Supplementary Table 1. Confidently identified rodent proteins for the stringently rinsed cells. Peptides were identified by the SEQUEST algorithm. Scores for a given protein were calculated as described in the Methods section. A score above 2.0 was considered as a confident positive identification based on calculated false positive rates. Any peptide with a score less than 2.0 was manually verified and only included in the table if the identification could be confirmed. Protein names and accession numbers correspond to UNI-PROT identifiers.*

Protein name	Accession No.	Peptides No.	Scans No.	Score	Peptide Coverage
Collagen alpha 1(I) chain	P11087	12	93	384.06	23.5%
Collagen alpha 2(I) chain	P02466	14	91	249.11	14.5%
Actin, cytoplasmic 1	P60711	4	87	196.43	11.2%
SPARC precursor (Osteonectin)	P07214	6	65	177.71	29.3%
Thrombospondin 1 precursor	Q03350	11	63	188.88	21.4%
Vimentin	P31000	9	62	84.37	9.2%
Fibronectin precursor	P04937	9	40	145.92	6.3%
Collagen alpha 1(I) chain	Q9XSJ7	5	22	43.85	11.3%
Plasminogen activator inhibitor-1	P20961	5	20	45.21	14.4%
Alpha-2-HS-glycoprotein precursor	P24090	6	18	46.57	18.6%
Alpha enolase	P04764	3	16	16.92	12.9%
L-lactate dehydrogenase A chain	P04642	3	14	11.05	11.5%
Desmin	P31001	2	13	10.10	6.5%
Histone	P22752	3	13	5.62	13.4%
Tropomyosin 1 alpha chain	P09495	4	12	16.97	12.4%
Transgelin	P31232	3	12	11.89	8.7%
Lumican precursor	P51886	2	12	8.21	10.1%
Profilin I	P62962	2	12	5.99	10.9%
Follistatin-related protein 1 precursor	Q62632	2	12	5.12	14.1%
Heat shock 70 kDa protein 1L	P55063	3	11	4.31	3.8%
Timeless homolog	Q9R1X4	4	9	17.76	4.5%
Biglycan precursor	P28653	1	9	3.20	2.6%
Actin, cytoplasmic 1 (Beta-actin 1)	Q91ZK5	3	8	9.30	4.1%
Periostin precursor (PN)	Q62009	3	8	7.58	4.6%
60S acidic ribosomal protein	P19945	2	8	3.46	3.8%
Serotransferrin precursor	P12346	5	6	11.96	6.7%
Protein kinase C inhibitor	P35213	3	6	7.10	8.4%
Actin, cytoplasmic 1	P60710	2	6	5.84	3.8%
Filamin A (Alpha-filamin)	Q8BTM8	2	6	3.65	0.8%
Actin, gamma	P63268	1	6	2.65	1.2%
Glyceraldehyde-3-phosphate	P04797	1	6	2.24	3.2%

Protein name	Accession No.	Peptides No.	Scans No.	Score	Peptide Coverage
Peripherin	P21807	1	6	2.17	1.8%
Elongation factor 2 (EF-2)	P05197	3	5	7.39	3.2%
Pyruvate kinase	P11980	2	5	4.69	7.8%
Cathepsin L precursor	P07154	2	5	4.47	6.3%
Peptidyl-prolyl cis-trans isomerase A	P10111	2	5	3.33	18.7%
Nucleobindin 1 precursor	Q02819	2	5	3.11	6.5%
Phosphoglycerate kinase 1	P16617	2	5	2.69	6.1%
Metalloproteinase inhibitor 1	P12032	3	5	2.57	7.9%
Apolipoprotein A-I precursor	P04639	1	5	2.29	2.4%
Tubulin alpha-1 chain	P68370	1	5	2.18	1.6%
47 kDa heat shock protein precursor	P29457	2	4	3.52	4.5%
Fibulin-2 precursor	P37889	2	4	3.13	0.4%
Lactadherin precursor	P70490	2	4	2.60	1.8%
Cystatin C precursor	P14841	1	4	1.87	4.5%
Elongation factor 1-beta (EF-1-beta)	O70251	1	4	1.62	6.6%
Alpha-actin 1	P68134	3	3	3.07	5.2%
Pigment epithelium-derived factor	P97298	3	3	2.28	6.1%
Peroxiredoxin 5, mitochondrial	Q9R298	2	3	2.18	5.2%
Nidogen precursor	P10493	2	3	2.16	0.7%
Annexin A1	P07150	1	3	1.44	1.2%
Nucleoside diphosphate kinase B	P70010	1	3	1.17	10.2%
Fructose-bisphosphate aldolase A	P05065	1	3	1.14	1.4%
Adenylyl cyclase-associated protein 1	Q08163	1	3	1.09	0.7%
Phosphoglycerate mutase 1	P25113	1	3	1.09	2.9%
Osteopontin precursor	P08721	1	3	1.03	5.1%
Tubulin beta-1 chain	Q9H4B7	2	2	2.59	0.5%
Ribonuclease inhibitor	P29315	2	2	1.36	6.9%
Myosin heavy chain	Q63862	2	2	1.15	0.3%
6-phosphogluconate dehydrogenase	Q9DCD0	1	2	0.99	0.5%
Annexin A5	P14668	1	2	0.95	1.4%
Annexin A2	Q07936	1	2	0.88	2.1%
Cofilin-1	P45592	1	2	0.76	8.4%
Rho GDP-dissociation inhibitor 1	Q99PT1	1	2	0.72	7.5%
Disabled homolog 2	O88797	1	2	0.62	0.6%
DnaJ homolog subfamily C	Q5FVM7	1	2	0.51	0.9%
DNA primase large subunit	P33610	1	2	0.42	1.8%

* UNI-Prot can be found at http://www.pir.uniprot.org/