

**Table: Akt Substrate Motif PhosphoScan® Final Results, SILAC**

**Study Design: Human squamous cell carcinoma (H1703) cell line; LysC/post-IAP trypsin Digest; Antibody: Akt Substrate Motif, RXXS\*/T\*; CST #1978, 5561**

**Treatments: Untreated (Heavy), Wortmannin (Light)**

Index	Fold Change (Wortmannin / Untreated)	Protein Name	Description	Phosphorylation Site	Peptide	Accession	kD	Count in Study	Intensity
1		<b>Adaptor/scaffold</b>							
2	1.0	AHNAK	AHNAK nucleoprotein isoform 1	\$210	TVIRLPSG*GSGAASPTGSVAVDIRAGAIASGPELQAGHSHK	Q09666	629	1	2.59E+06
3	1.0	AHNAK	AHNAK nucleoprotein isoform 1	\$212	TVIRLPSGS*GAASPTGSVAVDIRAGAIASGPELQAGHSHK	Q09666	629	1	2.88E+06
4	-1.2	AHNAK	AHNAK nucleoprotein isoform 1	\$5780	S*NSFSDEREFSGPSTPTGTLEFEGEVSLGGK	Q09666	629	2	1.11E+06
5	-1.3	AHNAK	AHNAK nucleoprotein isoform 1	\$5782	HRSNS*FSDEREFSGPSTPTGTLEFEGEVSLGGK	Q09666	629	2	2.97E+06
6	-1.0	AKAP12	A kinase (PRKA) anchor protein 12 isoform 1	\$627	RVRRPS*ESDKDELDK	Q02952	191	3	5.82E+06
7	-1.0	AKAP12	A kinase (PRKA) anchor protein 12 isoform 1	\$629	RVRRPSES*DKEDELDK	Q02952	191	1	1.12E+06
9	1.0	FRS2	fibroblast growth factor receptor substrate 2	503	TRHNS*TDLPM	Q8WU20	57	1	4.89E+06
10	1.3	LMO7; LMO7 iso2; LMO7 iso3	LIM domain only 7	\$805; \$805; \$471	RM#YS*FDDVLEEGK	Q8WW11; Q8WW11-2; Q8WW11-3	193; 191; 154	1	6.48E+05
11	12.5	PACS-1	phosphofurin acidic cluster sorting protein 1	320, 321, 322	TRRKLTS*T*S*AIRQPNIK	Q6VY07	105	1	9.33E+05
12	-1.3	liprin beta 1; liprin beta 1 iso2	PTPRF interacting protein binding protein 1 isoform 1	\$601; \$595	LRRSQS*TFNPDDMSEPEFK	Q86W92; Q86W92-2	114; 113	8	4.51E+06
13	-4.6	Rictor	rapamycin-insensitive companion of mTOR	1135	IRTLT*EPSVDFNHSDDFPISTVQK	Q6R327	192	1	1.30E+06
14	-1.2	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1 isoform a	\$212, \$214	KRKLS*SS*EPYEEDEFNDQSIK	Q9H4L7	117	1	2.70E+05
15	-2.2	tensin 3	tensin 3	\$776	KLS*LGQYDNDAGGLPFPSK	Q68C22	155	1	3.89E+05
16		<b>Adhesion or extracellular matrix protein</b>							
17	-8.1	atadin iso3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 isoform 2	\$1718	LFS*QGQDVSNKVK	P55196-3	198	2	7.01E+05
18		<b>Apoptosis</b>							
19	-5.8	Akt1S1	AKT1 substrate 1 (proline-rich)	\$246	ALVLRFAEDTQVFGDLPRPLNT*SDFQK	Q96B36	27	6	1.24E+07
20	1.0	PEA-15	phosphoprotein enriched in astrocytes 15	\$116	DIROPS*EEIIKLAPPKKA	Q15121	15	6	9.67E+06
21		<b>Cell cycle regulation</b>							
22	-1.4	KAB1	centrosomal protein 170kDa isoform beta	1205	ANS*ISRLSDSK	Q5SW79	175	1	1.11E+06
23	1.3	CLASP1; CLASP1 iso3	CLIP-associating protein 1	\$646; \$646	RQS*SGSATNAVSTPNRGR	Q7Z460; Q7Z460-3	169; 165	3	1.20E+05
24	1.9	SPECC1L	SPECC1-like	\$832	RSS*TSSEPTPTVK	Q69YQ0	125	2	6.12E+05
25		<b>Cell development/differentiation</b>							
26	-1.0	NDRG3	N-myc downstream-regulated gene 3 isoform b	\$329, \$335	SRT*HSTSSS*LGSGESPFSR	Q9UGV2	41	1	4.24E+05
27	1.1	NDRG3	N-myc downstream-regulated gene 3 isoform b	\$331	SRTHS*TSSSLGSGESPFSR	Q9UGV2	41	2	2.04E+06
28	-1.0	NDRG3	N-myc downstream-regulated gene 3 isoform b	\$332, \$334, \$335	SRHST*SS*S*LGSGESPFSR	Q9UGV2	41	1	3.29E+05
29		<b>Chaperone</b>							
30	1.5	SGTA	small glutamine-rich tetra-ricopeptide	\$305	SRTPS*ASNDQQE	Q43765	34	4	2.51E+04
31		<b>Chromatin, DNA-binding, DNA repair or DNA replication protein</b>							
32	-1.3	MLH1	MutL protein homolog 1	\$477	RHREDS*DVEM#VEDDSRK	P40692	85	2	1.02E+06
33	-1.1	APRIN	PDS5, regulator of cohesion maintenance, homolog B	\$1213, \$1218	GRLDSS*EMDHS*ENEDYTM#SSPLPGK	Q9NTI5	168	2	3.20E+05
34	-1.5	Rif1	RAP1 interacting factor 1	\$1422	RRS*EVVESTTESQDK	Q5UIP0	274	1	7.38E+04
36	-2.2	ZNF185; ZNF185 iso1	zinc finger protein 185	153; 18	LAPYNIRRS*TSGDTEEEEEEEVVPFSSDEQK	NP_009081; O15231	74; 49	2	1.13E+06
37	-1.4	ZNF185; ZNF185 iso1	zinc finger protein 185	153, 155; 18, 20	RSS*TS*GDTEEEEEEEVVPFSSDEQK	NP_009081; O15231	74; 49	1	1.47E+06
38	-1.2	ZNF185; ZNF185 iso1	zinc finger protein 185	155; 20	RSSTS*GDTEEEEEEEVVPFSSDEQK	NP_009081; O15231	74; 49	1	5.85E+05
40		<b>Cytoskeletal protein</b>							
41	-1.0	DBNL; DBNL iso2	drebrin-like isoform b	\$269; \$270	ERAMS*TTSSISPPQPGK	Q9UJU6; Q9UJU6-2	48; 48	4	9.33E+06
42	-1.3	DBNL; DBNL iso2	drebrin-like isoform b	\$269, \$275; \$270, \$276	ERAMS*TTSSISS*PQPGK	Q9UJU6; Q9UJU6-2	48; 48	3	8.55E+06
43	-1.5	KIF23; KIF23 iso2	kinesin family member 23 isoform 2	\$911; \$807	RRS*STVAPAQDGAESEWTVETR	Q02241; Q02241-2	110; 98	2	8.50E+05
46	-1.5	PSRC2; PSRC2 iso5	proline/serine-rich coiled-coil 2	\$1046; \$1055	RRS*FLESNYFTKPNLK	Q60293; BAA25472	226; 218	1	2.58E+06
47	-1.5	PSRC2; PSRC2 iso5	proline/serine-rich coiled-coil 2	\$352; \$361	RIS*TSILSEK	Q60293; BAA25472	226; 218	1	1.83E+06
48		<b>Enzyme, misc.</b>							
50	-1.3	PICH	excision repair protein ERCC6-like	\$1028	IVS*DGEDDDSKFDTSSINPFTSLFQFSSVK	Q2NKX8	141	1	3.16E+05
51	1.2	GFAT; GFAT iso2	glucosamine-fructose-6-phosphate aminotransferase	\$260; \$243	KGSCNLSRVDST*TCCLFPVEEK	Q06210; Q06210-2	79; 77	4	5.89E+07
52	1.2	GFAT; GFAT iso2	glucosamine-fructose-6-phosphate aminotransferase	\$261; \$244	KGSCNLSRVDST*TCCLFPVEEK	Q06210; Q06210-2	79; 77	1	4.67E+06

LEGEND: \$ = published site; \* = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

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Index	Fold Change (Wortmannin / Untreated)	Protein Name	Description	Phosphorylation Site	Peptide	Accession	kD	Count in Study	Intensity
53		<b>G protein or regulator</b>							
56	-1.5	GARNL1	GTPase activating Rap/RanGAP domain-like 1 isoform 1	\$754	SIVRQKT*VDIDDAQLPR	Q66YQ0	230	1	3.30E+05
57	-1.3	GARNL1	GTPase activating Rap/RanGAP domain-like 1 isoform 1	\$773	VRHFS*QSEETGNEVFGALNEEQPLPR	Q66YQ0	230	1	6.37E+05
58	-1.3	GARNL1	GTPase activating Rap/RanGAP domain-like 1 isoform 1	\$797	SSS*TSDILEPFTVERAK	Q66YQ0	230	1	1.30E+06
59	-1.2	RALBP1	ralA binding protein 1	\$28	RVEHGSLTRTPS*SEEIPTK	Q15311	76	1	4.55E+05
60	-1.2	RapGEF6	PDZ domain-containing guanine nucleotide exchange factor I	\$1094	RSS*LLNAK	Q8TEU7	179	1	8.95E+05
61	1.2	RIN2	Ras and Rab interactor 2	332, 337	LARTETQT*SMPET*VNHNK	Q8WYP3	100	1	1.29E+05
62	-3.4	TBC1D4	TBC1 domain family, member 4	\$318	CSS*VTGVQR	Q60343	147	1	7.73E+05
63	-2.2	TBC1D4; TBC1D4 iso3	TBC1 domain family, member 4	\$642; \$154	AHT*FSHPPSSTK	Q60343; Q5JU47	147; 31	3	2.56E+06
64	-2.2	tuberin; tuberin iso3	tuberous sclerosis 2 isoform 1	\$1798; \$1754	RLIS*SVEDTFEV	P49815; P49815-3	201; 196	1	5.90E+05
67		<b>Phosphatase</b>							
68	-1.6	CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	\$104	VRRKS*QVNGEAGSYEMTNOQHVK	Q8IY19	53	5	1.25E+07
69	-1.3	MYPT1	protein phosphatase 1, regulatory (inhibitor) subunit 12A	\$507	RLAS*TSDIIEK	Q14974	115	2	1.55E+06
71	-1.1	MYPT1	protein phosphatase 1, regulatory (inhibitor) subunit 12A	\$696	RST*QGVTLTLDQEAEK	Q14974	115	1	3.72E+05
72	-1.3	SSH3	slingshot homolog 3	\$649, \$653	VVRQAS*VHDS*GEEGEA	Q8TE77	73	1	3.42E+05
73		<b>Protein kinase, Ser/Thr (non-receptor)</b>							
75	1.2	AAK1	AP2 associated kinase 1	\$637	RILS*DVTHSAVGVPAK	Q2M218	94	3	2.97E+06
76	-3.9	GSK3A	glycogen synthase kinase 3 alpha	\$21	ARTSS*FAEPGGGGGGGGPGGSASGPGGTGGGK	P49840	51	2	1.93E+06
78	1.3	PKAc; PKAc iso2; PKAcB; PKAcG	cAMP-dependent protein kinase catalytic subunit alpha isoform 1	\$197; \$190; \$197; \$197	GRTWT*LCGTPEYLPAEILSK	P17612; P17612-2; P22694; P22612	40; 40; 40; 40	2	2.53E+06
79	-3.4	Trío	triple functional domain (PTPRF interacting)	1726, 1727	RLS*S*GKADGHVK	Q75962	342	1	7.26E+04
80		<b>Protein kinase, Tyr (receptor)</b>							
81	3.8	ROS	proto-oncogene c-ros-1 protein precursor	1273, 1274	NS*T*ISFSVYPLLSR	P08922	264	1	2.44E+06
82		<b>Protein kinase, atypical</b>							
83	-1.1	TIF1-gamma	tripartite motif-containing 33 protein isoform alpha	\$1119	LKS*DERPVHIK	Q9UPN9	123	1	1.49E+06
84	1.1	ChaK1	transient receptor potential cation channel, subfamily M, member 7	\$1505	ISRRPST*EDTHEVDSK	Q96QT4	213	1	2.60E+05
85		<b>Protein kinase, regulatory subunit</b>							
86	-1.2	Dbf4	activator of S phase kinase	\$273	LRIQT*DGDK	Q9UBU7	77	1	2.71E+06
87		<b>RNA processing</b>							
88	-2.5	EDC3	enhancer of mRNA decapping 3	\$161	HNS*WSSSRHPNQATPK	Q96F86	56	2	5.63E+05
90	-1.7	LARP5	La ribonucleoprotein domain family, member 5	731, \$736	RLSREQS*TPPKS*PQ	Q92615	81	2	2.45E+06
93	1.3	SRm160; SRm160 iso3	serine/arginine repetitive matrix 1	\$748, \$752, \$756; \$757, \$761, \$765	RVS*SSRS*VSGS*PEPAAK	Q8IYB3; A921X7	102; 103	1	1.27E+05
94		<b>Receptor, channel, transporter or cell surface protein</b>							
96	-1.0	HSPC274	hypothetical protein LOC29058 isoform 1	\$24	YSRLSS*TDGYIDLQFKK	Q96A57	13	1	1.01E+06
98	-6.5	MICB	MHC class I polypeptide-related sequence B	99, 101, 112	RT*LT*HIKDKGGLHS*LQEIR	Q29980	43	1	4.25E+05
99	-1.3	RELL1	receptor expressed in lymphoid tissues like 1	268	SLM#SVSGAETVNGEVPATPKRERS*GTE	Q8IUW5	29	1	3.82E+05
100	-1.3	RELL1	receptor expressed in lymphoid tissues like 1	270	SLMSVSGAETVNGEVPATPKRERSGT*E	Q8IUW5	29	2	5.91E+05
101	-3.5	SEMA4B	semaphorin 4B precursor	\$825	VRLGS*EIRDVV	Q9NPR2	92	1	2.09E+07
102	1.3	SLC4A7; SLC4A7 iso3	solute carrier family 4, sodium bicarbonate cotransporter, member 7	\$403, \$407; \$189, \$193	SGEIKNGSGGS*RENS*TVDFSK	Q9Y6M7; Q9Y6M7-3	136; 114	1	2.80E+05
103		<b>Transcriptional regulator</b>							
104	1.2	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	\$17	NRTPS*DVKELVDNSR	P39687	29	1	1.32E+06
106	-1.4	BRCA1	breast cancer 1, early onset isoform 1	\$509	RRPT*SGLHPEDFIK	P38398	208	1	6.16E+06
107	-1.7	FLNA	filamin A, alpha isoform 2	\$2152	RAPS*VANVGSCHDLCLK	P21333	281	9	3.33E+07
108	-1.7	FRYL	furry-like	\$1959	RSNT*LDIM#DGRINHSSSLAR	Q94915	340	3	7.90E+05
109	-1.2	PNN	pinin, desmosome associated protein	\$95, \$99	TRRES*ROES*DPEDDDVK	Q9H307	81	3	3.48E+05
110	-1.7	HBXAP	remodeling and spacing factor 1	\$1295	LHRIET*DEEESCDNAHGDNQPARDSPR	Q96T23	161	5	9.84E+05
111	-1.0	PC4	activated RNA polymerase II transcription cofactor 4	\$49	TGETSRALS*SSK	P53999	14	1	4.97E+04
112	-1.9	TCF12	transcription factor 12 isoform b	558	GRTS*STNEDEDLNPEQKIEREK	Q99081	73	1	2.69E+05
113	-2.4	TCF12	transcription factor 12 isoform b	\$560	VSSRGRTSST*NEDEDLNPEQKIEREK	Q99081	73	1	2.70E+05
114	-1.1	treacle; treacle iso2	Treacher Collins-Franceschetti syndrome 1 isoform b	\$1350; \$1312	KLS*GDQPAAR	Q13428; A0JLU0	152; 144	4	2.91E+04

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Index	Fold Change (Wortmannin / Untreated)	Protein Name	Description	Phosphorylation Site	Peptide	Accession	kD	Count in Study	Intensity
115	-1.4	TAZ	WW domain containing transcription regulator 1	58, 66, 69	KILPESFFKEPDS*GSHSRQSS*TDSSGGHPGPR	Q9GZV5	44	1	8.01E+05
116	-1.4	TAZ	WW domain containing transcription regulator 1	60, 67, 69	KILPESFFKEPDSGS*HSRQSS*TDSSGGHPGPR	Q9GZV5	44	1	1.77E+06
117	1.0	TAZ	WW domain containing transcription regulator 1	\$89	SHS*SPASLQLGTGAGAAGSPAQQHAHLR	Q9GZV5	44	2	4.72E+05
118	-1.0	YAP1; YAP1 iso2	Yes-associated protein 1, 65kDa isoform 1	\$103, \$109; \$103, \$109	KLDPDSFFKPPPEPKS*HSRQAS*TDAGTAGALTPQHVR	P46937; Q7Z574	49; 53	1	2.89E+06
119	1.1	YAP1; YAP1 iso2	Yes-associated protein 1, 65kDa isoform 1	\$103, \$110; \$103, \$110	S*HSRQAST*TAGTAGALTPQHVR	P46937; Q7Z574	49; 53	1	2.07E+06
122	1.1	YAP1; YAP1 iso2	Yes-associated protein 1, 65kDa isoform 1	\$105, \$110; \$105, \$110	SHS*ROAST*TAGTAGALTPQHVR	P46937; Q7Z574	49; 53	2	1.95E+06
123	-1.3	YAP1; YAP1 iso2	Yes-associated protein 1, 65kDa isoform 1	\$109; \$109	SHSRQAS*TDAGTAGALTPQHVR	P46937; Q7Z574	49; 53	3	3.03E+06
124	-1.1	YAP1; YAP1 iso2	Yes-associated protein 1, 65kDa isoform 1	\$127; \$127	AHS*SPASLQLGVSPGLTPTGVVSGPAATPTAQHLR	P46937; Q7Z574	49; 53	2	1.24E+06
126	1.2	YAP1; YAP1 iso2	Yes-associated protein 1, 65kDa isoform 1	\$164; \$164	QSS*FEIPDDVPLPAGWEM#AK	P46937; Q7Z574	49; 53	2	1.31E+06
127	-1.3	YAP1; YAP1 iso2	Yes-associated protein 1, 65kDa isoform 1	\$94, \$109; \$94, \$109	KLDPDS*FFKPPPEKSHSRQAS*TDAGTAGALTPQHVR	P46937; Q7Z574	49; 53	1	3.83E+05
128	<b>Translation</b>								
130	2.3	eIF4G; eIF4G iso3	eukaryotic translation initiation factor 4 gamma, 1 isoform 4	\$1188; \$1148	TPATKRFSFS*K	Q04637; Q04637-3	176; 172	1	2.80E+05
131	-1.3	eIF5B	eukaryotic translation initiation factor 5B	\$182, \$183, \$186	ERSRINS*S*GES*GDESEDFLQSRK	O60841	139	1	2.22E+05
132	-3.8	S6	ribosomal protein S6	\$235	RLS*SLRASTSK	P62753	29	1	2.06E+07
133	-7.7	S6	ribosomal protein S6	\$235, \$236	RLS*S*LRASTSK	P62753	29	1	8.66E+06
134	-45.6	S6	ribosomal protein S6	\$235, \$236, \$240	RLS*S*LRAS*TSK	P62753	29	3	3.90E+06
135	-20.4	S6	ribosomal protein S6	\$235, \$240, \$244	LS*SLRAS*TSKS*ESSQK	P62753	29	1	4.73E+05
136	-20.7	S6	ribosomal protein S6	\$235, \$241	LS*SLRAST*SKSESSQK	P62753	29	1	2.46E+06
137	-9.7	S6	ribosomal protein S6	\$235, \$242	RLS*SLRASTSK	P62753	29	1	9.39E+06
138	-4.0	S6	ribosomal protein S6	\$236	LSS*LRAS*TSK	P62753	29	4	1.10E+08
139	-19.3	S6	ribosomal protein S6	\$236, \$240	LSS*LRAS*TSK	P62753	29	3	2.63E+07
140	-49.2	S6	ribosomal protein S6	\$236, \$241, \$244	LSS*LRAS*SKS*ESSQK	P62753	29	1	5.55E+06
141	-20.0	S6	ribosomal protein S6	\$236, \$244, \$247	LSS*LRAS*SKS*ESS*QK	P62753	29	1	4.73E+05
142	-4.6	S6	ribosomal protein S6	\$242	LSS*LRAS*SKSESSQK	P62753	29	1	2.31E+05
143	<b>Ubiquitin conjugating system</b>								
144	1.3	UBR4	retinoblastoma-associated factor 600	\$1760, 1762	ISESLVRHAS*TS*SPADK	Q5T4S7	574	1	1.02E+06
145	1.0	UBR4	retinoblastoma-associated factor 600	1761	ESAFQSEPRISESLVRHAST*SPPADK	Q5T4S7	574	1	4.28E+05
146	-1.2	UBXD2	UBX domain containing 2	\$489	IYRLRT*QDDGEDENNTWNGNSTQQM#	Q92575	57	1	2.64E+05
147	<b>Unknown function</b>								
149	5.2	C9orf42	hypothetical protein LOC116224	\$62	RNS*TIFFPSR	Q96E09	31	1	3.66E+06
151	3.9	FLJ44003; FLJ44003 iso2	hypothetical protein LOC159090	24; 24	SS*SAFLIHGLSDLSQVFPQPYTLR	Q7Z309; BAC86380	27; 29	1	1.09E+06
152	4.5	FLJ44003; FLJ44003 iso2	hypothetical protein LOC159090	\$25; \$25	SSS*APLIHGLSDLSQVFPQPYTLR	Q7Z309; BAC86380	27; 29	1	7.80E+06
153	5.2	FLJ44003; FLJ44003 iso2	hypothetical protein LOC159090	\$50; \$50	RNS*TTIMSR	Q7Z309; BAC86380	27; 29	1	1.30E+07
155	-1.0	NIFUN	iron-sulfur cluster assembly enzyme isoform ISCU1	\$14	RVAS*ALLLR	Q9H1K1	18	1	6.77E+05
159	2.0	NHSL1	PREDICTED: similar to hCG18281	1450, 1458	QVGS*IQRSIRKS*STSSDNFKALLLK	Q5SYE7	175	1	1.15E+05
162	-1.4	ubiquitin 1	ubiquitin 1	\$493	MLEEEKDKQDRDRICS*DEEEDEEK	Q9P1P7	122	1	5.65E+06
164	-1.1	ZC3H11A	zinc finger CCH-type containing 11A	\$758	TRRLS*SASTGKPPPLSVEDDFEK	Q75152	89	1	4.73E+05
165	-1.1	ZC3H11A	zinc finger CCH-type containing 11A	\$759	TRRLSS*ASTGKPPPLSVEDDFEK	Q75152	89	1	8.32E+05
166	<b>Vesicle protein</b>								
167	1.1	CSP	Dnaj (Hsp40) homolog, subfamily C, member 5	\$10	SLS*TSGESLYHLVGLDK	Q9H3Z4	22	2	2.14E+07
168	1.1	CSP	Dnaj (Hsp40) homolog, subfamily C, member 5	\$8	S*LS*TSGESLYHLVGLDK	Q9H3Z4	22	1	2.02E+07
169	-1.2	RABEP1	rabaptin, RAB GTPase binding effector protein 1 isoform 2	\$407	DGLRRAQS*TDLSLGTSGSLQSK	Q15276	99	4	2.25E+06
170	1.6	RABEP1	rabaptin, RAB GTPase binding effector protein 1 isoform 2	\$407, \$410	DGLRRAQS*TDSS*LGTSGLQSK	Q15276	99	3	4.17E+06
171	-1.1	REPS1	RALBP1 associated Eps domain containing 1 isoform b	\$657	RLKS*EDELPRPEVDEHTQK	Q96D71	81	4	1.63E+07
172	-6.7	STX7	syntaxin 7	\$124, \$128	VRAS*SRVSGSFPEDSSK	Q15400	30	2	5.13E+05
173	-6.7	STX7	syntaxin 7	\$125, \$128	VRASS*RVSGSFPEDSSK	Q15400	30	2	2.46E+06

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