTVLSGGTTMYPGIADR-	2344.63	3 1076.67	2.92	0.5	712	25/84
jmravminigg200mmnaci,1634	-KDYANTVLSGGTTMYPGIADR-	2344.63	3 755.69	3.29	0.4	420	5/17
jml5minigrawlowonic,1638	-VAPEEHPVLLTEAPLNPK-	1955.24	2 14140.30	4.05	0.5	572	9/17
jmravminigg200mmnaci,1638	-KDYANTVLSGGTTMYPGIADR-	2344.63	3 4616.92	2.48	0.4	510	23/84
jml5minigrawlowonic,1642	-VAPEEHPVLLTEAPLNPK-	1955.24	2 10639.73	2.96	0.5	689	19/34
jmgg450rawphag3007,1740	-SYELPDGQVITIGNER-	1791.94	2 8171.38	2.57	0.5	724	8/15
jmlgG300rawphag3007,1750	-SYELPDGQVITIGNER-	1791.94	2 11078.70	3.50	0.4	1286	7/10
jmlgG400rawphag3007,1752	-SYELPDGQVITIGNER-	1791.94	2 8316.90	2.50	0.5	683	3/5
AJRAWActinG_June13,1756-1758	-KDYANTVLSGGTTMYPGIADR-	2344.63	3 10826.63	3.87	0.4	893	13/42
jmlgG350nacr1rawphag3007,1763-1765	-SYELPDGQVITIGNER-	1791.94	2 14649.15	3.68	0.5	1358	11/15
jmrav5miniggg500mmnaci,1782-1784	-SYELPDGQVITIGNER-	1791.94	2 17104.53	4.40	0.5	1485	7/10
jmlgG250rawphag3007,1786-1788	-SYELPDGQVITIGNER-	1791.94	2 14314.01	3.97	0.4	1654	23/30
jmravminigg200mmnaci,1804-1806	-SYELPDGQVITIGNER-	1791.94	2 14868.15	4.45	0.4	1330	23/30
jmrav5miniggg250mmnaci,1820-1822	-KDYANTVLSGGTTMYPGIADR-	2344.63	3 402.93	1.51	0.1	43	5/28
jmravminigg200mmnaci,1894-1896	-TTGVMDSDGQVTHTVPIYEGYALPHAILR-	3185.60	3 30885.94	5.89	0.6	1622	41/116
jml5minigrawlowonic,1918-1920	-KDYANTVLSGGTTMYPGIADR-	2344.63	3 4070.13	2.48	0.3	458	1/4
AJRAWActinG_June13,1924-1926	-SYELPDGQVITIGNER-	1791.94	2 15899.61	4.36	0.5	1482	11/15
jmrav5miniggg250mmnaci,1984-1986	-SYELPDGQVITIGNER-	1791.94	2 11003.90	3.34	0.5	1013	16/30
AJRAWActinG_June13,1992-1994	-TTGVMDSDGQVTHTVPIYEGYALPHAILR-	3185.60	3 24002.15	4.61	0.6	1808	16/58
jml5minigrawlowonic,2086-2088	-SYELPDGQVITIGNER-	1791.94	2 12499.20	3.98	0.4	1475	11/15
jml5minigrawlowonic,2100	-SYELPDGQVITIGNER-	1791.94	3 371.57	1.27	0.1	221	1/4
jml5minigrawlowonic,2174-2176	-TTGVMDSDGQVTHTVPIYEGYALPHAILR-	3185.60	3 1810.80	2.11	0.2	499	13/58
IPP_MOUSE Actin-binding protein IPP (MIPP protein) (Murine iAP-promoted place							
jmlg5minicnt200mmnaci,478-480	-WSPLPMGTR-	1142.36	3 745.21	1.59	0.0	469	17/36
AJRAWActinG_June13,1279	-RVSPPLMAGTR-	1454.73	2 487.77	1.00	0.2	128	3/11
jmlg5minicnt200mmnaci,480-482	-RKHVLEDPVR-	1447.71	2 311.65	0.27	0.0	231	9/22
jmlg5minicnt200mmnaci,482-484	-RVSPPLMAGTR-	1298.54	2 357.19	1.17	0.0	305	9/20
jmlg5minicnt200mmnaci,484-486	-LLKYIEGVDFNL-	1667.93	2 1221.21	1.52	0.2	234	9/26
similar to actin [Mus musculus] sculus] orvegi							
JMFAGNACL10_1B2IE3,494	-QEMTAAAR-	908.02	2 346.17	1.01	0.1	258	4/7
jmlg5minigbead_030528200105,1977	-MDLHEGRWNEDDSNGR-	1989.03	3 327.35	1.35	0.0	235	13/64
jmlg5minigbead_030528200105,1977	-ALLQSSFLQIESCGIHETTFIMK-	2751.18	3 460.31	1.31	0.0	360	8/24
jmlg5minigbead_030528200105,1977	-PCYVYALDFQEMTAAARSSSLEK-	2664.01	3 1514.58	1.99	0.2	307	11/46
actin monomer-binding protein [Mus musculus]							
jmlg5minigbead_030528200105,1977	-LPSSEQVILDK-	1429.64	2 398.32	1.61	0.0	244	11/24
jmlg5minigbead_030528200105,1977	-REPDSNGGGPTTGGPAAEAAQRPR-	2663.76	3 693.05	1.93	0.1	237	21/104
jmlg5minigbead_030528200105,1977	-LPSSEQVILDK-	1429.64	2 1492.47	2.07	0.1	628	1/2
similar to Actin monomer-binding protein [Mus musculus]							
jmlg5minigbead_030528200105,1977	-QLLEEKEEALSDGHSWETLK-	2528.71	3 429.69	1.56	0.0	262	23/84
jmlg5minigbead_030528200105,1977	-QLLEEKEEALSDGHSWETLK-	2528.71	3 520.27	1.59	0.1	248	11/42
actin [Rattus norvegicus]							
jmlg5minigbead_030528200105,1977	-FHLLEPQGRVLTGSTR-	1968.25	2 415.85	1.81	0.0	230	11/32
jmlg5minigbead_030528200105,1977	-FHLLEPQGRVLTGSTR-	1968.25	2 269.67	1.40	0.1	129	5/16
jmlg5minigbead_030528200105,1977	-FHLLEPQGRVLTGSTR-	1968.25	2 132.28	1.22	0.1	73	7/32
jmlg5minigbead_030528200105,1977	-FHLLEPQGRVLTGSTR-	1968.25	2 1684.76	1.83	0.3	247	13/32
jmlg5minigbead_030528200105,1977	-PAGRTQSPHSSPGPGPEAPPPQPPAPEAERAR-	3451.71	2 55.19	0.73	0.1	36	1/11
SWI/SNF related, matrix associated, actin dependent regulator of chrom							
JMFAGNACL10_1B2IE3,450-452	-DLKIITDVIGNPEER-	1842.04	3 484.26	1.42	0.1	259	4/15
jmlg5minigbead_030528200105,1977	-KFLTK-	714.88	2 444.24	1.14	0.0	381	7/10
jmlg5minigbead_030528200105,1977	-LDRLARLLGVHTQTR-	1847.16	2 1486.46	1.84	0.2	407	13/30
phagrawF250_dec22,2177	-MPMAGLQVGPAGSFGTAAPLR-	2224.64	3 1054.61	1.50	0.2	378	23/88
phagrawF800_Dec23,2536	-LLVPQAQPPMPAQR-	1703.05	2 439.78	1.15	0.1	260	11/28
SWI/SNF related, matrix associated, actin dependent regulator of chroma							
phagrawF400_dec20,1066	-FONTEAGSPITISVLK-	1693.88	3 552.52	1.44	0.0	382	3/10
phagrawFchf_dec23,1522	-AGGVGLNLCARSRLFLMDPAWPAEADQCQFDR-	3481.93	3 150.23	1.11	0.0	123	17/124
rawextr_200bead_Mar04,864	-DLAAGAFATK-	965.09	2 919.36	1.64	0.1	532	11/18
similar to SWI/SNF related, matrix associated, actin dependent regulat							
phagrawFuchf_dec23,2026	-MVLVFPDSQVSTEFACWYMEAFK-	2863.35	3 1565.49	1.96	0.2	260	4/23
phagrawF300_dec20,1435	-LIVKDSVEENMLK-	1518.80	2 292.08	1.19	0.1	180	1/3
rawextr_actinbeadig_Mar04,813	-CHRLQKQEMITK-	1742.15	3 408.19	1.27	0.1	250	15/52
rawextr_350beadig2_Mar04,1696	-ASGVFTPLDGSMAQKKR-	1941.24	3 423.95	1.45	0.0	280	15/68
rawextr_400beadig_Mar04,2068	-DSVEENMLKIGTQXDLAAGAFGTK-	2895.04	3 535.33	1.58	0.1	223	17/96

Table 2 continued

rawextr_60MeOHbeadigg_Mar04, 2134	-EAGIKYVFGQHVK-	1620.84	2 68.09	1.28	0.0	41	3/13
SWI/SNF related, matrix associated, actin dependent regulator of chrom	-TLQITSLGVMK-	1368.67	3 763.00	1101.95	40254124.0	6	
rawextr_chifbeadigg_Mar04, 157	-KWWPTLRSVLQIGDK-	1718.09	2 192.00	1.09	0.0	163	17/44
FFbeads500_dec19, 2708	-TLQITSLGVMKHYRNIPGPHMLVVK-	3108.76	2 146.06	0.98	0.1	44	5/14
FFbeads300_Dec19, 3652				0.98	0.1	44	7/52
SWI/SNF related matrix associated, actin dependent regulator of chromatin				6684.24	9055348.0	18	
rawextr_800beadigg_Mar04, 676	-EGVSFAISK-	1094.25	2 365.81	1.60	0.0	212	11/18
rawextr_150beadigg2_Mar04, 726	-EKFLVFAHHKVIDLDAVK-	2066.48	3 406.08	1.38	0.0	282	9/34
rawextr_500beadigg_Mar04, 902	-MNVVNPGRISRR-	1315.57	2 492.83	1.22	0.2	164	7/22
rawextr_700beadigg_Mar04, 1210	-QSIDSFYVLGGK-	1401.55	2 509.72	1.33	0.1	316	11/24
rawextr_300beadigg_Mar04, 1230-1232	-VLPFSLPENINVVVTGK-	1854.14	3 501.77	1.45	0.1	320	9/32
rawextr_450beadigg_Mar04, 1626	-GSGIDSFYVLGGKTPRTGGR-	2199.41	3 927.04	1.42	0.2	179	4/19
FFbeads150_Dec19, 1713	-VLGEAGLSEINFSEMTATDYVHKAPKQK-	3182.51	3 348.35	1.20	0.1	140	15/112
rawphag2007chfbaad2, 1022-1024	-FLVFAHHKVIDLDAVK-	1809.19	2 631.52	2.39	0.0	269	11/30
RawPhag200760MeOHbeadadgest, 2198	-QLKTPFKVVIDESHFLK-	2143.56	3 487.72	1.11	0.0	490	21/68
JMFAGNACL10_1B21E3, 500	-RLKSDVLSLPK-	1455.73	3 482.84	1.78	0.1	220	5/16
jmfag5minigg1000mmncl, 678	-QVQLDPLPK-	1038.22	2 786.49	1.33	0.1	456	5/8
jmfag5minigg400mmncl, 1018	-LKADVPADLSGVDAKLVSSLMFPQR-	2788.21	3 382.66	1.59	0.0	240	19/100
JMFAGNACL5B21E3, 2274	-FEVDYGYSEAVILPK-	1788.03	2 431.19	1.32	0.1	149	4/15
jmfag5minigg300mmncl, 2940	-VLGEAGLSEINFSEMTATDYVHKAPKQK-	3182.51	2 72.73	0.84	0.0	74	1/7
jmfag5miniggbead_030528200105, 3035	-LSTVSLKPLDEAGSGVGGQSLPSAPSLTFVTGK-	3303.71	2 177.48	1.00	0.1	90	3/22
SWI/SNF related, matrix associated, actin dependent regulator of chromatin				3980.73	3478564.0	5	
rawextr_actinbead_Mar04, 1898	-AAGRYFTGTVLAHYADVLGLLR-	2721.15	2 142.71	0.97	0.1	79	3/16
rawextr_500phagigg_Mar04, 1018	-VKEDSKFALTFFASATQR-	2047.30	3 820.94	1.78	0.0	461	21/68
rawextr_700phagigg_Mar04, 1359	-INALMHALIER-	1394.71	2 1487.96	1.50	0.3	316	5/11
phagrawF350_dec20, 2528	-SEVHLNFYVYGGPRDIRDSAWLSK-	2917.23	2 146.59	0.90	0.1	39	3/23
phagrawF350_dec20, 3818	-LRQICHTHLLTNGMSSSGPSRSDTPEELR-	3327.72	2 165.94	1.14	0.1	19	7/58
rawextr_300beadigg_Mar04, 844	-QEVITK-	830.99	1 714.62	1.22	0.2	118	1/2
rawextr_150beadigg2_Mar04, 1308	-DSVEENMLKIGNTK-	1849.85	2 307.30	1.13	0.0	259	9/26
rawextr_500beadigg_Mar04, 1600	-ILISGSDSEACALCDLSLTPVTHCAHVCK-	3454.02	2 24.45	0.72	0.0	34	3/51
rawextr_200beadigg_Mar04, 1971	-KGMSSMECEACTDGER-	1866.13	2 120.23	1.16	0.0	104	7/32
T30847 actin binding protein ACF7, neural isoform 2 - mouse (fragment)				2388.57	7513584.0	4	
jmfag5minigg200mmncl, 1166	-GAIEMASRVESQYVK-	1697.90	3 1247.89	2.17	0.1	526	19/56
jmfag5miniggbead, 1541	-HQGGSSSGKSLCAEFKVDLK-	2226.50	3 1120.69	1.29	0.2	603	1/4
actin-related protein 5 [Mus musculus]				2295.68	21313172.0	4	
JMMAAGTUBE1B16E3.616-618	-EAIRINRVGKLLTNHLK-	1990.38	3 1542.16	2.04	0.1	711	13/34
jmfag5minigg500mmncl, 988	-EAIRINRVGKLLTNHLK-	1990.38	3 753.52	1.29	0.1	641	21/68
ADVL_1009E Adylin [Actin-binding protein DOCB]				2234.82	14547960.0	13	
jmfag5minigg200mmncl, 1234	-GALSTAQEVVLTHPSGR-	1787.96	2 648.64	1.50	0.2	191	11/32
jmfag5minigg1000mmncl, 1438	-TQAEHYLYWYKSGSSGDER-	2085.18	3 243.41	1.16	0.1	167	3/17
JMFAGNACL10_2B21E3, 1782	-GATVKEQQAAMSK-	1349.58	2 139.25	0.80	0.0	169	1/3
JMFAGNACL10_1B21E3, 2464	-QGIYKKGAVSGMIK-	1537.85	2 239.70	0.87	0.1	161	2/7
jmfag5minigg250mmncl, 1294	-DELAASAYRAVEVDQDFRAPVQVR-	2835.08	3 963.82	1.53	0.2	282	19/96
ARPS actin-related protein 8 homolog; actin-related protein 8 homolog				5119.25	13837389.0	8	
jmfag5minigg1000mmncl, 2782	-HPDSPALLYQFRLGDEK-	1987.21	1 1736.05	1.21	0.4	185	5/16
rawphag2007chfbaad1, 1302	-YYPICLLIPDYNYK-	1788.15	3 1014.79	1.51	0.1	470	17/52
rawextr_300phagigg_Mar04, 1121	-CILLIPIDYNYKQVVK-	1798.19	2 206.09	1.13	0.0	177	9/28
rawextr_1000phagigg_Mar04, 1213-1215	-YYPICLLIPDYNYK-	1788.15	3 627.80	1.80	0.1	316	9/26
rawextr_700phagigg_Mar04, 1429	-RSGQLNIHPPGPGSLTAVLADIEVWVSHAIQK-	3279.74	3 482.07	1.56	0.1	236	3/20
phagrawF600_dec20, 2440	-LIAWKGGAVALCLDTQELWIYQR-	2750.21	2 219.14	0.57	0.1	80	4/23
phagrawF150_dec22, 2664	-CILLIPIDYNYKQVVK-	1798.19	2 333.32	1.59	0.2	285	3/7
ARP1 actin-related protein 1 homolog A, contractin alpha; ARP1 [actin-]				1849.20	5031568.0	3	
jmfag5mincon250mmncl, 828	-EYEEEDGAR-	968.95	3 550.42	1.32	0.1	380	1/2
jmfbeads150rawphag3007, 1280-1282	-AEHRGLLSIRYMEHGIVK-	2336.70	3 315.38	2.19	0.1	93	7/38
rawextr_chifphagigg_Mar04, 654	-LAPKDYKVR-	1040.29	2 130.92	0.78	0.0	168	7/16
rawextr_chifphagigg_Mar04, 1806	-KEGYDHSSEFEVVK-	1903.04	2 440.17	1.56	0.0	269	11/50
phagrawF350_dec20, 2424	-EGYDFHSSSEFEVVK-	2087.27	3 220.63	1.38	0.0	152	7/34
phagrawF200_dec22, 2987	-EYEEEDGARSHIRK-	1590.68	2 191.67	0.82	0.0	234	3/8
ARP1 actin-related protein 1 homolog B [Mus musculus]				2781.93	22122615.0	10	
phagrawF350MeOH_dec23, 1348	-EYEEEDGSRAHR-	1462.51	2 339.18	1.03	0.1	287	1/2
rawextr_350phagigg_Mar04, 1524	-TLFSNVLSGSGSLTFK-	1684.96	2 765.82	1.41	0.2	314	11/30
phagrawFchf_dec23, 2092	-EYEEEDGSRAHR-	1462.51	2 381.75	1.62	0.1	165	9/22
jmfbeads150rawphag3007, 1080	-LLLRKGGADPHTSAEFEVVR-	2318.62	3 929.24	1.60	0.1	507	6/19
jmfag5mincon400_030531151834, 1358	-DLQQTFSSEHPLVLTAPLNSPK-	2594.86	3 385.95	1.60	0.0	241	15/88
actin related protein 2/3 complex, subunit 3; actin related protein 2/3				1625.53	9790141.0	4	
JMMAEGNEB16D3, 170-172	-SQPKGAPPR-	988.13	3 454.06	1.27	0.1	237	11/32
jmfag5minigg200mmncl, 452	-QFMNKLSPGQ-	1294.46	3 1171.45	1.65	0.1	603	17/44
capping protein (actin filament) muscle Z-line, alpha 2; capping protein				1515.38	6971672.0	3	
JMFAGNACL15B21E3, 1228	-LLLNNDNLLR-	1198.40	2 1515.38	1.90	0.2	423	5/9
similar to cortactin isoform b; oncogene EMS1; cortactin [Mus musculus]				1512.21	38084311.0	7	
jmfag5minigg150mmncl, 886	-YAVGYEQSK-	1158.28	2 743.53	1.65	0.1	285	1/2
JMFAGNACL15B21E3, 946	-VQKMAKESGEKEX-	1548.79	2 523.38	1.61	0.1	191	3/8
JMFAGNACL15B21E3, 1472	-ASAGHAVISQTDDR-	1426.49	2 245.25	1.03	0.1	184	4/13
cortactin, p80p85 [mice, BALB/c 3T3 cells, Peptide, 546 aa]				1443.39	438621.0	11	
JMMAAGTUBE1B16E3, 1474	-ELETGPKASHGYGKFGVEQDR-	2363.53	2 694.27	1.30	0.2	144	13/42
jmfag5mincon10min_030601202502, 1406-1408	-TVPIEAVTSKTSNIRANFENLAK-	2504.83	3 749.12	1.77	0.0	413	19/88
AS4728 actin alpha, cardiac - mouse (fragment)				1289.18	627834.0	2	
jmfag5mincon2, 5minigg, 2134	-DDEETALVCDNGSLVK-	1866.98	2 1269.18	1.40	0.3	149	11/34
TRIO and F-actin binding protein [Mus musculus] X&				1192.17	27503073.0	12	
jmfag5mincon2, 5minigg, 284	-DELQVIQDK-	1216.37	3 240.99	1.60	0.0	149	7/18
jmfag5mincon5mincon, 440	-KWFESTDGR-	1126.20	2 143.65	1.20	0.0	110	1/2
jmfag5miniggbead_030528200105, 1335	-PTKQEDLERDLAQR-	1699.85	2 361.10	1.31	0.1	108	7/26
jmfag5mincon2, 5mincon, 1772	-LAMAALQEKAEVRSNLAEL-	1945.23	3 358.21	1.06	0.0	331	15/68
JMMAAGTUBE1B16E3, 2046	-IGEQRTSGEIVGRGPR-	1769.94	2 88.21	1.27	0.0	70	9/32
similar to ARP1 actin-related protein 1 homolog A; actin-related prote				2106.25	3806491.0	5	
jmfag5minigg350mmncl, 885	-HPVLLTEALLSPR-	1446.72	3 987.86	1.37	0.2	414	1/3
JMFAGNACL15B21E3, 2868	-MRSVAFANRAGISFLGK-	1954.29	1 97.30	0.88	0.0	98	1/4
rawextr_150beadigg2_Mar04, 326	-LSEVKLVVK-	1141.43	2 1024.09	1.82	0.1	507	2/3
actin-related protein T1 [Mus musculus]				1319.87	13386318.0	4	
jmfag5minigg150mmncl, 676	-LDNPAVIFDNGSLCK-	1663.88	3 1316.87	2.00	0.1	611	1/3
SWI/SNF related, matrix associated, actin dependent regulator of chrom				4437.68	30678388.0	12	
rawextr_350bead_Mar04, 344	-TSNVCVR-	778.90	2 178.41	1.04	0.0	171	1/2
rawextr_200bead_Mar04, 1130	-TIGYVVPNPEIPNPAIAQR-	2235.58	3 533.04	1.71	0.0	297	1/4
rawextr_150bead_Mar04, 2553	-DDKQSLISVGYDR-	1496.61	2 553.44	1.24	0.1	340	5/12
jmfbeads250rawphag3007, 274	-MVNMLPKADRAK-	1374.70	3 265.89	1.61	0.0	182	7/22
jmfag5mincon10min_030601202502, 1406-1408	-VSEKIPK-	888.08	2 634.89	1.16	0.2	251	5/7
jmfbeads150rawphag3007, 1620	-LGTVEWIEPK-	1286.47	1 128.64	0.99	0.1	34	3/10
jmfbeads500rawphag3007, 2596	-EEGAAATAETGTTATEKGEK-	1229.98	2 185.85	0.91	0.1	123	4/19
rawphag2007chfbaad2, 94	-SEKEMDPEYEK-	1514.59	3 236.17	1.07	0.0	220	1/4
rawphag2007chfbaad3, 973	-EMDPEYEK-	1170.23	2 225.51	1.01	0.0	162	7/16

Table 2 continued

phagrawF60MaOH_dec23_2372	-LGTVEVIEPPKRR-	1710.66	2 85.57	0.89	0.0	85	3/13
rawscrtp_800phagig_Mar04_826	-EGGAAAATGGTATEKGEK-	1922.98	2 54.25	0.83	0.0	63	7/38
phagrawFusc450_dec20_1492	-SPTSPLNNKLAR-	1315.57	2 472.20	1.33	0.0	346	5/11
phagrawFusc350_dec20_1860	-EVEGKSPEEVMEYSVFWER-	2402.62	3 712.31	1.51	0.1	384	5/19
rawscrtp_700phagig_Mar04_2569	-AAFRDEMPGEWDOCVTYSVMVKEK-	3179.70	2 140.90	0.89	0.1	84	2/13
B2519 actin, fetal skeletal/adult cardiac muscle - mouse (fragment)					580477.27	80263.0	5
mfag5miniggbad_043-045	-YPIEGHITNWDDMEK-	1962.17	3 10029.44	4.22	0.4	1144	13/30
mfag5miniggbad_949	-YPIEGHITNWDDMEK-	1962.17	2 5488.19	3.38	0.3	785	17/30
mfag5miniggbad_1037-1039	-YPIEGHITNWDDMEK-	1962.17	3 11773.73	3.95	0.4	1538	9/20
mfag5miniggbad_1054-1056	-YPIEGHITNWDDMEK-	1962.17	3 8115.00	3.73	0.3	1204	9/20
mfag5miniggbad_1080-1082	-YPIEGHITNWDDMEK-	1962.17	2 10030.71	3.90	0.4	712	17/30
JMFAGNACL10_2B21E3_1062	-YPIEGHITNWDDMEK-	1962.17	3 3097.34	2.02	0.3	611	1/3
JMFAGNACL10_2B21E3_1074	-YPIEGHITNWDDMEK-	1962.17	3 2836.80	2.61	0.2	471	17/60
mfag1mnacl0minig_1078-1080	-YPIEGHITNWDDMEK-	1962.17	3 7747.41	3.72	0.3	1030	9/20
mfag5miniggbad_030528200105_1143	-YPIEGHITNWDDMEK-	1962.17	3 10618.86	4.70	0.3	1237	9/20
JMMAAGNEGB18D3_1146-1148	-YPIEGHITNWDDMEK-	1962.17	2 7245.02	3.58	0.3	838	8/15
mfag5miniggbad_030528200105_1147	-YPIEGHITNWDDMEK-	1962.17	2 12357.51	4.49	0.4	854	3/5
JMFAGNACL10_1B21E3_1282	-YPIEGHITNWDDMEK-	1962.17	3 10677.74	3.58	0.4	1159	7/15
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 2730.27	2.82	0.1	922	7/20
JMMAAGNEGB18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 4730.30	2.88	0.2	1341	9/20
JMMAAGTUBE18E3_1172	-YPIEGHITNWDDMEK-	1962.17	3 10189.47	3.49	0.4	1156	2/5
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 6948.96	2.89	0.4	622	8/15
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	2 7973.36	3.14	0.4	803	17/30
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 8556.08	3.69	0.4	551	1/2
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 12166.31	3.95	0.4	1588	7/15
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 7230.19	3.42	0.3	1377	13/30
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	2 10699.08	3.60	0.4	1279	16/30
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 15327.59	4.25	0.5	1535	29/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 2022.03	1.84	0.2	523	19/60
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 8460.62	3.44	0.4	1034	23/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	2 10687.87	4.42	0.4	825	8/15
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 10558.34	3.47	0.5	762	8/15
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	2 5187.36	3.11	0.3	635	7/15
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 7744.79	3.18	0.4	636	8/15
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 8620.62	2.82	0.4	1080	13/30
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 3070.10	1.98	0.3	778	11/30
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 5605.85	2.61	0.3	1213	13/30
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 9787.95	3.56	0.4	1378	9/20
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 4647.28	2.83	0.3	997	23/60
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 1962.31	2.18	0.2	586	19/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	2 7180.53	3.43	0.4	763	8/15
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 3083.59	2.67	0.2	615	7/20
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 2941.31	2.28	0.2	930	23/60
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 8413.94	2.88	0.4	809	23/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 7776.51	3.75	0.3	1140	13/30
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 3889.10	2.91	0.2	693	11/30
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 7041.73	2.91	0.3	1721	29/60
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 8771.33	3.24	0.3	2023	29/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 8475.44	2.95	0.3	1065	2/5
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 6145.59	2.91	0.3	1163	2/5
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 2197.59	2.44	0.1	603	11/30
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 2382.72	2.51	0.1	771	23/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 5263.06	2.58	0.3	893	23/60
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 4391.90	2.86	0.1	1311	5/12
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 9789.94	3.32	0.4	1036	2/5
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 8008.57	3.33	0.4	575	7/15
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	2 3032.31	2.55	0.3	438	13/30
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 2904.30	2.52	0.2	448	3/10
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 6370.01	2.82	0.2	1333	9/20
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 9320.18	3.62	0.3	1514	7/15
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 8742.20	3.41	0.4	1121	5/12
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 10126.04	3.83	0.4	883	2/5
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 10978.69	4.21	0.4	1298	9/20
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 7446.51	3.04	0.4	1003	13/30
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 8086.90	3.26	0.4	1238	7/15
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 788.25	1.21	0.2	84	9/58
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	0 0616.43	3.08	0.4	648	1/2
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	0 8350.07	3.29	0.3	1486	9/20
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 9425.79	3.47	0.4	898	2/5
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 4628.57	2.96	0.3	481	3/10
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 8010.45	3.34	0.3	841	23/60
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 1304.68	2.62	0.0	468	19/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	2 13444.55	4.29	0.5	1060	3/5
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 2730.78	2.49	0.3	347	13/30
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 6321.60	2.38	0.3	925	2/5
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 1910.42	1.77	0.3	412	19/68
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 8051.07	3.53	0.3	1202	2/5
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 4096.74	3.02	0.2	974	23/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 2859.03	2.45	0.2	615	7/20
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 6323.09	3.34	0.4	630	1/2
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	2 4650.69	2.78	0.3	593	7/15
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 3309.53	2.16	0.3	631	19/60
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 6754.34	3.41	0.3	817	7/20
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 9232.00	3.40	0.4	890	5/12
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 6018.36	3.20	0.2	1281	13/30
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 5144.18	2.86	0.3	792	11/30
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 1833.97	3.95	0.3	954	2/5
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 6303.28	2.98	0.3	1461	13/30
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 2884.45	2.81	0.2	552	1/3
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	2 5504.71	3.05	0.3	631	12/2
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 291.47	1.08	0.0	289	1/4
mfag5miniggbad_030528200105_1153	-YPIEGHITNWDDMEK-	1962.17	3 807.99	1.90	0.1	387	1/4
JMMAAGTUBE18E3_1168	-YPIEGHITNWDDMEK-	1962.17	3 807.99	1.90	0.1	387	1/4
alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens]					5708.05	4501581.0	1
mfag1mnacl0minig_732	-QYDEAGPSIVHR-	1501.58	2 553.00	1.72	0.1	270	3/8
mfag5miniggbad_030528200105_837	-QYDEAGPSIVHR-	1501.58	2 557.57	1.68	0.0	319	5/12
mfag5miniggbad_030528200105_837	-QYDEAGPSIVHR-	1501.58	2 764.23	1.46	0.1	415	11/24
mfag5miniggbad_030528200105_837	-QYDEAGPSIVHR-	1501.58	2 981.11	1.72	0.2	320	5/12
mfag5miniggbad_030528200105_837	-QYDEAGPSIVHR-	1501.58	2 781.88	1.64	0.1	281	3/8
mfag5miniggbad_030528200105_837	-QYDEAGPSIVHR-	1501.58	2 571.56	1.47	0.1	340	3/8
mfag5miniggbad_030528200105_837	-QYDEAGPSIVHR-	1501.58	2 633.75	1.65	0.1	401	11/24

Table 2 continued

jmfag5mincon500m mnacl, 1390	-QEYDEAGPSIVHR-	1501.55	2 564.99	1.53	0.0	370	11/24
similar to actin, gam ma, cytoplasmic [Mus musculus]	-AGFAGDDAPR-	977.01	2 8647.26	2.98	0.4	1432	8/9
jmfag1mnacl2.5minngg, 146	-HQDVMVMGKG KDSYVGDK-	1905.23	1 92.06	0.98	0.0	89	7/34
jmfag1mnacl7.5minngg, 1832	-GYSFTTAKR-	1132.25	2 2311.12	2.16	0.2	564	2/3
rewextr_300beadigg_Mar4, 924	-VLTVDLMKILTER-	1505.93	3 302.92	1.72	0.0	178	5/18
jmfag5mincon350, 434	-AGFAGDDAPR-	977.01	2 2198.65	1.65	0.2	878	7/9
jmfag1mecon10m in_030801230741, 918	-AGFAGDDAPR-	977.01	2 2945.27	2.17	0.2	968	7/9
jmfag1mecon10m in_030801230741, 924	-AGFAGDDAPR-	977.01	2 2056.46	1.63	0.3	582	2/3
jmfag1mecon10m in_030801202502, 1008	-AGFAGDDAPR-	977.01	2 1547.29	1.62	0.1	792	2/3
jmfag1mecon10m in_030801202502, 1012	-AGFAGDDAPR-	977.01	2 3211.06	1.84	0.3	936	2/3
rewextr_300beadigg_Mar04,361-363	-AGFAGDDAPR-	977.01	2 6702.89	2.97	0.3	1092	8/9
rewextr_300beadigg_Mar4, 924	-GYSFTTAKR-	1132.25	2 2311.12	2.16	0.2	564	2/3
actin-like [Mus musculus]	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 6610.63	2.77	0.4	445	23/84
jmfag5minnggbead, 1009	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 539.76	1.87	0.0	287	3/14
jmfag5minngg350m mnacl, 1103	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 6303.52	3.19	0.4	470	2/7
jmfag1mnacl2.5minngg, 1204-1206	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 5984.02	2.69	0.4	478	5/21
jmfag5minnggbead_030528200105, 1209-1211	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 1432.25	3.86	0.5	910	9/28
JMMAGT ube1B16E3, 1228-1230	-KDLVANTVLSGGT TMYPLADR-	2344.63	2 37138.96	5.37	0.7	2347	9/14
JMMAGT ube1B16E3, 1238-1240	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 4855.45	2.76	0.4	501	23/84
jmfag1mnacl5mincon, 1418-1420	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 4642.09	2.56	0.3	755	13/42
jmfag5minngg450m mnacl_030527025134, 1872	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 8470.44	2.92	0.4	774	9/28
jmfag5minngg450m mnacl_030527025134, 1878	-KDLVANTVLSGGT TMYPLADR-	2344.63	3 15301.57	4.28	0.5	560	25/84
jmfag5mincon500m mnacl, 1886	-KDLVANTVLSGGT TMYPLADR-	2344.63	2 225.49	1.03	0.1	96	5/27
jmfag1mnacl7.5minngg, 2514	-CDVDIKDLV ANT VLSGGT TMYPLADR-	3046.43	2 225.49	1.03	0.1	96	5/27
similar to KIAA0825 protein [Mus musculus] actin	-VLSIEROK-	1086.31	2 304.07	1.01	0.1	140	9/16
jmfag1mnacl5mincon, 1430	-NLHSLSSA TYVSQR-	1678.86	3 737.88	1.73	0.1	363	19/56
JMFAGNACL5B21E3, 1490	-WNLLDT LLHS GGLPRLKSSK-	2696.24	3 8238.55	3.16	0.5	429	25/82
jmfag5minngg200m mnacl, 1826	-WNLLDT LLHS GGLPRLKSSK-	2696.24	3 1524.88	2.08	0.2	314	11/46
jmfag1mnacl5minngg, 1900	-GAVHALVSP ECGS KERR-	1868.11	3 280.14	1.16	0.0	225	15/64
jmfag5minngg500m mnacl, 1994	-LQNVQALDFLQK -	1696.98	3 927.78	1.93	0.1	390	4/13
microtubule-actin crosslinkin g factor 1 [Mus musculus]	-RWTDLSK-	1019.18	2 188.43	0.65	0.0	195	3/7
jmfag5minngg350m mnacl, 475	-LETVALP LQGLLEDAADRMR-	2326.66	3 1030.50	1.55	0.2	324	9/40
jmfag1mnacl0minngg, 468	-IHQRIHKA NEEINR-	2226.57	3 688.27	1.84	0.0	357	9/34
jmfag5minngg600m mnacl, 671	-EALAGLLK-	814.99	2 081.34	1.95	0.0	494	11/14
JMMAGNEG B18D3, 842	-WDTVCGK-	808.93	2 233.36	0.95	0.0	236	7/12
jmfag5minngg250m mnacl, 900	-DQDGKIT ROEFIDG ILASK-	2135.36	3 455.11	1.85	0.1	276	5/24
jmfag5minnggbead, 1021	-PSSRAASPT R-	1030.12	2 233.62	1.27	0.1	241	1/2
JMMAGT ube1B16E3, 1370	-ALERHOGGASR-	1182.28	2 598.16	1.20	0.2	169	9/20
jmfag1mnacl0minngg, 1336	-ALERHOGGASR-	1847.67	2 107.06	1.19	0.1	137	1/4
JMFAGNACL5B21E3, 1442-1444	-ALERHOGGASR-	1182.28	2 1607.35	1.61	0.3	247	11/20
JMMAGT ube1B16E3, 1464	-ALERHOGGASR-	1182.28	2 1074.76	1.72	0.2	335	3/5
jmfag5minngg1000m mnacl, 2028	-LAELSQRFOQLQ LQQEKESNLK-	2788.11	3 617.90	1.68	0.0	350	19/68
jmfag5minngg400m mnacl, 2284	-FQNLCSLDER-	1312.44	2 329.04	1.24	0.1	165	3/10
jmfag5mincon500m mnacl, 2374	-ELEEA VTSALQOQ EK-	1805.92	2 94.47	1.01	0.0	89	4/15
jmfag1mnacl7.5minngg, 2768	-VDEIDAALQRSQQYQADAELA VWAETKR-	3406.66	2 488.82	0.89	0.2	70	9/58
Coronin, actin binding protein 1A [Mus musculus]	-NLNIAVQK-	900.06	2 3115.91	2.24	0.3	484	11/14
JMFAGNACL5B21E3, 164	-NLNIAVQK-	900.06	2 3080.69	2.21	0.3	414	5/7
jmfag1mnacl2.5minngg, 166	-LDRLLEETVQAK-	1302.46	3 2674.63	2.70	0.2	617	19/40
JMFAGNACL5B21E3, 422	-NLNIAVQK-	900.06	2 1328.90	2.08	0.1	525	11/14
jmfag1mecon10m in_030801202502, 1076	-YFEITSEAPFLHYLSMFSSK-	2398.72	3 6077.20	2.99	0.4	488	11/38
coronin, actin binding protein 1A; coronin-like actin binding protein;	-KCEPIVMTVPRK-	1401.77	3 677.97	1.60	0.0	419	4/11
jmfag1mecon10m in_030801202502, 2848	-DLVRSRR-	874.02	2 528.08	1.23	0.1	348	7/12
coronin, actin binding protein 1B; coronin 1b ; coronin 2 [Mus musculus]	-RCSLIKHPLASNV LSCGVLDK-	2554.08	0 680.53	0.60	0.1	339	8
jmbbeads300ravphag3007, 151	-PHEGARFLRAVFTADG K-	1823.05	2 609.32	1.45	0.1	127	2
jmfag5mincon350, 764	-PVHAVFVSEGGKILT GFSSR-	2046.36	3 457.26	1.42	0.0	305	17/72
coronin [Hemicentrotus pulcherrimus] ing protein 1	-MQEITIAPPERK-	1526.83	2 580.62	1.61	0.1	326	11/24
jmfag1mecon2.5m in.1962.1962.3	-VAPEEHVLLT KVLPSLK-	1971.37	3 452.81	1.35	0.1	306	19/68
coronin, actin binding protein 6 isoform A; coronin 6; clpin E [Mus m	-ASGRGLQPK-	914.05	2 640.01	1.19	0.1	450	5/8
jmfag1mecon10m in_030801202502, 2072	-ASGRGLQPK-	914.05	2 503.63	1.42	0.1	302	5/8
p57 coren in [Mus musculus]	-ASGRGLQPK-	914.05	2 1473.04	1.79	0.2	534	11/16
jmbbeads250ravphag3007, 906	-FNGSHVGSPPKVR-	1551.74	3 672.57	1.72	0.0	373	15/52
similar to actin, gam ma, cytoplasmic [Mus musculus]	-VIVLFAQHQSISPFVNDK-	2328.70	3 276.17	1.48	0.0	168	17/80
rewextr_250beadigg_Mar04, 1180	-VHAQGPGLK-	907.05	2 369.51	0.85	0.1	229	7/16
FPbeads150_Dec19, 1219	-CLATG PGIAPTVKT GEEVGFVDAKTAGK-	2818.24	2 164.41	0.96	0.1	43	1/8
FLNB_MOUSE Filamin B (FLN-B) (Beta-filamin) (Actin-bind ing like protein) (ABP	-ASGRGLQPK-	914.05	2 1150.10	1.76	0.1	627	3/4
jmfag5minngg200m mnacl, 432	-ETADPKVDT KAAGSGELGVT VK-	2224.45	3 1789.23	2.61	0.1	657	25/84
jmfag1mnacl5mincon, 432-434	-FADEHVPGSPFTVMSIGEG R-	2131.33	3 477.69	1.07	0.0	448	5/19
jmfag5minngg1000m mnacl, 438	-YSYAVTW GGHHPKSPFEVQV GPEAGMQK-	3138.55	2 328.67	1.05	0.2	76	1/7
jmfag5minngg200m mnacl, 596	-VKVFGPGRVERGLK-	1473.75	3 215.65	1.08	0.0	166	1/4
JMFAGNACL10_2B21E3, 696	-ANEPTHT VDOT EAGEGDVSGVIGKCDAR-	2923.14	3 351.21	1.79	0.0	191	19/108
jmfag5minngg250m mnacl, 702	-EAFTHKSNVFT VTRGAGGGLG IVEGPSSEK-	3324.69	2 97.88	0.95	0.1	77	9/84
jmfag5minngg350m mnacl, 909	-VMYTPMAPNGVLYGVKGGPNHISRPK-	3196.74	2 42.70	0.79	0.0	34	3/28
jmfag5minngg250m mnacl, 960	-RCSQVGLKGAADFLDISD LSTLTASIK-	3184.61	2 104.10	0.75	0.0	138	11/58
jmfag1mnacl2.5minngg, 1250-1252	-HLWDYTFGPEK-	1363.53	3 2552.49	2.14	0.2	677	17/40
jmfag5minnggbead, 1369	-RKHMVFLGAVLADIMK-	1887.35	3 4293.32	2.36	0.3	644	11/32
jmfag1mnacl0minngg, 1726	-HLWDYTFGPEK-	1363.53	2 740.95	1.32	0.1	383	3/5
jmfag1mnacl7.5minngg, 1732	-RLDIAGRDIT R-	1286.47	2 97.81	0.91	0.0	107	3/10
jmfag5minngg300m mnacl, 2040-2042	-DLIVGDEASEL-	1335.47	2 401.41	1.09	0.1	288	5/11
jmfag5minngg150m mnacl, 2108	-MSDQQLDCALDLIR-	1639.90	3 289.06	1.28	0.0	213	1/4
jmfag5minngg400m mnacl, 2744	-MSDQQLDCALDLIR-	1639.90	3 430.93	1.58	0.0	271	4/13
jmfag5minngg400m mnacl, 3084	-SPWSENKYDPLLEDG AMPARS-	2219.42	3 6007.66	2.76	0.4	829	13/38
actin-related prote in 2; ARP2 (actin-related protein 2, yeast) homolog	-AVFPSSIV GRPR-	1199.43	2 3626.53	1.85	0.4	431	3/5
jmfag5minngg350m mnacl, 355	-AVFPSSIV GRPR-	1199.43	2 1206.91	1.78	0.2	359	1/2
jmfag1mnacl0minngg, 874	-AVFPSSIV GRPR-	1199.43	3 407.52	1.25	0.1	150	13/40
jmfag1mnacl7.5minngg, 1158	-AVFPSSIV GRPR-	1199.43	0 220.49	1.25	0.1	148	3/10
jmfag5minngg500m mnacl, 1492	-AVFPSSIV GRPR-	1199.43	2 867.94	1.49	0.1	536	3/5
jmfag5minngg250m mnacl, 1560	-MSDQQLDCALDLIR-	1639.90	3 289.06	1.28	0.0	213	1/4
CAPB_MOUSE F-actin capping protein beta su bunit (Cap Z beta)	-MSDQQLDCALDLIR-	1639.90	3 430.93	1.58	0.0	271	4/13
JMFAGNACL5B21E3, 666	-SPWSENKYDPLLEDG AMPARS-	2219.42	3 6007.66	2.76	0.4	829	13/38
jmfag1mnacl2.5minngg, 670	-AVFPSSIV GRPR-	1199.43	2 3626.53	1.85	0.4	431	3/5
JMFAGNACL5B21E3, 1014	-AVFPSSIV GRPR-	1199.43	2 1206.91	1.78	0.2	359	1/2
S53793 actin - mouse (fragments) A14; EST A1449046 [Mus musc	-AVFPSSIV GRPR-	1199.43	3 407.52	1.25	0.1	150	13/40
JMFAGNACL10_2B21E3, 678	-AVFPSSIV GRPR-	1199.43	0 220.49	1.25	0.1	148	3/10
JMFAGNACL10_1B21E3, 836	-AVFPSSIV GRPR-	1199.43	2 867.94	1.49	0.1	536	3/5
jmfag5minngg500m mnacl, 1098							
jmfag1mecon7.5m in.1230.1232.3							
AJRAW SoluteConfr_june13, 572							

Table 2 continued

AJRAWSoluteContr_june13, 560	-AVFSPVGRPR-	1199.43	3 170.07	1.32	0.0	113	1/4
jmfagtimecont10min_030601202502.1372-1374	-AVFSPVGRPR-	1199.43	2 4839.96	2.48	0.3	788	13/20
rawphag2007chfbad3, 615	-PRVPEEHPVSELP-	1720.91	3 328.55	1.37	0.0	230	1/4
rawsuctrfp_60MeOHPphagig_Mar04, 746	-AVFSPVGRPR-	1199.43	3 1626.74	1.55	0.3	202	13/40
rawsuctrfp_60MeOHPphagig_Mar04, 750	-AVFSPVGRPR-	1199.43	2 3036.57	2.12	0.3	512	13/20
rawsuctrfp_300phagigig_Mar04, 822	-AVFSPVGRPR-	1199.43	2 5686.91	2.62	0.4	670	7/10
rawsuctrfp_900phagigig_Mar04, 835	-AVFSPVGRPR-	1199.43	2 1067.82	1.39	0.2	335	1/2
rawsuctrfp_600phagigig_Mar04, 958	-AVFSPVGRPR-	1199.43	2 1277.26	1.51	0.2	312	1/2
rawsuctrfp_700phagigig_Mar04, 980	-AVFSPVGRPR-	1199.43	2 2321.00	1.81	0.3	358	1/2
actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub	-AVFSPVGRPR-	1199.43	2 549.98	1.05	0.2	226	1/2
JMMAGNEGB16D3, 1168	-ELLQPVITSR-	1260.52	2 2742.43	2.11	0.3	526	7/10
JMMAGTube1B16E3, 1198	-ELLQPVITSR-	1269.52	2 1744.83	1.47	0.2	760	13/20
JMMAGNEGB16D3, 1738-1740	-EISEMK-	736.86	1 188.08	1.26	0.0	149	3/5
similar to actin related protein 2/3 complex, subunit 5; actin related	-VLUSFKANDIEKAVQSLDK-	2119.45	3 1185.88	1.49	0.2	465	1/4
rawsuctrfp_450phagigig_Mar04, 1364	-NQEESIDAR-	1062.07	2 425.91	1.12	0.0	362	5/8
cytoskeletal actin-modulating protein [Mus musculus]	-ACSAIAVNLN-	1155.36	2 535.37	1.76	0.0	287	1/2
jmfag1mnacl5minig, 282	-ACSAIAVNLN-	1155.36	2 763.70	1.57	0.1	269	9/20
JMMAGNEGB16D3, 860	-ACSAIAVNLN-	1155.36	2 569.86	1.65	0.0	600	13/20
JMFAGNACL10_1B21E3, 774	-ACSAIAVNLN-	1155.36	1721.02	1.34	0.0	195	1/4
JMFAGNACL1B21E3,806-808	-TDQIKADTALFLPR-	957.15	1 944.02	1.47	0.1	582	9/14
jmfag5mincon500mnacl, 508	-LFRCSNEK-	2196.68	3 500.23	1.29	0.1	309	17/72
JMMAGTube1B16E3, 1480	-PKVELMPCMRLLQLSLDTR-	1155.36	2 766.42	1.74	0.0	440	3/5
JMFAGNACL10_1B21E3, 1638	-ACSAIAVNLN-	1155.36	2 1216.19	2.19	0.2	329	1/2
rawextr_400bead_Mar04,761-763	-VGLGLGYLEPQINYLKSEVHK-	2600.05	3 128.14	1.45	0.0	83	2/11
rawextr_900bead_Mar04,780-782	-GGYPFENVKAMTSLR-	1670.92	2 560.56	1.27	0.2	104	2/7
rawextr_150bead_Mar04, 1551	-LYKVLGLGYLEPQINYLKSEVHK-	2876.39	3 791.32	1.99	0.1	258	17/66
rawextr_300bead_Mar04, 1820	-ACSAIAVNLN-	1155.36	2 1108.66	1.91	0.2	335	11/20
rawextr_450bead_Mar04, 1950	-ACSAIAVNLN-	1155.36	2 1096.15	1.82	0.2	238	9/20
rawextr_500beadig_Mar04,782-784	-ACSAIAVNLN-	1155.36	2 495.78	1.42	0.0	348	11/20
rawextr_1000_beadig_Mar04, 796	-ACSAIAVNLN-	1155.36	2 746.25	1.45	0.1	434	3/5
rawextr_900beadig_Mar04,804-806	-ACSAIAVNLN-	1155.36	2 612.76	1.53	0.0	388	3/5
rawextr_900beadig_Mar04, 824	-ACSAIAVNLN-	1155.36	2 1380.79	1.74	0.2	390	11/20
rawextr_450beadig_Mar04,874-876	-KNIKLEPVPLK-	1279.60	1 97.37	0.88	0.0	110	7/20
rawextr_250beadig_Mar04, 892	-AFTRCFHAWSTFR-	1630.56	2 320.61	1.32	0.0	216	3/8
FPbead150_Dec19, 975	-ACSAIAVNLN-	1155.36	0 1192.07	0.2	0.4	343	11/20
rawextr_60MeOHbeadig_Mar04, 982	-PKWWDVLTVDVTR-	1772.94	0 1173.53	1.36	0.2	291	9/26
jmfagtimecon7.5min.716.716.2	-ACSAIAVNLN-	1155.36	2 416.82	1.46	0.1	203	9/20
jmfagtimecon7.5min.3158.3158.2	-NOLTSLSAICK-	1275.50	2 180.70	1.08	0.0	167	7/22
jmfagcon5minn600mnacl, 717	-CSNEKGYFAVEK-	1476.64	2 259.64	1.27	0.0	203	1/3
AJRAWActinContr_june13, 732	-ACSAIAVNLN-	1155.36	2 1364.77	1.79	0.2	449	3/5
jmfagcon5min10.00mnacl_030601180404, 792	-PYDDDAEYMK-	1155.36	2 531.03	1.59	0.1	252	9/20
jmfbead500rawphag3007, 814	-QLPAMMALQTLHLR-	1247.31	2 124.41	1.15	0.0	236	4/5
jmfbead500rawphag3007, 828	-QLPAMMALQTLHLR-	1624.01	2 930.92	1.61	0.2	178	4/13
jmfag5mincon450mnacl, 898	-NTQRTQSNLPTSLEGLSNLSOVLSCNDLTR-	3393.84	2 58.55	0.84	0.0	60	7/60
jmfbead5150rawphag3007, 1956	-QLPAMMALQTLHLR-	1624.01	2 232.75	1.01	0.0	218	9/26
jmfagtimecon10min, 3080	-ACSAIAVNLN-	1155.36	2 752.29	1.86	0.1	322	11/20
rawphag2007chfbad2, 304	-ACSAIAVNLN-	1155.36	2 872.54	1.57	0.0	543	13/20
rawphag2007chfbad2, 528	-ACSAIAVNLN-	1155.36	2 662.86	1.66	0.1	279	1/2
RawPhg2007Etslutiondigest, 605	-ACSAIAVNLN-	1155.36	2 978.88	1.83	0.1	369	3/5
rawphag2007chfso1, 1138	-ACSAIAVNLN-	1155.36	2 1384.49	2.11	0.1	446	13/20
rawphag2007chfso1, 1176	-ACSAIAVNLN-	1155.36	3 142.05	1.13	0.0	126	13/56
rawphag2007chfso1, 1176	-ACSAIAVNLN-	1155.36	2 803.71	1.48	0.1	473	3/5
phagrawFsu150_dec22, 48	-ACSAIAVNLN-	1155.36	2 350.09	1.47	0.0	234	9/20
phagrawFsu150_dec23, 514	-ACSAIAVNLN-	1155.36	2 619.46	1.73	0.0	358	11/20
rawsuctrfp_300phagigig_Mar04, 816	-ACSAIAVNLN-	1155.36	2 655.06	1.71	0.0	378	11/20
rawsuctrfp_150phagigig_Mar04,935-937	-ACSAIAVNLN-	1155.36	2 666.20	1.71	0.1	383	11/20
rawsuctrfp_450phagigig_Mar04,946-948	-ACSAIAVNLN-	1155.36	1 278.50	1.32	0.0	211	9/20
rawsuctrfp_700phagigig_Mar04, 966	-LAGASPTVAAMAAVSGSK-	1667.85	2 236.16	0.99	0.1	138	9/38
rawsuctrfp_700phagigig_Mar04, 968	-ACSAIAVNLN-	1155.36	2 2040.02	1.88	0.3	356	11/20
rawsuctrfp_800phagigig_Mar04, 974							
rawsuctrfp_400phagigig_Mar04, 985							
similar to beta actin [Mus musculus] [usculus] X&							
jmfag5minig350mnacl, 589-571	-IWHHTFYNELR-	1516.69	3 7343.21	3.48	0.2	1525	5/8
jmfag5minig600mnacl, 586-588	-IWHHTFYNELR-	1516.69	3 10871.40	3.53	0.4	1090	23/40
JMFAGNACL5B21E3, 624	-IWHHTFYNELR-	1516.69	3 7194.25	3.15	0.4	627	19/40
jmfag5minig400mnacl, 604	-IWHHTFYNELR-	1516.69	3 8261.02	3.02	0.4	1048	3/5
jmfag5minig400mnacl, 704	-IWHHTFYNELR-	1516.69	3 10458.41	2.97	0.5	1140	3/5
jmfagtimecon2.5min.724.724.3	-IWHHTFYNELR-	1516.69	0 7196.13	2.84	0.4	965	11/20
jmfagtimecon7.5min.947.946.3	-IWHHTFYNELR-	1516.69	0 8095.55	3.34	0.4	932	11/20
jmfagtimecon7.5min.952.854.3	-IWHHTFYNELR-	1516.69	0 4753.65	3.00	0.2	979	21/40
jmfagtimecon2.5min.738.738.3	-IWHHTFYNELR-	1516.69	0 4403.97	2.43	0.3	728	1/2
jmfag5mincon1150mnacl, 611	-IWHHTFYNELR-	1516.69	3 1640.96	2.15	0.2	433	7/20
jmfagcon5minn600mnacl, 791	-IWHHTFYNELR-	1516.69	3 7661.70	3.10	0.4	1283	3/5
jmfagcon5minn600mnacl, 795	-IWHHTFYNELR-	1516.69	3 4622.87	2.17	0.4	840	21/40
jmfagtimecon10min_030601230741, 1084	-IWHHTFYNELR-	1516.69	3 1704.35	1.67	0.2	653	9/20
jmfagcon5minn600mnacl, 1947-1949	-MXKEIALAPSTMIKIK-	1746.22	2 394.02	1.74	0.0	212	3/10
jmfagcon5minn600mnacl, 2843	-ALESDGGGGSGLLHGDEAGSKRGIPTLK-	2913.17	2 75.16	1.01	0.0	74	5/28
SAC2 [suppressor of actin mutations 2, homolog]-like [Mus musculus]							
jmfag5minig350mnacl, 495-497	-AELINIHLMVELKKHK-	2054.49	3 980.45	1.63	0.2	351	19/64
jmfag5minig600mnacl, 502	-LMKVQYEEVAEK-	1467.71	3 717.24	1.26	0.1	427	4/11
JMFAGNACL5B21E3, 504-506	-AELINIHLMVELKKHK-	2054.49	3 801.19	1.77	0.1	237	17/64
jmfag5minig600mnacl, 506-508	-AELINIHLMVELKKHK-	2054.49	3 1116.61	2.35	0.1	361	21/64
JMFAGNACL10_2B21E3, 508	-AELINIHLMVELKKHK-	2054.49	3 2227.18	1.86	0.3	250	16/64
jmravigg5minbeadsfreezeshaw,512-514	-AELINIHLMVELKKHK-	2054.49	3 1682.43	2.22	0.2	321	5/16
jmravigg5min150mnacl, 518-520	-AELINIHLMVELKKHK-	2054.49	3 488.89	1.45	0.0	338	5/16
jmfag1mnacl2.5minig,554-556	-AELINIHLMVELKKHK-	2054.49	3 3980.17	2.27	0.4	498	11/32
jmfag1mnacl7.5minig,558-560	-AELINIHLMVELKKHK-	2054.49	3 556.65	1.52	0.1	258	9/32
jmfag5minig400mnacl, 578	-AELINIHLMVELKKHK-	2054.49	3 352.41	1.50	0.0	222	15/64
jmfag5minig400mnacl, 580	-AELINIHLMVELKKHK-	2054.49	3 1195.38	1.82	0.2	398	19/64
jmfag5minig200mnacl, 606	-AELINIHLMVELKKHK-	2054.49	3 2216.74	2.07	0.3	323	19/64
jmfag5minig100mnacl, 606	-AELINIHLMVELKKHK-	2054.49	3 882.32	1.55	0.1	471	11/32
jmfag5minig100mnacl, 610	-AELINIHLMVELKKHK-	2054.49	3 278.21	1.33	0.1	177	7/32
JMFAGNACL15B21E3, 628	-AELINIHLMVELKKHK-	2054.49	3 364.46	1.39	0.0	240	17/64
jmfag5minig600mnacl, 770	-AELINIHLMVELKKHK-	2054.49	3 1387.26	1.74	0.2	313	19/64
jmfag5minig600mnacl, 972	-VLSQPLRALPAR-	1449.73	3 695.11	1.46	0.0	469	17/48
jmfag5minig500mnacl, 978	-AELINIHLMVELKKHK-	2054.49	3 565.15	1.24	0.1	429	21/64
jmfag1mnacl5minig, 1036	-AELINIHLMVELKKHK-	2054.49	3 517.04	1.50	0.1	216	17/64
jmgG40rawphag3007, 1040	-DEYVETLSK-	1084.16	2 137.32	1.15	0.0	119	3/8
	-AELINIHLMVELKKHK-	2054.49	3 770.32	1.58	0.1	449	5/16

Table 2 continued

jmlg350na drawphag3007, 104 1-1043	-AELINIHMLMVELKHKH-	2054.49	3 542.48	1.81	0.0	329	19/84
jmfag5minig300m mnacl, 1179-1180	-AELINIHMLMVELKHKH-	2054.49	3 580.25	1.69	0.1	281	5/16
jml5minigrawfowicac, 1228-1230	-AELINIHMLMVELKHKH-	2054.49	3 385.69	1.53	0.1	185	15/64
jmfagfrench20minig1mnacl, 1524	-YAEFSSALVSI NOTIPNER-	2140.34	3 1282.10	1.70	0.2	276	17/72
jmravag5min1mnacl, 2015	-RYAEFSSALVSI NOTIPNER-	2296.53	3 513.68	1.53	0.1	231	17/76
jmfag5minig150m mnacl, 2698	-GKLGELVDGLV PSALVTAI LEAPVT EPR-	2945.44	2 132.67	0.91	0.1	88	1/7
jmfag5minig150m mnacl, 2912	-HLESYLADCYDAIAVFLCHIVLRF-	3082.63	2 187.42	1.03	0.1	91	9/50
JMMAG Tube 1B16E3, 264	-LGGLDTR-	731.82	2 670.31	1.25	0.0	529	3/4
jmfag5minigbead, 441-443	-AELINIHMLMVELKHKH-	2054.49	3 882.20	1.88	0.1	281	9/32
JMMAG NEGB16D3, 484	-AELINIHMLMVELKHKH-	2054.49	3 359.04	1.35	0.0	285	19/84
JMMAG Tube 1B16E3, 502	-AELINIHMLMVELKHKH-	2054.49	3 1988.31	1.55	0.3	403	8/32
jmfag5minigbead, 03052:8200105, 603	-AELINIHMLMVELKHKH-	2054.49	3 807.19	1.74	0.1	287	19/64
jmfag1mnacl5mincon, 632-634	-AELINIHMLMVELKHKH-	2054.49	3 2024.14	2.05	0.3	257	16/64
jmag5mincon500m mnacl, 1200-1202	-AELINIHMLMVELKHKH-	2054.49	3 1095.66	1.71	0.2	316	19/64
jmfagtimecon2.5m in. 604, 606.3	-AELINIHMLMVELKHKH-	2054.49	3 1045.14	1.68	0.2	256	19/64
jmfagtimecon7.5m in. 436, 436.3	-AELINIHMLMVELKHKH-	2054.49	0 348.42	1.83	0.1	155	15/64
jmfagcon5m inn600mnacl, 425	-AELINIHMLMVELKHKH-	2054.49	0 581.45	1.61	0.0	358	5/16
jmfag5mincon400, 03053 1151834, 466	-AELINIHMLMVELKHKH-	2054.49	3 274.14	1.35	0.0	198	15/64
jmbeads400rawphag3007, 488	-AELINIHMLMVELKHKH-	2054.49	3 1525.47	1.55	0.3	173	7/32
jmbeads400rawphag3007, 476	-AELINIHMLMVELKHKH-	2054.49	3 810.08	1.99	0.2	216	17/64
jmfag5mincon150m mnacl, 495-497	-AELINIHMLMVELKHKH-	2054.49	3 367.80	1.28	0.1	148	15/64
jmfag5mincon350, 538-541 mnacl, 620-622	-AELINIHMLMVELKHKH-	2054.49	3 1625.29	1.98	0.2	352	5/16
jmfag5mincon450m mnacl, 918	-AELINIHMLMVELKHKH-	2054.49	3 587.32	1.71	0.1	250	9/32
jmfag5mincon250m mnacl, 996-998	-AELINIHMLMVELK-	2054.49	3 2804.58	2.05	0.3	258	19/64
jmfagtimecon10m in, 0306012 30741, 105 6-1058	-AELINIHMLMVELKHKH-	1661.01	3 604.82	1.53	0.0	395	17/52
jmbeads350rawphag30072nd, 1128-1130	-AELINIHMLMVELKHKH-	2054.49	3 1001.56	1.59	0.2	382	21/64
jmfag5mincon300mnacl, 1164-1166	-AELINIHMLMVELKHKH-	2054.49	3 965.68	2.03	0.1	321	19/64
jmfagtimecon10m in, 030601 202502, 1224-1226	-AELINIHMLMVELKHKH-	2054.49	3 579.88	1.82	0.0	357	21/64
phagrawF350_dec20, 1018	-AELINIHMLMVELKHKH-	2054.49	3 1124.08	2.07	0.1	357	19/64
phagrawF350_dec20, 1574	-AELINIHMLMVELKHKH-	2054.49	3 978.78	1.93	0.2	247	17/64
phagrawF350_dec22, 1810	-KPM TNYQI PQA ALLK-	1717.07	3 367.26	1.69	0.0	213	13/56
nactin, nF actin binding protein [Mus musculus]	-SF TNRFG TSIQIGALTQ LQLYHR-	2880.25	3 303.51	1.44	0.1	160	1/6
rawextr_600bead_Mar04, 896	-PSLRGNTI FTGLTR-	1719.97	2 214.68	1.01	0.1	164	2/7
rawextr_200bead_Mar04, 1234	-KSESPFT HK-	1061.17	3 437.04	1.37	0.0	319	7/16
rawextr_200bead_Mar04, 1396-1398	-EEEEENFGLSR-	1426.43	2 210.72	1.00	0.1	167	4/11
FPbeads150_Dec16, 697	-MRYEE ECRVLK-	1456.72	2 356.72	1.37	0.0	256	2/5
rawextr_400beadig_Mar04, 1236	-KSESPFT HK-	1061.17	3 501.48	1.55	0.0	319	1/2
rawextr_350beadig2_Mar04, 1818	-QKMEERR-	1106.24	2 434.45	1.21	0.0	354	9/14
jmfag5mincon350, 448	-CLSLVMDDETE AK-	1454.65	2 432.82	1.07	0.1	306	11/24
jmfag5mincon200mnacl, 1154	-RSGSIQAKNLK-	1202.39	3 1309.47	1.66	0.1	714	19/40
jmbeads300rawphag3007, 1812	-RT EERR-	978.03	2 300.48	1.27	0.0	224	2/3
jmfag5mincon200mnacl, 1940	-FEKUGQSEKEV QK-	1663.90	2 487.64	1.33	0.0	344	11/26
phagrawF150_dec22, 518	-EDEEE EEGSVNGST TEDEE QTR-	2613.51	3 761.99	2.07	0.0	348	19/88
phagrawF350_dec20, 1716	-KSESPFT HK-	1061.17	3 202.34	1.09	0.1	100	1/4
phagrawF800_Dec23, 2240	-EDEEE EEGSVNGST TEDEE QTR-	2613.51	3 671.38	1.84	0.1	263	9/44
phagrawF800_Dec23, 2244	-EDEEE EEGSVNGST TEDEE QTR-	2613.51	3 1897.97	2.16	0.2	283	5/22
phagrawF800_Dec23, 2244	-EDEEE EEGSVNGST TEDEE QTR-	2613.51	3 1668.11	2.28	0.2	416	1/4
fascin homolog 2, actin-bundling protein, retinal [Strongylocentrotus]	-DGAYQIGRR-	1036.13	2 135.54	0.88	0.1	86	3/8
rawextr_60MeOHbead_Mar04, 508	-STYDVHLSFRDQ AYGIR-	2176.38	3 470.22	1.65	0.0	284	1/4
rawextr_700bead_Mar04, 1125	-GLDGFVCPRRGS NCLDTR-	2106.31	3 370.35	1.25	0.1	223	5/24
rawextr_600bead_Mar04, 2088	-PLLVLRLGLDFG VCPR-	1656.03	3 1052.82	1.88	0.1	513	19/56
rawextr_450beadig_Mar04, 610	-AGYAGE DCPKVDFFT AIGV/LER-	2408.72	3 846.94	1.88	0.1	420	21/88
rawextr_150beadig2_Mar04, 550	-GKVLGFR-	776.95	2 1006.15	1.02	0.3	178	1/2
kaptin; actin-binding protein [Mus musculus]	-PEYDEAGPSI VHR-	1470.57	2 575.15	1.41	0.1	302	11/24
jmfag5mincon300mnacl, 268	-DMWITNHEYLEIG PSVIFRR-	2477.83	3 315.09	2.12	0.0	148	17/76
actin, gamma 2 prepeptide; actin, alpha-3 [Homo sapiens]	-EMAKVSPDF CVK-	1453.75	2 515.73	1.05	0.2	149	1/3
AJRAW ActinContr_june13, 696	-TELNYYPYPSRG ATNWDNVEK-	2615.00	3 633.73	1.38	0.1	357	19/84
similar to actin-12 [Mus musculus]	-ANPGIIMLTLE SIMS CEK-	1975.34	1 155.52	0.90	0.1	73	7/34
phagrawF350chf1bead_dec23, 1020-1022	-GAGTDDHTLIR-	1156.23	2 1120.12	1.83	0.0	812	13/20
rawphag2007chf1bead, 1418	-QEIAQEFK-	993.10	2 1321.94	1.86	0.2	265	5/7
phagrawF350chf1bead, 1808	-QEIAQEFK-	993.10	2 984.19	1.62	0.2	240	9/14
RawPhag2007EL Beadslip, 030718 152 503, 2454	-QEIAQEFK-	993.10	2 2273.65	2.22	0.3	305	5/7
Anz6 protein [Mus musculus] d domain protein 1 [M]	-QEIAQEFK-	993.10	2 258.44	1.68	0.1	280	9/14
jmfag1mnacl5mincon, 116	-QEIAQEFK-	993.10	2 836.93	1.84	0.1	321	11/14
jmfag1mnacl0minig, 248	-QEIAQEFK-	993.10	2 1595.60	1.72	0.3	246	9/14
jmfag1mnacl0minig, 260	-QEIAQEFK-	993.10	2 2088.94	1.95	0.3	375	5/7
jmfag1mnacl5minig, 264	-QEIAQEFK-	993.10	2 1078.34	1.58	0.2	285	5/7
jmfag1mnacl5mincon, 270	-TPPELSAIK-	988.12	2 1948.24	1.78	0.3	357	11/16
jmfag1mnacl5minig, 270	-TPPELSAIK-	988.12	2 8275.82	2.94	0.4	1124	15/16
jmfag1mnacl5mincon, 284	-TPPELSAIK-	988.12	2 4101.95	2.62	0.2	1082	15/16
jmfag1mnacl2.5minig, 376-378	-TPPELSAIK-	988.12	2 3809.54	2.36	0.3	736	13/16
jmfag1mnacl7.5minig, 384	-TPPELSAIK-	988.12	2 3672.58	2.00	0.2	1223	15/16
jmfag1mnacl7.5minig, 542	-TPPELSAIK-	988.12	2 5343.84	2.37	0.4	655	13/16
jmfag1mnacl2.5minig, 546-548	-TPPELSAIK-	988.12	2 5382.52	2.92	0.3	1044	7/8
jmfag1mnacl7.5minig, 548	-TPPELSAIK-	988.12	2 2575.43	2.11	0.3	544	3/4
jmfag5minig400m mnacl, 564-566	-LYDAYELK-	1015.14	2 1063.95	1.98	0.1	507	13/14
jmfag1mnacl5mincon, 566	-LYDAYELK-	1015.14	2 1752.85	1.87	0.2	629	6/7
jmfag5minig200m mnacl, 614	-VLTEIASR-	1002.19	2 5094.25	3.37	0.2	950	15/16
jmfag1mnacl5minig, 618	-VLTEIASR-	1002.19	2 1006.49	1.60	0.2	300	9/16
jmfag1mnacl5minig, 622	-VLTEIASR-	1002.19	2 4306.91	2.86	0.2	946	7/8
jmfag1mnacl0minig, 724	-LYDAYELK-	1015.14	2 1915.11	1.60	0.3	448	11/14
jmfag1mnacl0minig, 728	-VLTEIASR-	1002.19	2 5034.44	2.88	0.3	996	13/16
jmfag1mnacl0minig, 778-780	-VLTEIASR-	1002.19	2 5250.08	2.58	0.3	864	7/8
jmfag5minig600m mnacl, 792	-GTVTDFPGFDGR-	1269.35	2 13380.36	3.57	0.5	986	9/11
jmfag1mnacl2.5minig, 848-850	-VLTEIASR-	1002.19	2 6104.49	2.50	0.4	903	15/16
jmfag1mnacl5minig, 934	-FITIFGTR-	955.14	2 1667.53	1.92	0.2	416	11/14
jmfag1mnacl5minig, 992-994	-GTVTDFPGFDGR-	1269.35	2 10548.58	2.93	0.5	1058	17/22
jmfag1mnacl5mincon, 1016	-GTVTDFPGFDGR-	1269.35	2 8453.62	2.72	0.5	818	17/22
jmfag1mnacl0minig, 1016-1018	-GTVTDFPGFDGR-	1269.35	2 348.75	1.15	0.0	291	9/22
jmfag1mnacl5mincon, 1020	-LYDAYELK-	1015.14	2 740.50	1.52	0.1	383	9/14
jmfag1mnacl0minig, 1086-1088	-FITIFGTR-	955.14	2 2468.73	2.18	0.2	510	6/7
jmfag1mnacl2.5minig, 1072-1074	-FITIFGTR-	955.14	2 2524.50	1.60	0.3	416	11/14
jmfag1mnacl7.5minig, 1086-1088	-GTVTDFPGFDGR-	1269.35	2 2837.83	1.75	0.3	551	7/11
jmfag5minigbead, 03052:8200105, 1087							
jmfag5minig500m mnacl, 1124							
jmfag1mnacl2.5minig, 1124-1126							
jmfag1mnacl7.5minig, 1154							
jmfag5minig1000mnacl, 1180							

Table 2 continued

jmfag5minig450m mnacl_030527025134, 1188	-TPEELSAIK-	988.12	2 2509.41	1.03	0.2	686	13/16
jmfag1mnacl5minig, 1236-1238	-GTVTDFPGFDGR-	1269.35	2 5296.22	2.28	0.3	1119	17/22
jmfag5minig600m mnacl, 1256	-SEIDFNIR-	1107.24	2 7218.06	2.69	0.4	1124	7/8
jmfag1mnacl5mincon, 1274-1276	-GTVTDFPGFDGR-	1269.35	2 6350.65	2.11	0.5	780	17/22
jmfag1mnacl0minig, 1292-1294	-SEIDFNIR-	1107.24	2 9654.04	3.37	0.4	1238	7/8
jmfag1mnacl5minig, 1296-1298	-FITIFGTR-	955.14	2 2668.67	2.51	0.2	567	6/7
jmfag1mnacl2,5minig, 1348-1350	-SEIDFNIR-	1107.24	2 10466.92	3.54	0.4	1310	7/8
jmfag1mnacl7,5minig, 1370	-SEIDFNIR-	1107.24	2 9773.86	3.29	0.4	1245	7/8
jmfag1mnacl0minig, 1380-1382	-SEIDFNIR-	1107.24	2 8115.10	3.26	0.4	1228	7/8
jmfag5minig450m mnacl_030527025134, 1420	-NFATSLYSMIK-	1275.50	2 6406.62	2.57	0.4	1080	4/5
jmfag5minig300m mnacl, 1426	-VLTEIASR-	1002.19	2 3268.30	2.32	0.2	832	7/8
jmfag5minig300m mnacl, 1434	-VLTEIASR-	1002.19	2 2163.22	2.09	0.2	850	13/16
jmfag5mincon500m mnacl, 1458-1460	-VLTEIASR-	1002.19	2 2304.85	2.00	0.2	631	3/4
jmfag1mnacl2,5minig, 1520	-VLTEIASR-	1002.19	2 3410.06	2.49	0.2	963	7/8
jmfag1mnacl7,5minig, 1530	-YMTISGFQIETIDR-	1804.02	2 387.04	1.61	0.1	169	5/14
jmfag1mnacl5minig, 1530-1532	-YMTISGFQIETIDR-	1804.02	2 4794.91	2.15	0.4	462	13/28
jmfag5minig250m mnacl, 1544	-SEIDFNIR-	1107.24	2 7152.98	3.38	0.3	1067	7/8
jmfag5minig250m mnacl, 1548	-GTVTDFPGFDGR-	1269.35	2 1883.75	1.45	0.3	621	7/11
jmfag5minig400m mnacl, 1552	-GTVTDFPGFDGR-	1269.35	2 2220.37	1.29	0.3	697	13/22
jmfag1mnacl5mincon, 1564	-YMTISGFQIETIDR-	1804.02	2 798.36	1.58	0.2	170	2/7
jmfag5minig350m mnacl, 1635	-SEIDFNIR-	1107.24	2 8970.16	3.05	0.4	1196	7/8
jmfag5minig250m mnacl, 1656	-DLVDLKLSELTGK-	1433.59	2 8634.28	2.55	0.5	1250	17/24
jmfag1mnacl5minig, 1704-1706	-FITIFGTR-	955.14	2 2128.45	1.89	0.3	299	9/14
jmfag5minig450m mnacl_030527025134, 1706-1708	-YMTISGFQIETIDR-	1804.02	2 371.57	1.85	0.1	140	5/14
jmfag5minig300m mnacl, 1724	-GTVTDFPGFDGR-	1269.35	2 4081.64	2.21	0.4	598	7/11
jmfag1mnacl0minig, 1732	-GTVTDFPGFDGR-	1269.35	2 5010.49	1.90	0.4	797	8/11
jmfag5minig300m mnacl, 1736	-DLVDLKLSELTGK-	1433.59	2 14584.66	3.34	0.5	2173	7/8
jmfag5mincon500m mnacl, 1742	-GTVTDFPGFDGR-	1269.35	2 602.99	1.50	0.1	348	1/2
jmfag5mincon500m mnacl, 1750	-GTVTDFPGFDGR-	1269.35	2 1478.44	1.43	0.2	587	13/22
jmfag5minig350m mnacl, 1763	-GTVTDFPGFDGR-	1269.35	2 5207.15	2.09	0.4	681	8/11
jmfag5minig350m mnacl, 1767	-GLGTDEDSILNLT SR-	1704.86	2 13079.66	3.91	0.5	876	8/15
jmfag1mnacl2,5minig, 1774	-GLGTDEDSILNLT SR-	1704.86	2 8348.76	3.62	0.3	1202	19/30
jmfag5minig500m mnacl, 1776-1778	-DLVDLKLSELTGK-	1433.59	3 1732.18	1.86	0.3	209	1/3
jmfag5minig600m mnacl, 1794	-SEIDFNIR-	1107.24	2 9639.09	3.25	0.4	1260	7/8
jmfag5minig600m mnacl, 1800	-GLGTDEDSILNLT SR-	1704.86	2 10777.82	3.70	0.3	1625	7/10
jmfag1mnacl0minig, 1818-1820	-GLGTDEDSILNLT SR-	1704.86	2 3497.96	1.80	0.4	559	1/2
jmfag5minig600m mnacl_030527025134, 1833	-SIPYLAETLYYAMK-	1735.04	2 16228.78	4.13	0.5	978	9/14
jmfag5mincon500m mnacl, 1836-1838	-SIPYLAETLYYAMK-	1735.04	2 7546.66	2.97	0.5	446	1/2
jmfag1mnacl0minig, 1856-1860	-FITIFGTR-	955.14	2 3048.77	2.52	0.3	346	9/14
jmfag1mnacl2,5minig, 1864	-GLGTDEDSILNLT SR-	1704.86	2 19359.88	4.85	0.5	1587	7/10
jmfag1mnacl2,5minig, 1872	-SIPYLAETLYYAMK-	1735.04	2 10598.04	3.01	0.5	636	17/28
jmfag1mnacl7,5minig, 1926	-SIPYLAETLYYAMK-	1735.04	2 12033.18	2.99	0.6	524	4/7
jmfag5minig400m mnacl, 1926	-GLGTDEDSILNLT SR-	1704.86	2 14929.15	4.32	0.5	1063	19/30
jmfag1mnacl7,5minig, 1930	-GLGTDEDSILNLT SR-	1704.86	2 15427.15	4.66	0.4	1358	19/30
jmfag5minig400m mnacl, 1932	-GLGTDEDSILNLT SR-	1704.86	2 12363.09	3.58	0.5	1021	17/30
jmfag1mnacl0minig, 1936	-GLGTDEDSILNLT SR-	1704.86	2 11386.43	3.81	0.5	958	17/30
jmfag1mnacl0minig, 1938	-GLGTDEDSILNLT SR-	1704.86	2 10715.94	3.87	0.4	1269	2/3
jmfag1mnacl0minig, 1940	-ETSQNLQQLLA VVK-	1614.87	2 14333.34	3.63	0.5	999	17/28
JMAGAGTUBE16E3, 1950	-ETSQNLQQLLA VVK-	1614.87	2 17175.77	4.00	0.6	1173	19/28
JMAGAGTUBE16E3, 1952	-GLGTDEDSILNLT SR-	1704.86	2 13121.38	4.36	0.4	1217	3/5
JMAGAGTUBE16E3, 1958	-GLGTDEDSILNLT SR-	1704.86	2 11376.02	3.90	0.4	1014	8/15
jmfag1mnacl5minig, 1960	-GLGTDEDSILNLT SR-	1704.86	2 11676.88	3.39	0.5	1254	3/5
jmfag1mnacl5minig, 1964	-DLVDLKLSELTGK-	1433.59	3 1165.05	1.91	0.2	301	3/8
jmfag1mnacl2,5minig, 1968	-DLVDLKLSELTGK-	1433.59	2 15354.49	3.77	0.5	1546	19/24
jmfag1mnacl5minig, 1970	-ETSQNLQQLLA VVK-	1614.87	2 1620.53	2.22	0.2	422	3/7
jmfag1mnacl2,5minig, 1972	-DLVDLKLSELTGK-	1433.59	2 9566.93	2.18	0.4	959	2/3
jmfag5minig1000m mnacl, 1972	-ETSQNLQQLLA VVK-	1614.87	2 11183.21	3.62	0.5	895	4/7
jmfag1mnacl2,5minig, 1974	-SIPYLAETLYYAMK-	1735.04	2 4769.71	2.50	0.4	556	4/7
jmfag1mnacl7,5minig, 2022-2004	-ETSQNLQQLLA VVK-	1614.87	3 8762.85	3.54	0.4	1196	27/56
jmfag5minig1000m mnacl, 2004-2006	-ETSQNLQQLLA VVK-	1614.87	2 11531.31	3.54	0.5	869	17/28
jmfag1mnacl5minig, 2050	-GLGTDEDSILNLT SR-	1704.86	2 17404.44	4.78	0.5	1120	2/3
jmfag1mnacl5minig, 2058	-SIPYLAETLYYAMK-	1735.04	2 835.02	1.52	0.2	237	3/7
jmfag5minig450m mnacl_030527025134, 2068	-SIPYLAETLYYAMK-	1735.04	2 14481.70	3.15	0.6	914	17/28
jmfag5mincon500m mnacl, 2070-2072	-SEIDFNIR-	1107.24	2 7978.37	2.56	0.4	1425	7/8
jmfag5minig1000m mnacl, 2074	-SEIDFNIR-	1107.24	2 6729.14	3.05	0.4	933	13/16
jmfag1mnacl5minig, 2074	-ETSQNLQQLLA VVK-	1614.87	2 8097.53	2.90	0.4	827	4/7
jmfag1mnacl5minig, 2098-2100	-YMTISGFQIETIDR-	1804.02	2 1005.12	1.70	0.1	377	5/14
jmfag1mnacl5mincon, 2122-2124	-GLGTDEDSILNLT SR-	1704.86	2 11028.34	4.43	0.4	1002	3/5
jmfag1mnacl5mincon, 2150-2152	-SIPYLAETLYYAMK-	1735.04	2 2418.08	1.86	0.3	408	3/7
jmfag1mnacl5minig, 2168-2170	-GLGTDEDSILNLT SR-	1704.86	2 14978.98	4.22	0.5	1427	19/30
jmfag1mnacl5minig, 2172-2174	-ETSQNLQQLLA VVK-	1614.87	2 12640.40	3.92	0.5	909	17/28
jmfag5mincon500m mnacl, 2180	-ETSQNLQQLLA VVK-	1614.87	3 10247.98	3.63	0.4	953	3/7
jmfag1mnacl5mincon, 2224-2226	-NFATSLYSMIK-	1275.50	2 1773.15	1.75	0.2	631	3/5
jmfag5minig500m mnacl, 2382	-ETSQNLQQLLA VVK-	1614.87	2 12510.59	3.81	0.5	1201	19/28
jmfag5minig500m mnacl, 2444	-SIPYLAETLYYAMK-	1735.04	2 746.38	1.12	0.1	484	1/2
jmfag5minig500m mnacl, 2498	-GLGTDEDSILNLT SR-	1704.86	2 3579.14	2.14	0.3	647	13/30
jmfag5minig250m mnacl, 2508-2510	-ETSQNLQQLLA VVK-	1614.87	2 6113.81	2.66	0.4	843	1/2
jmfag5minig250m mnacl, 2564	-SIPYLAETLYYAMK-	1735.04	2 305.16	1.77	0.0	172	2/7
jmfag5minig450m mnacl_030527025134, 2648	-ETSQNLQQLLA VVK-	1614.87	2 7438.10	2.94	0.4	1292	17/30
jmfag5mincon500m mnacl, 2698	-SIPYLAETLYYAMK-	1735.04	2 11145.04	3.35	0.5	1144	9/14
jmfag5mincon500m mnacl, 2702	-GLGTDEDSILNLT SR-	1704.86	2 9811.92	2.78	0.5	647	17/28
jmfag5minig450m mnacl_030527025134, 2718	-GLGTDEDSILNLT SR-	1704.86	2 4623.39	2.37	0.3	905	8/15
jmfag5minig450m mnacl_030527025134, 2726	-GLGTDEDSILNLT SR-	1704.86	2 4859.37	2.76	0.3	988	8/15
jmfag5minig300m mnacl, 2754	-GLGTDEDSILNLT SR-	1704.86	2 13260.09	4.02	0.5	946	8/15
jmfag5mincon500m mnacl, 2760-2762	-GLGTDEDSILNLT SR-	1704.86	2 9232.80	3.43	0.4	709	7/15
jmfag5minig450m mnacl_030527025134, 2772-2774	-GLGTDEDSILNLT SR-	1704.86	2 10351.10	3.77	0.4	1292	19/30
jmfag1mnacl0minig, 3379	-ETSQNLQQLLA VVK-	1614.87	2 10991.41	3.32	0.5	688	4/7
jmrarwminig200m mnaclsyndnas, 1016	-DPDTAIDQVELDA QALFQAGELK-	1614.87	2 8845.71	3.07	0.5	623	15/28
jmrarwminig200m mnaclsyndnas, 1064	-TPEELSAIK-	988.12	2 1974.58	1.70	0.2	630	13/16
jmlgG250rawphag3007, 1236	-GTVTDFPGFDGR-	1269.35	2 3879.35	1.67	0.4	481	13/22
jmlgG150rawphag3007, 1464-1466	-VLTEIASR-	1002.19	2 1175.03	1.36	0.1	693	13/16
jmlgG250rawphag3007, 1496-1498	-GTVTDFPGFDGR-	1269.35	2 506.32	1.39	0.1	266	5/11
jmlgG300rawphag3007, 1506	-GTVTDFPGFDGR-	1269.35	2 2135.06	1.87	0.3	425	6/11
jmrarwminig200m mnaclsyndnas, 1514	-GTVTDFPGFDGR-	1269.35	2 5127.65	2.36	0.4	596	13/22
jmrarwminig200m mnaclsyndnas, 1524	-GTVTDFPGFDGR-	1269.35	2 1388.77	1.63	0.2	488	1/2
jmrarwminig200m mnaclsyndnas, 1742	-GTVTDFPGFDGR-	1269.35	2 2721.60	1.92	0.3	368	1/2
jmrarwminig200m mnaclsyndnas, 1888	-WGTDDEKFIITGTRSVSHLR-	2480.76	3 485.99	1.86	0.0	262	17/80
jmlgG350nactrawphag3007, 2163	-GLGTDEDSILNLT SR-	1704.86	2 11388.10	3.61	0.5	844	8/15
	-DLVDLKLSELTGKFEK-	1838.05	3 4017.43	2.53	0.4	278	1/3

Table 2 continued

jmlgG300rawphag3007, 2194	-DLVDDLKSELTKGFEK-	1838.05	3 316.29	1.50	0.1	103	1160
jmlgG250rawphag3007, 2214	-DLVDDLKSELTKGFEK-	1838.05	3 2080.88	2.01	0.3	488	2/5
jmlrawminig200mmnacsyringdnas, 2250	-DLVDDLKSELTKGFEK-	1838.05	3 1722.25	2.11	0.2	275	3/10
jmlrawminig200mmnacsyringdnas, 2450-2452	-GLGTDEDSILNLLTSR-	1704.86	2 6965.12	3.41	0.3	1281	3/5
jml5minigrawowiconic, 2738	-GLGTDEDSILNLLTSR-	1704.86	2 7691.04	2.91	0.4	826	3/5
jml5minigrawowiconic, 2740	-GLGTDEDSILNLLTSR-	1704.86	2 10919.93	3.76	0.4	1460	2/3
rawextr_400bead_Mar04, 705	-TPELSAIK-	988.12	2 3103.03	1.86	0.3	625	7/8
rawextr_actinbead_Mar04, 876	-QEIAQEFK-	993.10	2 661.32	1.87	0.1	288	5/7
rawextr_actinbead_Mar04, 882	-QEIAQEFK-	993.10	2 2081.08	1.87	0.3	476	8/7
rawextr_actinbead_Mar04, 1092	-VLTEIASR-	1002.19	2 4629.91	2.49	0.3	137	15/16
rawextr_actinbead_Mar04, 1336-1338	-GTVTDFPGDGR-	1269.35	2 7150.89	2.68	0.4	775	17/22
rawextr_200bead_Mar04, 1414-1418	-GLGTDEDSILNLLTSR-	1269.35	2 5933.09	1.91	0.4	1039	9/11
rawextr_800bead_Mar04, 1662	-GLGTDEDSILNLLTSR-	1704.86	2 5268.70	3.32	0.3	690	8/15
rawextr_800bead_Mar04, 1686	-GLGTDEDSILNLLTSR-	1704.86	2 15579.89	4.33	0.4	1638	2/3
rawextr_actinbead_Mar04, 1764	-WGTDDEKFIITGTR-	1800.99	2 4603.30	2.23	0.4	349	11/28
rawextr_450bead_Mar04, 1860	-GLGTDEDSILNLLTSR-	1704.86	2 6880.80	3.63	0.3	1253	3/5
rawextr_450bead_Mar04, 1864	-GLGTDEDSILNLLTSR-	1704.86	2 4686.91	2.93	0.3	608	7/15
rawextr_350bead_Mar04, 1918	-GLGTDEDSILNLLTSR-	1704.86	2 7781.25	3.72	0.3	1221	3/5
rawextr_600bead_Mar04, 1974	-GLGTDEDSILNLLTSR-	1704.86	2 13669.76	4.07	0.5	1001	17/30
rawextr_250bead_Mar04, 1980	-GLGTDEDSILNLLTSR-	1704.86	2 6375.16	3.12	0.4	787	1/2
rawextr_250bead_Mar04, 1986	-GLGTDEDSILNLLTSR-	1704.86	2 1466.84	2.09	0.1	607	7/15
rawextr_chifbead_Mar04, 1996	-GLGTDEDSILNLLTSR-	1704.86	2 858.75	1.63	0.0	403	2/5
rawextr_chifbead_Mar04, 2006	-GLGTDEDSILNLLTSR-	1704.86	2 2940.47	2.44	0.3	278	7/15
rawextr_actinbead_Mar04, 2068	-SIPAYLAETLYYAM K-	1735.04	2 11429.34	3.03	0.8	749	9/14
rawextr_actinbead_Mar04, 2122-2124	-GLGTDEDSILNLLTSR-	1704.86	2 8671.46	3.56	0.4	943	17/30
rawextr_200bead_Mar04, 2130	-SIPAYLAETLYYAM K-	1735.04	2 12630.13	3.06	0.6	809	4/7
rawextr_200bead_Mar04, 2134	-SIPAYLAETLYYAM K-	1735.04	2 6605.01	2.40	0.4	861	17/28
rawextr_actinbead_Mar04, 2138	-ETSGNLEQLLAVVK-	1614.87	2 2123.24	2.35	0.2	326	11/28
rawextr_200bead_Mar04, 2158-2160	-GLGTDEDSILNLLTSR-	1704.86	2 12179.42	4.24	0.4	1146	3/5
rawextr_200bead_Mar04, 2164	-GLGTDEDSILNLLTSR-	1704.86	2 12396.78	4.09	0.5	900	3/5
rawextr_actinbead_Mar04, 2480	-YMTISGPIQIEHIDRETSNGLEQLLAVVK-	1704.86	3 1456.42	1.67	0.2	444	25/18
rawextr_actinbead_Mar04, 2642	-GLGTDEDSILNLLTSR-	1704.86	2 1776.18	1.74	0.2	415	11/30
rawextr_actinbead_Mar04, 603	-QEIAQEFK-	993.10	2 638.54	1.36	0.2	164	4/7
rawextr_actinbead_Mar04, 611	-QEIAQEFK-	993.10	2 1516.05	1.77	0.2	276	11/14
FPbeads150_Dec19, 673	-TPELSAIK-	988.12	2 841.82	1.53	0.1	393	5/8
rawextr_actinbead_Mar04, 673-675	-TPELSAIK-	988.12	2 5771.22	2.70	0.4	874	7/8
rawextr_300bead_Mar4, 684	-GDTSGDYKALLCGGEDD-	2071.25	3 475.66	1.86	0.0	254	5/19
rawextr_200bead_Mar04, 843-845	-VLTEIASR-	1002.19	2 5534.58	2.68	0.3	971	15/18
rawextr_actinbead_Mar04, 863-865	-VLTEIASR-	1002.19	2 3123.77	2.24	0.2	959	15/16
rawextr_200bead_Mar04, 1063-1085	-GTVTDFPGDGR-	1269.35	2 9441.75	2.72	0.5	833	9/11
rawextr_actinbead_Mar04, 1121-1123	-GTVTDFPGDGR-	1269.35	2 5290.75	2.91	0.3	950	17/22
rawextr_250bead_Mar04, 1250-1252	-GTVTDFPGDGR-	1269.35	2 6730.31	2.64	0.4	761	8/11
rawextr_200bead_Mar04, 1337	-SEIDLFINR-	1107.24	2 7817.06	2.72	0.4	1138	7/8
rawextr_200bead_Mar04, 1341	-SEIDLFINR-	1107.24	2 5946.88	3.16	0.3	1061	13/16
rawextr_actinbead_Mar04, 1365	-SEIDLFINR-	1107.24	2 6621.90	2.91	0.3	1269	15/16
rawextr_actinbead_Mar04, 1371	-SEIDLFINR-	1107.24	2 6055.15	3.03	0.3	1067	13/16
rawextr_200bead_Mar04, 1417	-NFATSLYSMIK-	1275.50	2 1768.63	1.61	0.1	569	7/10
rawextr_200bead_Mar04, 1501	-WGTDDEKFIITGTR-	1800.99	2 7619.44	2.82	0.5	485	13/28
rawextr_200bead_Mar04, 1709	-DLVDDLKSELTKGFEK-	1838.05	3 6042.04	3.33	0.4	470	5/12
rawextr_200bead_Mar04, 1711-1713	-DLVDDLKSELTKGFEK-	1838.05	2 18916.61	4.44	0.8	1041	2/3
rawextr_200bead_Mar04, 1717	-DLVDDLKSELTKGFEK-	1838.05	3 4573.17	2.88	0.3	576	7/20
FPbeads150_Dec19, 1721	-DLVDDLKSELTKG-	1433.59	2 10380.54	3.01	0.4	1458	3/4
rawextr_500bead_Mar04, 1740	-GLGTDEDSILNLLTSR-	1704.86	2 13672.34	4.27	0.5	1025	17/30
rawextr_actinbead_Mar04, 1745	-DLVDDLKSELTKGFEK-	1838.05	3 7639.44	2.61	0.5	257	1/3
rawextr_500bead_Mar04, 1748	-GLGTDEDSILNLLTSR-	1704.86	2 3742.11	2.53	0.3	793	1/2
rawextr_actinbead_Mar04, 1751	-DLVDDLKSELTKGFEK-	1838.05	3 8840.43	3.28	0.5	555	9/20
rawextr_actinbead_Mar04, 1755-1757	-DLVDDLKSELTKGFEK-	1838.05	2 19658.69	4.61	0.6	1134	2/3
rawextr_actinbead_Mar04, 1783	-GLGTDEDSILNLLTSR-	1433.59	2 11675.24	3.25	0.4	1732	5/6
rawextr_700bead_Mar04, 1788-1790	-DLVDDLKSELTKG-	1704.86	2 10916.16	3.78	0.4	1543	7/10
rawextr_actinbead_Mar04, 1789	-GLGTDEDSILNLLTSR-	1433.59	2 11525.97	3.43	0.5	1294	3/4
rawextr_200bead_Mar04, 1795-1797	-SIPAYLAETLYYAM K-	1735.04	2 15319.76	3.66	0.6	1154	5/7
rawextr_actinbead_Mar04, 1833-1835	-SIPAYLAETLYYAM K-	1735.04	2 2512.55	2.20	0.3	396	1/2
rawextr_200bead_Mar04, 1837-1839	-GLGTDEDSILNLLTSR-	1704.86	2 17476.27	4.88	0.5	1251	19/30
rawextr_200bead_Mar04, 1861	-GLGTDEDSILNLLTSR-	1704.86	3 2169.92	2.89	0.2	512	17/60
rawextr_actinbead_Mar04, 1881-1883	-GLGTDEDSILNLLTSR-	1704.86	2 16143.29	4.52	0.5	1246	19/30
rawextr_200bead_Mar04, 1889-1891	-ETSGNLEQLLAVVK-	1614.87	2 10208.36	3.41	0.5	824	17/28
rawextr_actinbead_Mar04, 1903	-GLGTDEDSILNLLTSR-	1704.86	1 455.82	1.41	0.1	622	3/10
rawextr_actinbead_Mar04, 1905	-GLGTDEDSILNLLTSR-	1704.86	3 2919.82	2.66	0.2	707	11/30
rawextr_actinbead_Mar04, 1926-1931	-GLGTDEDSILNLLTSR-	1614.87	2 7285.13	3.32	0.4	755	17/28
rawextr_450bead_Mar04, 1966-1968	-GLGTDEDSILNLLTSR-	1704.86	2 10058.61	3.89	0.4	1351	19/30
rawextr_250bead_Mar04, 1990	-GLGTDEDSILNLLTSR-	1704.86	2 16882.93	4.68	0.5	1267	2/3
rawextr_250bead_Mar04, 1994	-GLGTDEDSILNLLTSR-	1704.86	2 24558.30	5.32	0.5	2018	11/15
rawextr_actinbead_Mar04, 2007	-GLGTDEDSILNLLTSR-	1704.86	2 1829.61	2.02	0.2	651	7/15
rawextr_400bead_Mar04, 2016-2018	-GLGTDEDSILNLLTSR-	1704.86	2 10408.47	4.14	0.4	968	3/5
rawextr_350bead_Mar04, 2114-2116	-GLGTDEDSILNLLTSR-	1704.86	2 13534.72	4.22	0.4	1511	7/10
rawextr_300bead_Mar04, 2130-2132	-GLGTDEDSILNLLTSR-	1704.86	2 13573.59	4.72	0.4	1550	2/3
rawextr_350bead_Mar04, 2187-2191	-GLGTDEDSILNLLTSR-	1704.86	2 23062.70	5.47	0.5	1288	19/30
FPbeads150_Dec19, 2354	-GLGTDEDSILNLLTSR-	1704.86	2 12049.01	3.70	0.5	1185	17/30
FPbeads250_Dec19, 2606	-GLGTDEDSILNLLTSR-	1704.86	2 4747.14	2.78	0.3	929	1/2
FPbeads300_Dec19, 2646	-GLGTDEDSILNLLTSR-	1704.86	2 7495.76	3.24	0.4	930	3/5
FPbeads300_Dec19, 2952	-GLGTDEDSILNLLTSR-	1704.86	2 5942.81	2.51	0.4	1034	8/15
jmfagtimecon2.5min.185.185.3	-SNAQROEIAQEFK-	1549.67	0 8847.31	3.38	0.4	1066	1/2
jmfagtimecon2.5min.2406.2408.2	-SIPAYLAETLYYAM K-	1735.04	0 13216.10	3.75	0.5	674	17/28
jmfagtimecon2.5min.2412.2412.3	-SIPAYLAETLYYAM K-	1735.04	0 2689.21	1.99	0.3	308	3/8
jmfagtimecon2.5min.2030.2030.3	-GLGTDEDSILNLLTSR-	1704.86	0 9084.10	3.85	0.3	1380	9/20
jmfagtimecon2.5min.2024.2026.2	-GLGTDEDSILNLLTSR-	1704.86	0 17476.05	4.73	0.5	1186	2/3
jmfagtimecon2.5min.1996.1996.2	-SIPAYLAETLYYAM K-	1735.04	0 6063.46	2.17	0.5	678	15/28
jmfagtimecon2.5min.1880.1882.3	-SNAQROEIAQEFK-	1549.67	0 5687.86	2.77	0.4	697	23/48
jmfagtimecon2.5min.938.938.2	-DLVDDLKSELTKGFEK-	1838.05	0 8775.48	3.26	0.5	462	23/60
jmfagtimecon2.5min.2434.2436.2	-VLTEIASR-	1002.19	0 6164.25	2.63	0.4	907	7/8
jmfagtimecon2.5min.1178.1180.2	-GLGTDEDSILNLLTSR-	1704.86	0 17406.96	5.07	0.5	1290	2/3
jmfagtimecon2.5min.2504.2506.2	-GTVTDFPGDGR-	1269.35	0 8505.31	3.25	0.4	898	15/22
jmfagtimecon2.5min.668.668.3	-ETSGNLEQLLAVVK-	1614.87	0 10799.49	3.50	0.5	754	4/7
jmfagtimecon2.5min.672.672.3	-LIVAMMKPSR-	1146.50	0 3774.72	2.17	0.4	257	5/12
jmfagtimecon2.5min.2304.2304.3	-LIVAMMKPSR-	1146.50	0 3875.31	2.16	0.4	279	1/2
jmfagtimecon2.5min.536.536.3	-DLVDDLKSELTKGFEK-	1838.05	0 997.19	2.23	0.1	327	1/3
jmfagtimecon2.5min.222.22.2	-LIVAMMKPSR-	1146.50	0 2952.82	2.33	0.3	320	19/36
jmfagtimecon2.5min.1650.1650.2	-QEIAQEFK-	993.10	0 912.85	1.58	0.2	220	9/14
jmfagtimecon2.5min.952.952.2	-GTVTDFPGDGR-	1269.35	0 7166.57	2.40	0.4	1151	9/11
	-VLTEIASR-	1002.19	0 2558.91	2.44	0.2	709	13/16

Table 2 continued

jmfagtimecon7.5m in. 386.38.2	-TPELSAIK.-	988.12	0.2857.70	2.32	0.2	851	7/8
jmfagtimecon7.5m in. 1586.1382.2	-VLTEIASR.-	1002.19	0.6370.46	2.87	0.4	904	15/16
jmfagtimecon7.5m in. 1642.1642.2	-GTVTDFPGFDGR.-	1269.35	0.5551.97	2.45	0.4	468	7/11
jmfagtimecon7.5m in. 1700.1700.2	-FITIFGTR.-	955.14	0.1150.01	1.81	0.2	384	5/7
jmfagtimecon7.5m in. 1914.1916.2	-SEIDLFNIR.-	1107.24	0.7641.15	3.13	0.4	1023	7/8
jmfagtimecon7.5m in. 544.544.3	-LIVAMMKPSR.-	1146.50	0.2261.68	2.04	0.3	132	1/3
jmfagtimecon7.5m in. 394.394.2	-TPELSAIK.-	988.12	0.2928.45	1.99	0.3	762	7/8
jmfagcon5m inn600m mnacl. 373	-TPELSAIK.-	988.12	2.2678.33	2.43	0.2	747	13/16
jmbeads250rawpba g3007. 448	-TPELSAIK.-	988.12	2.3206.31	2.03	0.3	848	13/16
jmfag5mincon400_030531151834. 478	-TPELSAIK.-	988.12	2.2042.85	2.11	0.2	517	3/4
jmfagcon5m in1000m mnacl_030601180404. 534	-TPELSAIK.-	988.12	2.3921.21	2.56	0.3	802	3/4
jmfag5mincon350. 562	-TPELSAIK.-	988.12	2.1068.09	1.29	0.1	685	11/16
jmfag5mincon400_030531151834.778-780	-TPELSAIK.-	988.12	2.1645.45	1.78	0.2	489	11/16
jmbeads250rawpba g3007. 974	-VLTEIASR.-	1002.19	2.6724.56	2.74	0.4	1107	15/16
jmfagcon5m inn600m mnacl. 1027	-GTVTDFPGFDGR.-	1269.35	2.6514.03	2.19	0.5	883	8/11
jmfag5mincon400_030531151834. 1010	-GTVTDFPGFDGR.-	1269.35	2.1314.24	1.46	0.2	465	13/22
jmfagcon5m inn600m mnacl. 1027	-VLTEIASR.-	1002.19	2.3535.86	2.15	0.3	820	7/8
jmfag5mincon450m mnacl. 1080	-TPELSAIK.-	988.12	2.2133.51	1.98	0.2	707	3/4
jmfag5mincon300m mnacl. 1066	-QEIAQEFK.-	993.10	2.211.32	1.02	0.0	207	9/14
jmfagtimecon10m in. 1138	-QEIAQEFK.-	993.10	2.464.56	1.66	0.0	292	5/7
jmfagtimecon10m in. 1146	-QEIAQEFK.-	993.10	2.810.61	1.45	0.2	210	4/7
jmbeads300rawpba g3007. 1150	-GTVTDFPGFDGRADAEVL.-	1002.19	3.1164.20	1.76	0.1	601	11/38
jmfagtimecon10m in. 030601202502. 1158	-QEIAQEFK.-	993.10	2.1677.61	1.52	0.3	238	4/7
jmfagtimecon10m in. 030601202502. 1164	-QEIAQEFK.-	993.10	2.681.99	1.60	0.1	250	5/7
jmfag5mincon300m mnacl. 1180	-TPELSAIK.-	988.12	2.1780.17	2.17	0.2	529	3/4
jmfag5mincon250m mnacl. 1220	-VLTEIASR.-	1002.19	2.1663.75	1.59	0.2	630	11/16
jmfagtimecon0m in. 030601230741. 1240	-LYDAYELK.-	1015.14	2.603.02	1.45	0.0	404	5/7
jmfagcon5m inn600m mnacl. 1267-1269	-GTVTDFPGFDGR.-	1269.35	2.6313.64	2.20	0.5	757	8/11
jmfag5mincon450m mnacl. 1278	-VLTEIASR.-	1002.19	2.1718.27	1.91	0.1	726	13/16
jmfagtimecon0m in. 030601230741. 1286-1288	-VLTEIASR.-	1002.19	2.4885.66	2.78	0.2	1135	15/16
jmfag5mincon300m mnacl. 1400	-VLTEIASR.-	1002.19	2.4883.96	2.19	0.3	1052	15/16
jmbeadsactinrawpba g3007. 1417	-ALLLCO GEDD.-	1119.27	2.301.63	1.13	0.1	178	2/5
jmfagtimecon10m in. 1418-1420	-LYDAYELK.-	1015.14	2.2679.39	2.56	0.2	756	13/14
jmfagtimecon10m in. 030601202502.1434-1436	-LYDAYELK.-	1015.14	2.3436.01	3.05	0.2	637	13/14
jmfagtimecon10m in. 1474	-VLTEIASR.-	1002.19	2.1371.59	1.93	0.1	640	13/16
jmfagtimecon10min_030601202502. 1492-1494	-VLTEIASR.-	1002.19	2.4653.58	3.01	0.2	1078	15/16
jmfag5mincon450m mnacl. 1504	-GTVTDFPGFDGR.-	1269.35	2.8841.47	2.67	0.5	1024	17/22
jmfag5mincon450m mnacl. 1512	-GTVTDFPGFDGR.-	1269.35	2.1323.44	1.41	0.2	351	1/2
jmfagtimecon0m in. 030601230741.1558-1560	-GTVTDFPGFDGR.-	1269.35	2.3049.77	1.98	0.3	472	7/11
jmbeads300rawpba g3007. 1582-1584	-DLVDDLK SELT GKFEK.-	1838.05	3.10886.27	3.32	0.5	620	13/20
jmbeads250rawpba g3007. 1594-1596	-DLVDDLK SELT GKFEK.-	1838.05	3.8599.90	3.62	0.5	806	5/12
jmfagtimecon0m in. 030601230741. 1664	-FITIFGTR.-	955.14	2.596.42	1.50	0.1	225	1/2
jmfagcon5m in1000m mnacl_030601180404. 1744-1746	-SIPAYLAETLYYAMK.-	1735.04	2.11337.77	3.11	0.5	729	17/28
jmfagtimecon10m in. 030601202502. 1786	-GLGTDSDIINLLTS R.-	1704.86	2.13796.67	4.44	0.4	1527	19/30
jmfagtimecon10m in. 030601202502. 1792	-GTVTDFPGFDGR.-	1269.35	2.2020.63	1.57	0.3	627	15/22
jmfagcon5m in1000m mnacl_030601180404. 1802	-GTVTDFPGFDGR.-	1269.35	2.2541.96	1.55	0.3	564	7/11
jmfagcon5m in1000m mnacl_030601180404. 1808	-ETSGNLEQLLAVVVK.-	1814.87	2.10407.33	2.94	0.5	588	15/28
jmfag5mincon400_030531151834. 1814	-ETSGNLEQLLAVVVK.-	1814.87	2.8127.00	2.90	0.5	524	15/28
jmfag5mincon400_030531151834. 1818	-GLGTDSDIINLLTS R.-	1704.86	2.9530.93	3.79	0.4	1251	19/30
jmfag5mincon450m mnacl. 1832	-GLGTDSDIINLLTS R.-	1704.86	2.12662.39	4.26	0.4	1368	7/10
jmfag5mincon400_030531151834. 1892	-GLGTDSDIINLLTS R.-	1704.86	2.11277.75	3.74	0.4	1029	3/5
jmfagtimecon0m in. 030601230741. 1898	-GLGTDSDIINLLTS R.-	1704.86	2.7668.05	3.07	0.4	1125	7/8
jmfagcon5m inn600m mnacl. 2023	-SEIDLFNIR.-	1107.24	2.2860.37	2.38	0.3	343	13/28
jmfagcon5m inn600m mnacl. 2059	-SEIDLFNIR.-	1107.24	2.7720.03	2.76	0.4	1212	7/8
jmfagcon5m inn600m mnacl. 2111	-SIPAYLAETLYYAMK.-	1735.04	2.8194.88	2.57	0.5	545	1/2
jmfagtimecon10m in. 2122	-GLGTDSDIINLLTS R.-	1704.86	2.7963.41	3.24	0.4	835	8/15
jmfagtimecon10m in. 030601202502. 2140	-ETSGNLEQLLAVVVK.-	1814.87	2.5302.77	2.46	0.4	577	15/28
jmfagtimecon10m in. 2214	-SEIDLFNIR.-	1107.24	2.4008.19	2.61	0.3	695	11/16
jmfagtimecon0m in. 030601230741. 2342	-SEIDLFNIR.-	1107.24	2.4744.34	2.86	0.2	1173	7/8
jmfagtimecon0m in. 030601230741. 2346	-NFATSLYSIMK.-	1275.50	2.1847.17	1.94	0.2	609	13/29
jmfagtimecon0m in. 030601230741. 2350	-DLVDDLK SELT GKFEK.-	1838.05	3.1307.15	2.06	0.2	357	2/5
jmfag5mincon450m mnacl.2458-2460	-DLVDDLK SELT GKFEK.-	1838.05	3.4893.51	2.51	0.4	285	1/3
jmfag5mincon250m mnacl. 2474	-GLGTDSDIINLLTS R.-	1704.86	2.107.02	0.97	0.0	110	3/10
jmfagtimecon0m in. 030601230741. 2482	-GLGTDSDIINLLTS R.-	1704.86	2.14456.55	4.54	0.4	1317	2/3
jmfag5mincon250m mnacl. 2486	-GLGTDSDIINLLTS R.-	1704.86	2.127.34	1.09	0.0	104	1/5
jmfag5mincon450m mnacl. 2526	-SIPAYLAETLYYAMK.-	1735.04	2.517.12	1.11	0.0	465	3/7
jmfagtimecon0m in. 030601230741. 2550	-GLGTDSDIINLLTS R.-	1704.86	2.7761.78	2.73	0.5	722	8/15
jmfagtimecon10m in. 2556	-ETSGNLEQLLAVVVK.-	1814.87	2.3958.91	2.17	0.4	579	13/28
jmfagtimecon0m in. 030601230741. 2558	-GLGTDSDIINLLTS R.-	1704.86	2.7446.86	2.95	0.4	846	17/30
jmfagtimecon10m in. 2562	-DLVDDLK SELT GKFEK.-	1838.05	3.3052.43	1.95	0.4	204	3/10
jmfagtimecon0m in. 030601230741. 2572	-GLGTDSDIINLLTS R.-	1704.86	2.13081.42	3.98	0.4	1422	19/30
jmfagtimecon10m in. 030601202502. 2598	-DLVDDLK SELT GKFEK.-	1838.05	3.4827.05	2.24	0.4	435	23/60
jmfagtimecon10m in. 030601202502. 2606	-GLGTDSDIINLLTS R.-	1704.86	1.3222.96	1.93	0.4	242	1/3
jmfagtimecon10m in. 030601202502. 2610	-DLVDDLK SELT GKFEK.-	1838.05	3.1223.75	1.68	0.2	294	3/10
jmfagtimecon10m in. 030601202502. 2614	-DLVDDLK SELT GKFEK.-	1838.05	2.5361.40	2.20	0.4	545	13/30
jmfag5mincon300m mnacl. 2668	-DLVDDLK SELT GKFEK.-	1838.05	3.1009.88	1.83	0.2	211	1/4
jmfag5mincon300m mnacl. 2674	-DLVDDLK SELT GKFEK.-	1838.05	2.443.51	1.12	0.2	146	3/10
jmfagtimecon10m in. 2686-2688	-GLGTDSDIINLLTS R.-	1704.86	2.11654.12	4.02	0.4	1407	19/30
jmfagtimecon10m in. 030601202502.2752-2754	-GLGTDSDIINLLTS R.-	1704.86	2.9963.97	3.35	0.4	1014	3/5
jmfagtimecon10m in. 2776-2778	-SIPAYLAETLYYAMK.-	1735.04	2.16206.84	3.76	0.8	960	19/28
jmfagtimecon10m in. 030601202502. 2818	-SIPAYLAETLYYAMK.-	1735.04	2.7874.30	3.04	0.5	610	15/28
jmfagtimecon10m in. 030601202502. 2822	-GLGTDSDIINLLTS R.-	1704.86	2.9034.20	3.54	0.4	854	17/30
rawphag2007chf bead1. 1582	-GLGTDSDIINLLTS R.-	1704.86	2.9168.30	3.71	0.4	1012	3/5
RawPhag2007E beadsdest_030718152503. 1782	-GLGTDSDIINLLTS R.-	1704.86	2.2607.82	2.21	0.2	636	8/15
rawscrpf_350phagi gg_Mar04.1404-1408	-ETSGNLEQLLAVVVK.-	1814.87	2.5778.92	2.26	0.4	604	15/28
ANX9_MOUSE Annexin A8 (Annexin VIII)	-GTVTDFPGFDGR.-	1269.35	2.456.75	1.32	0.1	286	5/11
phagrawFsu400_dec20. 3678	-SIRSPAYLAETLYYAMKAGTDDHTLIR.-	3228.67	2.206.03	0.85	0.1	50	1/8
MOES_MOUSE Moesin (Membrane-organizing extension spike protein)	-SEIDLFNIR.-	1235.42	2.347.82	1.39	0.1	97	1/3
rawextr_700bead gg_Mar04. 1868	-CIEDFSKSETHGSLEEAMLTW/KCTR.-	2915.31	2.97.47	0.57	0.0	86	4/25
rawextr_350bead gg_Mar04. 2318	-TISVRVTTMDALEFAIOPNTTGK.-	2823.97	3.469.72	1.31	0.1	105	15/92
ezrin, pp61-tyrosine-phosphorylated band 4.1 cytosolic protein homolog [mi	-TISVRVTTMDALEFAIOPNTTGK.-	2823.97	3.529.34	1.67	0.0	308	15/92
phagrawF300_dec20. 1365	-KQLFDQVE.-	1007.12	2.430.79	1.12	0.1	325	4/7
erythrocyte protein band 4.1-like 2; generally expressed protein 4.1 [	-VTLPLFPQASSHETLNVVEEK.-	2579.99	3.709.76	1.98	0.1	286	2/11
rawextr_300bead gg_Mar4. 1856	-IAPSPVSKFVK.-	1315.63	3.466.89	1.40	0.1	303	17/44
erythrocyte protein band 4.1-like 4a; erythrocyte protein band 4.1-like	-LPCPVNAAQMGAYAIAELGDHDPYK.-	2887.28	2.124.62	0.94	0.1	67	2/13
jmfag5minigggbead_030528200105. 2039							

Table 2 continued

phagrawFauc150_dec22_40	-FGSISYK-	801.91	1 481.38	0.91	0.1	312	7/12
phagrawF350_dec20_714	-IHKTLMGQAPSEAEINLYR-	2172.49	3 437.05	1.58	0.1	203	19/72
phagrawFauc800_dec23_1164	-AHNSG EDS DLKQRR-	1613.68	2 87.13	0.99	0.1	43	7/26
jmfagfrench5minig1m nacltdt_517	-ETQFELR-	923.01	2 517.11	1.40	0.0	368	3/4
rawextr_600bead_Mar04_672	-IHKTLMGQAPSEAEINLYR-	2172.49	3 267.76	1.48	0.0	173	2/9
jmfagtimecon10min_1584	-FGSISYK HRYR-	1414.60	2 634.15	1.06	0.1	378	1/2
RawPhag2007E1Beads digest_030718152503_1214	-IIAPSPVK-	825.03	2 120.02	0.93	0.0	119	3/7
similar to erythrocyte membrane protein band 4.1 like 4B; EHM2 gene; F							
rawphag2007chf bead3_503	-KPVSLATSEFYDLR-	1626.84	2 445.96	1.14	0.1	327	5/13
rawphag2007chi fsd2_746	-ALTTAFER-	909.82	3 146.33	1.10	0.0	131	1/4
phagrawFchf1bead_dec23_1815	-SCCANPAA SILP GLT DECCA PIK-	2435.85	3 772.89	1.53	0.0	485	21/92
AJRAW ActinContr_june13_474	-FSQYLALKA KDAS YR-	1711.94	2 294.41	1.06	0.1	105	1/4
Snz27 protein [Mus musculus] rane protein band 4.1				873.74	3242586.0		8
rawscurfp_600phagi gg_Mar04_2000	-GIHPSA PHRNG GGGGSGSLHCA GNGGGGGGPRVVR-	3175.42	2 513.67	1.05	0.2	63	4/35
rawscurfp_400phagi gg_Mar04_2155	-GDRILEVNG VNVEGATHK-	1909.09	2 160.08	0.95	0.0	168	9/34
erythrocyte protein band 4.1-like 4b; expressed in high-metastatic cell				2436.21	9506567.0		5
jmfagactinrawphag3007_904	-GAAGLGDE RDGG PR-	1328.37	3 1530.85	1.57	0.1	831	21/52
jmravwigg5minbeads yringdnase_1420	-EYRGKSPAQAEISLYNK-	1955.16	3 142.44	1.09	0.0	130	11/64
jmrav5minig5500m mnacld_1560	-ASNPIAAQLCSK-	1316.55	2 174.72	1.23	0.0	141	7/24
jmrav5minig5500m mnacld_1720	-ASNPIAAQLCSK-	1316.55	2 515.53	1.32	0.1	188	3/6
jmravwigg5minbeads freezehaw_2788	-TSASGDSGHFD YYQDQNRNLG GAYS VTYY-	3295.40	2 72.67	0.85	0.0	85	9/58
erythrocyte protein band 4.1-like 1 [Mus musculus]				2792.84	7305020.0		7
phagrawF250_dec22_1205	-GACSTPEMPQFESVVK-	1611.82	3 501.50	1.29	0.0	387	2/7
jmfag1mnac12.5minig_646	-APESDT GDEDDOGER-	1692.59	3 829.61	1.74	0.1	380	9/28
AJRAW SoluteContr_june13_746	-APESDT GDEDDOGER-	1692.59	3 581.87	1.43	0.0	408	9/28
jmbeads600naci rawphag3007_1579	-SLDVAEF SRPASFVSENHDA GPDGDK-	2559.60	3 445.68	1.32	0.1	257	3/16
jmfagG350naci rawphag3007_1269	-IITGDVEDVDQDALALAIK-	2142.39	3 434.27	1.24	0.0	346	1/4
E4L2_MOUSE Band 4.1-like protein 2 (Generally expressed protein 4.1) (4.1G)				124.36	17432886.0		3
AJRAW ActinG_june13_2838	-ATPLPAEGKKNLTLR-	1496.74	2 124.36	1.05	0.0	118	5/13
erythrocyte protein band 4.1-like 3; DAL1P [Mus musculus]				5842.45	7305031.0		7
rawextr_60MeO Hbead_Mar04_854	-KAEATPVTLAR-	1288.46	3 1061.19	1.85	0.0	573	17/44
rawextr_1000bead_Mar04_1628	-VIELKSHRG MTPAEAMHFLNAK-	2877.29	3 469.55	1.45	0.1	266	11/48
jmbeads400rawphag3007_1249	-RVITGADQDHDQALQAIK-	2264.52	3 363.26	1.48	0.1	231	17/60
FBbeads150_Dec19_751	-PKSMQCK-	822.03	1 219.75	1.14	0.1	159	5/12
phagrawF450_dec20_1202	-SGAWHFSFNVKFPYPPDQALSEDITR-	3011.28	2 1056.00	1.00	0.3	146	11/50
jmfag5minig350m mnac1_435	-LLLPAPPKKFLTLGSK-	1853.28	3 220.29	1.18	0.0	187	15/64
jmravwigg5min350m mnac1 yringdnase_1043	-AEEATPVTLALRHE GKTDSER-	2198.34	3 872.58	1.81	0.1	307	21/76
ajrawphag1MNaCl_20_1272	-LMDGSSEILSLESAR-	1364.88	3 465.14	1.33	0.1	271	2/7
jmfagfrench5minig1m nacltdt_1571	-DSVSAEAVGTGQYATTKGISQNLITVTPEK-	3269.56	2 29.95	0.64	0.0	47	7/62
jmravminig200m mnac1 yringdnase_2674	-QQPALEQFPFAAAHSTPVKREIGDK-	2749.03	2 1184.75	1.18	0.3	145	3/16
erythrocyte protein band 4.1 [Mus musculus]				5878.14	38570129.0		5
phagrawFauc150bead_dec23_678	-ASNGDTPTHEDLT K-	1486.52	3 571.99	1.17	0.1	414	15/52
jmbeads250rawphag3007_662	-DVPVHTETK-	1139.28	2 137.59	0.80	0.1	136	1/3
jmfagcon5minig600m mnac1_3147	-QVRGVNPNVTFWVKFYPPDPAQLTEDITR-	2364.52	2 118.43	0.88	0.0	113	9/65
FBbeads250_Dec19_1580	-THTETVTPVTSNGDQTK-	1843.93	3 247.17	1.15	0.0	209	7/32
FBbeads700_Dec19_1619	-SRPSTAPAAQSOVTEGGRPIK-	2446.75	2 57.60	0.72	0.0	62	7/46
rawextr_60MeO Hbeadig_Mar04_1832	-AKDLEGVDDIGVCSGLLYVKDK-	2565.97	3 1134.57	1.53	0.2	303	17/62
rawextr_700beadig_Mar04_2402	-TQTVTISDTANAVKSEIPTKDPVHTETK-	3225.59	2 60.78	0.81	0.0	63	4/29
FBbeads1000_Dec19_3218	-LDGENEYIRHNSLM LEDLKS QEEIK-	3104.44	2 164.66	1.09	0.1	67	4/25
ajrawphagiun20actinDPI_649-650	-PKSVQSEEE GR-	1246.31	2 252.30	1.03	0.1	80	9/20
jmrav5minig600m mnacld_1330	-LGENEYIR-	1903.22	2 290.14	1.13	0.0	254	1/2
ajrawphag1MNaCl_20_1732	-TLNIGNVPTGDDGPRPLVK-	1821.07	3 649.93	1.57	0.1	205	4/17
phagrawFauc150_dec22_808	-ERLDG ENYIRHNSLMLEDLD K-	2674.97	3 789.43	1.26	0.2	214	4/21
rawscurfp_500phagi gg_Mar04_1594	-EVESEKIEGEGGQK-	1534.61	2 380.51	1.61	0.1	236	9/26
JMFAGNACL1521E_3_124	-LIRNRPFWPK-	1327.61	2 233.95	1.20	0.1	129	1/3
jmfag5minig350m mnac1_283-285	-ISSKRSSFVK-	1300.53	3 637.71	1.42	0.0	448	3/8
JMFAGNACL521E3_1636	-RVCEHLNLLIE DYFGLALWDSATSK-	2911.24	3 442.77	1.93	0.0	229	17/66
similar to Cofilin, non-muscle isoform [Mus musculus]				1078.04	38060273.0		2
rawextr_800bead_Mar04_562	-NWSGNNASGVADSDVVK-	1866.99	3 1078.04	1.87	0.1	356	19/68
cofilin 1, non-muscle [Mus musculus]				34282.87	6880924.0		3
jmfag1mnac15mincon_482-484	-HELOANCYEEVK-	1463.80	2 10696.62	4.43	0.5	1476	19/22
jmfag1mnac12.5minig_1102	-LGGSAVISLEGKPL-	1341.58	2 1593.75	1.63	0.2	548	15/26
JMFAGNACL521E_3_1106	-LGGSAVISLEGKPL-	1341.58	2 349.78	1.10	0.1	240	11/26
jmfag1mnac12.5minig_1108	-LGGSAVISLEGKPL-	1341.58	2 572.02	1.39	0.1	196	9/26
jmfag5minig400m mnac1_1152	-LGGSAVISLEGKPL-	1341.58	2 309.24	1.05	0.3	478	7/13
jmfag5minig1000m mnac1_1168	-LGGSAVISLEGKPL-	1341.58	2 784.81	1.57	0.1	406	6/13
jmfag1mnac15minig_1284-1286	-LGGSAVISLEGKPL-	1341.58	2 516.49	2.80	0.3	728	8/13
jmfagtimecon0min_030601230741_1612	-LGGSAVISLEGKPL-	1341.58	2 1717.76	1.64	0.2	504	15/28
jmfagtimecon5min_1682	-LGGSAVISLEGKPL-	1341.58	2 1362.41	1.49	0.2	485	15/26
cofilin 2, muscle [Mus musculus]				135.49	6971746.0		1
rawextr_1000_beadig_Mar04_1550	-KAVFLCSD DK-	1239.47	2 135.49	0.90	0.1	86	1/4
FERM, RhoGEF and pleckstrin domain protein 2 [Mus musculus]				13282.41	21704022.0		29
FBbeads350_Dec19_715	-TRTSLHALTVOLPK-	1552.80	2 323.84	1.10	0.0	291	11/26
rawextr_200beadig_Mar04_847-849	-HDEVLTELEKATKHCK-	1882.13	3 359.90	2.00	0.0	167	1/5
rawextr_450bead_Mar04_896	-MFFLFSDMLLYTSK-	1744.11	2 206.93	1.11	0.1	95	4/13
rawextr_chf1beadig_Mar04_990	-QLVDYVKDGGMKR-	1506.78	2 268.35	1.17	0.1	157	3/8
rawextr_700beadig_Mar04_1630	-LTELQ RDLVGVENLIA PGREFIR-	2640.03	3 2822.39	2.30	0.3	523	23/88
rawextr_600bead_Mar04_1792-1794	-LTELQ RDLVGVENLIA PGREFIR-	2640.03	3 1463.98	2.48	0.2	252	19/88
FBbeads250_Dec19_1878	-QLVDYVKDGGMKR-	1509.76	2 79.53	0.88	0.0	84	5/24
phagrawF350_dec20_634-636	-VCYLP LNTFLK-	1424.78	2 365.12	1.55	0.1	210	0/22
phagrawF500_dec20_735	-YLFAQLKLR-	1152.41	1 264.06	0.96	0.0	276	9/16
phagrawFauc450_dec20_1332-1334	-VCYLP LNTFLK-	1424.78	2 354.85	1.55	0.0	253	9/22
rawscurfp_chf1phagig_Mar04_1336	-GLQGRMFLFSDMLLYTSK-	2326.77	3 315.51	1.38	0.0	227	1/4
rawscurfp_300phagi gg_Mar04_1520	-LTELQ RDLVGVENLIA PGREFIR-	2640.03	3 1138.86	2.10	0.1	330	19/88
rawscurfp_600phagi gg_Mar04_1716-1718	-LTELQ RDLVGVENLIA PGREFIR-	2640.03	3 592.54	1.85	0.1	242	9/44
phagrawFauc400_dec20_2788	-VKLLDS TVELFDIEPK-	1847.14	2 573.86	1.41	0.2	175	3/10
JMMAG Tube1B16E3_384	-NSNGWOK-	833.87	2 630.54	1.02	0.0	429	3/4
jmfag5minig250m mnac1_854-856	-KLEMYGIR-	1010.24	3 283.24	1.08	0.1	69	8/28
JMFAGNACL10_2B21E3_2946	-LLLSRLCAHY SPGHRDYA DCEALK-	2670.29	3 262.45	1.10	0.0	235	17/68
jmf5minigrawlowionic_890	-YSGRQTK-	839.92	2 71.68	0.72	0.0	81	5/12
jmfag1000naci rawphag3007_2468	-LTELQ RDLVGVENLIA PGREFIR-	2640.03	3 1282.23	1.75	0.2	274	9/44
jmravwigg5minbeads freezehaw_2518	-LEAVYKEF ELQKVCYLP LNTFLK-	2903.47	2 131.88	0.92	0.1	64	9/46
jmrav5minigglowionic_2597-2599	-PKAKAVFFSR-	1151.39	2 141.67	0.92	0.0	136	1/3
jmfagtimecon5min_137	-GDHQRIGDILRNMR-	1795.06	2 208.32	1.02	0.0	204	9/28
jmfag5mincon350_1448	-MFRFLSDMLLYTSKVS TGASHFR-	2687.13	3 501.64	1.68	0.0	297	17/88
jmbeads250rawphag3007_1746	-EFELQKVCYLP LNTFLKVPQR-	2680.20	3 455.21	1.67	0.1	241	17/84
jmfag5mincon400_0305311518_34_2066	-STAERSSG PSSSDGSP TSQAHLP GPVPLR-	2935.11	2 106.03	0.87	0.0	111	5/29
jmfagtimecon0min_030601230741_2146	-LLDSTV ELFDIEPK CDGQ VLLTQVVK-	2991.45	2 74.72	0.88	0.1	43	4/25
FERM domain containing 3 [Mus musculus]				848.14	27370318.0		7
jmfag5mincon450m mnac1_1982	-EARQLWSYSILTGHVWNLVK-	2770.18	3 451.01	1.56	0.0	283	9/46

Table 2 continued

jmfag5minnag250mmnaci, 2758	-EWWAGKVNVL YMLGCS-	1883.27	2 195.11	1.21	0.0	157	9/32
jmfag1mnnaci0minng, 268	-VSDATGGMNLT TK-	1265.42	2 1325.09	80477.06	6680842.0	7	
jmfag1mnnaci5minnaci, 302	-VSDATGGMNLT TK-	1265.42	2 5754.67	1.49	0.1	679	13/22
jmfag1mnnaci5minnaci, 316	-VSDATGGMNLT TK-	1265.42	2 6448.84	2.90	0.4	999	17/22
jmfag1mnnaci5minnaci, 326	-VSDATGGMNLT TK-	1265.42	2 3397.37	1.91	0.2	1483	9/11
JMMAAGNEGB16D3, 352	-VSDATGGMNLT TK-	1265.42	2 3236.32	2.01	0.3	978	15/22
JMMAAGTube1B18E3, 362	-VSDATGGMNLT TK-	1265.42	2 3535.89	2.42	0.2	1210	9/11
jmfag5minnag600mmnaci, 368	-VSDATGGMNLT TK-	1265.42	2 5050.06	2.48	0.3	1080	15/22
jmfag1mnnaci2.5minnag, 406	-VSDATGGMNLT TK-	1265.42	2 4891.13	2.05	0.4	964	8/11
jmfag1mnnaci2.5minnag, 410	-VSDATGGMNLT TK-	1265.42	2 4174.01	2.34	0.3	968	8/11
jmfag1mnnaci7.5minnag, 414	-VSDATGGMNLT TK-	1265.42	2 4861.48	2.39	0.2	935	8/11
jmfag5minnag350mmnaci, 1003	-QAAQLQADGFSR-	1376.54	2 7881.09	2.42	0.5	765	5/8
jmfag1mnnaci7.5minnag, 1142	-EGNFEDITADGTNAQAAALYK-	2350.44	3 934.34	1.62	0.1	549	11/42
jmfag1mnnaci5minnag, 1276	-QAAQLQADGFSR-	1376.54	2 6901.22	2.28	0.5	773	2/3
jmfag5minnag400mmnaci, 1320	-ELQGNESDLFMSYFRGLK-	2232.50	3 288.83	1.24	0.1	201	5/24
jmfag1mnnaci5minnaci, 1326	-EGNFEDITADGTNAQAAALYK-	2350.44	2 12680.59	3.43	0.6	607	17/44
jmfag5minnag500mmnaci, 1494	-QAAQLQADGFSR-	1376.54	2 7143.35	2.31	0.5	653	5/8
jmfag5minnag300mmnaci, 1776-1778	-QAAQLQADGFSR-	1376.54	2 1695.43	1.94	0.2	457	7/12
JMFAGNACL15B21E3, 2938	-DEGGACAVLAVHLNLTGERPVQHR-	2728.09	3 295.35	1.32	0.0	223	17/86
profilin 1; actin binding protein [Mus musculus]				23229.88	6755046.0	10	
JMFAGNACL15B21E3, 594	-TLVLLMGK-	875.16	2 257.29	1.07	0.0	232	1/2
jmfag5minnag150mmnaci, 1014	-DSPSVWAAVPGK-	1214.35	2 389.89	1.68	0.3	1209	15/22
jmfag5minnag600mmnaci, 1172	-SSFFVNGLTGGQK-	1455.64	2 1050.62	3.11	0.5	1005	9/13
jmfag1mnnaci5minnag, 1328	-STGGAPTFNVTMTAK-	1683.91	2 211.48	1.52	0.0	139	9/32
jmfag5minnag350mmnaci, 1413	-TFVSIPTAEVGLVGKDR-	1617.91	2 7830.80	2.63	0.5	753	3/5
JMFAGNACL15B21E3, 1424	-TFVSIPTAEVGLVGKDR-	1889.19	3 283.92	1.57	0.0	178	9/34
jmfag5minnag250mmnaci, 1482-1484	-DSPSVWAAVPGK-	1214.35	2 3567.48	1.89	0.3	1037	8/11
jmfag1mnnaci0minnag, 1466	-TFVSIPTAEVGLVGKDR-	1617.91	2 10209.81	2.81	0.5	941	11/15
jmfag5minnag200mmnaci, 1516	-SSFFVNGLTGGQK-	1455.64	2 4722.71	2.12	0.4	425	6/13
jmfag5minnag450mmnaci, 030527025134, 1632	-TLVLLMGK-	875.16	2 171.10	1.92	0.2	449	11/14
JMMAAGTube1B18E3, 1816	-DSLLODGEFTMDLR-	1640.80	2 3159.92	2.24	0.3	326	5/13
jmravwg5minbeadsfreezethaw, 1390-1392	-TFVSIPTAEVGLVGKDR-	1889.19	3 803.95	1.80	0.1	254	1/4
jmravwg5minbeadsfreezethaw, 1516	-TFVSIPTAEVGLVGKDR-	1617.91	2 14304.61	3.46	0.6	604	3/5
jmravwminnag200mmnaci5yrindnas, 1854	-TFVSIPTAEVGLVGKDR-	1889.19	3 1641.82	1.96	0.3	175	15/68
jmravwminnag200mmnaci5yrindnas, 2002	-TFVSIPTAEVGLVGKDR-	1617.91	2 1814.70	2.10	0.2	336	13/30
jr5minnagrawwlonic, 2132-2134	-TFVSIPTAEVGLVGKDR-	1889.19	3 1489.58	2.09	0.2	209	9/34
jmrfreebeadsrawphag3007, 1122	-SSFFVNGLTGGQK-	1455.64	2 10519.74	3.24	0.5	814	15/26
jmfagtlmecon2.5min, 1368-1368.2	-SSFFVNGLTGGQK-	1455.64	0 10259.25	3.21	0.5	662	15/26
jmfagtlmecon2.5min, 1358-1358.2	-TFVSIPTAEVGLVGKDR-	1617.91	2 550.91	2.50	0.4	651	17/38
jmfagtlmecon7.5min, 1824-1826.2	-SSFFVNGLTGGQK-	1455.64	0 13415.82	3.54	0.5	792	8

Table 2 continued

jmftg1mecon2.5m in. 1826.2	-EPPSRGAAPPPPPMIR-	1768.08	0 301.99	1.07	0.0	276	11/32
jmftg1mecon5m in. 717	-EKPLPTPGQR-	1220.40	2 78.10	0.85	0.0	83	9/10
jmftgcon5m in1000m mnacl_030601180404, 1876-1878	-KTPGPVRGLAPFPPTSATPSLLSNR-	2512.89	3 564.15	1.86	0.0	286	7/32
RawPhg2007M e3thmeth3d1 gest, 3474	-AARGAPPLPPILR-	1329.62	2 62.35	0.70	0.0	89	5/24
WASP family 1 [Mus musculus]				3755.01	13984209.0		3
jmftg1mnacl0m ingg, 634	-OKNLDRIPEK-	1491.64	2 740.94	1.68	0.1	343	1/2
AJRAWActinlgG_june13, 984	-YAEIDIFGELFNEAHSFSSR-	2280.44	3 979.81	1.69	0.1	377	17/72
rawextr_actinbead_Mar04, 480	-KGILQR-	714.88	2 268.41	1.06	0.0	252	3/5
rawextr_900bead_Mar04, 1316-1318	-PTPTCISSATGLIENRNPQSPAAQR-	2425.71	2 217.23	1.29	0.1	56	4/23
jmftgcon5m inn600m mnacl, 729	-NIDPRHLCHTA LPR-	1643.90	3 1396.37	1.62	0.0	840	11/26
jmftgcon5m in1000m mnacl_030601180404, 1084	-QLSSLSK YAEIDIFGELFNEAHSF SFR-	3024.29	3 152.26	1.01	0.1	110	13/100
N-WASP protein [Mus musculus] uculus] 6				573.23	15706272.0		2
jmftg5mincon300m mnacl, 774	-GAPPPP PPSR-	876.00	2 448.41	1.21	0.0	362	5/8
phagraw F5uc500_dec 20, 1690	-GAPPPP PPSRG GPPPPP PPSHSG PPPPPP PARGR-	3229.65	3 124.82	1.16	0.0	102	17/128
Wiskott-Aldrich syndrome homolog; Wiskott-Aldrich syndrome protein [Mus				26773.21	6678881.0		5
jmftg5min300m mnacl5yringednas.e, 557	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4979.03	2.27	0.3	1358	5/12
jmftg5min400m mnacl5d, 583	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5236.90	2.13	0.3	1525	37/84
jmftg1mnacl0m ingg, 646-648	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5998.14	2.77	0.1	2065	19/42
jmftg5min300m mnacl, 651-653	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5855.63	2.43	0.2	1891	19/42
jmftg5min300m mnacl, 658	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5500.02	2.27	0.2	1875	37/84
jmftg5min300m mnacl, 662	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5680.34	2.22	0.3	1848	3/7
jmftg5minbeads freezehaw, 696-698	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 7284.94	2.30	0.2	2687	11/21
JMFAGNACL5B21E 3,712-714	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4938.15	1.79	0.2	2431	41/84
jmftg1mnacl2.5min ingg, 724	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 1839.17	1.52	0.1	1019	31/84
jmftg5min150m mnacl, 750-752	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3815.18	2.07	0.1	1655	3/7
jmftg5min400m mnacl, 772-774	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 6878.55	2.40	0.3	2528	13/28
jmftg5min300m mnacl5yringednas, 1082	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 6907.74	2.57	0.3	1269	31/84
jmftg5min300m mnacl5yringednas, 1086	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4956.37	2.24	0.1	2035	19/42
jmftg5min300m mnacl5yringednas.e, 1269-1288	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3578.67	1.98	0.1	1613	3/7
jmftg5min450m mnacl_030527025134, 1292	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5648.67	2.21	0.2	2118	37/84
jm5min1grawlowionc, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 2804.15	1.66	0.0	1681	3/7
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 7624.63	2.65	0.3	2087	13/28
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 6248.47	2.48	0.1	2489	37/84
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 2280.95	1.47	0.0	1535	11/28
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 2575.40	1.00	0.0	1336	8/21
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4805.83	2.07	0.2	1957	19/42
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4714.35	2.44	0.1	1731	19/42
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4448.21	2.12	0.2	1521	5/12
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3798.44	2.83	0.3	2444	10/21
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 2838.50	1.51	0.0	1657	3/7
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4786.44	2.28	0.2	1648	37/84
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 2826.89	1.75	0.1	1570	19/42
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5813.03	2.51	0.2	1732	19/42
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 6676.43	2.48	0.2	2314	10/21
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 6579.79	2.53	0.3	1817	13/28
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4615.15	2.45	0.2	1300	17/42
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3445.63	1.91	0.1	1589	5/12
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 686.41	1.70	0.1	361	13/62
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3968.42	2.38	0.0	1873	5/12
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3968.43	1.67	0.1	2350	13/28
jmftg5min300m mnacl, 1338-1340	-RSRVHSSDEGEDTGEDEDEDDDD-	3051.81	2 95.22	0.81	0.1	82	7/50
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 10557.28	2.69	0.4	2473	1/2
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3112.43	1.74	0.0	1772	5/12
jmftg5min300m mnacl, 1338-1340	-VHSSDEGEDTGEDEDEDDDD-	2652.46	2 120.94	1.02	0.0	100	2/11
jmftg5min300m mnacl, 1338-1340	-GGPPPPPPATGR-	1196.36	2 340.43	1.23	0.1	185	1/3
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 7383.37	2.68	0.2	2345	1/2
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5889.50	2.67	0.2	1862	19/42
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5951.18	2.36	0.3	1770	37/84
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 5565.35	2.10	0.2	2367	41/84
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	0 2332.31	1.91	0.1	1087	8/21
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	0 5988.55	2.43	0.2	1909	19/42
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4520.62	2.03	0.3	1509	5/12
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3660.39	1.99	0.1	1729	37/84
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3580.35	1.68	0.1	1658	19/42
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 2572.03	1.86	0.1	1306	5/12
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4235.30	2.05	0.3	1423	5/12
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 2829.08	1.55	0.1	1749	37/84
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 6246.99	2.46	0.2	2185	10/21
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 11554.63	2.87	0.4	2707	10/21
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 4488.59	2.22	0.1	1811	19/42
jmftg5min300m mnacl, 1338-1340	-YRGLPAPGPPTDKK-	1554.78	3 521.83	1.26	0.0	411	19/56
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 3774.22	2.03	0.2	1367	5/12
jmftg5min300m mnacl, 1338-1340	-GGGGGGGGGGGGGGGGGGGGGQPLR-	1540.54	3 2501.76	1.79	0.1	1336	17/42
Wiskott-Aldrich syndrome-like [Mus musculus] Squ				4401.95	39083702.0		8
jmftg5min300m mnacl, 438	-NELRRQAPPPPPPSR-	1712.94	3 1819.22	1.73	0.2	525	19/56
JMFAGNACL5B21E 3, 494	-TG GVEAVK-	760.86	2 358.60	1.42	0.0	252	6/14
JMFAGNACL5B21E 3, 766	-GRGAAPPPPPXR-	1089.28	2 292.63	1.13	0.0	251	1/2
jmftg5mincon350, 528	-TG GVEAVK-	760.86	2 1156.53	1.54	0.2	458	5/7
jmftg5mincon200m mnacl, 640	-TG GVEAVK-	760.86	2 774.68	1.33	0.1	391	9/7
Wiskott-Aldrich syndrome homolog (human) binding protein [Mus musculus]				5671.46	13507988.0		2
rawphag2007chf bead1, 1004	-RAAPTTPPPPVK-	1388.64	3 489.15	1.22	0.1	354	1/3
rawextr_200bead_Mar04, 158	-AAPTTTTPPPVK-	1078.27	3 1440.90	1.26	0.2	712	17/40
rawextr_250bead_Mar04, 1938	-RQGPESHPTLRQVCHDQQR-	2273.48	3 498.18	1.37	0.0	364	1/4
phagraw F300_dec20, 1293	-NTGLSHELCRVAIAVWVWTSR-	2387.71	3 228.38	1.54	0.0	146	17/80
phagraw F5uc150_dec 22, 2582	-LQGMEDQVQLNDRAIEAVNTAMRDGK-	1368.58	2 236.40	0.91	0.1	85	6/58
jmftgcon5m inn600m mnacl, 261	-AAPTTTTPPPVK-	1078.27	3 446.89	1.40	0.0	316	3/8
jmftg5min300m mnacl, 1680	-DMQDTQDQK-	1347.40	2 572.90	1.02	0.0	541	1/2
JMFAGNACL5B21E 3, 658	-DREALVSGSGGR-	1317.44	3 657.85	1.41	0.0	458	3/8
jmftg5min300m mnacl5yringednas.e, 1381	-VAIAVWVWTSRPPCSQLTYHGAGPPLAGR-	3080.51	2 744.45	0.90	0.0	80	9/58
JMFAGNACL5B21E 3, 1468	-ALIAVHNTAMR-	1213.39	2 380.26	1.31	0.0	290	11/20
JMFAGNACL5B21E 3, 1648	-LILLNRGD DPVRI FR-	1611.28	3 148.06	0.85	0.0	153	1/5
jmftg5min300m mnacl, 2287	-PPCSQLTYHGAGPPLAGRQGPESHPTLR-	3082.45	2 771.65	0.95	0.2	123	5/28
jmftg5min300m mnacl, 1315	-RAAPTTPPPPVK-	1388.64	2 146.12	0.93	0.0	143	7/24
Hemopoietic cell specific Lyn substrate 1 [Mus musculus]				15568.70	13638627.0		11
jmftg1mnacl5min ingg, 354	-SAVGHEYVADVEK-	1404.51	3 720.99	1.94	0.1	335	3/8
jmftg1mnacl5min con, 378	-SAVGHEYVADVEK-	1404.51	3 4792.17	2.53	0.4	631	1/2
jmftg1mnacl0m ingg, 696	-KTTPIEAASSGARGLK-	1587.80	2 1478.87	1.89	0.0	780	17/30
jmftg1mnacl5min ingg, 2740	-EEEEKAQMARQQRER-	2019.14	3 1205.68	2.08	0.0	578	7/20
jmftg300rawphag3007, 1214	-DRVMD SAVGFNEM EAPTAYK-	2330.56	3 231.35	1.20	0.0	191	17/80
jmftg5min300m mnacl, 1356	-ELES GPKASHGVGGR-	1545.64	2 311.51	1.18	0.1	208	5/14

Table 2 continued

jmlgG250rawphag3007.2318-2320	-HSSQ2DAARGFGGKGYVER-	2024.14	3 593.03	1.56	0.0	379	5/18
jmlfreebeadsrawphag3007.1212-1214	-KTTPIEAASSGARGLK-	1587.80	2 1821.17	2.19	0.1	629	7/15
jmravwigg5minigfreebead, 880	-SAVGFNE MEAPTTAYK-	1716.89	2 2714.07	2.22	0.3	545	1/2
FPbeads300_Dec19, 1510	-KTTPIEAASSGARGLK-	1587.80	2 576.32	1.43	0.0	368	2/5
AJRAW/SoluteContr June13, 736	-TTPIEAASSGARGLK-	1459.63	2 482.59	1.70	0.0	265	5/14
jmfag5mincon250mmnacl, 1324	-QSPQLNHLEDNEEPALPPR-	2282.46	3 660.97	1.58	0.0	416	9/38
hematopoietic cell specific Lyn substrate 1 [Mus musculus]				4156.79	6680187.0	2	
rawextr_450beadigg_Mar04, 864	-ELESQPKASHGYGQGFVER-	2106.24	3 664.90	1.59	0.1	325	9/38
rawextrfp_350pHagigg_Mar04, 1428	-KTTPIEAASSGARGLK-	1587.80	2 617.64	1.44	0.0	309	2/5
rawextrfp_600pHagigg_Mar04, 1450-1452	-KTTPIEAASSGARGLK-	1587.80	2 500.89	1.48	0.0	335	1/3
phagrawF200_dec22, 1617	-ISSEVWPPAESHLPPESQVRSRR-	2743.03	3 371.74	1.45	0.0	240	9/46
phagrawFuc450_dec20, 2178	-KTTPIEAASSGARGLK-	1587.80	2 2001.81	1.67	0.2	643	13/30
similar to cytoplasmic beta-actin [Mus musculus]				493.52	39061104.0	4	
rawextrfp_500pHagigg_Mar04, 1648	-EITALAPS TMKIKIITPPR-	2210.67	3 493.52	1.48	0.1	261	1/4
similar to cytoplasmic beta-actin [Mus musculus]				1725.40	38052880.0	7	
jmfag1mmnacl2.5minig, 1256	-YGSARRMTSTPTPTSTAN ASR-	2287.46	3 548.09	1.44	0.0	380	1/4
JMFAGNACL10_1821E3, 2618	-ELADITLOS PONGS PGTKVDNLSEYR-	2867.10	3 537.29	1.44	0.0	373	1/5
rawextr_actinbead_Mar04, 986	-ETITLVPS TMK-	1218.40	2 357.75	1.16	0.0	306	1/2
rawextr_150bead_Mar04, 1059-1061	-AEHQRVTRQWTK-	1559.74	3 175.43	1.37	0.0	108	13/44
FPbeads1000_Dec19, 2864	-RSMTSTPTPTSTANASR WTEQQTAK-	2725.93	3 106.84	1.03	0.0	95	11/66
similar to mutant beta-actin (beta-actin) [Mus musculus]				4912.85	3808842.0	4	
jmfag5minig1000mmnacl, 152-154	-RGILTLK-	801.01	2 2250.90	2.12	0.2	673	11/12
jmfag5minig600mmnacl, 164-166	-RGILTLK-	801.01	2 1177.67	2.26	0.1	367	3/4
jmfag1mmnacl5mincon, 608	-LCYVALDFK-	1072.30	3 400.49	1.30	0.0	298	13/32
jmfag5minig450mmnacl_030527025134, 1000-1002	-RGILTLK-	801.01	2 1083.88	1.98	0.1	522	11/12
AnkA1 protein				58217.77	4502101		
ajmembphagigGDIPIJune18, 962	-GGPGSAVSPYF TPNPSSOVAALHK-	2357.56	3 7670.87	3.42	0.4	514	
ajmembphagigGDIPIJune19, 1214-1216	-DLAKDITSD TSGDFR-	1641.72	3 2978.07	2.60	0.2	730	
ajmembphagigGDIPIJune19, 1788	-GVDEATIDILTKR-	1544.78	2 7013.92	2.03	0.5	518	
ajmembphagigGGPIJune19, 2522	-GVDEATIDILTKR-	1544.78	3 1843.39	2.03	0.2	246	
ajmembphagigGDIPIJune19, 1954-1956	-GVDEATIDILTKR-	1388.59	2 13791.86	2.22	0.4	1477	
ajmembphagigGDIPIJune19, 2008	-GLGTDEDTLIEILASR-	1703.87	2 13229.97	2.03	0.4	2007	
ajmembphagigGGPIJune19, 2326	-GTDVNVFNTLITR-	1551.73	2 8789.79	2.03	0.4	1120	
AnkA2 protein				13 435 564			
rawextr_250beadigg_Mar04, 1156	WISIMTER	1036.23	2 1.64	10.1	1.639	0.26	365.4
AnkA4 protein				33 416 550			
rawextr_250beadigg_Mar04, 1662	SETSGSFED ALLAIK	1667.84	2 3.68	10.2	3.676	0.48	1652.6
FMS-like tyrosine kinase 1				3622.38	34 328 190		
rawextr_chifbead_Mar04, 708	-POIYKSVSS LPSPYLPLGSR-	2416.76	3 312.66	3622.37	1.50	0.0	204
rawextr_350beadigg2_Mar04, 1056	-QPVPQETTAGRR-	1243.36	2 211.06	3622.37	1.10	0.1	107
FPbeads600_Dec19, 1124	-MATTQDYSITLN LVIKNVLSDESGTYACRAR-	3435.88	3 993.86	3622.37	1.67	0.2	183
rawextr_150bead_Mar04, 1325	-LKGSL GRGAFGK-	1191.41	2 128.48	3622.37	0.88	0.1	103
rawextr_300bead_Mar04, 1659	-VGMSSWNYPAKTKR-	1666.93	2 190.57	3622.37	1.15	0.1	104
rawextr_actinbead_Mar04, 2000	-MPAEGED LKLSGVVFLYR-	2313.73	3 1785.74	3622.37	2.47	0.2	459
ras-GTPase-activating protein SH3 domain binding protein				26117.53	7 305 075		
rawextr_200bead_Mar04, 1516	-FKMQTFVLAPEGSAVK-	1740.02	2 2190.74	41199.84	2.34	0.2	317
rawextr_60MeOHbeadigg_Mar04, 1632	-PEKIPGDSQIPQRPQR-	1861.05	2 237.63	41199.84	1.31	0.1	131
FPbeads150_Dec19, 1677	-LPNFQGV VFDDESPQVK-	1936.16	2 18803.69	41199.84	4.18	0.6	1249
rawextr_350bead_Mar04, 1830	-DFFQNFQGV VFLR-	1585.75	2 4439.27	41199.84	2.52	0.3	964
rawextr_actinbead_Mar04, 2106	-GGPGSGMGRPPR GGMVQK-	1727.01	2 328.15	41199.84	1.35	0.1	197
rawextr_actinbead_Mar04, 2604	-EFVQRYVY LLNQAPDMLHRYGK-	2891.30	2 109.08	41199.84	0.96	0.0	108
Rho GTPase-activating protein				2417.66	28 893 538		
FPbeads400_Dec19, 1178	-KSPVGVSW RSFFNL GK-	1710.66	2 559.97	2417.66	1.59	0.2	97
rawextr_200bead_Mar04, 1194	-NESEPEMK-	1051.11	2 553.94	2417.66	1.06	0.1	384
rawextr_60MeOHbeadigg_Mar04, 2334	-PHHSELTKDSMPSTLPRDK-	2361.62	3 193.42	2417.66	1.32	0.0	147
rawextr_700bead_Mar04, 2564	-ELPNPLLTLYQLEK FSDAVSAATDEERLIK-	3455.86	2 59.87	2417.66	0.82	0.1	39
rawextr_chifbeadigg_Mar04, 2698	-SVPIRSRTVEPPD DEPAVCYRPVYQYK-	3008.35	2 1050.46	2417.66	1.31	0.3	132
RAB25, member RAS oncogene family y				781.41	31 990 838		
jmrav5minigglowicon, 513	-VVLIGESGVGKTLN LLSRFR-	2147.51	3 781.41	781.41	1.75	0.0	428
FKBP96 binding protein 12-rapamycin associated protein 1				6210.96	9 910 228		
jmfagfrench5minig1mmnacl, 1123	-POGYRHTEAEK-	1721.85	2 343.30	3541.04	1.37	0.0	237
jmlgG450rawphag3007, 1472	-YCKDMLGFGTKR-	1516.81	2 190.36	3541.04	0.98	0.0	192
jmrav5minig500mmnacl, 2098	-ETSFNQAYGR DLMSEAQVCRK-	2563.81	3 528.44	3541.04	1.81	0.0	288
jmgg600rawphage3007, 2276	-VYLPRLVDIRAAL PPK-	1955.39	2 897.09	3541.04	2.08	0.2	185
jmfagfrench20minig1mmnacl, 2618	-LHWEVEDALVAYDK-	1589.73	2 810.13	3541.04	1.16	0.2	245
jmlgG300rawphag3007, 2780	-KYPTLLLEVLNLFKTEQNGTR-	2607.00	2 150.46	3541.04	1.06	0.1	121
ajrawphagactin20, 2966	-LIHQTLTDIGR-	1279.51	2 112.19	3541.04	0.79	0.1	117
jmravminig200mmnacl, 2376	-SSQGDAL ASGPVETGPMKK LHVSTINLQK-	2995.40	2 240.73	3541.04	1.04	0.1	81
FPbeads600_Dec19, 852	-VYLPRLVDIRAAL PPK-	1701.69	3 1114.99	2837.35	1.46	0.1	656
FPbeads500_Dec19, 1340	-VIALDLKTLTLLVYPAV QOFFRSILSR-	2142.64	2 143.28	2837.35	1.02	0.0	130
FPbeads400_Dec19, 1396	-PLVGRILHOLLTDIGR-	1802.16	2 260.53	2837.35	1.07	0.1	182
rawextr_800bead_Mar04, 1876	-GFDETLAKEGMNLR-	1566.79	2 339.15	2837.35	0.82	0.1	219
rawextr_60MeOHbead_Mar04, 2124	-STAMDTLSSLVFLQGLK-	1698.96	2 284.41	2837.35	1.16	0.0	237
rawextr_chifbeadigg_Mar04, 2690	-KAGTTPVESIHSGIGDLVKPEALNK-	2710.08	3 497.65	2837.35	1.69	0.1	230
jmrav5minbeadfreezethaw, 996	-EOSARMLGHVLSNAPR-	1767.01	3 169.35	3541.04	1.22	0.0	131
WAVE (WASP family prote in member 1)				3755.01	13 994 299		
jmfagcon5min1000mmnacl, 729	-NIDPRHLCTALPR-	1643.90	3 1366.37	1548.63	1.62	0.0	840
jmfagcon5min1000mmnacl_030601180404, 1084	-QLSSLKSYAEDIFGELFN EAHSPFSR-	3024.29	3 152.26	1548.63	1.01	0.1	110
jmfag1mmnacl0minig, 634	-QKNDLRHPEPK-	1491.64	2 740.94	740.94	1.86	0.1	343
AJRAW/ActinG June13, 984	-YAEIDFGLFNEAHSFSFR-	2280.44	3 979.81	1720.75	1.89	0.1	377
rawextr_actinbead_Mar04, 480	-KIQGLR-	714.88	2 268.41	485.64	1.06	0.0	252
rawextr_900bead_Mar04, 1318-1318	-PTPTCISSATGL IENRQSPAPAGR-	2425.71	2 217.23	485.64	1.29	0.1	56
Arp2/3 complex				28902.80	5 631 595		
FPbeads150_Dec19, 1767	-VSAIKQAD EIEKILCHK-	2025.40	3 333.84	474.05	1.02	0.1	300
FPbeads300_Dec19, 3958	-PYLSAIVRAIL QALCLFNFSQSVVERHNK-	3246.89	3 140.21	474.05	1.15	0.1	93
JMMAQNEGB1803, 1168	-ELLQPYTISR-	1269.52	2 2742.43	4675.33	2.11	0.3	526
JMMAQNEGB1803, 1738-1740	-EISEMK-	736.26	1 188.08	4675.33	1.26	0.0	149
jmbbeads250rawphag3007, 1548	-PVEGYDISFUTNFHTEQMYK-	2533.34	3 1250.34	11268.94	2.17	0.2	278
jmsminigrawlowicon, 3162	-HNKPEVEVRSK-	1410.56	2 344.58	3153.52	0.94	0.2	135
AJRAW/SoluteContr June13, 1034	-LVDFVHFMEIDEIK-	1736.03	3 535.42	11268.94	1.36	0.1	370
jmfag5mincon250mmnacl, 3160	-LVDFVHFMEIDEIKSEIMK-	2453.86	3 9483.18	11268.94	3.55	0.5	532
ajmembphagigGGPIRJune182nd_030622052702, 1078	-QQNIPMLAL QAAKNPPINTK-	2082.41	3 3463.05	42493.42	2.44	0.3	715
ajmembphagigGGPIRJune19, 798	-ALAGGVGSVVR-	1071.28	2 10421.79	42493.42	2.98	0.5	909
PAK (p21 (CDKN1A)-activated kinase 1				396.42	6 754 979		
jmfag1mmnacl5minig, 2626	-IGGGASGTYYTAMD VATG QEVAIKQMLQQQPK-	3464.92	2 396.42	396.42	0.93	0.2	84
LIM kinase				1093.84	8 754 540		
rawextr_200bead_Mar04, 76	-KRYTVVGNPNYVMAPEMINGR-	2383.78	3 691.05	1433.95	1.20	0.2	162
FPbeads400_Dec19, 2114	-FDEETQR TFLKEVK-	1770.87	2 372.78	1433.95	1.16	0.1	245
Anx6 protein [Mus musculus] ein [Mus musculus] X8				10383.01	13542782.0	12	
JMFAGNACL15B21E3, 1026	-SELDMLDIREIFR-	1637.68	3 965.88	1.74	0.0	311	1/3 3
jmfag5minig500mmnacl, 1444	-DAISGIGTDEK LIEILASR-	2105.40	3 495.94	1.41	0.1	211	7/38 1
jmbbeads250rawphag3007, 1172	-TNAIRIRAINAEYKEDYHK-	2106.34	3 758.30	1.46	0.2	236	4/17 2
jmbbeads150rawphag3007, 1632	-FRTVLCTRSYPHLR-	1725.08	2 306.27	1.08	0.1	184	9/26 2
jmfagmecon0min_03061230741, 2122	-GSVHDPFPEFDANQDAEAL YTMK-	2557.73	8 6394.53	2.82	0.4	805	23/68 3
RawPhg2007MeEhmmlh3dgest, 1266	-QTFKSHFGR-	1108.24	2 130.87	0.82	0.0	142	1/2 3
rawextr_150bead_Mar04, 1635	-VELKGTVCVCA ANDFNPDADAK-	2079.28	3 481.15	1.21	0.0	399	1/4 3
rawextr_250beadigg_Mar04, 1694	-GSVHDPFPEFDANQDAEAL YTMK-	2557.73	3 1390.26	1.87	0.1	515	23/88 3
ANX6_MOUSE Anxin6 (Anxin6) (P68) (P70) (Protein III) (C				1325.93	113963.0	3	
rawextr_200beadigg_Mar04, 751	-EEGGENRQQAQEDAQVA EILEIADTPSGDK-	3287.36	3 1325.93	1.79	0.2	317	1/5 1