Supplementary Table 1: List of phosphopeptides quantified by mass spectrometry that did not change significantly with dDAVP exposure. Mean and standard error (SE) values are calculated from log2(D/C), where D and C are areas of the reconstructed ion chromatograms for dDAVP-treated and control samples, respectively. Note: Phosphorylation sites were not scored, despite confidence in phosphopeptide identification.

#	Name	Sequence	Accession #	Mean ± SE
1	NFkB interacting protein 1	R.IPMPPSSPQPRS*T*PRQRPIPLS*MIFK.L(+3)	XP_001075705	-0.56 ± 0.24
2	hsp 90kDa alpha (cytosolic), class B member 1	K.IEDVGS*DEEDDSGKDKK.K(+2)	NP_001004082	-0.55 ± 0.35
3	EPS8-like 2	R.QSILPPPQS*PAPIPFQRQPGDS*PQAK.N(+3)	NP_001101978	-0.55 ± 0.34
4	scaffold attachment factor B	R.APTAAPS*PEPR.D(+2)	NP_071789	-0.53 ± 0.23
5	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	K.MEGPGVDIDS*PDVNIEGPEGK.L(+3)	XP_001078032	-0.49 ± 0.17
6	calnexin	K.AEEDEILNRS*PR.N(+2)	NP_742005	-0.48 ± 0.25
7	PREDICTED: PDZ domain containing 10	K.QSATT*LLVGPRHGISHVIDLK.T(+3)	XP_001053582	-0.48 ± 0.7
8	PREDICTED: PDZ-domain protein scribble	R.MVEPENAVTITPLRPEDDY*SPR.E(+3)	XP_001074724	-0.48 ± 0.41
9	PREDICTED: serine/arginine repetitive matrix 2	K.AAEIPAVASCWVGPQVS*PEHK.E(+3)	XP_001056343	-0.47 ± 0.17
10	thyroid hormone receptor associated protein 3	R.ASVSDLS*PR.E(+2)	NP_001009693	-0.45 ± 0.08
11	oxidative-stress responsive 1	R.LHKTEDGGWEWS*DDEFDEESEEGKAAISQLR.S(+4)	NP_001101664	-0.45 ± 1.59
12	PREDICTED: tensin	R.HLGGSGSVVPGS*PSLDR.H(+2)	XP_237286	-0.44 ± 0.05
13	lethal giant larvae homolog 2	R.S*QSDGAETKPGPVMEHALLSDAWVLK.E(+3)	NP_001121021	-0.43 ± 0.64
14	monocarboxylate transporter	R.SIIQIYLTT*GVIT*GLGLALNFQPS*LIMLNRYFNK.R(+4)	NP_110461	-0.43 ± 0.73
15	PREDICTED: Epithelial protein lost in neoplasm (mEPLIN)	R.TSSVKS*PKPLS*PSLRK.G(+3)	XP_217039	-0.43 ± 0.1
16	LIM domain containing preferred translocation partner in lipoma	R.RSS*LDAEIDSLTSILADLECSSPYKPR.A(+3)	NP_001013886	-0.42 ± 1.05
17	Ste-20 related kinase	K.TEDGDWEWS*DDEMDEKSEEGK.A(+3)	NP_062235	-0.42 ± 0.65
18	PREDICTED: GrpE protein homolog 2, mitochondrial precursor (Mt-GrpE#2)	R.S*LWAVQRLQRLLASGAVS*ES*R.G(+3)	XP_001058643	-0.41 ± 0.92
19	matrin 3	R.RDS*FDDRGPSLNPVLDYDHGSR.S(+3)	NP_062022	-0.4 ± 0.3
20	PREDICTED: CAP-binding protein complex interacting protein 1	K.S*RPVALGRVQK.V(+2)	XP_001077962	-0.4 ± 0.39
21	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	K.MYFPDVEFDIKS*PK.F(+3)	XP_001078032	-0.4 ± 0.13
22	actin-binding LIM protein 1	R.TLS*PTPSAEGFQDGR.D(+2)	NP_001037859	-0.39 ± 0.21
23	ladinin	R.LPS*VEEAEVSKPSPPASKDEGEEFQAILR.T(+3)	NP_001101412	-0.39 ± 0.62
24	tight junction protein 3	R.AIAEPES*PGESR.Y(+2)	NP_001101543	-0.39 ± 0.15
25	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	K.FKAEAALPS*PK.L(+2)	XP_001078032	-0.39 ± 0.12
26	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	K.MEGPGVDIDS*PDVNIEGPEGK.L(+2)	XP_001078032	-0.39 ± 0.09
27	PREDICTED: PDZ-domain protein scribble	R.MVEPENAVTITPLRPEDDYS*PR.E(+3)	XP_001074724	-0.38 ± 0.53
28	periplakin	R.S*IVVIDPDTGRELSPEEAHR.A(+3)	NP_001100446	-0.37 ± 0.21
29	protein C	K.TIVPICLPNSGLAQELSQAGQETVVT*GWGY*QS*DK.V(+4)	NP_036935	-0.37 ± 0.45
30	endosulfine alpha isoform 2	K.YFDS*GDYNMAK.A(+2)	NP_068614	-0.37 ± 0.12
31	septin 2	R.ILDEIEEHSIKIYHLPDAES*DEDEDFKEQTR.L(+4)	NP_476489	-0.37 ± 0.74
32	PREDICTED: neuron navigator 1	K.GQLTNIVSPT*AAT*TPR.I(+3)	XP_001063421	-0.37 ± 0.17
33	PREDICTED: tensin	R.AINPTMAAPGS*PSLSHR.Q(+3)	XP_237286	-0.37 ± 0.17
34	calnexin	K.AEEDEILNRS*PR.N(+3)	NP_742005	-0.36 ± 0.17
35	PREDICTED: tensin	R.TVGTNTPPS*PGFGR.R(+2)	XP_237286	-0.36 ± 0.13
36	heat shock protein 90kDa alpha (cytosolic), class B member 1	K.IEDVGS*DEEDDSGKDK.K(+2)	NP_001004082	-0.35 ± 0.31
37	mitogen-activated protein kinase 6	R.ES*ADVVDKLNDLNSSVSQLEM#KSLISK.S(+3)	NP_113810	-0.35 ± 0.15
38	EPS8-like 2	K.HSLSSEPQVPEDVAPPGS*SPHANR.G(+3)	NP_001101978	-0.34 ± 0.04
39	EPS8-like 2	K.HSLSSEPQVPEDVAPPGSS*PHANR.G(+3)	NP_001101978	-0.34 ± 0.04
40	PREDICTED: Epithelial protein lost in neoplasm (mEPLIN)	K.GENEETLGRPAQPPSAGETPHS*PGVEDAPIAK.V(+3)	XP_217039	-0.34 ± 0.23

41	PREDICTED: Epithelial protein lost in neoplasm (mEPLIN)	K.GWSEPEPEQSEEFGGGTVTQTES*PRPSR.E(+3)	XP_217039	-0.34 ± 0.38
42	PREDICTED: tensin-like SH2 domain containing 1	R.WDS*YENMSADGEVLHTQGPVDGSLYAK.V(+3)	XP_341257	-0.34 ± 0.5
43	BCL2-associated transcription factor 1	R.IDIS*PSALR.K(+2)	NP_001041317	-0.33 ± 0.18
44	mannose receptor, C type 1	K.GSSKAAGVVIVVLLIVIGAGVAAY*FFY*KK.R(+3)	NP_001099593	-0.33 ± 0.36
45	hypothetical protein LOC300783	R.WLDES*DAEMELR.A(+2)	NP_001100301	-0.33 ± 0.26
46	fibronectin leucine rich transmembrane protein 1	R.NS*LAAPPLNLPSAHLQK.L(+2)	NP_001102630	-0.32 ± 0.78
47	heterogeneous nuclear ribonucleoprotein K	R.RDYDDMS*PR.R(+2)	NP_476482	-0.32 ± 0.05
48	PCTAIRE protein kinase 3	R.RAS*LSDIGFGK.L(+2)	NP_001093976	-0.31 ± 0.49
49	actinin, alpha 1	K.NY*ITGDELR.R(+2)	NP_112267	-0.31 ± 0.34
50	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	K.VPDVDIS*SPGVNVEAPDIHVK.A(+3)	XP_001078032	-0.31 ± 0.27
51	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	K.VPDVDISS*PGVNVEAPDIHVK.A(+3)	XP_001078032	-0.31 ± 0.27
52	PREDICTED: Ras-GTPase-activating protein binding protein 1	K.SAS*PAPADVAPAQEDLR.T(+2)	XP_340803	-0.31 ± 0.07
53	heat shock protein 90kDa alpha (cytosolic), class B member 1	K.IEDVGS*DEEDDSGKDK.K(+3)	NP_001004082	-0.3 ± 0.3
54	microtubule-associated protein 4	K.VGS*LDNVGHLPAGGTVK.T(+3)	NP_001019449	-0.3 ± 0.07
55	PREDICTED: tensin	R.HLGGSGSVVPGS*PSLDR.H(+3)	XP_237286	-0.3 ± 0.08
56	ADNP homeobox 2	K.ERHHVMPT*VHT*MLR.S(+2)	NP_001120845	-0.29 ± 0.17
57	calcium regulated heat stable protein 1	R.DRS*PS*PLRGNVVPS*PLPTR.R(+3)	NP_690003	-0.29 ± 0.2
58	calcium regulated heat stable protein 1	R.DRS*PS*PLRGNVVPSPLPT*R.R(+3)	NP_690003	-0.29 ± 0.2
59	PREDICTED: cyclin fold protein 1	R.S*ASADNLILPR.W(+2)	XP_341546	-0.29 ± 0.1
60	aquaporin 4 isoform 1	K.GSYMEVEDNRS*QVETEDLILKPGVVHVIDIDR.G(+4)	NP_036957	-0.28 ± 0.4
61	PREDICTED: ribosomal protein L27a	K.LWTLVS*KQTLVSAAKNK.T(+3)	XP_001055169	-0.28 ± 0.2
62	NEL-like 1	R.CVSDPCLAGNIAY*DIR.K(+2)	NP_112331	-0.27 ± 0.15
63	PREDICTED: serine/arginine repetitive matrix 2	K.ELS*HSPPRDNSFESLEFR.N(+3)	XP_001056343	-0.27 ± 0.24
64	PREDICTED: serine/arginine repetitive matrix 2	K.ELSHS*PPRDNSFESLEFR.N(+3)	XP_001056343	-0.27 ± 0.24
65	PREDICTED: Epithelial protein lost in neoplasm (mEPLIN)	K.GENEETLGRPAQPPSAGETPHS*PGVEDAPIAK.V(+4)	XP_217039	-0.27 ± 0.16
66	eukaryotic translation initiation factor 4B	K.SLENETLNKEEDCHS*PTSKPPKPDQPLK.V(+4)	NP_001008325	-0.26 ± 0.15
67	eukaryotic translation initiation factor 4B	K.SLENETLNKEEDCHSPT*SKPPKPDQPLK.V(+4)	NP_001008325	-0.26 ± 0.15
68	RNA binding motif protein 39	K.DKS*PVREPIDNLTPEER.D(+3)	NP_001013225	-0.26 ± 0.2
69	solute carrier family 9 (sodium/hydrogen exchanger), member 1	R.IGS*DPLAYEPK.A(+2)	NP_036784	-0.26 ± 0.19
70	phosphatidylethanolamine binding protein	K.FKVES*FR.K(+2)	NP_058932	-0.26 ± 0.34
71	synaptosomal-associated protein 23	K.ATWGDGGDSS*PSNVVSK.Q(+2)	NP_073180	-0.26 ± 0.17
72	PREDICTED: putative pheromone receptor (Go-VN3)	K.HQRRY*LIVLT*GPPWLTS*YK.L(+3)	XP_001060597	-0.26 ± 0.39
73	PREDICTED: tankyrase 1-binding protein of 182 kDa	K.ENYEDQEPLAGQES*PITLATR.E(+3)	XP_215763	-0.26 ± 0.07
74	PREDICTED: cyclin fold protein 1	R.SAS*ADNLILPR.W(+2)	XP_341546	-0.26 ± 0.12
75	myeloid/lymphoid (trithorax homolog, Drosophila); translocated to, 4	K.QGAIYHGLATLLNQPS*PMMQR.I(+3)	NP_037349	-0.25 ± 0.21
76	heat shock protein 1	R.QLS*SGVSEIR.Q(+2)	NP_114176	-0.25 ± 0.09
77	PREDICTED: Syntaxin-binding protein 5-like (Tomosyn-2)	R.GQRLGELEEKTAGMMT*SAEAFSK.H(+2)	XP_001070379	-0.25 ± 0.24
78	PREDICTED: eIF-5B isoform 2	K.SVPTIDS*GNEDDDSSFK.I(+2)	XP_001071547	-0.25 ± 0.12
79	PREDICTED: CAP-binding protein complex interacting protein 1	K.S*RPVALGRVQK.V(+1)	XP_001077962	-0.25 ± 0.74
80	epsin 3	R.TPVLPSGPPITDPWAPSS*PTPK.L(+3)	NP_001019962	-0.24 ± 0.12
81	epsin 3	R.TPVLPSGPPITDPWAPSSPT*PK.L(+3)	NP_001019962	-0.24 ± 0.12
82	ladinin	R.LPS*VEEAEVSKPSPPASKDEGEEFQAILR.T(+4)	NP_001101412	-0.24 ± 0.31
83	calcium channel, voltage-dependent, alpha2/delta subunit 1 isoform 3	R.RRPWY*IQGAASPKDM#LILVDVS*GSVSGLTLK.L(+3)	NP_001104317	-0.24 ± 0.32
84	aquaporin 2 (collecting duct)	R.RQS*VELHSPQS*LPR.G(+3)	NP_037041	-0.24 ± 1.17
85	hepatoma-derived growth factor	R.AGDMLEDS*PKRPK.E(+2)	NP_446159	-0.24 ± 0.19
86	heterogeneous nuclear ribonucleoprotein K	R.DYDDMS*PR.R(+2)	NP_476482	-0.24 ± 0.04

87	alpha-spectrin 2	R.WRS*LQQLAEER.S(+2)	NP_741984	-0.23 ± 0.13
88	PREDICTED: Oxysterol-binding protein-related protein 3 (ORP-3)	R.LHS*SNPNLSTLDFGEEK.S(+3)	XP_342684	-0.23 ± 0.13
89	PREDICTED: Oxysterol-binding protein-related protein 3 (ORP-3)	R.LHSS*NPNLSTLDFGEEK.S(+3)	XP_342684	-0.23 ± 0.13
90	catenin (cadherin-associated protein), alpha 1, 102kDa	R.TPEELDDS*DFETEDFDVR.S(+2)	NP_001007146	-0.22 ± 0.12
91	solute carrier family 9 (sodium/hydrogen exchanger), member 1	K.ITNYLTVPAHKLDS*PTMSR.A(+3)	NP_036784	-0.22 ± 0.14
92	solute carrier family 9 (sodium/hydrogen exchanger), member 1	K.ITNYLTVPAHKLDSPTMS*R.A(+3)	NP_036784	-0.22 ± 0.14
93	myosin, heavy chain 9, non-muscle	R.KGTGDCS*DEEVDGKADGADAK.A(+2)	NP_037326	-0.22 ± 0.23
94	adenosine monophosphate deaminase 3	K.GPPSVSPAMSPT*T*PLVLGAASKPGLAPYDMPEYQR.A(+4)	NP_113732	-0.22 ± 0.18
95	calnexin	K.QKS*DAEEDGGTGS*QDEEDSKPK.A(+3)	NP_742005	-0.22 ± 0.48
96	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	R.ELEKPIQSKPQS*PVIQATAGS*PK.F(+3)	NP_851597	-0.22 ± 0.08
97	PREDICTED: CG5937-PA	R.GPDS*PLLQRPQHLIDQGQMR.H(+3)	XP_001072524	-0.22 ± 0.19
98	PREDICTED: tensin	K.VSSS*PVANGMAS*PSGSSTVSFSHTLPDFSK.Y(+3)	XP_237286	-0.22 ± 0.25
99	branched chain keto acid dehydrogenase E1, alpha polypeptide	R.IGHHS*TSDDSSAYRS*VDEVNYWDKQDHPISR.L(+4)	NP_036914	-0.21 ± 0.13
100	protein kinase, cAMP dependent regulatory, type II alpha	R.RVS*VCAETFNPDEEEDNDPR.V(+3)	NP_062137	-0.21 ± 0.07
101	drebrin-like	K.LRS*PFLQK.Q(+2)	NP_112642	-0.21 ± 0.06
102	adenosine monophosphate deaminase 3	K.GPPSVS*PAMS*PTTPLVLGAASKPGLAPYDMPEYQR.A(+3)	NP_113732	-0.21 ± 0.3
103	hepatoma-derived growth factor	R.AGDM#LEDS*PKRPK.E(+3)	NP_446159	-0.21 ± 0.13
104	PREDICTED: (NUANCE protein)	R.LTSHTPGLDDEKEAS*ENETDIEDPREIPADSWR.K(+4)	XP_001080795	-0.21 ± 0.12
105	PREDICTED: splicing factor, arginine/serine-rich 1 (ASF/SF2)	R.VKVDGPRS*PSYGR.S(+3)	XP_001081187	-0.21 ± 0.09
106	PREDICTED: Epithelial protein lost in neoplasm (mEPLIN)	R.SEAQQPIYTKPLS*PDAR.T(+2)	XP_217039	-0.21 ± 0.12
107	epsin 3	R.TPVLPSGPPITDPWAPS*SPTPK.L(+3)	NP_001019962	-0.2 ± 0.09
108	p21-activated kinase 4	R.SNS*LRRES*PPPPAR.A(+3)	NP_001099708	-0.2 ± 0.13
109	vinculin	K.GWLRDPNAS*PGDAGEQAIR.Q(+3)	NP_001100718	-0.2 ± 0.07
110	PREDICTED: NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	K.YKPAPLAALPSTLDSVEY*DVSPETRK.A(+3)	XP_001056198	-0.2 ± 0.75
111	PREDICTED: (PDHE1-A type I) isoform 1	R.Y*HGHSM#SDPGVS*YR.T(+3)	XP_001060860	-0.2 ± 0.25
112	PREDICTED: (PDHE1-A type I) isoform 1	R.YHGHS*M#SDPGVS*YR.T(+3)	XP_001060860	-0.2 ± 0.25
113	Cobl-like 1	R.QSS*LNFQSSDPEHIR.Q(+3)	NP_001101203	-0.19 ± 0.06
114	erythrocyte protein band 4.1-like 1 isoform L	R.RLPSS*PAS*PSPK.G(+2)	NP_067713	-0.19 ± 0.08
115	plectin 1	R.T*QLASWSDPTEETGPVAGILDTETLEK.V(+3)	NP_071796	-0.19 ± 0.28
116	plectin 1	R.TQLAS*WSDPTEETGPVAGILDTETLEK.V(+3)	NP_071796	-0.19 ± 0.28
117	reticulon 4	R.GPLPAAPPAAPERQPS*WER.S(+2)	NP_114019	-0.19 ± 0.17
118	solute carrier family 14 (urea transporter), member 2 isoform 2	K.LYESELSS*PTWPSSSQDTHPALPLLEMPEEK.D(+3)	NP_808877	-0.19 ± 0.47
119	proteasome subunit alpha type 3-like	K.ESLKEEDES*DDDNM#.-(+2)	NP_001004094	-0.18 ± 0.13
120	catenin (cadherin-associated protein), alpha 1, 102kDa	R.T*PEELDDSDFETEDFDVR.S(+3)	NP_001007146	-0.18 ± 0.22
121	catenin (cadherin-associated protein), alpha 1, 102kDa	R.TPEELDDS*DFETEDFDVR.S(+3)	NP_001007146	-0.18 ± 0.22
122	ladinin	K.GRPEETAAQQKS*PVSEKTPVSAK.R(+4)	NP_001101412	-0.18 ± 0.14
123	cingulin-like 1	R.RQDS*AGPILDGAR.S(+2)	NP_001101634	-0.18 ± 0.11
124	galectin-related protein	K.LDDGHLNNSLGS*PVQADVYFPR.L(+3)	NP_001128202	-0.18 ± 0.21
125	heterogeneous nuclear ribonucleoprotein A1	K.SES*PKEPEQLR.K(+3)	NP_058944	-0.18 ± 0.24
126	PREDICTED: zinc finger CCCH-type containing 5	K.LHS*LQS*QLRLDLEAVDGVIFQLRAK.Q(+3)	XP_001059160	-0.18 ± 0.25
127	heat shock protein 90kDa alpha (cytosolic), class B member 1	K.IEDVGS*DEEDDSGKDKK.K(+3)	NP_001004082	-0.17 ± 0.21
128	RAS p21 protein activator (GTPase activating protein) 1	K.WPTNNTMRT*RVVS*GFVFLR.L(+3)	NP_037267	-0.17 ± 0.1
129	SH3-domain kinase binding protein 1	R.S*IEVENDFLPVEK.T(+2)	NP_445812	-0.17 ± 0.04
130	septin 2	K.IYHLPDAES*DEDEDFKEQTR.L(+4)	NP_476489	-0.17 ± 0.09
131	PREDICTED: AHNAK nucleoprotein isoform 2 isoform 1	R.KGDRS*PEPGQTWAHEVFSSR.S(+3)	XP_001078152	-0.17 ± 0.08

132	heat shock 105kDa	K.IES*PKLER.T(+2)	NP_001011901	-0.16 ± 0.07
133	BCL2-associated transcription factor 1	R.RIDIS*PSALR.K(+2)	NP_001041317	-0.16 ± 0.17
134	family with sequence similarity 83, member H	R.KGS*PTPAYPER.K(+2)	NP_001124037	-0.16 ± 0.07
135	erythrocyte protein band 4.1-like 1 isoform L	R.RLPSSPAS*PSPK.G(+2)	NP_067713	-0.16 ± 0.07
136	programmed cell death 4	R.DSGRGDS*VSDNGSEAVR.S(+3)	NP_071601	-0.16 ± 0.09
137	drebrin-like	K.LRS*PFLQK.Q(+3)	NP_112642	-0.16 ± 0.13
138	nucleobindin 1	R.AQRLS*QETEALGR.S(+2)	NP_445915	-0.16 ± 0.13
139	PREDICTED: Beta-2-syntrophin isoform 2	R.LVHSGS*GCRSPSLGSDLTFATR.T(+3)	XP_001071043	-0.16 ± 0.1
140	PREDICTED: Beta-2-syntrophin isoform 2	R.LVHSGSGCRS*PSLGSDLTFATR.T(+3)	XP_001071043	-0.16 ± 0.1
141	PREDICTED: mitogen-activated protein kinase kinase kinase 10	R.S*DSDEAAPTAPSPPPS*LLPPSPS*T*NPLVDVELESFKK.D(+4)	XP_001073032	-0.16 ± 0.17
142	PREDICTED: microsomal glutathione S-transferase 3	R.AKM#AVLSKEY*GFVLLTGAASFVMVLHLAINVGK.A(+3)	XP_001076104	-0.16 ± 0.48
143	PREDICTED: dynein heavy chain domain 3	R.YPPNAPFY*KIM#VPT*VDT*VR.Y(+3)	XP_220603	-0.16 ± 0.37
144	PCTAIRE protein kinase 3	R.NEDGRDEPGQLS*PGVQYQQR.Q(+3)	NP_001093976	-0.15 ± 0.04
145	catenin (cadherin associated protein), alpha 2	R.SRT*SVQTEDDQLIAGQSAR.A(+3)	NP_001100068	-0.15 ± 0.08
146	catenin (cadherin associated protein), alpha 2	R.SRTS*VQTEDDQLIAGQSAR.A(+3)	NP_001100068	-0.15 ± 0.08
147	catenin (cadherin associated protein), delta 1	R.VGGS*SVDLHR.F(+3)	NP_001101210	-0.15 ± 0.33
148	branched chain keto acid dehydrogenase E1, alpha polypeptide	R.IGHHS*TSDDS*SAYRSVDEVNYWDKQDHPISR.L(+4)	NP_036914	-0.15 ± 0.13
149	ankyrin 3, epithelial isoform 1	R.AEEPVS*PLTAYQK.S(+2)	NP_113993	-0.15 ± 0.12
150	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	R.VGWSTM#QAS*LDLGTDKFGFGFGGTGKK.S(+3)	NP_445866	-0.15 ± 0.1
151	PREDICTED: tankyrase 1-binding protein of 182 kDa	R.KEIPAS*PDRLWGSR.L(+3)	XP_215763	-0.15 ± 0.07
152	PREDICTED: Dystroglycan precursor (Dystrophin-associated glycoprotein 1)	R.IVPTPTSPAIAPPTET*MAPPVR.D(+2)	XP_343484	-0.15 ± 0.25
153	LIM domain 7	R.EVSRS*PDQFSDMR.I(+3)	NP_001001515	-0.14 ± 0.03
154	serine/arginine repetitive matrix 1	R.KETES*EAEDDNLDDLER.H(+3)	NP_001101456	-0.14 ± 0.07
155	solute carrier family 14 (urea transporter), member 2 isoform 2	K.LYESELSS*PTWPSSSQDTHPALPLLEMPEEK.D(+4)	NP_808877	-0.14 ± 0.9
156	translocase of outer mitochondrial membrane 70 homolog A	R.AS*PALGSGPDGSGDSLEMSSLDR.A(+2)	NP_997684	-0.14 ± 0.13
157	PREDICTED: Nucleophosmin	K.CGSGPVHISGQHLVAVEEDAES*EDEDEEDVKLLGMSGK.R(+4)	XP_001071367	-0.14 ± 0.31
158	Rho guanine nucleotide exchange factor (GEF) 12	R.VCLEDTPERTEGVQDADTQSLVGS*PSTR.G(+3)	NP_001013264	-0.13 ± 0.2
159	nuclear cap binding protein subunit 1, 80kDa	R.RKT*SDANETEDHLESLICK.V(+4)	NP_001014785	-0.13 ± 0.06
160	epsin 3	R.TPVLPSGPPITDPWAPSS*PTPK.L(+2)	NP_001019962	-0.13 ± 0.17
161	serine/arginine repetitive matrix 1	R.KET*ESEAEDDNLDDLER.H(+3)	NP_001101456	-0.13 ± 0.07
162	family with sequence similarity 83, member H	R.KGS*PTPAYPER.K(+3)	NP_001124037	-0.13 ± 0.08
163	thymopoietin	K.GPPDFSSDEEREPT*PVLGSGASVGR.G(+3)	NP_037019	-0.13 ± 0.09
164	USO1 homolog, vesicle docking protein	K.LKDLGHPVEEEDES*GDQEDDDDELDDGDRDQDI.-(+4)	NP_062252	-0.13 ± 0.08
165	sorting nexin 16	K.FT*VY*KILVKESPEESWVVFR.R(+3)	NP_071625	-0.13 ± 0.31
166	PREDICTED: Transcription initiation factor TFIID 105 kDa subunit (TAFII-105) (TAFII105)	K.VTVAPVKSLTQIGTTVATTAS*SASS*GQTVLENVK.K(+3)	XP_001073245	-0.13 ± 0.32
167	paxillin	R.YAHQQPPS*PSPIYSSSTK.N(+3)	NP_001012147	-0.12 ± 0.09
168	Structure specific recognition protein 1	K.EGINPGYDDYADS*DEDQHDAYLER.M(+3)	NP_112383	-0.12 ± 0.08
169	Structure specific recognition protein 1	K.EGINPGYDDYADSDEDQHDAY*LER.M(+3)	NP_112383	-0.12 ± 0.08
170	calcium regulated heat stable protein 1	R.TFS*ATVR.A(+2)	NP_690003	-0.12 ± 0.2
171	solute carrier family 14 (urea transporter), member 2 isoform 2	R.YKLYESELS*SPTWPSSSQDTHPALPLLEMPEEK.D(+4)	NP_808877	-0.12 ± 0.35
172	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	K.MYFPDVEFDIKS*PK.F(+2)	XP_001078032	-0.12 ± 0.13
173	transforming acidic coiled coil 2 isoform 2	K.TPEKLDNTPAS*PPRS*PAEPSDIPIAK.G(+3)	NP_001004418	-0.11 ± 0.14
174	thyroid hormone receptor associated protein 3	R.IDIS*PSTFR.K(+2)	NP_001009693	-0.11 ± 0.06
175	serine/arginine repetitive matrix 1	K.KPPAPPSPVQS*QS*PSTNWS*PAAPAKK.A(+3)	NP_001101456	-0.11 ± 0.13
176	lethal giant larvae homolog 2	R.VAVGCRLS*NGEAE.-(+2)	NP_001121021	-0.11 ± 0.08
177	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	R.NRTPS*DVKELVLDNCR.S(+3)	NP_037035	-0.11 ± 0.15

178	heterogeneous nuclear ribonucleoprotein A1	K.SES*PKEPEQLRK.L(+3)	NP_058944	-0.11 ± 0.12
179	erythrocyte protein band 4.1-like 1 isoform L	R.RSEAEEGEVRT*PTK.I(+3)	NP_067713	-0.11 ± 0.05
180	nucleoporin 98kDa	K.NLNNSNLFSPVNHDSEDLAS*PSEYPENGER.F(+3)	NP_112336	-0.11 ± 0.41
181	zinc finger, RAN-binding domain containing 2	R.ENVEYIEREES*DGEYDEFGR.K(+3)	NP_113804	-0.11 ± 0.18
182	alpha-spectrin 2	R.WRS*LQQLAEER.S(+3)	NP_741984	-0.11 ± 0.21
183	thyroid hormone receptor associated protein 3	R.RIDIS*PSTFR.K(+2)	NP_001009693	-0.1 ± 0.1
184	connector enhancer of kinase suppressor of Ras 1	K.KIPVPETPSKT*PPDS*PQR.L(+3)	NP_001034100	-0.1 ± 0.21
185	adaptor-related protein complex 3, delta 1 subunit	R.VDIITEEMPENALPS*DEDDKDPNDPYR.A(+3)	NP_001094189	-0.1 ± 0.21
186	protein phosphatase 4, regulatory subunit 2	R.AEETETAS*SPPEKDRENR.T(+3)	NP_001100083	-0.1 ± 0.15
187	erythrocyte protein band 4.9	R.KGAEEEEEEEDDDS*EEEIKAIR.E(+3)	NP_001101855	-0.1 ± 0.15
188	ATP-binding cassette, sub-family F (GCN20), member 1	R.LKQLSVPAS*DEEDEVPVPVPR.G(+3)	NP_001103353	-0.1 ± 0.34
189	USO1 homolog, vesicle docking protein	K.LKDLGHPVEEEDES*GDQEDDDDELDDGDRDQDI.-(+3)	NP_062252	-0.1 ± 0.12
190	PDZ and LIM domain 5	K.GEPKEVVKPVPIT*SPAVSKVT*STTNM#AYNK.V(+3)	NP_445778	-0.1 ± 0.22
191	StAR-related lipid transfer (START) domain containing 10	R.AGGAGEGS*DDDTSLT.-(+2)	NP_001013087	-0.09 ± 0.05
192	epsin 3	K.GKS*PS*PVELDPFGDSSPSCK.Q(+3)	NP_001019962	-0.09 ± 0.16
193	Cd4 molecule	R.LLQGQSLTLILDS*NPK.V(+3)	NP_036837	-0.09 ± 0.33
194	crystallin, alpha B	R.APS*WIDTGLSEMR.M(+2)	NP_037067	-0.09 ± 0.16
195	myeloid/lymphoid (trithorax homolog, Drosophila); translocated to, 4	K.TQVLS*PDSLFTAK.F(+2)	NP_037349	-0.09 ± 0.07
196	adenosine monophosphate deaminase 3	K.GPPSVSPAMS*PT*TPLVLGAASKPGLAPYDMPEYQR.A(+4)	NP_113732	-0.09 ± 0.09
197	hepatoma-derived growth factor	R.RAGDMLEDS*PKRPK.E(+3)	NP_446159	-0.09 ± 0.03
198	PREDICTED: RNA-binding protein 14 (RNA-binding motif protein 14)	R.TRLS*PPR.A(+2)	XP_001072105	-0.09 ± 0.15
199	eukaryotic translation initiation factor 3, subunit 9 (eta)	R.AKPAAQSEEETAAS*PAAS*PTPQSAQEPSAPGKAEAGGEQAR.H(+4)	NP_001026810	-0.08 ± 0.32
200	human immunodeficiency virus type I enhancer binding protein 1	R.LSGLDGQRDSSSSS*S*KTR.T(+3)	NP_001099221	-0.08 ± 0.07
201	tight junction protein 3	K.ASPASGHQLS*DQEEADHGR.G(+3)	NP_001101543	-0.08 ± 0.26
202	LSM14A, SCD6 homolog A	R.S*SPQLDPLRKS*PTMEQAVQTASAHLPAPAPVGR.R(+4)	NP_001121024	-0.08 ± 0.23
203	LSM14A, SCD6 homolog A	R.SS*PQLDPLRKSPT*MEQAVQTASAHLPAPAPVGR.R(+4)	NP_001121024	-0.08 ± 0.23
204	parvin, alpha	K.SPSVPKS*PTPKS*PPSR.K(+3)	NP_065707	-0.08 ± 0.06
205	tight junction protein 2	R.RQQYS*DQEYHSSTEK.L(+3)	NP_446225	-0.08 ± 0.06
206	PREDICTED: tankyrase 1-binding protein of 182 kDa	K.TWVTSSADPVS*EHGVSTSPVLLAK.V(+3)	XP_215763	-0.08 ± 0.16
207	PREDICTED: Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1)	R.VMTIPYQPMPASS*PVICAGGQDR.C(+3)	XP_575592	-0.08 ± 0.08
208	thyroid hormone receptor associated protein 3	R.ERS*PALKS*PLQSVVVR.R(+3)	NP_001009693	-0.07 ± 0.1
209	leucine rich repeat (in FLII) interacting protein 1	K.AENQRPVEDSALS*PGPLAGAK.C(+3)	NP_001014291	-0.07 ± 0.11
210	syntrophin, acidic 1	K.NSAGGTSVGWDS*PPAS*PLQR.Q(+2)	NP_001094371	-0.07 ± 0.13
211	ladinin	K.GRPEETAAQQKS*PVSEK.T(+3)	NP_001101412	-0.07 ± 0.29
212	serine/arginine repetitive matrix 1	K.KPPAPPS*PVQS*QSPSTNWS*PAAPAKK.A(+3)	NP_001101456	-0.07 ± 0.1
213	EPS8-like 2	R.RAEDSYSNVHTS*PEAEGAPHL.-(+3)	NP_001101978	-0.07 ± 0.12
214	myosin, heavy chain 9, non-muscle	R.KGTGDCS*DEEVDGKADGADAK.A(+4)	NP_037326	-0.07 ± 0.13
215	splicing factor 1 isoform 2	R.TGDLGIPPNPEDRS*PS*PEPIYNSEGK.R(+3)	NP_478117	-0.07 ± 0.13
216	calnexin	K.QKSDAEEDGGT*GSQDEEDSKPK.A(+3)	NP_742005	-0.07 ± 0.62
217	calnexin	K.QKSDAEEDGGTGS*QDEEDSKPK.A(+3)	NP_742005	-0.07 ± 0.62
218	PREDICTED: (PDHE1-A type I) isoform 1	R.YHGHS*MSDPGVS*YR.T(+2)	XP_001060860	-0.07 ± 0.18
219	PREDICTED: RAB11 family interacting protein 5 (class I) isoform 1	R.TYS*DEASQLR.A(+2)	XP_001073801	-0.07 ± 0.08
220	PREDICTED: myosin XVIIIa	K.SLAPDLS*DDEHDPVDSISRPR.F(+3)	XP_001080824	-0.07 ± 0.09
221	PREDICTED: tankyrase 1-binding protein of 182 kDa	K.TWVTSSADPVSEHGVS*TSPVLLAK.V(+3)	XP_215763	-0.07 ± 0.16
222	PREDICTED: tankyrase 1-binding protein of 182 kDa	K.TWVTSSADPVSEHGVST*SPVLLAK.V(+3)	XP_215763	-0.07 ± 0.16
223	PREDICTED: tankyrase 1-binding protein of 182 kDa	K.TWVTSSADPVSEHGVSTS*PVLLAK.V(+3)	XP_215763	-0.07 ± 0.16

224	histone deacetylase 1	R.MLPHAPGVQMQAIPEDAIPEES*GDEDEEDPDKR.I(+4)	NP_001020580	-0.06 ± 0.11
225	syntrophin, acidic 1	K.NSAGGTSVGWDS*PPAS*PLQR.Q(+3)	NP_001094371	-0.06 ± 0.12
226	EF hand domain family, member B	R.APLGKSHDQTPGLPKGMDVINTT*LGTPT*IR.E(+3)	NP_001100349	-0.06 ± 0.3
227	ladinin	R.SVERLPS*VEEAEVSKPS*PPASKDEGEEFQAILR.T(+4)	NP_001101412	-0.06 ± 0.17
228	erythrocyte protein band 4.9	K.ST*SPPPS*PEVWAESR.T(+2)	NP_001101855	-0.06 ± 0.07
229	PREDICTED: OTU domain containing 4 protein isoform 1	R.LQRPKEES*S*EDENEVSNILR.S(+3)	XP_001074219	-0.06 ± 0.23
230	PREDICTED: U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform b	R.GAKEEHGGLIRS*PR.H(+3)	XP_218195	-0.06 ± 0.13
231	protein kinase, cAMP dependent regulatory, type II beta	R.RAS*VCAEAYNPDEEEDDAESR.I(+3)	NP_001025191	-0.05 ± 0.18
232	non-SMC condensin II complex, subunit D3	R.T*Y*AAQS*LVQLLS*KLPSK.E(+3)	NP_001029172	-0.05 ± 0.46
233	utrophin	K.NVRPQPPT*SPEGR.T(+2)	NP_037202	-0.05 ± 0.05
234	utrophin	K.NVRPQPPTS*PEGR.T(+2)	NP_037202	-0.05 ± 0.05
235	protein kinase, cAMP dependent regulatory, type I, alpha	R.TDSREDEIS*PPPPNPVVK.G(+3)	NP_037313	-0.05 ± 0.13
236	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	R.GPDRT*PPSEEDSAEAER.L(+3)	NP_073194	-0.05 ± 0.12
237	myosin, heavy chain 10, non-muscle	R.QLHIEGASLELS*DDDTESK.T(+3)	NP_113708	-0.05 ± 0.46
238	chloride channel, nucleotide-sensitive, 1A	R.FGEESKEPFS*DEDEDDNDDVEPISEFR.F(+3)	NP_113907	-0.05 ± 0.44
239	septin 2	K.IYHLPDAES*DEDEDFKEQTR.L(+3)	NP_476489	-0.05 ± 0.02
240	PREDICTED: topoisomerase (DNA) II beta	K.KTSFDQDS*DVDIFPSDFTSEPPALPR.T(+3)	XP_001067768	-0.05 ± 0.24
241	PREDICTED: Epithelial protein lost in neoplasm (mEPLIN)	R.SEAQQPIYTKPLS*PDAR.T(+3)	XP_217039	-0.05 ± 0.08
242	proteasome subunit alpha type 3-like	K.ESLKEEDES*DDDNM.-(+2)	NP_001004094	-0.04 ± 0.04
243	eukaryotic translation elongation factor 1 delta	K.GATPAEDDEDNDIDLFGS*DEEEEDKEAAR.L(+3)	NP_001013122	-0.04 ± 0.11
244	catenin (cadherin associated protein), delta 1	R.LRS*YEDMIGEEVPPDQYYWAPLAQHER.G(+3)	NP_001101210	-0.04 ± 0.29
245	catenin (cadherin associated protein), delta 1	R.VGGS*SVDLHR.F(+2)	NP_001101210	-0.04 ± 0.27
246	golgi autoantigen, golgin subfamily a, 3	K.DKFMLQAKVS*ELK.N(+3)	NP_001101317	-0.04 ± 0.41
247	serine/arginine repetitive matrix 1	R.RYS*PPIQR.R(+2)	NP_001101456	-0.04 ± 0.05
248	EPS8-like 2	K.YWGPAS*PTHK.L(+2)	NP_001101978	-0.04 ± 0.29
249	EPS8-like 2	K.YWGPASPT*HK.L(+2)	NP_001101978	-0.04 ± 0.29
250	phosphoglucomutase 1	K.AIGGIILTAS*HNPGGPNGDFGIK.F(+3)	NP_058729	-0.04 ± 0.16
251	reticulon 4	R.GPLPAAPPAAPERQPS*WER.S(+3)	NP_114019	-0.04 ± 0.05
252	tripartite motif-containing 28	R.SRS*GEGEVSGLMR.K(+2)	NP_446368	-0.04 ± 0.06
253	calnexin	K.QKS*DAEEDGGTGSQDEEDSKPK.A(+3)	NP_742005	-0.04 ± 0.6
254	progesterone receptor membrane component 2	R.LLKPGEEPS*EYTDEEDTKDHSKQD.-(+3)	NP_001008375	-0.03 ± 0.11
255	phosphoglucomutase 1	K.AIGGIILT*ASHNPGGPNGDFGIK.F(+3)	NP_058729	-0.03 ± 0.15
256	heat shock protein 1	R.SPS*WEPFR.D(+2)	NP_114176	-0.03 ± 0.15
257	NSFL1 (p97) cofactor (p47)	R.KKS*PNELVDDLFK.G(+3)	NP_114187	-0.03 ± 0.06
258	p21-activated kinase 2	K.YLS*FTPPEKDGFPSGTPALNTK.G(+3)	NP_445758	-0.03 ± 0.21
259	PREDICTED: tankyrase 1-binding protein of 182 kDa	K.SSGSLS*PGLETEDPLEAR.E(+2)	XP_215763	-0.03 ± 0.05
260	PREDICTED: tetracycline transporter-like protein	R.AS*S*VTLGFHT*AANLLS*PLALLR.F(+3)	XP_223533	-0.03 ± 0.24
261	hypothetical protein LOC287534	K.KKGDGVLDS*PDSGLPPS*PSPSHWGLAAATGGGGER.A(+4)	NP_001007612	-0.02 ± 0.15
262	RNA binding motif protein 39	R.YRS*PYSGPK.F(+2)	NP_001013225	-0.02 ± 0.08
263	WD repeat domain 42A	R.VHGHS*DEEEEEEQPR.H(+3)	NP_001014253	-0.02 ± 0.33
264	nuclear cap binding protein subunit 1, 80kDa	R.KTS*DANETEDHLESLICK.V(+3)	NP_001014785	-0.02 ± 0.16
265	leucine rich repeat containing 47	R.RES*GEGEEEVADSAR.L(+3)	NP_001129138	-0.02 ± 0.16
266	phosphatidylethanolamine binding protein	K.VLTPTQVMNRPS*SISWDGLDPGK.L(+3)	NP_058932	-0.02 ± 0.25
267	heat shock protein 1	R.SPS*WEPFRDWYPAHSR.L(+4)	NP_114176	-0.02 ± 0.25
268	hepatoma-derived growth factor	R.AGDMLEDS*PKRPK.E(+3)	NP_446159	-0.02 ± 0.06
269	kinesin 13B	R.LEVTS*DSEDASEVPEWLR.E(+2)	NP_998791	-0.02 ± 0.19
270	PREDICTED: SAPS domain family, member 3	R.IQQFDDGGS*DEEDIWEEK.H(+2)	XP_001067905	-0.02 ± 0.16

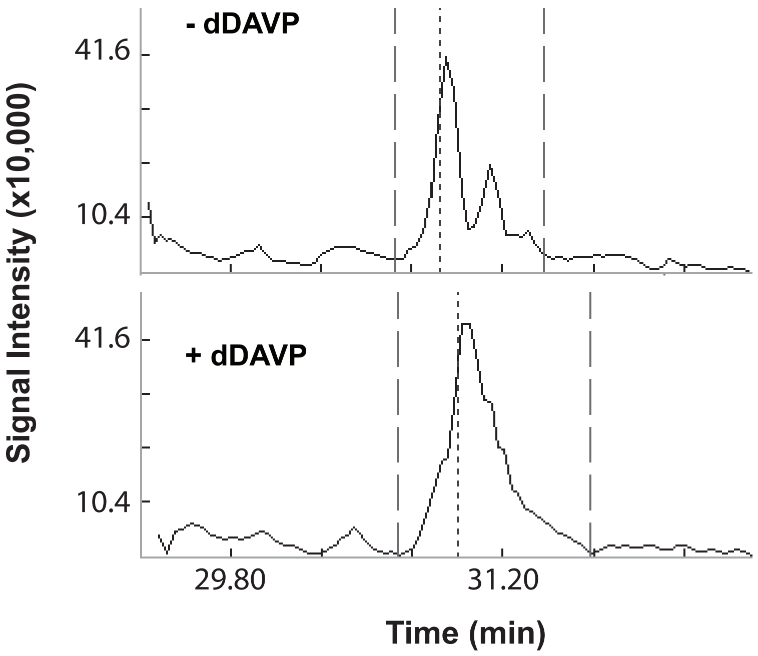
271	PREDICTED: AHNAK nucleoprotein isoform 2 isoform 1	R.KGDRS*PEPGQTWAHEVFSSR.S(+4)	XP_001078152	-0.02 ± 0.08
272	estrogen receptor binding site associated, antigen, 9	R.KLS*GDQITLPTTVDYSSVPK.Q(+3)	NP_001009665	-0.01 ± 0.07
273	estrogen receptor binding site associated, antigen, 9	R.KLSGDQIT*LPTTVDYSSVPK.Q(+3)	NP_001009665	-0.01 ± 0.07
274	eukaryotic translation elongation factor 1 delta	K.KGATPAEDDEDNDIDLFGS*DEEEEDKEAAR.L(+3)	NP_001013122	-0.01 ± 0.07
275	elongation factor Tu GTP binding domain containing 1	R.LM#AAMYTCDIMATSDVLGRVYAVLS*K.R(+3)	NP_001101004	-0.01 ± 0.38
276	kinase insert domain protein receptor	K.NKTVST*LVIQAAYVS*ALYK.C(+3)	NP_037194	-0.01 ± 0.07
277	hepatoma-derived growth factor	K.GNAEGS*S*DEEGKLVIDEPAKEK.N(+3)	NP_446159	-0.01 ± 0.24
278	mitogen-activated protein kinase 1	R.VADPDHDHTGFLTEY*VATR.W(+3)	NP_446294	-0.01 ± 0.08
279	heterogeneous nuclear ribonucleoprotein K	K.IIPTLEEGLQLPS*PTATSQLPLESDAVECLNYQHYK.G(+4)	NP_476482	-0.01 ± 0.08
280	dynein cytoplasmic 1 light intermediate chain 1	R.DFQEYVEPGEDFPAS*PQRR.A(+3)	NP_665715	-0.01 ± 0.04
281	solute carrier family 14 (urea transporter), member 2 isoform 2	K.EMSDNNRS*PLLPEPLSSR.Y(+3)	NP_808877	-0.01 ± 0.21
282	kinesin 13B	R.LEVTSDS*EDASEVPEWLR.E(+2)	NP_998791	-0.01 ± 0.2
283	PREDICTED: nuclear mitotic apparatus protein 1	R.LGS*PDDSNSALLSLPGYRPTTR.S(+3)	XP_218972	-0.01 ± 0.12
284	nucleobindin 1	K.SGKLS*QELDFVSHNVR.T(+3)	NP_445915	0 ± 0.09
285	PREDICTED: ribosomal protein L27a	K.LWT*LVSKQTLVSAAKNK.T(+3)	XP_001055169	0 ± 0.75
286	PREDICTED: (PDHE1-A type I) isoform 1	R.YGMGTS*VER.A(+2)	XP_001060860	0 ± 0.02
287	tight junction protein 1	K.FNHNLLPSETVHKPELSS*KPPPSPK.T(+4)	NP_001099736	0 ± 0.13
288	tight junction protein 1	K.FNHNLLPSETVHKPELSSKPPPS*PK.T(+4)	NP_001099736	0 ± 0.13
289	catenin (cadherin associated protein), delta 1	R.GSLAS*LDSLRK.G(+2)	NP_001101210	0 ± 0.25
290	synapse associated protein 1	K.SSSRDDNLPLTEAVRPKT*PPVVIK.S(+4)	NP_001004253	0.01 ± 0.27
291	thyroid hormone receptor associated protein 3	K.HGLTHEELKS*PREPGYK.A(+4)	NP_001009693	0.01 ± 0.11
292	paxillin	K.TGSSS*PPGGLSKPGSQLDSMLGSLQSDLNK.L(+3)	NP_001012147	0.01 ± 0.3
293	eukaryotic translation elongation factor 1 delta	K.KGATPAEDDEDNDIDLFGS*DEEEEDKEAAR.L(+4)	NP_001013122	0.01 ± 0.14
294	high-mobility group nucleosome binding domain 1	K.QAEVADQQTTDLPAENGETENQS*PAS*EEEKEAK.S(+3)	NP_001013202	0.01 ± 0.24
295	ankyrin 3, epithelial isoform 2	R.RQS*FTSLALR.K(+2)	NP_001029156	0.01 ± 0.22
296	oxysterol binding protein	K.GDMS*DEDDENEFFDAPEIITMPENLGHK.R(+3)	NP_001102397	0.01 ± 0.29
297	hypothetical protein LOC500552	K.KLQLERPVS*PEAQADLQR.N(+3)	NP_001128101	0.01 ± 0.11
298	leucine rich repeat containing 47	R.RES*GEGEEEVADSAR.L(+2)	NP_001129138	0.01 ± 0.09
299	heterogeneous nuclear ribonucleoprotein U	R.AKS*PQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I(+4)	NP_476480	0.01 ± 0.1
300	numb homolog	R.RTPS*EADRWLEEVSK.S(+3)	NP_579821	0.01 ± 0.07
301	solute carrier family 14 (urea transporter), member 2 isoform 2	K.EMS*DNNRSPLLPEPLSSR.Y(+3)	NP_808877	0.01 ± 0.22
302	zinc finger, CCCH-type with G patch domain	R.ITDVDNGYY*TVK.F(+2)	NP_001009656	0.02 ± 0.13
303	BCL2-associated transcription factor 1	K.LKELFDYS*PPLHK.S(+3)	NP_001041317	0.02 ± 0.12
304	cingulin-like 1	R.NCFPKPCGS*QPNS*PTPEDLAK.T(+3)	NP_001101634	0.02 ± 0.08
305	utrophin	K.NVRPQPPTS*PEGR.T(+3)	NP_037202	0.02 ± 0.03
306	histone deacetylase 2	R.MLPHAPGVQMQAIPEDAVHEDS*GDEDGEDPDKR.I(+4)	NP_445899	0.02 ± 0.13
307	PREDICTED: Beta-2-syntrophin isoform 2	R.GLGPPS*PPAPPRGPAGEASAS*PPVRR.V(+3)	XP_001071043	0.02 ± 0.14
308	PREDICTED: Myocyte-specific enhancer factor 2B	R.NLRTQVPVLGNLAS*SS*RGSAVHPPHR.T(+3)	XP_574970	0.02 ± 0.65
309	LIM domain 7	R.SAS*VNKEPICLTGIMR.R(+3)	NP_001001515	0.03 ± 0.02
310	paxillin	K.T*GSSSPPGGLSKPGSQLDSMLGSLQSDLNK.L(+3)	NP_001012147	0.03 ± 0.31
311	spectrin, beta, non-erythrocytic 1	K.VSEEAESQQWDTSKGDQVSQNGLPAEQGS*PR.M(+3)	NP_001013148	0.03 ± 0.28
312	B-cell linker	R.FTEGGS*PAADGPVPSFPFNSTFADQEAELHGKPWYAGACDR.K(+4)	NP_001020938	0.03 ± 0.14
313	eukaryotic translation initiation factor 3, subunit 9 (eta)	R.AKPAAQSEEETAAS*PAAS*PTPQSAQEPSAPGK.A(+3)	NP_001026810	0.03 ± 0.24
314	myosin, heavy chain 9, non-muscle	K.GTGDCS*DEEVDGKADGADAK.A(+3)	NP_037326	0.03 ± 0.06

315	carnitine palmitoyltransferase 1B	R.SPIM#VDSNY*Y*AMDFVLIKNTSQQAAR.L(+3)	NP_037332	0.03 ± 0.12
316	adducin 1 (alpha)	K.SPPDQSAVPNT*PPS*TPVKLEGGLPQEPTSR.D(+3)	NP_058686	0.03 ± 0.09
317	adducin 1 (alpha)	K.SPPDQSAVPNT*PPST*PVKLEGGLPQEPTSR.D(+3)	NP_058686	0.03 ± 0.09
318	matrin 3	R.RDS*FDDRGPSLNPVLDYDHGSR.S(+4)	NP_062022	0.03 ± 0.09
319	PREDICTED: DNA2 DNA replication helicase 2-like	K.DY*TLIVGM#PGT*GKTTT*ICALVR.I(+3)	XP_001080557	0.03 ± 0.12
320	phosphoprotein enriched in astrocytes 15A	K.YKDIIRQPS*EEEIIK.L(+3)	NP_001013249	0.04 ± 0.14
321	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	R.KSS*FSNSADDIK.S(+2)	NP_001100267	0.04 ± 0.09
322	serine/arginine repetitive matrix 1	R.RLS*PS*ASPPR.R(+2)	NP_001101456	0.04 ± 0.07
323	DNA segment, Chr 4, ERATO Doi 22, expressed isoform 1	R.ILGSAS*PEEEQEKPILDRPTR.I(+3)	NP_001108071	0.04 ± 0.11
324	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	K.ITSVS*TGNLCTEEQT*PPPRPEAYPIPTQTYTR.E(+3)	NP_037349	0.04 ± 0.25
325	PREDICTED: pleckstrin homology domain containing, family A member 6	R.YIDLEPVAPLS*PEELKEK.Q(+3)	XP_001060716	0.04 ± 0.16
326	PREDICTED: PDHE1-A type I isoform 1	R.YHGHS*MSDPGVS*YR.T(+3)	XP_001060860	0.04 ± 0.14
327	tight junction protein 1	K.VQIPVSHPDPDPVS*DNEDDSY*DEDVHDPR.S(+3)	NP_001099736	0.05 ± 0.06
328	serine/arginine repetitive matrix 1	R.RRS*PS*PAPPPPPPPPPR.R(+3)	NP_001101456	0.05 ± 0.09
329	calnexin	K.QKSDAEEDGGTGS*QDEEDSKPKAEEDEILNR.S(+4)	NP_742005	0.05 ± 0.15
330	PREDICTED: TBC1 domain family member 4 (Akt substrate of 160 kDa) (AS160) isoform 1	R.HAS*APSHVQPSDSEK.N(+3)	XP_001074155	0.05 ± 0.09
331	PREDICTED: splicing factor, arginine/serine-rich 1 (ASF/SF2)	R.VKVDGPRS*PS*YGR.S(+3)	XP_001081187	0.05 ± 0.11
332	PREDICTED: tankyrase 1-binding protein of 182 kDa	R.NMAPGAGCS*PGEPR.E(+2)	XP_215763	0.05 ± 0.17
333	PRP4 pre-mRNA processing factor 4 homolog B	K.LCDFGSASHVADNDITPY*LVSR.F(+3)	NP_001011923	0.06 ± 0.08
334	cingulin-like 1	R.S*RSVDSAFPFGLQGNTEYLTEFSR.N(+3)	NP_001101634	0.06 ± 0.38
335	plectin 1	R.SSS*VGSSSSYPISSAVPR.T(+2)	NP_071796	0.06 ± 0.11
336	calpastatin isoform a	K.LLEKNEAITGPLPDS*PKPMGIDHAIDALSSDFTCSS*PTGK.Q(+4)	NP_445747	0.06 ± 0.27
337	hepatoma-derived growth factor-related protein 2	R.KRS*EGLSLDR.K(+3)	NP_598232	0.06 ± 0.1
338	kinesin 13B	R.RRS*SGLQPQGAPEAR.R(+3)	NP_998791	0.06 ± 0.52
339	PREDICTED: hypothetical protein	R.RDT*ATEIQDVGVPR.N(+3)	XP_001077427	0.06 ± 0.07
340	PREDICTED: tensin	R.QGSPT*PALPEKR.R(+3)	XP_237286	0.06 ± 0.12
341	BCL2-associated transcription factor 1	K.KAEGEPQEES*PLKSK.S(+3)	NP_001041317	0.07 ± 0.08
342	tight junction protein 1	K.VQIPVSHPDPDPVS*DNEDDS*YDEDVHDPR.S(+4)	NP_001099736	0.07 ± 0.1
343	NCK adaptor protein 1	K.RKPS*VPDTASPADDSFVDPGER.L(+3)	NP_001100321	0.07 ± 0.09
344	hypothetical protein LOC308341	K.NAKRPT*TQPPGIPIT*KRPR.V(+3)	NP_001128017	0.07 ± 0.15
345	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	K.ITSVST*GNLCTEEQT*PPPRPEAYPIPTQTYTR.E(+3)	NP_037349	0.07 ± 0.24
346	plectin 1	R.SS*SVGSSSSYPISSAVPR.T(+2)	NP_071796	0.07 ± 0.11
347	heat shock protein 1	R.SPS*WEPFRDWYPAHSR.L(+3)	NP_114176	0.07 ± 0.13
348	PREDICTED: vacuolar protein sorting 13B isoform 1	K.CT*CT*IFM#AEFNLLDRLLPVIMGGK.N(+3)	XP_001058951	0.07 ± 0.37
349	ladinin	R.SVERLPS*VEEAEVSKPSPPASKDEGEEFQAILR.T(+4)	NP_001101412	0.08 ± 0.21
350	protein phosphatase 1, regulatory subunit 2	K.IDEPDTPYHNMIGDDEDVCS*DSEGNEVMTPEILAK.K(+3)	NP_620178	0.08 ± 0.09
351	PREDICTED: hypothetical protein isoform 2	K.LGGNEALS*PTS*PSKESRPGEWR.T(+3)	XP_001065403	0.08 ± 0.16
352	PREDICTED: Septin-4 (Peanut-like protein 2) (Brain protein H5)	K.IYQFPDCDS*DEDEDFKLQDQALK.E(+3)	XP_001081164	0.08 ± 0.11
353	spectrin, beta, non-erythrocytic 1	R.T*SSKESS*PVPS*PTSDRK.A(+3)	NP_001013148	0.09 ± 0.15
354	spectrin, beta, non-erythrocytic 1	R.TSS*KES*SPVPS*PTSDRK.A(+3)	NP_001013148	0.09 ± 0.15
355	spectrin, beta, non-erythrocytic 1	R.TSS*KESS*PVPS*PTSDRK.A(+3)	NP_001013148	0.09 ± 0.15
356	catenin (cadherin associated protein), delta 1	R.GSLAS*LDS*LRK.G(+2)	NP_001101210	0.09 ± 0.28
357	PREDICTED: hypothetical protein isoform 2	K.LGGNEALSPT*S*PSKESRPGEWR.T(+3)	XP_001065403	0.09 ± 0.16
358	PREDICTED: Semaphorin-4B precursor (Semaphorin C) (Sema C)	R.VRLGS*EIRDSVV.-(+2)	XP_001065984	0.09 ± 0.23

359	progesterone receptor membrane component 2	R.LLKPGEEPSEYT*DEEDTKDHSKQD.-(+4)	NP_001008375	0.1 ± 0.11
360	protein phosphatase 1, regulatory (inhibitor) subunit 12B	R.RLS*GTSDIEEKENR.E(+3)	NP_001100648	0.1 ± 0.09
361	pinin, desmosome associated protein	R.RGFS*DSGGGPPAK.Q(+2)	NP_001102493	0.1 ± 0.16
362	ATP-binding cassette, sub-family F (GCN20), member 1	K.GAEQGS*EEEKEEKEGEVK.A(+3)	NP_001103353	0.1 ± 0.14
363	phosphatidylethanolamine binding protein	K.VLTPTQVMNRPSS*ISWDGLDPGK.L(+3)	NP_058932	0.1 ± 0.18
364	signal transducer and activator of transcription 1 isoform alpha	R.LQSTENLLPMS*PEEFDEMSK.I(+2)	NP_116001	0.1 ± 0.24
365	zyxin	R.S*PGGPGPLTLK.E(+2)	NP_446213	0.1 ± 0.43
366	protein phosphatase 1, regulatory (inhibitor) subunit 12A	R.RLGS*TSDIEEKENR.E(+3)	NP_446342	0.1 ± 0.09
367	phosphoribosyl pyrophosphate synthetase-associated protein 2	R.LGIAVIHGEAQDAESDLVDGRHS*PPMVR.S(+4)	NP_476472	0.1 ± 0.07
368	PREDICTED: Secretory carrier-associated membrane protein 3	R.EPPPAY*EPPAPAPAPLPPPS*APS*VQSS*RK.L(+3)	XP_342280	0.1 ± 0.19
369	solute carrier family 14 (urea transporter), member 2 isoform 2	K.LYESELS*SPTWPSSSQDTHPALPLLEMPEEK.D(+3)	NP_808877	0.11 ± 0.24
370	BTB (POZ) domain containing 7	R.EILS*SLLPFVRIEHILPMNS*EVLSDAM#KR.G(+3)	NP_001102190	0.11 ± 0.33
371	BTB (POZ) domain containing 7	R.EILSS*LLPFVRIEHILPMNS*EVLSDAM#KR.G(+3)	NP_001102190	0.11 ± 0.33
372	myosin, heavy chain 9, non-muscle	R.KGTGDCS*DEEVDGKADGADAK.A(+3)	NP_037326	0.11 ± 0.07
373	heterogeneous nuclear ribonucleoprotein A1	K.SES*PKEPEQLR.K(+2)	NP_058944	0.11 ± 0.32
374	heterogeneous nuclear ribonucleoprotein D isoform a	K.IDASKNEEDEGHSNSS*PR.H(+3)	NP_077380	0.11 ± 0.23
375	PREDICTED: PDHE1-A type I isoform 1	R.YHGHS*M#SDPGVSYR.T(+3)	XP_001060860	0.11 ± 0.17
376	related RAS viral (r-ras) oncogene homolog 2	R.KFQEQECPPS*PEPTRK.E(+3)	NP_001013452	0.12 ± 0.06
377	BCL2-associated transcription factor 1	K.GRTDGDWDDQEVLDYFS*DKESAK.Q(+3)	NP_001041317	0.12 ± 0.13
378	eukaryotic translation elongation factor 1 beta 2	K.YGPVSVADTTGSGAADAKDDDDIDLFGS*DDEEESEDAKR.L(+4)	NP_001102269	0.12 ± 0.17
379	hypothetical protein LOC500552	K.ASSLAASESPGNALPTGAPETEPRS*PQS*PASK.A(+3)	NP_001128101	0.12 ± 0.13
380	mitogen activated protein kinase 3	R.IADPEHDHTGFLT*EYVATR.W(+3)	NP_059043	0.12 ± 0.06
381	mitogen activated protein kinase 3	R.IADPEHDHTGFLTEY*VATR.W(+3)	NP_059043	0.12 ± 0.06
382	cortactin isoform B	R.AKKQT*PPAS*PSPQPAEDRPPSS*PIYEDAAPLK.A(+4)	NP_068640	0.12 ± 0.17
383	cortactin isoform B	R.AKKQT*PPAS*PSPQPAEDRPPSSPIY*EDAAPLK.A(+4)	NP_068640	0.12 ± 0.17
384	cysteine string protein	R.S*LSTSGESLYHVLGLDK.N(+2)	NP_077075	0.12 ± 0.2
385	heterogeneous nuclear ribonucleoprotein D isoform a	K.IDASKNEEDEGHSNS*SPR.H(+3)	NP_077380	0.12 ± 0.23
386	spectrin, beta, non-erythrocytic 1	R.TSS*KESSPVPS*PTSDRK.A(+3)	NP_001013148	0.13 ± 0.22
387	histone deacetylase 1	R.MLPHAPGVQMQAIPEDAIPEES*GDEDEEDPDKR.I(+3)	NP_001020580	0.13 ± 0.14
388	coiled-coil domain containing 43	K.AALLAQYADVT*DEEDEADEKADPGASTANIGSDK.S(+3)	NP_001094198	0.13 ± 0.15
389	tight junction protein 1	K.KVQIPVSHPDPDPVS*DNEDDS*YDEDVHDPR.S(+4)	NP_001099736	0.13 ± 0.11
390	tight junction protein 1	K.KVQIPVSHPDPDPVS*DNEDDSY*DEDVHDPR.S(+4)	NP_001099736	0.13 ± 0.11
391	Cdc42-binding protein kinase beta	K.HSTPSNSSNPSGPPS*PNS*PHR.S(+3)	NP_446072	0.13 ± 0.33
392	heterogeneous nuclear ribonucleoprotein K	K.IIPTLEEGLQLPS*PTATSQLPLESDAVECLNYQHYK.G(+3)	NP_476482	0.13 ± 0.11
393	PREDICTED: FCH domain only 2	K.LSGINEIPRPFS*PPITS*NTSPPPTAPLAR.A(+3)	XP_219503	0.13 ± 0.13
394	PREDICTED: Apoptotic chromatin condensation inducer in the nucleus (Acinus)	K.SSSFSEEKGES*DDEKPR.K(+3)	XP_240178	0.13 ± 0.08
395	RNA binding motif protein 17	R.RPDPDS*DEDEDYERER.R(+3)	NP_001013076	0.14 ± 0.14
396	chordin-like 2	R.HFQAIGMGGT*TIKIILK.E(+2)	NP_001101007	0.14 ± 0.66
397	receptor (chemosensory) transporter protein 4	R.SPSPSPSPSPKSHS*SSPS*R.S(+3)	NP_001101791	0.14 ± 0.25
398	aquaporin 2 (collecting duct)	R.RQS*VELHSPQSLPR.G(+3)	NP_037041	0.14 ± 0.35
399	PREDICTED: caspase recruitment domain family, member 14	R.LQGATLDDTDT*DLEFEMLDGADLS*QT*EDSLQGSSR.S(+4)	XP_001081765	0.14 ± 0.12
400	PREDICTED: FCH domain only 2	K.LSGINEIPRPFS*PPITSNTS*PPPTAPLAR.A(+3)	XP_219503	0.14 ± 0.13
401	nucleosome assembly protein 1-like 4	R.EFITGDVEPTDAESAWHS*ENEEDDKLAGDMK.N(+3)	NP_001012170	0.15 ± 0.16

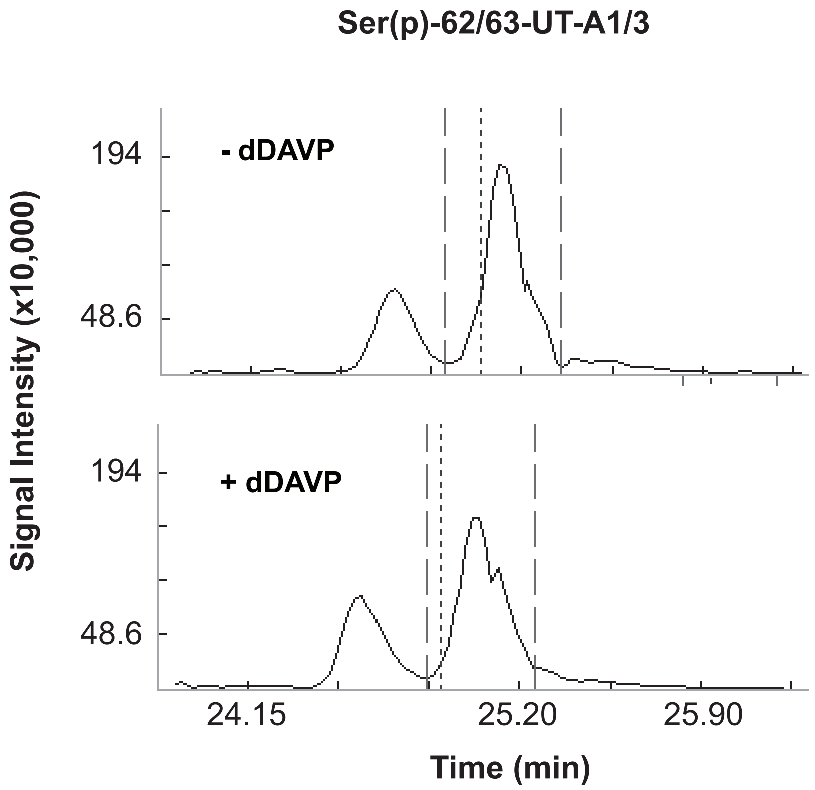
402	aquaporin 4 isoform 1	K.GSYMEVEDNRS*QVETEDLILKPGVVHVIDIDRGDEK.K(+4)	NP_036957	0.15 ± 0.12
403	PREDICTED: serine/arginine repetitive matrix 2	R.S*RTPPSAPSQSR.M(+3)	XP_001056343	0.15 ± 0.19
404	actin-binding LIM protein 1	K.LRPT*RTSSESIYSRPGSSIPGS*PGHTIYAK.V(+4)	NP_001037859	0.16 ± 0.17
405	death-associated protein	K.DKDDQEWESTS*PPKPTVYISGVIAR.G(+3)	NP_071971	0.16 ± 0.15
406	calpastatin isoform a	K.NEAITGPLPDS*PKPMGIDHAIDALSSDFTCSS*PTGK.Q(+4)	NP_445747	0.16 ± 0.43
407	PREDICTED: PDHE1-A type I isoform 1	R.YHGHSMS*DPGVSYR.T(+3)	XP_001060860	0.16 ± 0.08
408	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	R.NRS*NS*FSDEREFSAPST*PTGTLEFAGGEGK.G(+3)	XP_001078032	0.16 ± 0.33
409	PREDICTED: Epithelial protein lost in neoplasm (mEPLIN)	K.DLWASKGENEETLGRPAQPPSAGETPHS*PGVEDAPIAK.V(+4)	XP_217039	0.16 ± 0.3
410	hypothetical protein LOC296179	K.NSKEPVIEDILNLESSSTSSGS*PVS*PGLYSK.T(+3)	NP_001099985	0.18 ± 0.47
411	hypothetical protein LOC300783	K.RPLFLAPDFDRWLDES*DAEMELR.A(+4)	NP_001100301	0.18 ± 0.36
412	hypothetical protein LOC500552	R.LKASSLAASESPGNALPTGAPETEPRS*PQS*PASK.A(+3)	NP_001128101	0.18 ± 0.32
413	cortactin isoform B	K.KQT*PPAS*PSPQPAEDRPPSS*PIYEDAAPLK.A(+4)	NP_068640	0.18 ± 0.3
414	heterogeneous nuclear ribonucleoprotein D isoform a	K.IDASKNEEDEGHSNS*S*PR.H(+3)	NP_077380	0.18 ± 0.43
415	PREDICTED: THUMP domain containing 1	K.FIDKDQQPS*GS*EGEDDDAEAALKK.E(+3)	XP_001079074	0.18 ± 0.19
416	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	R.KHS*PS*PPPPTATESR.K(+3)	NP_001100331	0.19 ± 0.13
417	heat shock protein 1	R.SPS*WEPFRDWYPAHSR.L(+2)	NP_114176	0.19 ± 1.35
418	PREDICTED: serine/arginine repetitive matrix 2	R.RQPS*PQPS*PRDQQSSER.V(+3)	XP_001056343	0.19 ± 0.27
419	Rho GTPase activating protein 1	K.SSS*PEPVTHLKWDDPYYDIAR.H(+3)	NP_001101217	0.2 ± 0.46
420	peroxisome biogenesis factor 1	K.EQGRT*VFVLSPILLQK.I(+2)	NP_001102690	0.2 ± 0.59
421	PC4 and SFRS1 interacting protein 1	K.NLAKPGVT*S*TSDSEEDDDQEGEKKR.K(+3)	NP_786941	0.22 ± 0.27
422	PC4 and SFRS1 interacting protein 1	K.NLAKPGVTS*T*SDSEEDDDQEGEKKR.K(+3)	NP_786941	0.22 ± 0.27
423	serine/arginine repetitive matrix 1	R.RYS*PS*PPPK.R(+2)	NP_001101456	0.23 ± 0.15
424	eukaryotic translation elongation factor 1 beta 2	K.YGPVSVADTTGSGAADAKDDDDIDLFGS*DDEEESEDAKR.L(+3)	NP_001102269	0.23 ± 0.26
425	cysteine string protein	R.SLS*TSGESLYHVLGLDK.N(+2)	NP_077075	0.23 ± 0.16
426	coiled-coil domain containing 105	K.FNQEM#Y*VTRGLIK.G(+3)	NP_001020945	0.24 ± 0.26
427	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	R.LGAPENSGIST*LER.G(+2)	NP_001100757	0.24 ± 0.22
428	myosin light chain, regulatory B	R.ATS*NVFAMFDQSQIQEFKEAFNMIDQNR.D(+3)	NP_059039	0.24 ± 0.44
429	phosphatidylinositol 4-kinase type 2 alpha	R.VAAAGS*GPSPPCS*PGHDRER.Q(+3)	NP_446187	0.24 ± 0.16
430	phosphatidylinositol 4-kinase type 2 alpha	R.VAAAGSGPS*PPCS*PGHDRER.Q(+3)	NP_446187	0.24 ± 0.16
431	myosin phosphatase-Rho interacting protein isoform 1	R.MDIDRS*PGLLGTPDLK.T(+3)	NP_446266	0.24 ± 0.12
432	estrogen receptor binding site associated, antigen, 9	R.KLS*GDQITLPTTVDYSSVPK.Q(+2)	NP_001009665	0.25 ± 0.2
433	olfactory receptor Olr611	R.LIS*S*K.L(+1)	NP_001000926	0.26 ± 0.35
434	catenin (cadherin associated protein), delta 1	R.FHPEPYGLEDDQRS*MGYDDLDYGMMSDYGTAR.R(+4)	NP_001101210	0.26 ± 0.15
435	myosin light chain, regulatory B	R.AT*SNVFAMFDQSQIQEFK.E(+3)	NP_059039	0.26 ± 0.34
436	myosin light chain, regulatory B	R.ATS*NVFAMFDQSQIQEFK.E(+3)	NP_059039	0.26 ± 0.34
437	myosin light chain, regulatory B	R.AT*SNVFAMFDQSQIQEFK.E(+2)	NP_059039	0.27 ± 0.25
438	myosin light chain, regulatory B	R.ATS*NVFAMFDQSQIQEFK.E(+2)	NP_059039	0.27 ± 0.25
439	hypothetical protein LOC296179	K.NSKEPVIEDILNLESSSTSSGSPVS*PGLYSK.T(+3)	NP_001099985	0.28 ± 0.16
440	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	R.KSSFS*NSADDIKSK.K(+3)	NP_001100267	0.28 ± 0.73
441	high mobility group AT-hook 1	K.KLEKEEEEGISQES*S*EEEQ.-(+3)	NP_647543	0.28 ± 0.33
442	PREDICTED: tankyrase 1-binding protein of 182 kDa	R.ASRVPS*S*DEEVVEEPQSR.R(+3)	XP_215763	0.28 ± 0.33
443	cortactin isoform B	K.KQT*PPAS*PSPQPAEDRPPS*SPIYEDAAPLK.A(+3)	NP_068640	0.29 ± 0.27
444	nuclear casein kinase and cyclin-dependent kinase substrate 1	K.VVDYSQFQES*DDADEDYGRDSGPPAKK.I(+3)	NP_073636	0.29 ± 0.37
445	nuclear casein kinase and cyclin-dependent kinase substrate 1	R.KVVDYSQFQES*DDADEDYGRDSGPPAK.K(+3)	NP_073636	0.29 ± 0.37

446	Structure specific recognition protein 1	R.GLKEGINPGYDDYADS*DEDQHDAYLER.M(+4)	NP_112383	0.29 ± 0.86
447	solute carrier family 14 (urea transporter), member 2 isoform 2	R.YKLYESELSS*PTWPSSSQDTHPALPLLEMPEEKDLR.S(+4)	NP_808877	0.29 ± 0.67
448	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	K.GDVDVSIPNVEGDLQGPS*LDIKSPK.L(+3)	XP_001078032	0.29 ± 0.42
449	PREDICTED: SH2 domain binding protein 1 (tetratricopeptide repeat containing)	R.RRPPKGEEGS*DDDETENGPKPK.K(+4)	XP_238127	0.29 ± 0.14
450	PREDICTED: E3 ubiquitin-protein ligase NEDD4-like protein (Nedd4-2) (NEDD4.2)	R.S*LSSPTVTLSAPLEGAK.D(+2)	XP_574161	0.3 ± 0.09
451	PREDICTED: E3 ubiquitin-protein ligase NEDD4-like protein (Nedd4-2) (NEDD4.2)	R.SLS*SPTVTLSAPLEGAK.D(+2)	XP_574161	0.3 ± 0.09
452	hypothetical protein LOC300783	K.RPLFLAPDFDRWLDES*DAEMELR.A(+3)	NP_001100301	0.31 ± 0.21
453	aquaporin 1	K.VWTSGQVEEYDLDADDINS*RVEMKPK.-(+4)	NP_036910	0.31 ± 0.38
454	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	R.SNS*FSDEREFSAPSTPTGTLEFAGGEGK.G(+3)	XP_001078032	0.31 ± 0.11
455	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	R.SNSFS*DEREFSAPSTPTGTLEFAGGEGK.G(+3)	XP_001078032	0.31 ± 0.11
456	catenin (cadherin associated protein), delta 1	R.FHPEPYGLEDDQRSMGY*DDLDYGMMSDYGTAR.R(+4)	NP_001101210	0.32 ± 0.14
457	PREDICTED: AHNAK nucleoprotein isoform 1 isoform 1	R.S*NSFSDEREFSAPSTPTGTLEFAGGEGK.G(+3)	XP_001078032	0.32 ± 0.11
458	PREDICTED: pleckstrin homology domain containing, family G, member 3	R.RPS*DRS*PTSVEKR.M(+3)	XP_001080822	0.32 ± 0.27
459	PCTAIRE protein kinase 3	R.RLS*LSVPRPETIEESLTEFTEQFNQLHTQR.N(+4)	NP_001093976	0.33 ± 0.33
460	hippocalcin	K.QNS*KLRPEM#LQDLR.E(+2)	NP_058818	0.33 ± 0.15
461	dyskeratosis congenita 1, dyskerin	R.KRDS*DS*DADEATPTTTPR.V(+3)	NP_596910	0.33 ± 0.24
462	PREDICTED: heterogeneous nuclear ribonucleoprotein U isoform a	R.S*KSPPPPEEEAKDEEEDQTLVNLDTYTSDLHFQISK.D(+4)	XP_001073417	0.34 ± 0.26
463	complement receptor related protein isoform 1	K.EDSCVQPQSLLTSQENNSTSSPARNSLT*QEV.-(+3)	NP_001005330	0.35 ± 0.17
464	PREDICTED: nuclear mitotic apparatus protein 1	R.AAQLQGS*PAPEKGEVLGDALQLDTLKQEAAK.L(+3)	XP_218972	0.35 ± 0.23
465	myosin, heavy chain 9, non-muscle	R.KGT*GDCS*DEEVDGKADGADAK.A(+3)	NP_037326	0.37 ± 0.12
466	MYST histone acetyltransferase (monocytic leukemia) 3	K.QS*T*VS*K.G(+1)	NP_001094040	0.38 ± 0.43
467	splicing factor, arginine/serine-rich 10	R.RRS*PS*PYYSR.G(+3)	NP_476460	0.38 ± 0.25
468	phosphofructokinase, liver	R.RTLS*IDKGF.-(+2)	NP_037322	0.39 ± 0.18
469	phosphofructokinase, liver	R.TLS*IDKGF.-(+2)	NP_037322	0.39 ± 0.09
470	solute carrier family 14 (urea transporter), member 2 isoform 2	K.LYESELSSPT*WPSSSQDTHPALPLLEMPEEKDLR.S(+4)	NP_808877	0.39 ± 0.25
471	aquaporin 1	K.VWTSGQVEEYDLDADDINS*RVEMKPK.-(+3)	NP_036910	0.4 ± 0.31
472	tight junction protein 2	R.LYQDTRGS*YGS*DPEEEEEYRQQLAAHSK.R(+4)	NP_446225	0.4 ± 0.16
473	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	K.SGVDFGSLLKKENEEAEPS*PVPGT*PTLR.N(+3)	NP_596902	0.4 ± 0.88
474	PREDICTED: topoisomerase (DNA) II beta	K.KT*SFDQDS*DVDIFPSDFTSEPPALPR.T(+3)	XP_001067768	0.4 ± 0.17
475	PREDICTED: heterogeneous nuclear ribonucleoprotein U isoform a	R.SKS*PPPPEEEAKDEEEDQTLVNLDTYTSDLHFQISK.D(+4)	XP_001073417	0.4 ± 0.28
476	PCTAIRE protein kinase 3	K.RLS*LPMDIR.L(+2)	NP_001093976	0.41 ± 0.14
477	oxysterol binding protein	K.MLAES*DES*GDEESVSQTDKTELQNTLR.T(+3)	NP_001102397	0.44 ± 0.36
478	aquaporin 2 (collecting duct)	R.RQSVELHS*PQS*LPR.G(+4)	NP_037041	0.44 ± 0.18
479	nuclear casein kinase and cyclin-dependent kinase substrate 1	K.NSQEDS*EDS*EEKDVK.T(+2)	NP_073636	0.44 ± 0.45
480	nuclear casein kinase and cyclin-dependent kinase substrate 1	K.NSQEDS*EDS*EEKDVK.T(+3)	NP_073636	0.5 ± 0.52
481	catenin (cadherin associated protein), delta 1	R.FHPEPYGLEDDQRS*MGYDDLDYGMMSDYGTAR.R(+3)	NP_001101210	0.52 ± 0.16
482	aquaporin 2 (collecting duct)	R.RQS*VELHS*PQSLPR.G(+3)	NP_037041	0.55 ± 0.06
483	mitogen activated protein kinase 1	R.VADPDHDHTGFLT*EY*VATR.W(+3)	NP_446294	0.58 ± 0.07



Ser(p)-10-UT-A1/3

Supplementary Figure 1: Reconstructed ion chromatograms for a UT-A1/3 phosphopeptide with the Ser-10 residue phosphorylated. There is no change in abundance in the presence of dDAVP.



Supplementary Figure 2: Reconstructed ion chromatograms for a UT-A1/3 phosphopeptide with *both* Ser-62 *and* Ser-63 phosphorylated. There is no change in abundance in the presence of dDAVP.