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Supplementary Table 1. List of total identified phosphopeptides in Urea (U) and Sodium Deoxycholate (NaDOC) containing trypsin digestion method

	prot_hit_num	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	pep_query	pep_rank	pep_isbold	pep_exp_mz	pep_exp_mr	pep_exp_z	pep_calc_mr	pep_delta	pep_miss	pep_score	pep_homol	pep_ident	pep_expect	pep_res_befor	pep_seq	pep_res_after	pep_var_mod	pep_var_mod_pos
NaDOC	1	IPI00791301	Tax_Id=9606 Gene_Symbol=TMPO 46 kDa protein	191	46335	5	628	1	0	884.0656	2649.175	3	2649.1708	0.0042	1	41.56	15	42	0.069	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000000000003000000000000.0
NaDOC	1	IPI00030131	Tax_Id=9606 Gene_Symbol=TMPO Isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma	191	50696	5	628	1	0	884.0656	2649.175	3	2649.1708	0.0042	1	41.56	15	42	0.069	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000000000003000000000000.0
NaDOC	1	IPI00181409	Tax_Id=9606 Gene_Symbol=TMPO Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	191	38771	5	628	1	0	884.0656	2649.175	3	2649.1708	0.0042	1	41.56	15	42	0.069	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000000000003000000000000.0
NaDOC	1	IPI00216230	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2 isoform alpha	191	76016	5	628	1	0	884.0656	2649.175	3	2649.1708	0.0042	1	41.56	15	42	0.069	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000000000003000000000000.0
NaDOC	1	IPI00873716	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2, isoforms beta/gamma variant (Fragment)	191	41895	5	628	1	0	884.0656	2649.175	3	2649.1708	0.0042	1	41.56	15	42	0.069	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000000000003000000000000.0
NaDOC	2	IPI00788993	Tax_Id=9606 Gene_Symbol=CTNNB1 46 kDa protein	175	46282	2	314	1	0	860.8899	1719.7652	2	1719.7288	0.0364	0	129	40	41	9.90E-11	R	R.TSMGGTQQQFVEGVR.M	M	Oxidation (M); Phospho (ST)	0.032000000000000.0
NaDOC	2	IPI00219893	Tax_Id=9606 Gene_Symbol=CTNNB1 56 kDa protein	175	56284	2	314	1	0	860.8899	1719.7652	2	1719.7288	0.0364	0	129	40	41	9.90E-11	R	R.TSMGGTQQQFVEGVR.M	M	Oxidation (M); Phospho (ST)	0.032000000000000.0
NaDOC	2	IPI00017292	Tax_Id=9606 Gene_Symbol=CTNNB1 Isoform 1 of Catenin beta-1	175	86069	2	314	1	1	860.8899	1719.7652	2	1719.7288	0.0364	0	129	40	41	9.90E-11	R	R.TSMGGTQQQFVEGVR.M	M	Oxidation (M); Phospho (ST)	0.032000000000000.0
NaDOC	3	IPI00008868	Tax_Id=9606 Gene_Symbol=MAP1B Microtubule-associated protein 1B	162	271651	9	211	1	1	697.8625	1393.7105	2	1393.6854	0.0251	1	43.69	39	41	0.028	K	K.VQSLEGEKLSPK.S	S	Phospho (ST)	0.000000000300.0
NaDOC	3	IPI00008868	Tax_Id=9606 Gene_Symbol=MAP1B Microtubule-associated protein 1B	162	271651	9	731	1	1	1073.7501	3218.2286	3	3218.2612	-0.0327	1	39.4	17	42	0.11	K	K.QGVDDIEKFEDEGAGFEESSETGDYEEK.A	A	Phospho (ST)	0.0000000000000000000003000000.0
NaDOC	3	IPI00008868	Tax_Id=9606 Gene_Symbol=MAP1B Microtubule-associated protein 1B	162	271651	9	242	1	1	751.8686	1501.7227	2	1501.7065	0.0162	0	40.95	28	41	0.057	K	K.SPSLSPSPPSPLEK.T	T	Phospho (ST)	0.00000000030000.0
NaDOC	3	IPI00008868	Tax_Id=9606 Gene_Symbol=MAP1B Microtubule-associated protein 1B	162	271651	9	688	1	1	968.4049	2902.1929	3	2902.1674	0.0255	0	47.97	28	43	0.016	R	R.SEQSSMSIEFGQESPEQSLAMDFSR.Q	Q	Oxidation (M); Phospho (ST)	0.0000020000000300000000000.0
NaDOC	5	IPI00024971	Tax_Id=9606 Gene_Symbol=OSBP Oxysterol-binding protein 1	156	90220	4	737	1	1	1092.4468	3274.3185	3	3274.2995	0.019	0	25.81	19	43	2.6	K	K.GDMSDEDDENEFFDAPEIITMPENLGHK.R	R	Phospho (ST)	0.0003000000000000000000000000.0
NaDOC	5	IPI00024971	Tax_Id=9606 Gene_Symbol=OSBP Oxysterol-binding protein 1	156	90220	4	738	1	1	1097.7652	3290.2739	3	3290.2945	-0.0205	0	30.45	17	42	0.85	K	K.GDMSDEDDENEFFDAPEIITMPENLGHK.R	R	Oxidation (M); Phospho (ST)	0.0023000000000000000000000000.0
NaDOC	10	IPI00782992	Tax_Id=9606 Gene_Symbol=SRRM2 Isoform 1 of Serine/arginine repetitive matrix protein 2	117	300179	8	522	1	0	748.6853	2243.0342	3	2242.9733	0.0609	1	48.07	22	42	0.014	R	R.QGSITSPQANEQSVTPQRR.S	S	2 Phospho (ST)	0.0000030000000030000.0
NaDOC	10	IPI00782992	Tax_Id=9606 Gene_Symbol=SRRM2 Isoform 1 of Serine/arginine repetitive matrix protein 2	117	300179	8	550	1	0	780.3414	2338.0025	3	2338.0032	-0.0007	1	61.06	19	42	0.00076	K	K.ELSNSPLRENSFGSPLEFR.N	N	2 Phospho (ST)	0.0000300000000300000.0
NaDOC	10	IPI00782992	Tax_Id=9606 Gene_Symbol=SRRM2 Isoform 1 of Serine/arginine repetitive matrix protein 2	117	300179	8	703	1	0	1004.7837	3011.3292	3	3011.3427	-0.0135	0	35.6	27	43	0.28	R	R.HGGSPQPLATTPLSQEPVNPPSEASPTR.D	D	2 Phospho (ST)	0.0003000000000000000000000030.0
NaDOC	10	IPI00782992	Tax_Id=9606 Gene_Symbol=SRRM2 Isoform 1 of Serine/arginine repetitive matrix protein 2	117	300179	8	682	1	0	957.7724	2870.2953	3	2870.272	0.0234	1	35.7	26	42	0.26	R	R.RGEGDAPFSEPGTTSTQRPSSPETATK.Q	Q	Phospho (ST)	0.000000000000000000003000000.0
NaDOC	10	IPI00785023	Tax_Id=9606 Gene_Symbol=SRRM2 Isoform 2 of Serine/arginine repetitive matrix protein 2	117	257122	8	522	1	1	748.6853	2243.0342	3	2242.9733	0.0609	1	48.07	22	42	0.014	R	R.QGSITSPQANEQSVTPQRR.S	S	2 Phospho (ST)	0.0000030000000030000.0
NaDOC	10	IPI00785023	Tax_Id=9606 Gene_Symbol=SRRM2 Isoform 2 of Serine/arginine repetitive matrix protein 2	117	257122	8	550	1	1	780.3414	2338.0025	3	2338.0032	-0.0007	1	61.06	19	42	0.00076	K	K.ELSNSPLRENSFGSPLEFR.N	N	2 Phospho (ST)	0.0000300000000300000.0
NaDOC	10	IPI00785023	Tax_Id=9606 Gene_Symbol=SRRM2 Isoform 2 of Serine/arginine repetitive matrix protein 2	117	257122	8	703	1	1	1004.7837	3011.3292	3	3011.3427	-0.0135	0	35.6	27	43	0.28	R	R.HGGSPQPLATTPLSQEPVNPPSEASPTR.D	D	2 Phospho (ST)	0.0003000000000000000000000030.0
NaDOC	10	IPI00785023	Tax_Id=9606 Gene_Symbol=SRRM2 Isoform 2 of Serine/arginine repetitive matrix protein 2	117	257122	8	682	1	1	957.7724	2870.2953	3	2870.272	0.0234	1	35.7	26	42	0.26	R	R.RGEGDAPFSEPGTTSTQRPSSPETATK.Q	Q	Phospho (ST)	0.000000000000000000003000000.0
NaDOC	13	IPI00006079	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 1 of Bcl-2-associated transcription factor 1	102	106173	4	117	1	1	541.2607	1080.5068	2	1080.5216	-0.0149	0	40.91	35	40	0.042	R	R.IDSPSTLR.K	K	Phospho (ST)	0.00300000.0
NaDOC	13	IPI00006079	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 1 of Bcl-2-associated transcription factor 1	102	106173	4	369	1	1	627.2622	1878.7647	3	1878.7815	-0.0168	0	31.64	25	42	0.57	R	R.YSPSQNSPIHHIPSR.R	R	2 Phospho (ST)	0.030000300000000.0
NaDOC	13	IPI00413671	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 2 of Bcl-2-associated transcription factor 1	102	105999	4	117	1	0	541.2607	1080.5068	2	1080.5216	-0.0149	0	40.91	35	40	0.042	R	R.IDSPSTLR.K	K	Phospho (ST)	0.00300000.0
NaDOC	13	IPI00413671	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 2 of Bcl-2-associated transcription factor 1	102	105999	4	369	1	0	627.2622	1878.7647	3	1878.7815	-0.0168	0	31.64	25	42	0.57	R	R.YSPSQNSPIHHIPSR.R	R	2 Phospho (ST)	0.030000300000000.0
NaDOC	13	IPI00413672	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 3 of Bcl-2-associated transcription factor 1	102	100286	4	117	1	0	541.2607	1080.5068	2	1080.5216	-0.0149	0	40.91	35	40	0.042	R	R.IDSPSTLR.K	K	Phospho (ST)	0.00300000.0
NaDOC	13	IPI00413672	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 3 of Bcl-2-associated transcription factor 1	102	100286	4	369	1	0	627.2622	1878.7647	3	1878.7815	-0.0168	0	31.64	25	42	0.57	R	R.YSPSQNSPIHHIPSR.R	R	2 Phospho (ST)	0.030000300000000.0
NaDOC	13	IPI00886854	Tax_Id=9606 Gene_Symbol=LOC731605 similar to BCL2-associated transcription factor 1 isoform 2	102	100251	4	117	1	0	541.2607	1080.5068	2	1080.5216	-0.0149	0	40.91	35	40	0.042	R	R.IDSPSTLR.K	K	Phospho (ST)	0.00300000.0
NaDOC	13	IPI00886854	Tax_Id=9606 Gene_Symbol=LOC731605 similar to BCL2-associated transcription factor 1 isoform 2	102	100251	4	369	1	0	627.2622	1878.7647	3	1878.7815	-0.0168	0	31.64	25	42	0.57	R	R.YSPSQNSPIHHIPSR.R	R	2 Phospho (ST)	0.030000300000000.0
NaDOC	15	IPI00328753	Tax_Id=9606 Gene_Symbol=KTN1 Isoform 1 of Kinectin	95	156464	3	406	1	1	664.6181	1990.8325	3	1990.8269	0.0056	0	41.98	28	42	0.055	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC	15	IPI00328753	Tax_Id=9606 Gene_Symbol=KTN1 Isoform 1 of Kinectin	95	156464	3	407	1	1	996.4352	1990.8559	2	1990.8269	0.029	0	60.16	24	42	0.00084	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC	15	IPI00337736	Tax_Id=9606 Gene_Symbol=KTN1 Isoform 2 of Kinectin	95	149804	3	406	1	0	664.6181	1990.8325	3	1990.8269	0.0056	0	41.98	28	42	0.055	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC	15	IPI00337736	Tax_Id=9606 Gene_Symbol=KTN1 Isoform 2 of Kinectin	95	149804	3	407	1	0	996.4352	1990.8559	2	1990.8269	0.029	0	60.16	24	42	0.00084	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC	15	IPI00783726	Tax_Id=9606 Gene_Symbol=KTN1 kinectin 1 isoform b	95	150545	3	406	1	0	664.6181	1990.8325	3	1990.8269	0.0056	0	41.98	28	42	0.055	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC	15	IPI00783726	Tax_Id=9606 Gene_Symbol=KTN1 kinectin 1 isoform b	95	150545	3	407	1	0	996.4352	1990.8559	2	1990.8269	0.029	0	60.16	24	42	0.00084	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC	16	IPI00009032	Tax_Id=9606 Gene_Symbol=SSB Lupus La protein	95	46979	4	524	1	1	750.9659	2249.8759	3	2249.8386	0.0372	0	28.58	21	42	1.3	K	K.FASDDEHDEHDENGATGPVK.R	R	Deamidated (NQ); Phospho (ST)	0.00300000000010000000.0
NaDOC	16	IPI00009032	Tax_Id=9606 Gene_Symbol=SSB Lupus La protein	95	46979	4	568	1	1	802.9959	2405.966	3	2405.9397	0.0262	1	38.34		42	0.14	K	K.FASDDEHDEHDENGATGPVKR.A	A	Deamidated (NQ); Phospho (ST)	0.003000000000100000000.0
NaDOC	16	IPI00009032	Tax_Id=9606 Gene_Symbol=SSB Lupus La protein	95	46979	4	567	1	1	602.4963	2405.9561	4	2405.9397	0.0163	1	54.19	20	42	0.0036	K	K.FASDDEHDEHDENGATGPVKR.A	A	Deamidated (NQ); Phospho (ST)	0.003000000000100000000.0
NaDOC	21	IPI00455423	Tax_Id=9606 Gene_Symbol=LOC440577 similar to nucleophosmin	87	20488	3	794	1	0	1040.4911	4157.9351	4	4157.8624	0.0727	1	50.21	19	42	0.0077	K	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGK.R	R	Phospho (ST)	0.0000000000000000000003000000000000000
NaDOC	21	IPI00549248	Tax_Id=9606 Gene_Symbol=NPM1 Isoform 1 of Nucleophosmin	87	32726	3	794	1	0	1040.4911	4157.9351	4	4157.8624	0.0727	1	50.21	19	42	0.0077	K	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGK.R	R	Phospho (ST)	0.0000000000000000000003000000000000000
NaDOC	21	IPI00220740	Tax_Id=9606 Gene_Symbol=NPM1 Isoform 2 of Nucleophosmin	87	29617	3	794	1	1	1040.4911	4157.9351	4	4157.8624	0.0727	1	50.21	19	42	0.0077	K	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGK.R	R	Phospho (ST)	0.0000000000000000000003000000000000000
NaDOC	21	IPI00658013	Tax_Id=9606 Gene_Symbol=NPM1 nucleophosmin 1 isoform 3	87	28497	3	794	1	0	1040.4911	4157.9351	4	4157.8624	0.0727	1	50.21	19	42	0.0077	K	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGK.R	R	Phospho (ST)	0.0000000000000000000003000000000000000
NaDOC	26	IPI00795920	Tax_Id=9606 Gene_Symbol=EEF1D 27 kDa protein	79	26604	1	775	1	0	915.1441	3656.5473	4	3656.5163	0.031	1	79.47	22	43	1.20E-05	K	K.KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR.E	E	Phospho (ST)	0.00000000000000000030000000000000.0
NaDOC	26	IPI00796284	Tax_Id=9606 Gene_Symbol=EEF1D 30 kDa protein	79	30487	1	775	1	0	915.1441	3656.5473	4	3656.5163	0.031	1	79.47	22	43	1.20E-05	K	K.KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR.E	E	Phospho (ST)	0.00000000000000000030000000000000.0
NaDOC	26	IPI00064086	Tax_Id=9606 Gene_Symbol=EEF1D EEF1D protein	79	28654	1	775	1	0	915.1441	3656.5473	4	3656.5163	0.031	1	79.47	22	43	1.20E-05	K	K.KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR.E	E	Phospho (ST)	0.00000000000000000030000000000000.0
NaDOC	26	IPI00023048	Tax_Id=9606 Gene_Symbol=EEF1D Elongation factor 1-delta	79	31217	1	775	1	1	915.1441	3656.5473	4	3656.5163	0.031	1	79.47	22	43	1.20E-05	K	K.KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR.E	E	Phospho (ST)	0.00000000000000000030000000000000.0
NaDOC	26	IPI00642971	Tax_Id=9606 Gene_Symbol=EEF1D eukaryotic translation elongation factor 1 delta isoform 1	79	71820	1	775	1	0	915.1441	3656.5473	4	3656.5163	0.031	1	79.47	22	43	1.20E-05	K	K.KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR.E	E	Phospho (ST)	0.00000000000000000030000000000000.0
NaDOC	29	IPI00479509	Tax_Id=9606 Gene_Symbol=- RcNSEP1 (Fragment)	74	35435	2	741	1	0	1113.1354	3336.3844	3	3336.3552	0.0292	1	43.07	20	43	0.051	R	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R	R	Phospho (ST)	0.00000000003000000000000000000.0
NaDOC	29	IPI00643807	Tax_Id=9606 Gene_Symbol=YBX1 24 kDa protein	74	23584	2	741	1	0	1113.1354	3336.3844	3	3336.3552	0.0292	1	43.07	20	43	0.051	R	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R	R	Phospho (ST)	0.00000000003000000000000000000.0
NaDOC	29	IPI00031812	Tax_Id=9606 Gene_Symbol=YBX1 Nuclease-sensitive element-binding protein 1	74	35903	2	741	1	1	1113.1354	3336.3844	3	3336.3552	0.0292	1	43.07	20	43	0.051	R	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R	R	Phospho (ST)	0.00000000003000000000000000000.0
NaDOC	29	IPI00643351	Tax_Id=9606 Gene_Symbol=YBX1 Protein	74	42333	2	741	1	0	1113.1354	3336.3844	3	3336.3552	0.0292	1	43.07	20	43	0.051	R	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R	R	Phospho (ST)	0.00000000003000000000000000000.0
NaDOC	31	IPI00299667	Tax_Id=9606 Gene_Symbol=VAMP4 Isoform 1 of Vesicle-associated membrane protein 4	72	16444	1	425	1	1	1033.4144	2064.8142	2	2064.8201	-0.0059	0	72.2	34	42	5.30E-05	R	R.NLLEDDSDEEEDFFLR.G	G	Phospho (ST)	0.0000003000000000.0
NaDOC	32	IPI00395887	Tax_Id=9606 Gene_Symbol=TXNDC1 Thioredoxin domain-containing protein 1 precursor	70	32170	1	593	1	1	840.0145	2517.0217	3	2516.9803	0.0414	1	70.38	28	42	8.80E-05	K	K.KVEEEQEADEEDVSEEEAESK.E	E	Phospho (ST)	0.000000000000030000000.0
NaDOC	38	IPI00788076	Tax_Id=9606 Gene_Symbol=ASMTL similar to N-acetylserotonin O-methyltransferase-like protein	62	42990	1	670	1	1	940.7469	2819.2188	3	2819.1923	0.0265	0	62.35	28	43	0.00058	K	K.HDPIPAADTFEDLSDVEGGGSEPTQR.D	D	Phospho (ST)	0.00000000000003000000000000.0
NaDOC	38	IPI00888266	Tax_Id=9606 Gene_Symbol=LOC100133578 similar to acetylserotonin O-methyltransferase-like	62	44599	1	670	1	0	940.7469	2819.2188	3	2819.1923	0.0265	0	62.35	28	43	0.00058	K	K.HDPIPAADTFEDLSDVEGGGSEPTQR.D	D	Phospho (ST)	0.00000000000003000000000000.0
NaDOC	42	IPI00306369	Tax_Id=9606 Gene_Symbol=NSUN2 tRNA	59	87214	1	720	1	1	1058.7637	3173.2692	3	3173.2435	0.0257	0	59.03	24	43	0.0013	R	R.AGEPNSPDAEEANSPDVTAGCDPAGVHPPR.-	-	2 Phospho (ST)	0.000003000000030000000000000000.0
NaDOC	43	IPI00792132	Tax_Id=9606 Gene_Symbol=- Mediator of DNA damage checkpoint 1 variant 2 (Fragment)	59	27618	1	428	1	0	1037.4489	2072.8833	2	2072.9191	-0.0358	0	58.55	25	42	0.0012	R	R.LLLAEDSEEEVDFLSER.R	R	Phospho (ST)	0.00000030000000000.0
NaDOC	43	IPI00641106	Tax_Id=9606 Gene_Symbol=MDC1 227 kDa protein	59	227641	1	428	1	0	1037.4489	2072.8833	2	2072.9191	-0.0358	0	58.55	25	42	0.0012	R	R.LLLAEDSEEEVDFLSER.R	R	Phospho (ST)	0.00000030000000000.0
NaDOC	43	IPI00552897	Tax_Id=9606 Gene_Symbol=MDC1 Isoform 1 of Mediator of DNA damage checkpoint protein 1	59	227669	1	428	1	0	1037.4489	2072.8833	2	2072.9191	-0.0358	0	58.55	25	42	0.0012	R	R.LLLAEDSEEEVDFLSER.R	R	Phospho (ST)	0.00000030000000000.0
NaDOC	43	IPI00470805	Tax_Id=9606 Gene_Symbol=MDC1 Isoform 2 of Mediator of DNA damage checkpoint protein 1	59	198448	1	428	1	1	1037.4489	2072.8833	2	2072.9191	-0.0358	0	58.55	25	42	0.0012	R	R.LLLAEDSEEEVDFLSER.R	R	Phospho (ST)	0.00000030000000000.0
NaDOC	44	IPI00847646	Tax_Id=9606 Gene_Symbol=TNKS1BP1 Isoform 2 of 182 kDa tankyrase 1-binding protein	58	83140	1	271	1	0	795.3229	1588.6312	2	1588.6195	0.0117	0	57.86	26	42	0.0013	R	R.SQEADVQDWEFR.K	K	Phospho (ST)	0.300000000000.0
NaDOC	45	IPI00419482	Tax_Id=9606 Gene_Symbol=CTNND1 catenin, delta 1 isoform 1B	58	106426	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00419482	Tax_Id=9606 Gene_Symbol=CTNND1 catenin, delta 1 isoform 1B	58	106426	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00845246	Tax_Id=9606 Gene_Symbol=CTNND1 catenin, delta 1 isoform 3B	58	93990	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00845246	Tax_Id=9606 Gene_Symbol=CTNND1 catenin, delta 1 isoform 3B	58	93990	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00845519	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1 of Catenin delta-1	58	102388	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00845519	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1 of Catenin delta-1	58	102388	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219870	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1A of Catenin delta-1	58	104662	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219870	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1A of Catenin delta-1	58	104662	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00182469	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1AB of Catenin delta-1	58	107923	2	146	1	1	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00182469	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1AB of Catenin delta-1	58	107923	2	186	1	1	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00182540	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1ABC of Catenin delta-1	58	108744	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00182540	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1ABC of Catenin delta-1	58	108744	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219868	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1AC of Catenin delta-1	58	105482	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219868	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1AC of Catenin delta-1	58	105482	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219872	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1B of Catenin delta-1	58	105579	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219872	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1B of Catenin delta-1	58	105579	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219869	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1BC of Catenin delta-1	58	106399	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219869	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1BC of Catenin delta-1	58	106399	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219873	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1C of Catenin delta-1	58	103208	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219873	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 1C of Catenin delta-1	58	103208	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219732	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2 of Catenin delta-1	58	96285	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219732	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2 of Catenin delta-1	58	96285	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219728	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2A of Catenin delta-1	58	98559	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219728	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2A of Catenin delta-1	58	98559	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219725	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2AB of Catenin delta-1	58	101750	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219725	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2AB of Catenin delta-1	58	101750	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219875	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2ABC of Catenin delta-1	58	102571	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219875	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2ABC of Catenin delta-1	58	102571	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219726	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2AC of Catenin delta-1	58	99379	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219726	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2AC of Catenin delta-1	58	99379	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219730	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2B of Catenin delta-1	58	99476	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219730	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2B of Catenin delta-1	58	99476	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219727	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2BC of Catenin delta-1	58	100296	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219727	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2BC of Catenin delta-1	58	100296	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219731	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2C of Catenin delta-1	58	97105	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219731	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 2C of Catenin delta-1	58	97105	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219742	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3 of Catenin delta-1	58	90914	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219742	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3 of Catenin delta-1	58	90914	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219738	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3A of Catenin delta-1	58	93188	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219738	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3A of Catenin delta-1	58	93188	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219734	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3AB of Catenin delta-1	58	96379	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219734	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3AB of Catenin delta-1	58	96379	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219733	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3ABC of Catenin delta-1	58	97200	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0

NaDOC	45	IPI00219733	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3ABC of Catenin delta-1	58	97200	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219735	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3AC of Catenin delta-1	58	94008	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219735	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3AC of Catenin delta-1	58	94008	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219739	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3B of Catenin delta-1	58	94105	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219739	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3B of Catenin delta-1	58	94105	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219737	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3BC of Catenin delta-1	58	94926	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219737	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3BC of Catenin delta-1	58	94926	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219741	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3C of Catenin delta-1	58	91734	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219741	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 3C of Catenin delta-1	58	91734	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219750	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4 of Catenin delta-1	58	66285	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219750	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4 of Catenin delta-1	58	66285	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219747	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4A of Catenin delta-1	58	68559	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219747	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4A of Catenin delta-1	58	68559	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219744	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4AB of Catenin delta-1	58	71751	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219744	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4AB of Catenin delta-1	58	71751	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219743	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4ABC of Catenin delta-1	58	72571	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219743	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4ABC of Catenin delta-1	58	72571	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219745	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4AC of Catenin delta-1	58	69380	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219745	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4AC of Catenin delta-1	58	69380	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219748	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4B of Catenin delta-1	58	69477	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219748	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4B of Catenin delta-1	58	69477	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219746	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4BC of Catenin delta-1	58	70297	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219746	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4BC of Catenin delta-1	58	70297	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00219749	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4C of Catenin delta-1	58	67106	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00219749	Tax_Id=9606 Gene_Symbol=CTNND1 Isoform 4C of Catenin delta-1	58	67106	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	45	IPI00848265	Tax_Id=9606 Gene_Symbol=CTNND1 Putative uncharacterized protein DKFZp781O2021	58	105510	2	146	1	0	589.744	1177.4734	2	1177.4781	-0.0047	0	44.25	27	40	0.023	R	R.GSLASLDSLR.K	K	2 Phospho (ST)	0.0300300000.0
NaDOC	45	IPI00848265	Tax_Id=9606 Gene_Symbol=CTNND1 Putative uncharacterized protein DKFZp781O2021	58	105510	2	186	1	0	653.7935	1305.5724	2	1305.5731	-0.0007	1	40.86	28	41	0.052	R	R.GSLASLDSLRK.G	G	2 Phospho (ST)	0.03003000000.0
NaDOC	48	IPI00477468	Tax_Id=9606 Gene_Symbol=CTR9 RNA polymerase-associated protein CTR9 homolog	55	134332	2	543	1	1	1154.4808	2306.9471	2	2306.9104	0.0367	0	30.64	19	42	0.83	K	K.GGEFDEFVNDDTDDDLPISK.K	K	Phospho (ST)	0.00000000000300000000.0
NaDOC	48	IPI00477468	Tax_Id=9606 Gene_Symbol=CTR9 RNA polymerase-associated protein CTR9 homolog	55	134332	2	573	1	1	812.6819	2435.0238	3	2435.0054	0.0184	1	44.5	22	42	0.034	K	K.KGGEFDEFVNDDTDDDLPISK.K	K	Phospho (ST)	0.000000000000300000000.0
NaDOC	49	IPI00008465	Tax_Id=9606 Gene_Symbol=ABCC1 166 kDa protein	54	167459	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00008463	Tax_Id=9606 Gene_Symbol=ABCC1 167 kDa protein	54	167945	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00843930	Tax_Id=9606 Gene_Symbol=ABCC1 ATP-binding cassette, sub-family C, member 1 isoform 5	54	165510	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00014985	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 1 of Multidrug resistance-associated protein 1	54	172877	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00008338	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 2 of Multidrug resistance-associated protein 1	54	166146	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00216262	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 3 of Multidrug resistance-associated protein 1	54	166858	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00216263	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 4 of Multidrug resistance-associated protein 1	54	165480	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00216264	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 5 of Multidrug resistance-associated protein 1	54	160128	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00216265	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 6 of Multidrug resistance-associated protein 1	54	158749	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00216266	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 7 of Multidrug resistance-associated protein 1	54	159462	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00216267	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 8 of Multidrug resistance-associated protein 1	54	152731	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00719178	Tax_Id=9606 Gene_Symbol=ABCC1 Isoform 9 of Multidrug resistance-associated protein 1	54	173925	1	260	1	0	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	49	IPI00872844	Tax_Id=9606 Gene_Symbol=ABCC1 Putative uncharacterized protein	54	135813	1	260	1	1	777.3302	1552.6459	2	1552.6406	0.0053	0	53.97	28	41	0.003	R	R.QLSSSSSYSGDISR.H	H	Phospho (ST)	0.00300000000000.0
NaDOC	52	IPI00218260	Tax_Id=9606 Gene_Symbol=NFIX Isoform 1 of Nuclear factor 1 X-type	52	55577	1	563	1	1	1198.4918	2394.969	2	2394.9563	0.0127	0	51.63	20	42	0.0065	K	K.SIDDSEMESPVDDVFYPGTGR.S	S	Phospho (ST)	0.300000000000000000000.0
NaDOC	52	IPI00221071	Tax_Id=9606 Gene_Symbol=NFIX Isoform 2 of Nuclear factor 1 X-type	52	51236	1	563	1	0	1198.4918	2394.969	2	2394.9563	0.0127	0	51.63	20	42	0.0065	K	K.SIDDSEMESPVDDVFYPGTGR.S	S	Phospho (ST)	0.300000000000000000000.0
NaDOC	52	IPI00306473	Tax_Id=9606 Gene_Symbol=NFIX Isoform 3 of Nuclear factor 1 X-type	52	49350	1	563	1	0	1198.4918	2394.969	2	2394.9563	0.0127	0	51.63	20	42	0.0065	K	K.SIDDSEMESPVDDVFYPGTGR.S	S	Phospho (ST)	0.300000000000000000000.0
NaDOC	52	IPI00221073	Tax_Id=9606 Gene_Symbol=NFIX Isoform 4 of Nuclear factor 1 X-type	52	54564	1	563	1	0	1198.4918	2394.969	2	2394.9563	0.0127	0	51.63	20	42	0.0065	K	K.SIDDSEMESPVDDVFYPGTGR.S	S	Phospho (ST)	0.300000000000000000000.0
NaDOC	52	IPI00395691	Tax_Id=9606 Gene_Symbol=NFIX Isoform 5 of Nuclear factor 1 X-type	52	49176	1	563	1	0	1198.4918	2394.969	2	2394.9563	0.0127	0	51.63	20	42	0.0065	K	K.SIDDSEMESPVDDVFYPGTGR.S	S	Phospho (ST)	0.300000000000000000000.0
NaDOC	52	IPI00747331	Tax_Id=9606 Gene_Symbol=NFIX Nuclear factor 1	52	45038	1	563	1	0	1198.4918	2394.969	2	2394.9563	0.0127	0	51.63	20	42	0.0065	K	K.SIDDSEMESPVDDVFYPGTGR.S	S	Phospho (ST)	0.300000000000000000000.0
NaDOC	57	IPI00015195	Tax_Id=9606 Gene_Symbol=CSTF3 Cleavage stimulation factor 77 kDa subunit	50	83325	2	675	1	1	712.3175	2845.2411	4	2845.2556	-0.0145	1	49.77	23	43	0.011	K	K.RPNEDSDEDEEKGAVVPPVHDIYR.A	A	Phospho (ST)	0.000003000000000000000000.0
NaDOC	63	IPI00555833	Tax_Id=9606 Gene_Symbol=MYEF2 Isoform 1 of Myelin expression factor 2	45	64367	1	575	1	0	816.0515	2445.1325	3	2445.0962	0.0364	0	44.81	21	42	0.03	K	K.AEVPGATGGDSPHLQPAEPPGEPR.R	R	Phospho (ST)	0.000000000030000000000000.0
NaDOC	63	IPI00386418	Tax_Id=9606 Gene_Symbol=MYEF2 Isoform 2 of Myelin expression factor 2	45	62176	1	575	1	0	816.0515	2445.1325	3	2445.0962	0.0364	0	44.81	21	42	0.03	K	K.AEVPGATGGDSPHLQPAEPPGEPR.R	R	Phospho (ST)	0.000000000030000000000000.0
NaDOC	63	IPI00555987	Tax_Id=9606 Gene_Symbol=MYEF2 Isoform 3 of Myelin expression factor 2	45	62087	1	575	1	0	816.0515	2445.1325	3	2445.0962	0.0364	0	44.81	21	42	0.03	K	K.AEVPGATGGDSPHLQPAEPPGEPR.R	R	Phospho (ST)	0.000000000030000000000000.0
NaDOC	63	IPI00292940	Tax_Id=9606 Gene_Symbol=MYEF2 Isoform 4 of Myelin expression factor 2	45	14203	1	575	1	1	816.0515	2445.1325	3	2445.0962	0.0364	0	44.81	21	42	0.03	K	K.AEVPGATGGDSPHLQPAEPPGEPR.R	R	Phospho (ST)	0.000000000030000000000000.0
NaDOC	67	IPI00395337	Tax_Id=9606 Gene_Symbol=FIP1L1 Isoform 1 of Pre-mRNA 3'-end-processing factor FIP1	39	66601	1	507	1	0	732.6185	2194.8337	3	2194.8358	-0.0021	1	38.77	18	42	0.12	R	R.DHSPTPSVFNSDEERYR.Y	Y	2 Phospho (ST)	0.00300000003000000.0
NaDOC	67	IPI00657863	Tax_Id=9606 Gene_Symbol=FIP1L1 Isoform 2 of Pre-mRNA 3'-end-processing factor FIP1	39	63124	1	507	1	0	732.6185	2194.8337	3	2194.8358	-0.0021	1	38.77	18	42	0.12	R	R.DHSPTPSVFNSDEERYR.Y	Y	2 Phospho (ST)	0.00300000003000000.0
NaDOC	67	IPI00008449	Tax_Id=9606 Gene_Symbol=FIP1L1 Isoform 3 of Pre-mRNA 3'-end-processing factor FIP1	39	58398	1	507	1	1	732.6185	2194.8337	3	2194.8358	-0.0021	1	38.77	18	42	0.12	R	R.DHSPTPSVFNSDEERYR.Y	Y	2 Phospho (ST)	0.00300000003000000.0
NaDOC	67	IPI00658114	Tax_Id=9606 Gene_Symbol=FIP1L1 Isoform 4 of Pre-mRNA 3'-end-processing factor FIP1	39	64931	1	507	1	0	732.6185	2194.8337	3	2194.8358	-0.0021	1	38.77	18	42	0.12	R	R.DHSPTPSVFNSDEERYR.Y	Y	2 Phospho (ST)	0.00300000003000000.0
NaDOC	73	IPI00657704	Tax_Id=9606 Gene_Symbol=TP53BP1 112 kDa protein	37	112679	1	351	1	0	906.4206	1810.8266	2	1810.8139	0.0128	0	37.05	23	41	0.16	R	R.STPFIVPSSPTEQEGR.Q	Q	Phospho (ST)	0.0000000030000000.0
NaDOC	73	IPI00029778	Tax_Id=9606 Gene_Symbol=TP53BP1 Isoform 1 of Tumor suppressor p53-binding protein 1	37	215495	1	351	1	1	906.4206	1810.8266	2	1810.8139	0.0128	0	37.05	23	41	0.16	R	R.STPFIVPSSPTEQEGR.Q	Q	Phospho (ST)	0.0000000030000000.0
NaDOC	73	IPI00742743	Tax_Id=9606 Gene_Symbol=TP53BP1 Isoform 2 of Tumor suppressor p53-binding protein 1	37	216038	1	351	1	0	906.4206	1810.8266	2	1810.8139	0.0128	0	37.05	23	41	0.16	R	R.STPFIVPSSPTEQEGR.Q	Q	Phospho (ST)	0.0000000030000000.0
NaDOC	73	IPI00657708	Tax_Id=9606 Gene_Symbol=TP53BP1 Uncharacterized protein TP53BP1	37	210886	1	351	1	0	906.4206	1810.8266	2	1810.8139	0.0128	0	37.05	23	41	0.16	R	R.STPFIVPSSPTEQEGR.Q	Q	Phospho (ST)	0.0000000030000000.0
NaDOC	74	IPI00013174	Tax_Id=9606 Gene_Symbol=RBM14 Isoform 1 of RNA-binding protein 14	37	69620	1	127	1	0	563.7629	1125.5113	2	1125.5009	0.0105	0	36.96	23	40	0.11	R	R.QPTPPFFGR.D	D	Phospho (ST)	0.003000000.0
NaDOC	74	IPI00556514	Tax_Id=9606 Gene_Symbol=RBM14 RNA binding motif protein 14 variant (Fragment)	37	55824	1	127	1	1	563.7629	1125.5113	2	1125.5009	0.0105	0	36.96	23	40	0.11	R	R.QPTPPFFGR.D	D	Phospho (ST)	0.003000000.0
NaDOC	77	IPI00021954	Tax_Id=9606 Gene_Symbol=GBF1 Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	36	208367	1	390	1	1	650.2778	1947.8115	3	1947.8	0.0115	0	35.99	18	42	0.22	R	R.GYTSDSEVYTDHGRPGK.I	I	Phospho (ST)	0.00030000000000000.0
NaDOC	78	IPI00784614	Tax_Id=9606 Gene_Symbol=SEPT9 Isoform 1 of Septin-9	36	65646	1	373	1	1	949.3991	1896.7837	2	1896.8142	-0.0306	0	35.77	18	42	0.22	R	R.SFEVEEVETPNSTPPR.R	R	Phospho (ST)	0.3000000000000000.0
NaDOC	78	IPI00784936	Tax_Id=9606 Gene_Symbol=SEPT9 Isoform 2 of Septin-9	36	63911	1	373	1	0	949.3991	1896.7837	2	1896.8142	-0.0306	0	35.77	18	42	0.22	R	R.SFEVEEVETPNSTPPR.R	R	Phospho (ST)	0.3000000000000000.0
NaDOC	78	IPI00784808	Tax_Id=9606 Gene_Symbol=SEPT9 Isoform 5 of Septin-9	36	64926	1	373	1	0	949.3991	1896.7837	2	1896.8142	-0.0306	0	35.77	18	42	0.22	R	R.SFEVEEVETPNSTPPR.R	R	Phospho (ST)	0.3000000000000000.0
NaDOC	79	IPI00020984	Tax_Id=9606 Gene_Symbol=CANX Calnexin precursor	36	67982	3	249	1	1	754.854	1507.6934	2	1507.6667	0.0267	1	25.51	25	41	2	K	K.AEEDEILNRSPR.N	N	Phospho (ST)	0.000000000300.0
NaDOC	83	IPI00852591	Tax_Id=9606 Gene_Symbol=SF1 12 kDa protein	31	12224	2	691	1	1	976.0921	2925.2546	3	2925.247	0.0075	1	29.66	20	43	1.1	R	R.TGDLGIPPNPEDRSPSPEPIYNSEGK.R	R	2 Phospho (ST)	0.00000000000003030000000000.0
NaDOC	83	IPI00386114	Tax_Id=9606 Gene_Symbol=SF1 Isoform 1 of Splicing factor 1	31	68514	2	691	1	0	976.0921	2925.2546	3	2925.247	0.0075	1	29.66	20	43	1.1	R	R.TGDLGIPPNPEDRSPSPEPIYNSEGK.R	R	2 Phospho (ST)	0.00000000000003030000000000.0
NaDOC	83	IPI00294627	Tax_Id=9606 Gene_Symbol=SF1 Isoform 2 of Splicing factor 1	31	68817	2	691	1	0	976.0921	2925.2546	3	2925.247	0.0075	1	29.66	20	43	1.1	R	R.TGDLGIPPNPEDRSPSPEPIYNSEGK.R	R	2 Phospho (ST)	0.00000000000003030000000000.0
NaDOC	83	IPI00386117	Tax_Id=9606 Gene_Symbol=SF1 Isoform 3 of Splicing factor 1	31	67576	2	691	1	0	976.0921	2925.2546	3	2925.247	0.0075	1	29.66	20	43	1.1	R	R.TGDLGIPPNPEDRSPSPEPIYNSEGK.R	R	2 Phospho (ST)	0.00000000000003030000000000.0
NaDOC	83	IPI00386118	Tax_Id=9606 Gene_Symbol=SF1 Isoform 4 of Splicing factor 1	31	59902	2	691	1	0	976.0921	2925.2546	3	2925.247	0.0075	1	29.66	20	43	1.1	R	R.TGDLGIPPNPEDRSPSPEPIYNSEGK.R	R	2 Phospho (ST)	0.00000000000003030000000000.0
NaDOC	83	IPI00386119	Tax_Id=9606 Gene_Symbol=SF1 Isoform 5 of Splicing factor 1	31	80797	2	691	1	0	976.0921	2925.2546	3	2925.247	0.0075	1	29.66	20	43	1.1	R	R.TGDLGIPPNPEDRSPSPEPIYNSEGK.R	R	2 Phospho (ST)	0.00000000000003030000000000.0
NaDOC	83	IPI00386120	Tax_Id=9606 Gene_Symbol=SF1 Isoform 6 of Splicing factor 1	31	62135	2	691	1	0	976.0921	2925.2546	3	2925.247	0.0075	1	29.66	20	43	1.1	R	R.TGDLGIPPNPEDRSPSPEPIYNSEGK.R	R	2 Phospho (ST)	0.00000000000003030000000000.0
NaDOC	86	IPI00787793	Tax_Id=9606 Gene_Symbol=- similar to FUS interacting protein (serine-arginine rich) 1 isoform 4	31	20016	1	207	1	0	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	86	IPI00786930	Tax_Id=9606 Gene_Symbol=- similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS	31	29235	1	207	1	0	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	86	IPI00645384	Tax_Id=9606 Gene_Symbol=FUSIP1 FUS interacting protein (Serine/arginine-rich) 1	31	20957	1	207	1	0	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	86	IPI00646643	Tax_Id=9606 Gene_Symbol=FUSIP1 FUS interacting protein (Serine/arginine-rich) 1	31	22236	1	207	1	0	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	86	IPI00412643	Tax_Id=9606 Gene_Symbol=FUSIP1 Isoform 2 of FUS-interacting serine-arginine-rich protein 1	31	31252	1	207	1	0	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	86	IPI00386662	Tax_Id=9606 Gene_Symbol=FUSIP1 Isoform 4 of FUS-interacting serine-arginine-rich protein 1	31	21045	1	207	1	0	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	86	IPI00074587	Tax_Id=9606 Gene_Symbol=FUSIP1;LOC642558 Isoform 1 of FUS-interacting serine-arginine-rich protein 1	31	31339	1	207	1	0	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	86	IPI00009071	Tax_Id=9606 Gene_Symbol=LOC642558;FUSIP1 Isoform 3 of FUS-interacting serine-arginine-rich protein 1	31	22323	1	207	1	1	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	86	IPI00887543	Tax_Id=9606 Gene_Symbol=LOC653884 hypothetical protein, partial	31	22123	1	207	1	0	684.2521	1366.4896	2	1366.4744	0.0151	1	31.14	25	41	0.51	R	R.SRSFDYNYR.R	R	2 Phospho (ST)	0.303000000.0
NaDOC	88	IPI00397526	Tax_Id=9606 Gene_Symbol=MYH10 Isoform 1 of Myosin-10	31	229824	1	497	1	1	722.9852	2165.9339	3	2165.9365	-0.0026	0	30.86	20	42	0.74	R	R.QLHLEGASLELSDDDTESK.T	T	Phospho (ST)	0.0000000000030000000.0
NaDOC	88	IPI00479307	Tax_Id=9606 Gene_Symbol=MYH10 Isoform 2 of Myosin-10	31	231603	1	497	1	0	722.9852	2165.9339	3	2165.9365	-0.0026	0	30.86	20	42	0.74	R	R.QLHLEGASLELSDDDTESK.T	T	Phospho (ST)	0.0000000000030000000.0
NaDOC	88	IPI00790503	Tax_Id=9606 Gene_Symbol=MYH10 Isoform 3 of Myosin-10	31	232192	1	497	1	0	722.9852	2165.9339	3	2165.9365	-0.0026	0	30.86	20	42	0.74	R	R.QLHLEGASLELSDDDTESK.T	T	Phospho (ST)	0.0000000000030000000.0
NaDOC	89	IPI00472779	Tax_Id=9606 Gene_Symbol=ANK3 Ankyrin-3	30	482387	2	542	1	0	1152.4891	2302.9636	2	2302.9157	0.048	0	30.29	21	42	0.9	K	K.MNVPETMNEVLDMSDDEVR.K	K	Phospho (ST)	0.0000000000000300000.0
NaDOC	89	IPI00333558	Tax_Id=9606 Gene_Symbol=ANK3 Putative uncharacterized protein DKFZp686I225	30	203674	2	542	1	1	1152.4891	2302.9636	2	2302.9157	0.048	0	30.29	21	42	0.9	K	K.MNVPETMNEVLDMSDDEVR.K	K	Phospho (ST)	0.0000000000000300000.0
NaDOC	89	IPI00640884	Tax_Id=9606 Gene_Symbol=ANK3 Putative uncharacterized protein DKFZp686P17114	30	203778	2	542	1	0	1152.4891	2302.9636	2	2302.9157	0.048	0	30.29	21	42	0.9	K	K.MNVPETMNEVLDMSDDEVR.K	K	Phospho (ST)	0.0000000000000300000.0
NaDOC	90	IPI00412260	Tax_Id=9606 Gene_Symbol=CCDC86 18 kDa protein	30	17664	2	623	1	0	879.0534	2634.1384	3	2634.1963	-0.0578	1	29.59	21	42	1.1	R	R.ALVEFESNPEETREPGSPPSVQR.A	A	Phospho (ST)	0.00000000000000003000000.0
NaDOC	90	IPI00012199	Tax_Id=9606 Gene_Symbol=CCDC86 Coiled-coil domain-containing protein 86	30	40325	2	623	1	1	879.0534	2634.1384	3	2634.1963	-0.0578	1	29.59	21	42	1.1	R	R.ALVEFESNPEETREPGSPPSVQR.A	A	Phospho (ST)	0.00000000000000003000000.0
NaDOC	91	IPI00012340	Tax_Id=9606 Gene_Symbol=SFRS9 Splicing factor, arginine/serine-rich 9	29	25640	1	291	1	1	807.8038	1613.5931	2	1613.6105	-0.0174	0	28.99	16	41	0.96	R	R.GSPHYFSPFRPY.-	-	2 Phospho (ST)	0.030000300000.0
NaDOC	93	IPI00025156	Tax_Id=9606 Gene_Symbol=STUB1 Isoform 1 of STIP1 homology and U box-containing protein 1	29	35290	1	348	1	1	896.9239	1791.8333	2	1791.8404	-0.007	1	28.86	24	42	1.1	R	R.LGAGGGSPEKSPSAQELK.E	E	Phospho (ST)	0.000000300000000000.0
NaDOC	95	IPI00301021	Tax_Id=9606 Gene_Symbol=SSR1 Isoform 1 of Translocon-associated protein subunit alpha precursor	29	32215	1	758	1	1	1152.5244	3454.5513	3	3454.5534	-0.0022	1	28.67	22	42	1.3	K	K.VEMGTSSQNDVDMSWIPQETLNQINKASPR.R	R	Phospho (ST)	0.000000000000000000000000000300.0
NaDOC	95	IPI00449669	Tax_Id=9606 Gene_Symbol=SSR1 Isoform 2 of Translocon-associated protein subunit alpha precursor	29	29355	1	758	1	0	1152.5244	3454.5513	3	3454.5534	-0.0022	1	28.67	22	42	1.3	K	K.VEMGTSSQNDVDMSWIPQETLNQINKASPR.R	R	Phospho (ST)	0.000000000000000000000000000300.0
NaDOC	97	IPI00249982	Tax_Id=9606 Gene_Symbol=DIDO1 Isoform 1 of Death-inducer obliterator 1	27	130526	1	667	1	1	939.3735	2815.0987	3	2815.111	-0.0123	0	27.16	16	42	1.9	R	R.QEAIPDLEDSPPVSDSEEQQESAR.A	A	2 Phospho (ST)	0.000000000300000300000000.0
NaDOC	97	IPI00619921	Tax_Id=9606 Gene_Symbol=DIDO1 Isoform 4 of Death-inducer obliterator 1	27	245434	1	667	1	0	939.3735	2815.0987	3	2815.111	-0.0123	0	27.16	16	42	1.9	R	R.QEAIPDLEDSPPVSDSEEQQESAR.A	A	2 Phospho (ST)	0.000000000300000300000000.0
NaDOC, U	1	IPI00830089	Tax_Id=9606 Gene_Symbol=- Thymopoietin zeta isoform	191	27428	5	627	1	1	884.0593	2649.1562	3	2649.1708	-0.0146	1	57.14	18	42	0.0019	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	1	IPI00830089	Tax_Id=9606 Gene_Symbol=- Thymopoietin zeta isoform	191	27428	5	628	1	1	884.0656	2649.175	3	2649.1708	0.0042	1	41.56	15	42	0.069	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000000000000300000000000.0
NaDOC, U	1	IPI00830089	Tax_Id=9606 Gene_Symbol=- Thymopoietin zeta isoform	191	27428	5	647	1	1	910.729	2729.1651	3	2729.1371	0.028	1	46.34	20	43	0.024	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000330000000000000000000.0
NaDOC, U	1	IPI00830089	Tax_Id=9606 Gene_Symbol=- Thymopoietin zeta isoform	191	27428	5	648	1	1	910.7357	2729.1853	3	2729.1371	0.0482	1	56.62	20	43	0.0022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000300000000300000000000.0
NaDOC, U	1	IPI00830089	Tax_Id=9606 Gene_Symbol=- Thymopoietin zeta isoform	191	27428	5	319	1	1	864.4141	1726.8136	2	1726.7775	0.0361	0	68.25	26	42	0.00012	R	R.SSTPLPTISSSAENTR.Q	Q	Phospho (ST)	0.0030000000000000.0
NaDOC, U	1	IPI00791301	Tax_Id=9606 Gene_Symbol=TMPO 46 kDa protein	191	46335	5	627	1	0	884.0593	2649.1562	3	2649.1708	-0.0146	1	57.14	18	42	0.0019	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	1	IPI00791301	Tax_Id=9606 Gene_Symbol=TMPO 46 kDa protein	191	46335	5	647	1	0	910.729	2729.1651	3	2729.1371	0.028	1	46.34	20	43	0.024	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000330000000000000000000.0
NaDOC, U	1	IPI00791301	Tax_Id=9606 Gene_Symbol=TMPO 46 kDa protein	191	46335	5	648	1	0	910.7357	2729.1853	3	2729.1371	0.0482	1	56.62	20	43	0.0022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000300000000300000000000.0
NaDOC, U	1	IPI00791301	Tax_Id=9606 Gene_Symbol=TMPO 46 kDa protein	191	46335	5	319	1	0	864.4141	1726.8136	2	1726.7775	0.0361	0	68.25	26	42	0.00012	R	R.SSTPLPTISSSAENTR.Q	Q	Phospho (ST)	0.0030000000000000.0
NaDOC, U	1	IPI00030131	Tax_Id=9606 Gene_Symbol=TMPO Isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma	191	50696	5	627	1	0	884.0593	2649.1562	3	2649.1708	-0.0146	1	57.14	18	42	0.0019	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	1	IPI00030131	Tax_Id=9606 Gene_Symbol=TMPO Isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma	191	50696	5	647	1	0	910.729	2729.1651	3	2729.1371	0.028	1	46.34	20	43	0.024	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000330000000000000000000.0
NaDOC, U	1	IPI00030131	Tax_Id=9606 Gene_Symbol=TMPO Isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma	191	50696	5	648	1	0	910.7357	2729.1853	3	2729.1371	0.0482	1	56.62	20	43	0.0022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000300000000300000000000.0
NaDOC, U	1	IPI00030131	Tax_Id=9606 Gene_Symbol=TMPO Isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma	191	50696	5	319	1	0	864.4141	1726.8136	2	1726.7775	0.0361	0	68.25	26	42	0.00012	R	R.SSTPLPTISSSAENTR.Q	Q	Phospho (ST)	0.0030000000000000.0

NaDOC, U	1	IPI00181409	Tax_Id=9606 Gene_Symbol=TMPO Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	191	38771	5	627	1	0	884.0593	2649.1562	3	2649.1708	-0.0146	1	57.14	18	42	0.0019	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	1	IPI00181409	Tax_Id=9606 Gene_Symbol=TMPO Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	191	38771	5	647	1	0	910.729	2729.1651	3	2729.1371	0.028	1	46.34	20	43	0.024	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000330000000000000000000.0
NaDOC, U	1	IPI00181409	Tax_Id=9606 Gene_Symbol=TMPO Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	191	38771	5	648	1	0	910.7357	2729.1853	3	2729.1371	0.0482	1	56.62	20	43	0.0022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000300000003000000000000.0
NaDOC, U	1	IPI00181409	Tax_Id=9606 Gene_Symbol=TMPO Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	191	38771	5	319	1	0	864.4141	1726.8136	2	1726.7775	0.0361	0	68.25	26	42	0.00012	R	R.SSTPLPTISSSAENTR.Q	Q	Phospho (ST)	0.0030000000000000.0
NaDOC, U	1	IPI00216230	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2 isoform alpha	191	76016	5	627	1	0	884.0593	2649.1562	3	2649.1708	-0.0146	1	57.14	18	42	0.0019	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	1	IPI00216230	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2 isoform alpha	191	76016	5	647	1	0	910.729	2729.1651	3	2729.1371	0.028	1	46.34	20	43	0.024	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000330000000000000000000.0
NaDOC, U	1	IPI00216230	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2 isoform alpha	191	76016	5	648	1	0	910.7357	2729.1853	3	2729.1371	0.0482	1	56.62	20	43	0.0022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000300000003000000000000.0
NaDOC, U	1	IPI00216230	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2 isoform alpha	191	76016	5	319	1	0	864.4141	1726.8136	2	1726.7775	0.0361	0	68.25	26	42	0.00012	R	R.SSTPLPTISSSAENTR.Q	Q	Phospho (ST)	0.0030000000000000.0
NaDOC, U	1	IPI00873716	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2, isoforms beta/gamma variant (Fragment)	191	41895	5	627	1	0	884.0593	2649.1562	3	2649.1708	-0.0146	1	57.14	18	42	0.0019	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	1	IPI00873716	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2, isoforms beta/gamma variant (Fragment)	191	41895	5	647	1	0	910.729	2729.1651	3	2729.1371	0.028	1	46.34	20	43	0.024	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000330000000000000000000.0
NaDOC, U	1	IPI00873716	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2, isoforms beta/gamma variant (Fragment)	191	41895	5	648	1	0	910.7357	2729.1853	3	2729.1371	0.0482	1	56.62	20	43	0.0022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	2 Phospho (ST)	0.00000300000003000000000000.0
NaDOC, U	1	IPI00873716	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2, isoforms beta/gamma variant (Fragment)	191	41895	5	319	1	0	864.4141	1726.8136	2	1726.7775	0.0361	0	68.25	26	42	0.00012	R	R.SSTPLPTISSSAENTR.Q	Q	Phospho (ST)	0.0030000000000000.0
NaDOC, U	2	IPI00788993	Tax_Id=9606 Gene_Symbol=CTNNB1 46 kDa protein	175	46282	2	310	1	0	852.8887	1703.7629	2	1703.7339	0.0291	0	80.26	28	42	7.60E-06	R	R.TSMGGTQQQFVEGVR.M	M	Phospho (ST)	0.300000000000000.0
NaDOC, U	2	IPI00219893	Tax_Id=9606 Gene_Symbol=CTNNB1 56 kDa protein	175	56284	2	310	1	0	852.8887	1703.7629	2	1703.7339	0.0291	0	80.26	28	42	7.60E-06	R	R.TSMGGTQQQFVEGVR.M	M	Phospho (ST)	0.300000000000000.0
NaDOC, U	2	IPI00017292	Tax_Id=9606 Gene_Symbol=CTNNB1 Isoform 1 of Catenin beta-1	175	86069	2	310	1	1	852.8887	1703.7629	2	1703.7339	0.0291	0	80.26	28	42	7.60E-06	R	R.TSMGGTQQQFVEGVR.M	M	Phospho (ST)	0.300000000000000.0
NaDOC, U	3	IPI00008868	Tax_Id=9606 Gene_Symbol=MAP1B Microtubule-associated protein 1B	162	271651	9	434	1	1	1047.4657	2092.9169	2	2092.8912	0.0257	0	55.59	27	42	0.0025	R	R.ASVSPMDEPVPDSESPIEK.V	V	Phospho (ST)	0.0003000000000000000.0
NaDOC, U	3	IPI00008868	Tax_Id=9606 Gene_Symbol=MAP1B Microtubule-associated protein 1B	162	271651	9	684	1	1	963.092	2886.2542	3	2886.1725	0.0817	0	73.79	32	43	4.20E-05	R	R.SEQSSMSIEFGQESPEQSLAMDFSR.Q	Q	Phospho (ST)	0.0000003000000000000000000.0
NaDOC, U	4	IPI00872944	Tax_Id=9606 Gene_Symbol=NUCKS1 34 kDa protein	158	33538	3	545	1	0	1159.4394	2316.8641	2	2316.8696	-0.0054	0	74.96	28	42	2.80E-05	K	K.VVDYSQFQESDDADEDYGR.D	D	Phospho (ST)	0.0000000003000000000.0
NaDOC, U	4	IPI00872944	Tax_Id=9606 Gene_Symbol=NUCKS1 34 kDa protein	158	33538	3	700	1	0	1000.7344	2999.1815	3	2999.1982	-0.0167	1	40.25	17	43	0.095	K	K.VVDYSQFQESDDADEDYGRDSGPPTK.K	K	Phospho (ST)	0.00000000030000000000000000.0
NaDOC, U	4	IPI00872944	Tax_Id=9606 Gene_Symbol=NUCKS1 34 kDa protein	158	33538	3	574	1	0	816.0031	2444.9876	3	2444.9646	0.023	1	87.78	22	42	1.60E-06	R	R.KVVDYSQFQESDDADEDYGR.D	D	Phospho (ST)	0.00000000003000000000.0
NaDOC, U	4	IPI00022145	Tax_Id=9606 Gene_Symbol=NUCKS1 Isoform 1 of Nuclear ubiquitous casein and cyclin-dependent kinases substrate	158	27280	3	545	1	1	1159.4394	2316.8641	2	2316.8696	-0.0054	0	74.96	28	42	2.80E-05	K	K.VVDYSQFQESDDADEDYGR.D	D	Phospho (ST)	0.0000000003000000000.0
NaDOC, U	4	IPI00022145	Tax_Id=9606 Gene_Symbol=NUCKS1 Isoform 1 of Nuclear ubiquitous casein and cyclin-dependent kinases substrate	158	27280	3	700	1	1	1000.7344	2999.1815	3	2999.1982	-0.0167	1	40.25	17	43	0.095	K	K.VVDYSQFQESDDADEDYGRDSGPPTK.K	K	Phospho (ST)	0.00000000030000000000000000.0
NaDOC, U	4	IPI00022145	Tax_Id=9606 Gene_Symbol=NUCKS1 Isoform 1 of Nuclear ubiquitous casein and cyclin-dependent kinases substrate	158	27280	3	574	1	1	816.0031	2444.9876	3	2444.9646	0.023	1	87.78	22	42	1.60E-06	R	R.KVVDYSQFQESDDADEDYGR.D	D	Phospho (ST)	0.00000000003000000000.0
NaDOC, U	5	IPI00024971	Tax_Id=9606 Gene_Symbol=OSBP Oxysterol-binding protein 1	156	90220	4	719	1	1	1058.0995	3171.2768	3	3171.284	-0.0072	1	87.87	24	43	1.70E-06	K	K.MLAESDESGDEESVSQTDKTELQNTLR.T	T	2 Phospho (ST)	0.000030030000000000000000000.0
NaDOC, U	5	IPI00024971	Tax_Id=9606 Gene_Symbol=OSBP Oxysterol-binding protein 1	156	90220	4	722	1	1	1063.4472	3187.3197	3	3187.2789	0.0408	1	74.22	23	43	4.00E-05	K	K.MLAESDESGDEESVSQTDKTELQNTLR.T	T	Oxidation (M); 2 Phospho (ST)	0.200030030000000000000000000.0
NaDOC, U	6	IPI00012442	Tax_Id=9606 Gene_Symbol=G3BP1 Ras GTPase-activating protein-binding protein 1	149	52189	2	397	1	1	982.9572	1963.8999	2	1963.8888	0.0112	0	103.68	37	42	3.60E-08	K	K.SSSPAPADIAQTVQEDLR.T	T	Phospho (ST)	0.003000000000000000.0
NaDOC, U	6	IPI00012442	Tax_Id=9606 Gene_Symbol=G3BP1 Ras GTPase-activating protein-binding protein 1	149	52189	2	739	1	1	1099.4584	3295.3534	3	3295.3242	0.0293	0	78.11	28	43	1.70E-05	R	R.YQDEVFGGFVTEPQEESEEEVEEPEER.Q	Q	Phospho (ST)	0.000000000000000030000000000.0
NaDOC, U	7	IPI00220739	Tax_Id=9606 Gene_Symbol=PGRMC1 Membrane-associated progesterone receptor component 1	135	21772	3	557	1	1	792.6604	2374.9593	3	2374.9325	0.0268	1	66.44	23	42	0.00021	K	K.EGEEPTVYSDEEEPKDESAR.K	K	Phospho (ST)	0.00000000300000000000.0
NaDOC, U	7	IPI00220739	Tax_Id=9606 Gene_Symbol=PGRMC1 Membrane-associated progesterone receptor component 1	135	21772	3	586	1	1	828.7194	2483.1364	3	2483.0966	0.0398	1	37.67	22	42	0.16	K	K.IVRGDQPAASGDSDDDEPPPLPR.L	L	Phospho (ST)	0.00000000000030000000000.0
NaDOC, U	7	IPI00220739	Tax_Id=9606 Gene_Symbol=PGRMC1 Membrane-associated progesterone receptor component 1	135	21772	3	454	1	1	1058.4345	2114.8544	2	2114.843	0.0114	0	77.65	25	42	1.50E-05	R	R.GDQPAASGDSDDDEPPPLPR.L	L	Phospho (ST)	0.00000000030000000000.0
NaDOC, U	8	IPI00789101	Tax_Id=9606 Gene_Symbol=PTGES3 19 kDa protein	132	19721	2	393	1	0	978.3343	1954.654	2	1954.62	0.0339	0	96.21	32	41	1.70E-07	K	K.DWEDDSDEDMSNFDR.F	F	Phospho (ST)	0.000003000000000.0
NaDOC, U	8	IPI00789101	Tax_Id=9606 Gene_Symbol=PTGES3 19 kDa protein	132	19335	2	393	1	0	978.3343	1954.654	2	1954.62	0.0339	0	96.21	32	41	1.70E-07	K	K.DWEDDSDEDMSNFDR.F	F	Phospho (ST)	0.000003000000000.0
NaDOC, U	8	IPI00789698	Tax_Id=9606 Gene_Symbol=PTGES3 19 kDa protein	132	19721	2	398	1	0	986.3188	1970.6231	2	1970.615	0.0082	0	65.56	28	40	0.00017	K	K.DWEDDSDEDMSNFDR.F	F	Oxidation (M); Phospho (ST)	0.000003000200000.0
NaDOC, U	8	IPI00789698	Tax_Id=9606 Gene_Symbol=PTGES3 19 kDa protein	132	19335	2	398	1	0	986.3188	1970.6231	2	1970.615	0.0082	0	65.56	28	40	0.00017	K	K.DWEDDSDEDMSNFDR.F	F	Oxidation (M); Phospho (ST)	0.000003000200000.0
NaDOC, U	8	IPI00015029	Tax_Id=9606 Gene_Symbol=PTGES3 Prostaglandin E synthase 3	132	18971	2	393	1	1	978.3343	1954.654	2	1954.62	0.0339	0	96.21	32	41	1.70E-07	K	K.DWEDDSDEDMSNFDR.F	F	Phospho (ST)	0.000003000000000.0
NaDOC, U	8	IPI00015029	Tax_Id=9606 Gene_Symbol=PTGES3 Prostaglandin E synthase 3	132	18971	2	398	1	1	986.3188	1970.6231	2	1970.615	0.0082	0	65.56	28	40	0.00017	K	K.DWEDDSDEDMSNFDR.F	F	Oxidation (M); Phospho (ST)	0.000003000200000.0
NaDOC, U	9	IPI00215948	Tax_Id=9606 Gene_Symbol=CTNNA1 Isoform 1 of Catenin alpha-1	118	100693	3	520	1	1	1119.9503	2237.8861	2	2237.8526	0.0336	0	93.3	32	42	4.40E-07	R	R.TPEELDDSDFETEDFDVR.S	S	Phospho (ST)	0.000000030000000000.0
NaDOC, U	9	IPI00215948	Tax_Id=9606 Gene_Symbol=CTNNA1 Isoform 1 of Catenin alpha-1	118	100693	3	602	1	1	854.6689	2560.9848	3	2560.952	0.0328	1	51.11	21	42	0.0074	R	R.TPEELDDSDFETEDFDVRSR.T	T	2 Phospho (ST)	0.00000003000000000030.0
NaDOC, U	9	IPI00473136	Tax_Id=9606 Gene_Symbol=CTNNA1 Isoform 2 of Catenin alpha-1	118	103426	3	520	1	0	1119.9503	2237.8861	2	2237.8526	0.0336	0	93.3	32	42	4.40E-07	R	R.TPEELDDSDFETEDFDVR.S	S	Phospho (ST)	0.000000030000000000.0
NaDOC, U	9	IPI00473136	Tax_Id=9606 Gene_Symbol=CTNNA1 Isoform 2 of Catenin alpha-1	118	103426	3	602	1	0	854.6689	2560.9848	3	2560.952	0.0328	1	51.11	21	42	0.0074	R	R.TPEELDDSDFETEDFDVRSR.T	T	2 Phospho (ST)	0.00000003000000000030.0
NaDOC, U	11	IPI00006865	Tax_Id=9606 Gene_Symbol=SEC22B Vesicle-trafficking protein SEC22b	107	24896	1	304	1	1	833.8905	1665.7665	2	1665.7723	-0.0059	0	106.95	31	41	1.60E-08	R	R.NLGSINTELQDVQR.I	I	Phospho (ST)	0.00030000000000.0
NaDOC, U	12	IPI00008998	Tax_Id=9606 Gene_Symbol=PTPLAD1 Protein tyrosine phosphatase-like protein PTPLAD1	106	44466	2	266	1	1	787.3145	1572.6145	2	1572.6167	-0.0022	0	76.88	25	41	1.60E-05	R	R.WLDESDAEMELR.A	A	Phospho (ST)	0.000030000000.0
NaDOC, U	12	IPI00008998	Tax_Id=9606 Gene_Symbol=PTPLAD1 Protein tyrosine phosphatase-like protein PTPLAD1	106	44466	2	270	1	1	795.3157	1588.6168	2	1588.6116	0.0052	0	50.14	18	41	0.0077	R	R.WLDESDAEMELR.A	A	Oxidation (M); Phospho (ST)	0.000030002000.0
NaDOC, U	12	IPI00879761	Tax_Id=9606 Gene_Symbol=PTPLAD1 similar to butyrate-induced transcript 1	106	26346	2	266	1	0	787.3145	1572.6145	2	1572.6167	-0.0022	0	76.88	25	41	1.60E-05	R	R.WLDESDAEMELR.A	A	Phospho (ST)	0.000030000000.0
NaDOC, U	12	IPI00879761	Tax_Id=9606 Gene_Symbol=PTPLAD1 similar to butyrate-induced transcript 1	106	26346	2	270	1	0	795.3157	1588.6168	2	1588.6116	0.0052	0	50.14	18	41	0.0077	R	R.WLDESDAEMELR.A	A	Oxidation (M); Phospho (ST)	0.000030002000.0
NaDOC, U	13	IPI00006079	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 1 of Bcl-2-associated transcription factor 1	102	106173	4	409	1	1	1001.3622	2000.7099	2	2000.6797	0.0303	0	60.3	25	42	0.00077	K	K.FNDSEGDDTEETEDYR.Q	Q	Phospho (ST)	0.0003000000000000.0
NaDOC, U	13	IPI00006079	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 1 of Bcl-2-associated transcription factor 1	102	106173	4	590	1	1	838.3357	2511.9854	3	2511.9955	-0.0101	1	46.83	18	42	0.02	R	R.AEGEWEDQEALDYFSDKESGK.Q	Q	Phospho (ST)	0.000000000000003000000.0
NaDOC, U	13	IPI00413671	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 2 of Bcl-2-associated transcription factor 1	102	105999	4	409	1	0	1001.3622	2000.7099	2	2000.6797	0.0303	0	60.3	25	42	0.00077	K	K.FNDSEGDDTEETEDYR.Q	Q	Phospho (ST)	0.0003000000000000.0
NaDOC, U	13	IPI00413671	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 2 of Bcl-2-associated transcription factor 1	102	105999	4	590	1	0	838.3357	2511.9854	3	2511.9955	-0.0101	1	46.83	18	42	0.02	R	R.AEGEWEDQEALDYFSDKESGK.Q	Q	Phospho (ST)	0.000000000000003000000.0
NaDOC, U	13	IPI00413672	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 3 of Bcl-2-associated transcription factor 1	102	100286	4	409	1	0	1001.3622	2000.7099	2	2000.6797	0.0303	0	60.3	25	42	0.00077	K	K.FNDSEGDDTEETEDYR.Q	Q	Phospho (ST)	0.0003000000000000.0
NaDOC, U	13	IPI00413672	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 3 of Bcl-2-associated transcription factor 1	102	100286	4	590	1	0	838.3357	2511.9854	3	2511.9955	-0.0101	1	46.83	18	42	0.02	R	R.AEGEWEDQEALDYFSDKESGK.Q	Q	Phospho (ST)	0.000000000000003000000.0
NaDOC, U	13	IPI00886854	Tax_Id=9606 Gene_Symbol=LOC731605 similar to BCL2-associated transcription factor 1 isoform 2	102	100251	4	409	1	0	1001.3622	2000.7099	2	2000.6797	0.0303	0	60.3	25	42	0.00077	K	K.FNDSEGDDTEETEDYR.Q	Q	Phospho (ST)	0.0003000000000000.0
NaDOC, U	13	IPI00886854	Tax_Id=9606 Gene_Symbol=LOC731605 similar to BCL2-associated transcription factor 1 isoform 2	102	100251	4	590	1	0	838.3357	2511.9854	3	2511.9955	-0.0101	1	46.83	18	42	0.02	R	R.AEGEWEDQEALDYFSDKESGK.Q	Q	Phospho (ST)	0.000000000000003000000.0
NaDOC, U	14	IPI00003419	Tax_Id=9606 Gene_Symbol=C11orf58 Small acidic protein	97	20377	2	635	1	1	891.0416	2670.1028	3	2670.0831	0.0198	1	59.63	23	43	0.0011	K	K.RSASPDDDLGSSNWEAADLGNEER.K	K	Phospho (ST)	0.000300000000000000000000.0
NaDOC, U	14	IPI00003419	Tax_Id=9606 Gene_Symbol=C11orf58 Small acidic protein	97	20377	2	591	1	1	839.0113	2514.0122	3	2513.982	0.0302	0	62.51	28	42	0.00053	R	R.SASPDDDLGSSNWEAADLGNEER.K	K	Phospho (ST)	0.00300000000000000000000.0
NaDOC, U	15	IPI00328753	Tax_Id=9606 Gene_Symbol=KTN1 Isoform 1 of Kinectin	95	156464	3	405	1	1	664.6175	1990.8306	3	1990.8269	0.0037	0	46.71	29	42	0.019	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC, U	15	IPI00337736	Tax_Id=9606 Gene_Symbol=KTN1 Isoform 2 of Kinectin	95	149804	3	405	1	0	664.6175	1990.8306	3	1990.8269	0.0037	0	46.71	29	42	0.019	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC, U	15	IPI00783726	Tax_Id=9606 Gene_Symbol=KTN1 kinectin 1 isoform b	95	150545	3	405	1	0	664.6175	1990.8306	3	1990.8269	0.0037	0	46.71	29	42	0.019	K	K.EIQNGNLHESDSESVPR.D	D	Deamidated (NQ); Phospho (ST)	0.00010000030000000.0
NaDOC, U	16	IPI00009032	Tax_Id=9606 Gene_Symbol=SSB Lupus La protein	95	46979	4	566	1	1	602.2347	2404.9096	4	2404.9557	-0.0461	1	56.07	25	42	0.0022	K	K.FASDDEHDEHDENGATGPVKR.A	A	Phospho (ST)	0.003000000000000000000.0
NaDOC, U	17	IPI00382995	Tax_Id=9606 Gene_Symbol=NDRG2 Cytoplasmic protein Ndr1	95	40076	1	227	1	0	715.3308	1428.6471	2	1428.6246	0.0225	0	94.64	30	41	2.50E-07	R	R.TASLTSAASVDGNR.S	S	Phospho (ST)	0.00300000000000.0
NaDOC, U	17	IPI00008994	Tax_Id=9606 Gene_Symbol=NDRG2 Isoform 1 of Protein NDRG2	95	41114	1	227	1	1	715.3308	1428.6471	2	1428.6246	0.0225	0	94.64	30	41	2.50E-07	R	R.TASLTSAASVDGNR.S	S	Phospho (ST)	0.00300000000000.0
NaDOC, U	17	IPI00218108	Tax_Id=9606 Gene_Symbol=NDRG2 Isoform 2 of Protein NDRG2	95	39607	1	227	1	0	715.3308	1428.6471	2	1428.6246	0.0225	0	94.64	30	41	2.50E-07	R	R.TASLTSAASVDGNR.S	S	Phospho (ST)	0.00300000000000.0
NaDOC, U	17	IPI00218109	Tax_Id=9606 Gene_Symbol=NDRG2 Isoform 3 of Protein NDRG2	95	39996	1	227	1	0	715.3308	1428.6471	2	1428.6246	0.0225	0	94.64	30	41	2.50E-07	R	R.TASLTSAASVDGNR.S	S	Phospho (ST)	0.00300000000000.0
NaDOC, U	17	IPI00384121	Tax_Id=9606 Gene_Symbol=NDRG2 Isoform 4 of Protein NDRG2	95	36371	1	227	1	0	715.3308	1428.6471	2	1428.6246	0.0225	0	94.64	30	41	2.50E-07	R	R.TASLTSAASVDGNR.S	S	Phospho (ST)	0.00300000000000.0
NaDOC, U	17	IPI00759789	Tax_Id=9606 Gene_Symbol=NDRG2 Isoform 5 of Protein NDRG2	95	37759	1	227	1	0	715.3308	1428.6471	2	1428.6246	0.0225	0	94.64	30	41	2.50E-07	R	R.TASLTSAASVDGNR.S	S	Phospho (ST)	0.00300000000000.0
NaDOC, U	18	IPI00004795	Tax_Id=9606 Gene_Symbol=CLNS1A Methylosome subunit pICln	92	26370	1	748	1	1	1132.1305	3393.3698	3	3393.3457	0.0241	1	91.63	29	43	7.10E-07	K	K.FEEESKEPVADEEEEDSDDDVEPITEFR.F	F	Phospho (ST)	0.0000000000000000300000000000.0
NaDOC, U	19	IPI00029400	Tax_Id=9606 Gene_Symbol=ZRANB2 Isoform 1 of Zinc finger Ran-binding domain-containing protein 2	88	37838	2	572	1	1	807.317	2418.929	3	2418.8959	0.0332	1	52.31	19	42	0.0055	K	K.EVEDKESEGEEEDEDEDLSK.Y	Y	Phospho (ST)	0.00000030000000000000.0
NaDOC, U	19	IPI00029400	Tax_Id=9606 Gene_Symbol=ZRANB2 Isoform 1 of Zinc finger Ran-binding domain-containing protein 2	88	37838	2	600	1	1	849.0128	2544.0165	3	2543.9965	0.02	1	56.08	22	42	0.0024	R	R.ENVEYIEREESDGEYDEFGR.K	K	Phospho (ST)	0.00000000003000000000.0
NaDOC, U	19	IPI00219866	Tax_Id=9606 Gene_Symbol=ZRANB2 Isoform 2 of Zinc finger Ran-binding domain-containing protein 2	88	36753	2	572	1	0	807.317	2418.929	3	2418.8959	0.0332	1	52.31	19	42	0.0055	K	K.EVEDKESEGEEEDEDEDLSK.Y	Y	Phospho (ST)	0.00000030000000000000.0
NaDOC, U	19	IPI00219866	Tax_Id=9606 Gene_Symbol=ZRANB2 Isoform 2 of Zinc finger Ran-binding domain-containing protein 2	88	36753	2	600	1	0	849.0128	2544.0165	3	2543.9965	0.02	1	56.08	22	42	0.0024	R	R.ENVEYIEREESDGEYDEFGR.K	K	Phospho (ST)	0.00000000003000000000.0
NaDOC, U	19	IPI00845348	Tax_Id=9606 Gene_Symbol=ZRANB2 Putative uncharacterized protein DKFZp686N09117	88	38569	2	572	1	0	807.317	2418.929	3	2418.8959	0.0332	1	52.31	19	42	0.0055	K	K.EVEDKESEGEEEDEDEDLSK.Y	Y	Phospho (ST)	0.00000030000000000000.0
NaDOC, U	19	IPI00845348	Tax_Id=9606 Gene_Symbol=ZRANB2 Putative uncharacterized protein DKFZp686N09117	88	38569	2	600	1	0	849.0128	2544.0165	3	2543.9965	0.02	1	56.08	22	42	0.0024	R	R.ENVEYIEREESDGEYDEFGR.K	K	Phospho (ST)	0.00000000003000000000.0
NaDOC, U	21	IPI00455423	Tax_Id=9606 Gene_Symbol=LOC440577 similar to nucleophosmin	87	20488	3	759	1	0	1154.1654	3459.4744	3	3459.4297	0.0447	0	50.25	19	43	0.01	K	K.CGSGPVHISGQHLVAVEEDAESEDEEEDVK.L	L	Phospho (ST)	0.000000000000000000000300000000.0
NaDOC, U	21	IPI00549248	Tax_Id=9606 Gene_Symbol=NPM1 Isoform 1 of Nucleophosmin	87	32726	3	759	1	0	1154.1654	3459.4744	3	3459.4297	0.0447	0	50.25	19	43	0.01	K	K.CGSGPVHISGQHLVAVEEDAESEDEEEDVK.L	L	Phospho (ST)	0.000000000000000000000300000000.0
NaDOC, U	21	IPI00220740	Tax_Id=9606 Gene_Symbol=NPM1 Isoform 2 of Nucleophosmin	87	29617	3	759	1	1	1154.1654	3459.4744	3	3459.4297	0.0447	0	50.25	19	43	0.01	K	K.CGSGPVHISGQHLVAVEEDAESEDEEEDVK.L	L	Phospho (ST)	0.000000000000000000000300000000.0
NaDOC, U	21	IPI00658013	Tax_Id=9606 Gene_Symbol=NPM1 nucleophosmin 1 isoform 3	87	28497	3	759	1	0	1154.1654	3459.4744	3	3459.4297	0.0447	0	50.25	19	43	0.01	K	K.CGSGPVHISGQHLVAVEEDAESEDEEEDVK.L	L	Phospho (ST)	0.000000000000000000000300000000.0
NaDOC, U	22	IPI00219774	Tax_Id=9606 Gene_Symbol=PRKAR2A cAMP-dependent protein kinase type II-alpha regulatory subunit	83	45832	2	607	1	0	864.3512	2590.0318	3	2590.0166	0.0151	1	52.45	26	43	0.0057	R	R.RVSVCAETYNPDEEEEDTDPR.V	V	Phospho (ST)	0.003000000000000000000.0
NaDOC, U	22	IPI00219774	Tax_Id=9606 Gene_Symbol=PRKAR2A cAMP-dependent protein kinase type II-alpha regulatory subunit	83	45832	2	622	1	0	878.353	2632.0373	3	2632.0466	-0.0094	1	56.85	27	42	0.002	R	R.VADAKGDSESEEDEDLEVPVPSR.F	F	2 Phospho (ST)	0.00000003030000000000000.0
NaDOC, U	22	IPI00063234	Tax_Id=9606 Gene_Symbol=PRKAR2A PRKAR2A protein	83	43382	2	607	1	1	864.3512	2590.0318	3	2590.0166	0.0151	1	52.45	26	43	0.0057	R	R.RVSVCAETYNPDEEEEDTDPR.V	V	Phospho (ST)	0.003000000000000000000.0
NaDOC, U	22	IPI00063234	Tax_Id=9606 Gene_Symbol=PRKAR2A PRKAR2A protein	83	43382	2	622	1	1	878.353	2632.0373	3	2632.0466	-0.0094	1	56.85	27	42	0.002	R	R.VADAKGDSESEEDEDLEVPVPSR.F	F	2 Phospho (ST)	0.00000003030000000000000.0
NaDOC, U	23	IPI00291946	Tax_Id=9606 Gene_Symbol=USP10 Ubiquitin carboxyl-terminal hydrolase 10	80	87707	1	710	1	1	1036.4176	3106.2309	3	3106.2061	0.0248	0	80.02	31	43	1.00E-05	K	K.NHSVNEEEQEEQGEGSEDEWEQVGPR.N	N	Phospho (ST)	0.00000000000000030000000000.0
NaDOC, U	24	IPI00514873	Tax_Id=9606 Gene_Symbol=C20orf30 17 kDa protein	80	17180	1	308	1	0	841.3701	1680.7256	2	1680.7284	-0.0028	0	79.95	27	41	7.90E-06	R	R.LSSTDDGYIDLQFK.K	K	Phospho (ST)	0.00300000000000.0
NaDOC, U	24	IPI00023023	Tax_Id=9606 Gene_Symbol=C20orf30 Chromosome 20 open reading frame 30	80	7987	1	308	1	1	841.3701	1680.7256	2	1680.7284	-0.0028	0	79.95	27	41	7.90E-06	R	R.LSSTDDGYIDLQFK.K	K	Phospho (ST)	0.00300000000000.0
NaDOC, U	24	IPI00746691	Tax_Id=9606 Gene_Symbol=C20orf30 Isoform 1 of UPF0414 transmembrane protein C20orf30	80	20069	1	308	1	0	841.3701	1680.7256	2	1680.7284	-0.0028	0	79.95	27	41	7.90E-06	R	R.LSSTDDGYIDLQFK.K	K	Phospho (ST)	0.00300000000000.0
NaDOC, U	24	IPI00641887	Tax_Id=9606 Gene_Symbol=C20orf30 Isoform 2 of UPF0414 transmembrane protein C20orf30	80	13180	1	308	1	0	841.3701	1680.7256	2	1680.7284	-0.0028	0	79.95	27	41	7.90E-06	R	R.LSSTDDGYIDLQFK.K	K	Phospho (ST)	0.00300000000000.0
NaDOC, U	27	IPI00179298	Tax_Id=9606 Gene_Symbol=HUWE1 482 kDa protein	75	485780	2	267	1	0	789.3115	1576.6085	2	1576.6042	0.0043	0	75.01	33	41	2.30E-05	R	R.GSGTASDDEFENLR.I	I	Phospho (ST)	0.00000300000000.0
NaDOC, U	27	IPI00746059	Tax_Id=9606 Gene_Symbol=HUWE1 HECT, UBA and WWE domain containing 1	75	376696	2	267	1	1	789.3115	1576.6085	2	1576.6042	0.0043	0	75.01	33	41	2.30E-05	R	R.GSGTASDDEFENLR.I	I	Phospho (ST)	0.00000300000000.0
NaDOC, U	27	IPI00456919	Tax_Id=9606 Gene_Symbol=HUWE1 Isoform 1 of E3 ubiquitin-protein ligase HUWE1	75	485523	2	267	1	0	789.3115	1576.6085	2	1576.6042	0.0043	0	75.01	33	41	2.30E-05	R	R.GSGTASDDEFENLR.I	I	Phospho (ST)	0.00000300000000.0
NaDOC, U	27	IPI00445401	Tax_Id=9606 Gene_Symbol=HUWE1 Isoform 2 of E3 ubiquitin-protein ligase HUWE1	75	483831	2	267	1	0	789.3115	1576.6085	2	1576.6042	0.0043	0	75.01	33	41	2.30E-05	R	R.GSGTASDDEFENLR.I	I	Phospho (ST)	0.00000300000000.0
NaDOC, U	27	IPI00643153	Tax_Id=9606 Gene_Symbol=HUWE1 Isoform 3 of E3 ubiquitin-protein ligase HUWE1	75	484651	2	267	1	0	789.3115	1576.6085	2	1576.6042	0.0043	0	75.01	33	41	2.30E-05	R	R.GSGTASDDEFENLR.I	I	Phospho (ST)	0.00000300000000.0
NaDOC, U	28	IPI00719821	Tax_Id=9606 Gene_Symbol=SAPS3 Isoform 1 of SAPS domain family member 3	74	98577	1	511	1	0	1110.4376	2218.8607	2	2218.858	0.0028	0	74.23	33	42	3.40E-05	R	R.IQQFDDGGSDEEDIWEEK.H	H	Phospho (ST)	0.000000003000000000.0
NaDOC, U	28	IPI00719553	Tax_Id=9606 Gene_Symbol=SAPS3 Isoform 2 of SAPS domain family member 3	74	97866	1	511	1	0	1110.4376	2218.8607	2	2218.858	0.0028	0	74.23	33	42	3.40E-05	R	R.IQQFDDGGSDEEDIWEEK.H	H	Phospho (ST)	0.000000003000000000.0
NaDOC, U	28	IPI00719345	Tax_Id=9606 Gene_Symbol=SAPS3 Isoform 3 of SAPS domain family member 3	74	89766	1	511	1	0	1110.4376	2218.8607	2	2218.858	0.0028	0	74.23	33	42	3.40E-05	R	R.IQQFDDGGSDEEDIWEEK.H	H	Phospho (ST)	0.000000003000000000.0
NaDOC, U	28	IPI00019540	Tax_Id=9606 Gene_Symbol=SAPS3 Isoform 4 of SAPS domain family member 3	74	89809	1	511	1	1	1110.4376	2218.8607	2	2218.858	0.0028	0	74.23	33	42	3.40E-05	R	R.IQQFDDGGSDEEDIWEEK.H	H	Phospho (ST)	0.000000003000000000.0
NaDOC, U	28	IPI00719725	Tax_Id=9606 Gene_Symbol=SAPS3 Isoform 5 of SAPS domain family member 3	74	99393	1	511	1	0	1110.4376	2218.8607	2	2218.858	0.0028	0	74.23	33	42	3.40E-05	R	R.IQQFDDGGSDEEDIWEEK.H	H	Phospho (ST)	0.000000003000000000.0
NaDOC, U	28	IPI00030624	Tax_Id=9606 Gene_Symbol=SAPS3 Isoform 6 of SAPS domain family member 3	74	95298	1	511	1	0	1110.4376	2218.8607	2	2218.858	0.0028	0	74.23	33	42	3.40E-05	R	R.IQQFDDGGSDEEDIWEEK.H	H	Phospho (ST)	0.000000003000000000.0
NaDOC, U	30	IPI00008527	Tax_Id=9606 Gene_Symbol=RPLP1 60S acidic ribosomal protein P1	74	11621	7	442	1	1	1055.3589	2108.7033	2	2108.6847	0.0186	1	51.55	18	41	0.0049	K	K.KEESEESDDDMGFGLFD.-	-	2 Phospho (ST)	0.00030030000000000.0
NaDOC, U	30	IPI00008527	Tax_Id=9606 Gene_Symbol=RPLP1 60S acidic ribosomal protein P1	74	11621	7	458	1	1	1063.36	2124.7054	2	2124.6796	0.0258	1	29.37		41	0.8	K	K.KEESEESDDDMGFGLFD.-	-	Oxidation (M); 2 Phospho (ST)	0.00030030002000000.0
NaDOC, U	30	IPI00008527	Tax_Id=9606 Gene_Symbol=RPLP1 60S acidic ribosomal protein P1	74	11621	7	443	1	1	1055.3594	2108.7043	2	2108.6847	0.0196	1	29.9	15	41	0.72	K	K.KEESEESDDDMGFGLFD.-	-	2 Phospho (ST)	0.00030030000000000.0
NaDOC, U	30	IPI00412779	Tax_Id=9606 Gene_Symbol=RPLP1 ribosomal protein P1 isoform 2	74	8912	7	442	1	0	1055.3589	2108.7033	2	2108.6847	0.0186	1	51.55	18	41	0.0049	K	K.KEESEESDDDMGFGLFD.-	-	2 Phospho (ST)	0.00030030000000000.0
NaDOC, U	30	IPI00412779	Tax_Id=9606 Gene_Symbol=RPLP1 ribosomal protein P1 isoform 2	74	8912	7	458	1	0	1063.36	2124.7054	2	2124.6796	0.0258	1	29.37		41	0.8	K	K.KEESEESDDDMGFGLFD.-	-	Oxidation (M); 2 Phospho (ST)	0.00030030002000000.0
NaDOC, U	30	IPI00412779	Tax_Id=9606 Gene_Symbol=RPLP1 ribosomal protein P1 isoform 2	74	8912	7	443	1	0	1055.3594	2108.7043	2	2108.6847	0.0196	1	29.9	15	41	0.72	K	K.KEESEESDDDMGFGLFD.-	-	2 Phospho (ST)	0.00030030000000000.0
NaDOC, U	30	IPI00008529	Tax_Id=9606 Gene_Symbol=RPLP2 60S acidic ribosomal protein P2	74	11658	7	442	1	0	1055.3589	2108.7033	2	2108.6847	0.0186	1	51.55	18	41	0.0049	K	K.KEESEESDDDMGFGLFD.-	-	2 Phospho (ST)	0.00030030000000000.0
NaDOC, U	30	IPI00008529	Tax_Id=9606 Gene_Symbol=RPLP2 60S acidic ribosomal protein P2	74	11658	7	458	1	0	1063.36	2124.7054	2	2124.6796	0.0258	1	29.37		41	0.8	K	K.KEESEESDDDMGFGLFD.-	-	Oxidation (M); 2 Phospho (ST)	0.00030030002000000.0
NaDOC, U	30	IPI00008529	Tax_Id=9606 Gene_Symbol=RPLP2 60S acidic ribosomal protein P2	74	11658	7	443	1	0	1055.3594	2108.7043	2	2108.6847	0.0196	1	29.9	15	41	0.72	K	K.KEESEESDDDMGFGLFD.-	-	2 Phospho (ST)	0.00030030000000000.0
NaDOC, U	33	IPI00639842	Tax_Id=9606 Gene_Symbol=KRI1 68 kDa protein	68	68260	1	546	1	0	1160.4989	2318.9832	2	2318.9427	0.0404	0	67.6	25	42	0.00016	R	R.AFVEDSEDEDGAGEGGSSLLQK.R	R	Phospho (ST)	0.0000030000000000000000.0
NaDOC, U	33	IPI00798034	Tax_Id=9606 Gene_Symbol=KRI1 Isoform 1 of Protein KRI1 homolog	68	83657	1	546	1	0	1160.4989	2318.9832	2	2318.9427	0.0404	0	67.6	25	42	0.00016	R	R.AFVEDSEDEDGAGEGGSSLLQK.R	R	Phospho (ST)	0.0000030000000000000000.0
NaDOC, U	33	IPI00186139	Tax_Id=9606 Gene_Symbol=KRI1 Isoform 2 of Protein KRI1 homolog	68	83062	1	546	1	1	1160.4989	2318.9832	2	2318.9427	0.0404	0	67.6	25	42	0.00016	R	R.AFVEDSEDEDGAGEGGSSLLQK.R	R	Phospho (ST)	0.0000030000000000000000.0
NaDOC, U	34	IPI00402231	Tax_Id=9606 Gene_Symbol=DNAJC5 Isoform 1 of DnaJ homolog subfamily C member 5	67	22933	1	371	1	0	943.4568	1884.8991	2	1884.887	0.0121	0	67.26	32	42	0.00016	R	R.SLSTSGESLYHVLGLDK.N	N	Phospho (ST)	0.00030000000000000.0
NaDOC, U	34	IPI00023780	Tax_Id=9606 Gene_Symbol=DNAJC5 Isoform 2 of DnaJ homolog subfamily C member 5	67	19587	1	371	1	1	943.4568	1884.8991	2	1884.887	0.0121	0	67.26	32	42	0.00016	R	R.SLSTSGESLYHVLGLDK.N	N	Phospho (ST)	0.00030000000000000.0
NaDOC, U	35	IPI00871851	Tax_Id=9606 Gene_Symbol=SEPT2 Septin	66	42886	1	592	1	0	839.6943	2516.0609	3	2516.038	0.0229	1	65.68	30	42	0.00026	K	K.IYHLPDAESDEDEDFKEQTR.L	L	Phospho (ST)	0.00000000300000000000.0

NaDOC, U	35	IPI00014177	Tax_Id=9606 Gene_Symbol=SEPT2 Septin-2	66	41689	1	592	1	1	839.6943	2516.0609	3	2516.038	0.0229	1	65.68	30	42	0.00026	K	K.IYHLPDAESDEDEDFKEQTR.L	L	Phospho (ST)	0.00000000300000000000.0
NaDOC, U	36	IPI00410079	Tax_Id=9606 Gene_Symbol=FAM82C Isoform 1 of Protein FAM82C	63	52542	2	417	1	1	1023.4546	2044.8947	2	2044.8739	0.0208	0	65.24	28	42	0.00026	R	R.SQSLPNSLDYTQTSDPGR.H	H	Phospho (ST)	0.003000000000000000.0
NaDOC, U	37	IPI00171422	Tax_Id=9606 Gene_Symbol=TMEM87A cDNA FLJ76697	63	63798	1	677	1	1	950.7911	2849.3516	3	2849.3008	0.0508	0	63.28	36	42	0.00042	K	K.WVEENVPSSVTDVALPALLDSDEER.M	M	Phospho (ST)	0.00000000000000000000030000.0
NaDOC, U	37	IPI00783698	Tax_Id=9606 Gene_Symbol=TMEM87A Isoform 1 of Transmembrane protein 87A precursor	63	63788	1	677	1	0	950.7911	2849.3516	3	2849.3008	0.0508	0	63.28	36	42	0.00042	K	K.WVEENVPSSVTDVALPALLDSDEER.M	M	Phospho (ST)	0.00000000000000000000030000.0
NaDOC, U	37	IPI00816013	Tax_Id=9606 Gene_Symbol=TMEM87A Isoform 3 of Transmembrane protein 87A precursor	63	57136	1	677	1	0	950.7911	2849.3516	3	2849.3008	0.0508	0	63.28	36	42	0.00042	K	K.WVEENVPSSVTDVALPALLDSDEER.M	M	Phospho (ST)	0.00000000000000000000030000.0
NaDOC, U	39	IPI00878314	Tax_Id=9606 Gene_Symbol=MAP4 110 kDa protein	60	109936	3	296	1	0	814.3956	1626.7766	2	1626.7576	0.019	1	53.53	34	41	0.0033	K	K.DMESPTKLDVTLAK.D	D	Phospho (ST)	0.00030000000000.0
NaDOC, U	39	IPI00878314	Tax_Id=9606 Gene_Symbol=MAP4 110 kDa protein	60	109936	3	302	1	0	822.3751	1642.7356	2	1642.7525	-0.0169	1	37.72	28	41	0.13	K	K.DMESPTKLDVTLAK.D	D	Oxidation (M); Phospho (ST)	0.02030000000000.0
NaDOC, U	39	IPI00871726	Tax_Id=9606 Gene_Symbol=MAP4 128 kDa protein	60	128795	3	296	1	0	814.3956	1626.7766	2	1626.7576	0.019	1	53.53	34	41	0.0033	K	K.DMESPTKLDVTLAK.D	D	Phospho (ST)	0.00030000000000.0
NaDOC, U	39	IPI00871726	Tax_Id=9606 Gene_Symbol=MAP4 128 kDa protein	60	128795	3	302	1	0	822.3751	1642.7356	2	1642.7525	-0.0169	1	37.72	28	41	0.13	K	K.DMESPTKLDVTLAK.D	D	Oxidation (M); Phospho (ST)	0.02030000000000.0
NaDOC, U	39	IPI00396171	Tax_Id=9606 Gene_Symbol=MAP4 Isoform 1 of Microtubule-associated protein 4	60	121457	3	296	1	0	814.3956	1626.7766	2	1626.7576	0.019	1	53.53	34	41	0.0033	K	K.DMESPTKLDVTLAK.D	D	Phospho (ST)	0.00030000000000.0
NaDOC, U	39	IPI00396171	Tax_Id=9606 Gene_Symbol=MAP4 Isoform 1 of Microtubule-associated protein 4	60	121457	3	302	1	0	822.3751	1642.7356	2	1642.7525	-0.0169	1	37.72	28	41	0.13	K	K.DMESPTKLDVTLAK.D	D	Oxidation (M); Phospho (ST)	0.02030000000000.0
NaDOC, U	39	IPI00220113	Tax_Id=9606 Gene_Symbol=MAP4 Isoform 2 of Microtubule-associated protein 4	60	103241	3	296	1	0	814.3956	1626.7766	2	1626.7576	0.019	1	53.53	34	41	0.0033	K	K.DMESPTKLDVTLAK.D	D	Phospho (ST)	0.00030000000000.0
NaDOC, U	39	IPI00220113	Tax_Id=9606 Gene_Symbol=MAP4 Isoform 2 of Microtubule-associated protein 4	60	103241	3	302	1	0	822.3751	1642.7356	2	1642.7525	-0.0169	1	37.72	28	41	0.13	K	K.DMESPTKLDVTLAK.D	D	Oxidation (M); Phospho (ST)	0.02030000000000.0
NaDOC, U	39	IPI00470852	Tax_Id=9606 Gene_Symbol=MAP4 Isoform 5 of Microtubule-associated protein 4	60	85485	3	296	1	1	814.3956	1626.7766	2	1626.7576	0.019	1	53.53	34	41	0.0033	K	K.DMESPTKLDVTLAK.D	D	Phospho (ST)	0.00030000000000.0
NaDOC, U	39	IPI00470852	Tax_Id=9606 Gene_Symbol=MAP4 Isoform 5 of Microtubule-associated protein 4	60	85485	3	302	1	1	822.3751	1642.7356	2	1642.7525	-0.0169	1	37.72	28	41	0.13	K	K.DMESPTKLDVTLAK.D	D	Oxidation (M); Phospho (ST)	0.02030000000000.0
NaDOC, U	39	IPI00888475	Tax_Id=9606 Gene_Symbol=MAP4 Isoform 6 of Microtubule-associated protein 4	60	120354	3	296	1	0	814.3956	1626.7766	2	1626.7576	0.019	1	53.53	34	41	0.0033	K	K.DMESPTKLDVTLAK.D	D	Phospho (ST)	0.00030000000000.0
NaDOC, U	39	IPI00888475	Tax_Id=9606 Gene_Symbol=MAP4 Isoform 6 of Microtubule-associated protein 4	60	120354	3	302	1	0	822.3751	1642.7356	2	1642.7525	-0.0169	1	37.72	28	41	0.13	K	K.DMESPTKLDVTLAK.D	D	Oxidation (M); Phospho (ST)	0.02030000000000.0
NaDOC, U	40	IPI00025512	Tax_Id=9606 Gene_Symbol=HSPB1 Heat shock protein beta-1	60	22826	1	140	1	1	578.2715	1154.5285	2	1154.5332	-0.0047	0	60.2	37	40	0.00056	R	R.QLSSGVSEIR.H	H	Phospho (ST)	0.0030000000.0
NaDOC, U	41	IPI00007764	Tax_Id=9606 Gene_Symbol=HN1 Isoform 1 of Hematological and neurological expressed 1 protein	60	16005	1	311	1	1	853.3721	1704.7296	2	1704.7356	-0.006	1	60.1	33	42	0.0008	R	R.RNSSEASSGDFLDLK.G	G	Phospho (ST)	0.003000000000000.0
NaDOC, U	41	IPI00384857	Tax_Id=9606 Gene_Symbol=HN1 Isoform 2 of Hematological and neurological expressed 1 protein	60	20360	1	311	1	0	853.3721	1704.7296	2	1704.7356	-0.006	1	60.1	33	42	0.0008	R	R.RNSSEASSGDFLDLK.G	K	Phospho (ST)	0.003000000000000.0
NaDOC, U	41	IPI00447316	Tax_Id=9606 Gene_Symbol=HN1 Isoform 3 of Hematological and neurological expressed 1 protein	60	11016	1	311	1	0	853.3721	1704.7296	2	1704.7356	-0.006	1	60.1	33	42	0.0008	R	R.RNSSEASSGDFLDLK.G	G	Phospho (ST)	0.003000000000000.0
NaDOC, U	44	IPI00304589	Tax_Id=9606 Gene_Symbol=TNKS1BP1 Isoform 1 of 182 kDa tankyrase 1-binding protein	58	182697	1	271	1	1	795.3229	1588.6312	2	1588.6195	0.0117	0	57.86	26	42	0.0013	R	R.SQEADVQDWEFR.K	K	Phospho (ST)	0.300000000000.0
NaDOC, U	44	IPI00855787	Tax_Id=9606 Gene_Symbol=TNKS1BP1 tankyrase 1-binding protein 1	58	182711	1	271	1	0	795.3229	1588.6312	2	1588.6195	0.0117	0	57.86	26	42	0.0013	R	R.SQEADVQDWEFR.K	K	Phospho (ST)	0.300000000000.0
NaDOC, U	46	IPI00299254	Tax_Id=9606 Gene_Symbol=EIF5B Eukaryotic translation initiation factor 5B	57	139171	2	452	1	1	705.2958	2112.8656	3	2112.8637	0.0019	0	57.04	22	42	0.0018	K	K.NKPGPNIESGNEDDDASFK.I	I	Phospho (ST)	0.0000000030000000000.0
NaDOC, U	47	IPI00013881	Tax_Id=9606 Gene_Symbol=HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	57	49484	2	336	1	1	882.8682	1763.7218	2	1763.7265	-0.0046	0	56.64	23	42	0.0017	K	K.HTGPNSPDTANDGFVR.L	L	Phospho (ST)	0.0000030000000000.0
NaDOC, U	47	IPI00479191	Tax_Id=9606 Gene_Symbol=HNRNPH1 HNRPH1 protein	57	51482	2	336	1	0	882.8682	1763.7218	2	1763.7265	-0.0046	0	56.64	23	42	0.0017	K	K.HTGPNSPDTANDGFVR.L	L	Phospho (ST)	0.0000030000000000.0
NaDOC, U	50	IPI00438229	Tax_Id=9606 Gene_Symbol=TRIM28 Isoform 1 of Transcription intermediary factor 1-beta	53	90261	1	231	1	1	722.8147	1443.6149	2	1443.6177	-0.0028	1	53.34	33	41	0.0032	R	R.SRSGEGEVSGLMR.K	K	Phospho (ST)	0.0030000000000.0
NaDOC, U	50	IPI00438230	Tax_Id=9606 Gene_Symbol=TRIM28 Isoform 2 of Transcription intermediary factor 1-beta	53	80621	1	231	1	0	722.8147	1443.6149	2	1443.6177	-0.0028	1	53.34	33	41	0.0032	R	R.SRSGEGEVSGLMR.K	K	Phospho (ST)	0.0030000000000.0
NaDOC, U	51	IPI00306301	Tax_Id=9606 Gene_Symbol=PDHA1 Mitochondrial PDHA1	52	48290	2	305	1	0	558.2271	1671.6596	3	1671.6501	0.0095	0	34.11	26	41	0.3	R	R.YHGHSMSDPGVSYR.T	T	Phospho (ST)	0.00003000000000.0
NaDOC, U	51	IPI00306301	Tax_Id=9606 Gene_Symbol=PDHA1 Mitochondrial PDHA1	52	48290	2	329	1	0	584.8717	1751.5933	3	1751.6164	-0.0231	0	46.21	31	41	0.017	R	R.YHGHSMSDPGVSYR.T	T	2 Phospho (ST)	0.00003000000300.0
NaDOC, U	51	IPI00642820	Tax_Id=9606 Gene_Symbol=PDHA1 Pyruvate dehydrogenase (Lipoamide) alpha 1	52	12580	2	305	1	1	558.2271	1671.6596	3	1671.6501	0.0095	0	34.11	26	41	0.3	R	R.YHGHSMSDPGVSYR.T	T	Phospho (ST)	0.00003000000000.0
NaDOC, U	51	IPI00642820	Tax_Id=9606 Gene_Symbol=PDHA1 Pyruvate dehydrogenase (Lipoamide) alpha 1	52	12580	2	329	1	1	584.8717	1751.5933	3	1751.6164	-0.0231	0	46.21	31	41	0.017	R	R.YHGHSMSDPGVSYR.T	T	2 Phospho (ST)	0.00003000000300.0
NaDOC, U	51	IPI00024087	Tax_Id=9606 Gene_Symbol=PDHA2 Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial precursc	52	43647	2	305	1	0	558.2271	1671.6596	3	1671.6501	0.0095	0	34.11	26	41	0.3	R	R.YHGHSMSDPGVSYR.T	T	Phospho (ST)	0.00003000000000.0
NaDOC, U	51	IPI00024087	Tax_Id=9606 Gene_Symbol=PDHA2 Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial precursc	52	43647	2	329	1	0	584.8717	1751.5933	3	1751.6164	-0.0231	0	46.21	31	41	0.017	R	R.YHGHSMSDPGVSYR.T	T	2 Phospho (ST)	0.00003000000300.0
NaDOC, U	54	IPI00791887	Tax_Id=9606 Gene_Symbol=TOMM70A 25 kDa protein	51	25378	2	577	1	0	817.3596	2449.0568	3	2449.0482	0.0087	0	47.16	18	42	0.019	R	R.ASPAPGSGHPEGPGAHLDMNSLDR.A	A	Phospho (ST)	0.0300000000000000000000000.0
NaDOC, U	54	IPI00015602	Tax_Id=9606 Gene_Symbol=TOMM70A Mitochondrial precursor proteins import receptor	51	68096	2	577	1	1	817.3596	2449.0568	3	2449.0482	0.0087	0	47.16	18	42	0.019	R	R.ASPAPGSGHPEGPGAHLDMNSLDR.A	A	Phospho (ST)	0.0300000000000000000000000.0
NaDOC, U	55	IPI00386569	Tax_Id=9606 Gene_Symbol=TTLL12 Putative uncharacterized protein	50	23944	1	638	1	1	895.7698	2684.2877	3	2684.2595	0.0281	0	50.34	23	42	0.0079	R	R.SSPGQTPEEGAQALAEFAALHGPALR.A	A	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	55	IPI00879002	Tax_Id=9606 Gene_Symbol=TTLL12 Tubulin tyrosine ligase-like family, member 12	50	74185	1	638	1	0	895.7698	2684.2877	3	2684.2595	0.0281	0	50.34	23	42	0.0079	R	R.SSPGQTPEEGAQALAEFAALHGPALR.A	A	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	55	IPI00029048	Tax_Id=9606 Gene_Symbol=TTLL12 Tubulin--tyrosine ligase-like protein 12	50	75154	1	638	1	0	895.7698	2684.2877	3	2684.2595	0.0281	0	50.34	23	42	0.0079	R	R.SSPGQTPEEGAQALAEFAALHGPALR.A	A	Phospho (ST)	0.00000300000000000000000000.0
NaDOC, U	56	IPI00306825	Tax_Id=9606 Gene_Symbol=TPD52L2 Isoform 1 of Tumor protein D54	50	22281	1	208	1	0	691.2983	1380.582	2	1380.5711	0.0109	1	50.2	25	41	0.0062	R	R.NSATFKSFEDR.V	V	Phospho (ST)	0.00000030000.0
NaDOC, U	56	IPI00221178	Tax_Id=9606 Gene_Symbol=TPD52L2 Isoform 2 of Tumor protein D54	50	19946	1	208	1	1	691.2983	1380.582	2	1380.5711	0.0109	1	50.2	25	41	0.0062	R	R.NSATFKSFEDR.V	V	Phospho (ST)	0.00000030000.0
NaDOC, U	56	IPI00399265	Tax_Id=9606 Gene_Symbol=TPD52L2 tumor protein D52-like 2 isoform a	50	24896	1	208	1	0	691.2983	1380.582	2	1380.5711	0.0109	1	50.2	25	41	0.0062	R	R.NSATFKSFEDR.V	V	Phospho (ST)	0.00000030000.0
NaDOC, U	56	IPI00399266	Tax_Id=9606 Gene_Symbol=TPD52L2 tumor protein D52-like 2 isoform b	50	22560	1	208	1	0	691.2983	1380.582	2	1380.5711	0.0109	1	50.2	25	41	0.0062	R	R.NSATFKSFEDR.V	V	Phospho (ST)	0.00000030000.0
NaDOC, U	56	IPI00399267	Tax_Id=9606 Gene_Symbol=TPD52L2 tumor protein D52-like 2 isoform c	50	23829	1	208	1	0	691.2983	1380.582	2	1380.5711	0.0109	1	50.2	25	41	0.0062	R	R.NSATFKSFEDR.V	V	Phospho (ST)	0.00000030000.0
NaDOC, U	56	IPI00399268	Tax_Id=9606 Gene_Symbol=TPD52L2 tumor protein D52-like 2 isoform d	50	21494	1	208	1	0	691.2983	1380.582	2	1380.5711	0.0109	1	50.2	25	41	0.0062	R	R.NSATFKSFEDR.V	V	Phospho (ST)	0.00000030000.0
NaDOC, U	56	IPI00743469	Tax_Id=9606 Gene_Symbol=TPD52L2 Uncharacterized protein TPD52L2 (Fragment)	50	23782	1	208	1	0	691.2983	1380.582	2	1380.5711	0.0109	1	50.2	25	41	0.0062	R	R.NSATFKSFEDR.V	V	Phospho (ST)	0.00000030000.0
NaDOC, U	59	IPI00217952	Tax_Id=9606 Gene_Symbol=GFPT1 Isoform 1 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	48	79555	1	285	1	1	802.8582	1603.7018	2	1603.6841	0.0177	0	47.8	26	41	0.013	R	R.VDSTTCLFPVEEK.A	A	Phospho (ST)	0.0003000000000.0
NaDOC, U	59	IPI00299506	Tax_Id=9606 Gene_Symbol=GFPT1 Isoform 2 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	48	77509	1	285	1	0	802.8582	1603.7018	2	1603.6841	0.0177	0	47.8	26	41	0.013	R	R.VDSTTCLFPVEEK.A	A	Phospho (ST)	0.0003000000000.0
NaDOC, U	60	IPI00289819	Tax_Id=9606 Gene_Symbol=IGF2R Cation-independent mannose-6-phosphate receptor precursor	47	281056	2	605	1	1	859.7319	2576.174	3	2576.1531	0.0209	0	51.56	26	42	0.0065	K	K.ALSSLHGDDQDSEDEVLTIPEVK.V	V	Phospho (ST)	0.00000000000300000000000.0
NaDOC, U	61	IPI00002349	Tax_Id=9606 Gene_Symbol=NUFIP2 Nuclear fragile X mental retardation-interacting protein 2	46	76132	1	176	1	1	638.756	1275.4974	2	1275.4921	0.0053	0	45.79	34	41	0.017	R	R.NDSWGSFDLR.A	A	Phospho (ST)	0.0030000000.0
NaDOC, U	62	IPI00016250	Tax_Id=9606 Gene_Symbol=FXR2 Fragile X mental retardation syndrome-related protein 2	46	77424	1	537	1	1	766.3353	2295.984	3	2295.9774	0.0066	1	45.64	22	42	0.025	R	R.TDGSISGDRQPVTVADYISR.A	A	2 Phospho (ST)	0.00030300000000000000.0
NaDOC, U	64	IPI00647720	Tax_Id=9606 Gene_Symbol=SRRM1 Isoform 1 of Serine/arginine repetitive matrix protein 1	44	102331	2	228	1	0	717.3486	1432.6827	2	1432.685	-0.0023	1	43.77	22	41	0.03	K	K.EKTPELPEPSVK.V	V	Phospho (ST)	0.003000000000.0
NaDOC, U	64	IPI00328293	Tax_Id=9606 Gene_Symbol=SRRM1 Uncharacterized protein SRRM1	44	103386	2	228	1	1	717.3486	1432.6827	2	1432.685	-0.0023	1	43.77	22	41	0.03	K	K.EKTPELPEPSVK.V	V	Phospho (ST)	0.003000000000.0
NaDOC, U	65	IPI00185919	Tax_Id=9606 Gene_Symbol=LARP1 Isoform 1 of La-related protein 1	40	123833	3	254	1	1	770.8604	1539.7062	2	1539.697	0.0091	0	38.38	28	41	0.11	R	R.SLPTTVPESPNYR.N	N	Phospho (ST)	0.0000000030000.0
NaDOC, U	65	IPI00643027	Tax_Id=9606 Gene_Symbol=LARP1 Isoform 2 of La-related protein 1	40	123320	3	254	1	0	770.8604	1539.7062	2	1539.697	0.0091	0	38.38	28	41	0.11	R	R.SLPTTVPESPNYR.N	N	Phospho (ST)	0.0000000030000.0
NaDOC, U	65	IPI00411690	Tax_Id=9606 Gene_Symbol=LARP1 Isoform 3 of La-related protein 1	40	116792	3	254	1	0	770.8604	1539.7062	2	1539.697	0.0091	0	38.38	28	41	0.11	R	R.SLPTTVPESPNYR.N	N	Phospho (ST)	0.0000000030000.0
NaDOC, U	69	IPI00104050	Tax_Id=9606 Gene_Symbol=THRAP3 Thyroid hormone receptor-associated protein 3	38	108658	1	123	1	1	558.2508	1114.4871	2	1114.506	-0.0189	0	37.83	30	40	0.094	R	R.IDISPSTFR.K	K	Phospho (ST)	0.000300000.0
NaDOC, U	70	IPI00003394	Tax_Id=9606 Gene_Symbol=LOC100133836;SMN2;SMN1;LOC100133835 Isoform SMN of Survival motor neuron protein	38	32285	1	435	1	1	1048.9251	2095.8355	2	2095.8024	0.0331	0	37.74	20	42	0.15	R	R.GTGQSDDSDIWDDTALIK.A	A	2 Phospho (ST)	0.0000300300000000000.0
NaDOC, U	70	IPI00219360	Tax_Id=9606 Gene_Symbol=LOC100133836;SMN2;SMN1;LOC100133835 Isoform SMN-delta5 of Survival motor neuron protein	38	28915	1	435	1	0	1048.9251	2095.8355	2	2095.8024	0.0331	0	37.74	20	42	0.15	R	R.GTGQSDDSDIWDDTALIK.A	A	2 Phospho (ST)	0.0000300300000000000.0
NaDOC, U	70	IPI00009598	Tax_Id=9606 Gene_Symbol=LOC100133836;SMN2;SMN1;LOC100133835 Isoform SMN-delta57 of Survival motor neuron protein	38	27460	1	435	1	0	1048.9251	2095.8355	2	2095.8024	0.0331	0	37.74	20	42	0.15	R	R.GTGQSDDSDIWDDTALIK.A	A	2 Phospho (ST)	0.0000300300000000000.0
NaDOC, U	70	IPI00009597	Tax_Id=9606 Gene_Symbol=LOC100133836;SMN2;SMN1;LOC100133835 Isoform SMN-delta7 of Survival motor neuron protein	38	30830	1	435	1	0	1048.9251	2095.8355	2	2095.8024	0.0331	0	37.74	20	42	0.15	R	R.GTGQSDDSDIWDDTALIK.A	A	2 Phospho (ST)	0.0000300300000000000.0
NaDOC, U	72	IPI00184330	Tax_Id=9606 Gene_Symbol=MCM2 DNA replication licensing factor MCM2	37	102516	1	399	1	1	987.4143	1972.814	2	1972.8051	0.0089	0	37.07	28	42	0.17	R	R.GLLYDSDEEDEERPAR.K	K	Phospho (ST)	0.0000030000000000.0
NaDOC, U	76	IPI00479786	Tax_Id=9606 Gene_Symbol=KHSRP Isoform 1 of Far upstream element-binding protein 2	36	73443	1	229	1	1	717.8335	1433.6525	2	1433.6552	-0.0027	0	36.29	23	41	0.17	K	K.VQISPDSGGLPER.S	S	Phospho (ST)	0.0003000000000.0
NaDOC, U	76	IPI00855957	Tax_Id=9606 Gene_Symbol=KHSRP Isoform 2 of Far upstream element-binding protein 2	36	73410	1	229	1	0	717.8335	1433.6525	2	1433.6552	-0.0027	0	36.29	23	41	0.17	K	K.VQISPDSGGLPER.S	S	Phospho (ST)	0.0003000000000.0
NaDOC, U	79	IPI00020984	Tax_Id=9606 Gene_Symbol=CANX Calnexin precursor	36	67982	3	248	1	0	754.8425	1507.6705	2	1507.6667	0.0037	1	37.01	29	41	0.14	K	K.AEEDEILNRSPR.N	N	Phospho (ST)	0.000000000300.0
NaDOC, U	80	IPI00240812	Tax_Id=9606 Gene_Symbol=PDS5B Isoform 1 of Sister chromatid cohesion protein PDS5 homolog B	35	165905	1	394	1	1	978.9374	1955.8603	2	1955.8361	0.0242	0	34.69	20	42	0.29	R	R.AESPESSAIESTQSTPQK.G	G	Phospho (ST)	0.003000000000000000.0
NaDOC, U	80	IPI00845446	Tax_Id=9606 Gene_Symbol=PDS5B Isoform 2 of Sister chromatid cohesion protein PDS5 homolog B	35	159435	1	394	1	0	978.9374	1955.8603	2	1955.8361	0.0242	0	34.69	20	42	0.29	R	R.AESPESSAIESTQSTPQK.G	G	Phospho (ST)	0.003000000000000000.0
NaDOC, U	81	IPI00292387	Tax_Id=9606 Gene_Symbol=NOLC1 Isoform Alpha of Nucleolar phosphoprotein p130	34	73560	1	326	1	1	873.9045	1745.7944	2	1745.7873	0.0071	1	33.58	17	42	0.36	R	R.GGSISVQVNSIKFDSE.-	-	Phospho (ST)	0.0000000000000030.0
NaDOC, U	81	IPI00216654	Tax_Id=9606 Gene_Symbol=NOLC1 Isoform Beta of Nucleolar phosphoprotein p130	34	74702	1	326	1	0	873.9045	1745.7944	2	1745.7873	0.0071	1	33.58	17	42	0.36	R	R.GGSISVQVNSIKFDSE.-	-	Phospho (ST)	0.0000000000000030.0
NaDOC, U	82	IPI00020060	Tax_Id=9606 Gene_Symbol=SLC9A1 Isoform 1 of Sodium/hydrogen exchanger 1	33	91218	1	632	1	1	887.3809	2659.1207	3	2659.1287	-0.0079	1	32.87	21	42	0.51	R	R.SKETSSPGTDDVFTPAPSDSPSSQR.I	I	Phospho (ST)	0.0000000000000000000300000.0
NaDOC, U	82	IPI00641616	Tax_Id=9606 Gene_Symbol=SLC9A1 Solute carrier family 9 (Sodium/hydrogen exchanger), member 1	33	36313	1	632	1	0	887.3809	2659.1207	3	2659.1287	-0.0079	1	32.87	21	42	0.51	R	R.SKETSSPGTDDVFTPAPSDSPSSQR.I	I	Phospho (ST)	0.0000000000000000000300000.0
NaDOC, U	82	IPI00646455	Tax_Id=9606 Gene_Symbol=SLC9A1 Solute carrier family 9 (Sodium/hydrogen exchanger), member 1	33	25073	1	632	1	0	887.3809	2659.1207	3	2659.1287	-0.0079	1	32.87	21	42	0.51	R	R.SKETSSPGTDDVFTPAPSDSPSSQR.I	I	Phospho (ST)	0.0000000000000000000300000.0
NaDOC, U	84	IPI00329791	Tax_Id=9606 Gene_Symbol=DDX46 cDNA FLJ78679, highly similar to Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 (DDX4t	31	117912	1	709	1	1	1036.1118	3105.3137	3	3105.3009	0.0128	0	31.38	19	43	0.76	K	K.AALGLQDSDDEDAAVDIDEQIESMFNSK.K	K	Phospho (ST)	0.0000000300000000000000000000.0
NaDOC, U	85	IPI00843991	Tax_Id=9606 Gene_Symbol=CCNY cyclin Y isoform 2	31	33525	1	164	1	0	612.7913	1223.568	2	1223.5547	0.0133	0	31.18	28	40	0.46	R	R.SASADNLTLPR.W	W	Phospho (ST)	0.30000000000.0
NaDOC, U	85	IPI00465457	Tax_Id=9606 Gene_Symbol=CCNY Isoform 1 of Cyclin-Y	31	39825	1	164	1	0	612.7913	1223.568	2	1223.5547	0.0133	0	31.18	28	40	0.46	R	R.SASADNLTLPR.W	W	Phospho (ST)	0.30000000000.0
NaDOC, U	85	IPI00334743	Tax_Id=9606 Gene_Symbol=CCNY Isoform 2 of Cyclin-Y	31	36994	1	164	1	1	612.7913	1223.568	2	1223.5547	0.0133	0	31.18	28	40	0.46	R	R.SASADNLTLPR.W	W	Phospho (ST)	0.30000000000.0
NaDOC, U	85	IPI00413625	Tax_Id=9606 Gene_Symbol=CCNY Isoform 3 of Cyclin-Y	31	33566	1	164	1	0	612.7913	1223.568	2	1223.5547	0.0133	0	31.18	28	40	0.46	R	R.SASADNLTLPR.W	W	Phospho (ST)	0.30000000000.0
NaDOC, U	87	IPI00292771	Tax_Id=9606 Gene_Symbol=NUMA1 Isoform 1 of Nuclear mitotic apparatus protein 1	31	239199	1	410	1	0	1002.4694	2002.9243	2	2002.8997	0.0246	0	31.08	19	42	0.66	R	R.TQPDGTSVPGEPASPISQR.L	L	Phospho (ST)	0.0000000000000300000.0
NaDOC, U	87	IPI00006196	Tax_Id=9606 Gene_Symbol=NUMA1 Isoform 2 of Nuclear mitotic apparatus protein 1	31	237456	1	410	1	1	1002.4694	2002.9243	2	2002.8997	0.0246	0	31.08	19	42	0.66	R	R.TQPDGTSVPGEPASPISQR.L	L	Phospho (ST)	0.0000000000000300000.0
NaDOC, U	87	IPI00030136	Tax_Id=9606 Gene_Symbol=NUMA1 NUMA1 protein	31	109896	1	410	1	0	1002.4694	2002.9243	2	2002.8997	0.0246	0	31.08	19	42	0.66	R	R.TQPDGTSVPGEPASPISQR.L	L	Phospho (ST)	0.0000000000000300000.0
NaDOC, U	87	IPI00872028	Tax_Id=9606 Gene_Symbol=NUMA1 NUMA1 variant protein	31	239172	1	410	1	0	1002.4694	2002.9243	2	2002.8997	0.0246	0	31.08	19	42	0.66	R	R.TQPDGTSVPGEPASPISQR.L	L	Phospho (ST)	0.0000000000000300000.0
NaDOC, U	92	IPI00251559	Tax_Id=9606 Gene_Symbol=RNF20 E3 ubiquitin-protein ligase BRE1A	29	114534	1	396	1	1	981.4415	1960.8684	2	1960.8415	0.0269	0	28.87	20	42	1.1	K	K.ALVVPEPEPDSDSNQER.K	K	Phospho (ST)	0.00000000000030000.0
NaDOC, U	94	IPI00013452	Tax_Id=9606 Gene_Symbol=EPRS Bifunctional aminoacyl-tRNA synthetase	29	172137	1	463	1	1	1063.4767	2124.9388	2	2124.9365	0.0023	0	28.68	22	42	1.2	K	K.EYIPGQPPLSQSSDSSPTR.N	N	Phospho (ST)	0.0000000000000003000.0
NaDOC, U	99	IPI00383807	Tax_Id=9606 Gene_Symbol=SLC4A4 Electrogenic Na+ bicarbonate cotransporter (Fragment)	26	75865	1	562	1	0	798.0363	2391.0872	3	2391.0607	0.0265	1	26.5	18	42	2.1	R	R.NLTSSSLNDISDKPEKDQLK.N	N	2 Phospho (ST)	0.00033000000000000000.0
NaDOC, U	99	IPI00411338	Tax_Id=9606 Gene_Symbol=SLC4A4 Isoform 2 of Electrogenic sodium bicarbonate cotransporter 1	26	116820	1	562	1	0	798.0363	2391.0872	3	2391.0607	0.0265	1	26.5	18	42	2.1	R	R.NLTSSSLNDISDKPEKDQLK.N	N	2 Phospho (ST)	0.00033000000000000000.0
NaDOC, U	99	IPI00658166	Tax_Id=9606 Gene_Symbol=SLC4A4 Isoform 3 of Electrogenic sodium bicarbonate cotransporter 1	26	72687	1	562	1	0	798.0363	2391.0872	3	2391.0607	0.0265	1	26.5	18	42	2.1	R	R.NLTSSSLNDISDKPEKDQLK.N	N	2 Phospho (ST)	0.00033000000000000000.0
NaDOC, U	99	IPI00016949	Tax_Id=9606 Gene_Symbol=SLC4A4 Isoform 4 of Electrogenic sodium bicarbonate cotransporter 1	26	113055	1	562	1	1	798.0363	2391.0872	3	2391.0607	0.0265	1	26.5	18	42	2.1	R	R.NLTSSSLNDISDKPEKDQLK.N	N	2 Phospho (ST)	0.00033000000000000000.0
NaDOC, U	99	IPI00410270	Tax_Id=9606 Gene_Symbol=SLC4A4 Solute carrier family 4 sodium bicarbonate cotransporter member 4 variant C	26	123900	1	562	1	0	798.0363	2391.0872	3	2391.0607	0.0265	1	26.5	18	42	2.1	R	R.NLTSSSLNDISDKPEKDQLK.N	N	2 Phospho (ST)	0.00033000000000000000.0
U	1	IPI00830089	Tax_Id=9606 Gene_Symbol=- Thymopoietin zeta isoform	173	27428	5	574	1	0	937.3711	2809.0914	3	2809.1034	-0.012	1	46.45	18	42	0.022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	3 Phospho (ST)	0.000003300000030000000000000.0
U	1	IPI00791301	Tax_Id=9606 Gene_Symbol=TMPO 46 kDa protein	173	46335	5	574	1	0	937.3711	2809.0914	3	2809.1034	-0.012	1	46.45	18	42	0.022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	3 Phospho (ST)	0.000003300000030000000000000.0
U	1	IPI00030131	Tax_Id=9606 Gene_Symbol=TMPO Isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma	173	50696	5	574	1	1	937.3711	2809.0914	3	2809.1034	-0.012	1	46.45	18	42	0.022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	3 Phospho (ST)	0.000003300000030000000000000.0
U	1	IPI00181409	Tax_Id=9606 Gene_Symbol=TMPO Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	173	38771	5	574	1	0	937.3711	2809.0914	3	2809.1034	-0.012	1	46.45	18	42	0.022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	3 Phospho (ST)	0.000003300000030000000000000.0
U	1	IPI00216230	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2 isoform alpha	173	76016	5	574	1	0	937.3711	2809.0914	3	2809.1034	-0.012	1	46.45	18	42	0.022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	3 Phospho (ST)	0.000003300000030000000000000.0
U	1	IPI00873716	Tax_Id=9606 Gene_Symbol=TMPO Lamina-associated polypeptide 2, isoforms beta/gamma variant (Fragment)	173	41895	5	574	1	0	937.3711	2809.0914	3	2809.1034	-0.012	1	46.45	18	42	0.022	K	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	S	3 Phospho (ST)	0.000003300000030000000000000.0
U	3	IPI00789101	Tax_Id=9606 Gene_Symbol=PTGES3 19 kDa protein	165	19721	4	637	1	0	1158.143	3471.4071	3	3471.3663	0.0408	1	51.4	22	43	0.0074	K	K.LNWLSVDFNNWKDWEDDSDEDMSNFDR.F	F	Phospho (ST)	0.000000000000000000300000000.0
U	3	IPI00789101	Tax_Id=9606 Gene_Symbol=PTGES3 19 kDa protein	165	19335	4	637	1	0	1158.143	3471.4071	3	3471.3663	0.0408	1	51.4	22	43	0.0074	K	K.LNWLSVDFNNWKDWEDDSDEDMSNFDR.F	F	Phospho (ST)	0.000000000000000000300000000.0
U	3	IPI00789698	Tax_Id=9606 Gene_Symbol=PTGES3 19 kDa protein	165	19721	4	638	1	0	1158.4818	3472.4237	3	3472.3503	0.0733	1	38.93	21	43	0.13	K	K.LNWLSVDFNNWKDWEDDSDEDMSNFDR.F	F	Deamidated (NQ); Phospho (ST)	0.000030000100000000000000000.0
U	3	IPI00789698	Tax_Id=9606 Gene_Symbol=PTGES3 19 kDa protein	165	19335	4	638	1	0	1158.4818	3472.4237	3	3472.3503	0.0733	1	38.93	21	43	0.13	K	K.LNWLSVDFNNWKDWEDDSDEDMSNFDR.F	F	Deamidated (NQ); Phospho (ST)	0.000030000100000000000000000.0
U	3	IPI00015029	Tax_Id=9606 Gene_Symbol=PTGES3 Prostaglandin E synthase 3	165	18971	4	637	1	1	1158.143	3471.4071	3	3471.3663	0.0408	1	51.4	22	43	0.0074	K	K.LNWLSVDFNNWKDWEDDSDEDMSNFDR.F	F	Phospho (ST)	0.000000000000000000300000000.0
U	3	IPI00015029	Tax_Id=9606 Gene_Symbol=PTGES3 Prostaglandin E synthase 3	165	18971	4	638	1	1	1158.4818	3472.4237	3	3472.3503	0.0733	1	38.93	21	43	0.13	K	K.LNWLSVDFNNWKDWEDDSDEDMSNFDR.F	F	Deamidated (NQ); Phospho (ST)	0.000030000100000000000000000.0
U	4	IPI00006079	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 1 of Bcl-2-associated transcription factor 1	164	106173	4	496	1	1	811.6371	2431.8894	3	2431.9078	-0.0184	1	88.16	24	42	1.30E-06	K	K.FNDSEGDDTEETEDYRQFR.K	K	Phospho (ST)	0.0003000000000000000.0
U	4	IPI00413671	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 2 of Bcl-2-associated transcription factor 1	164	105999	4	496	1	0	811.6371	2431.8894	3	2431.9078	-0.0184	1	88.16	24	42	1.30E-06	K	K.FNDSEGDDTEETEDYRQFR.K	K	Phospho (ST)	0.0003000000000000000.0
U	4	IPI00413672	Tax_Id=9606 Gene_Symbol=BCLAF1 Isoform 3 of Bcl-2-associated transcription factor 1	164	100286	4	496	1	0	811.6371	2431.8894	3	2431.9078	-0.0184	1	88.16	24	42	1.30E-06	K	K.FNDSEGDDTEETEDYRQFR.K	K	Phospho (ST)	0.0003000000000000000.0
U	4	IPI00886854	Tax_Id=9606 Gene_Symbol=LOC731605 similar to BCL2-associated transcription factor 1 isoform 2	164	100251	4	496	1	0	811.6371	2431.8894	3	2431.9078	-0.0184	1	88.16	24	42	1.30E-06	K	K.FNDSEGDDTEETEDYRQFR.K	K	Phospho (ST)	0.0003000000000000000.0
U	7	IPI00647720	Tax_Id=9606 Gene_Symbol=SRRM1 Isoform 1 of Serine/arginine repetitive matrix protein 1	146	102331	3	355	1	0	972.9009	1943.7872	2	1943.7884	-0.0012	1	98.64	32	42	1.20E-07	K	K.KETESEAEDNLDDLEK.H	H	Phospho (ST)	0.0000300000000000.0
U	7	IPI00647720	Tax_Id=9606 Gene_Symbol=SRRM1 Isoform 1 of Serine/arginine repetitive matrix protein 1	146	102331	3	380	1	0	1012.8963	2023.7781	2	2023.7548	0.0233	1	78.09	31	42	1.40E-05	K	K.KETESEAEDNLDDLEK.H	H	2 Phospho (ST)	0.0030300000000000.0
U	7	IPI00328293	Tax_Id=9606 Gene_Symbol=SRRM1 Uncharacterized protein SRRM1	146	103386	3	355	1	1	972.9009	1943.7872	2	1943.7884	-0.0012	1	98.64	32	42	1.20E-07	K	K.KETESEAEDNLDDLEK.H	H	Phospho (ST)	0.0000300000000000.0
U	7	IPI00328293	Tax_Id=9606 Gene_Symbol=SRRM1 Uncharacterized protein SRRM1	146	103386	3	380	1	1	1012.8963	2023.7781	2	2023.7548	0.0233	1	78.09	31	42	1.40E-05	K	K.KETESEAEDNLDDLEK.H	H	2 Phospho (ST)	0.0030300000000000.0
U	8	IPI00215948	Tax_Id=9606 Gene_Symbol=CTNNA1 Isoform 1 of Catenin alpha-1	139	100693	3	452	1	1	1111.4828	2220.9511	2	2220.9413	0.0098	1	50.02	25	42	0.0095	R	R.SRTSVQTEDDQLIAGQSAR.A	A	2 Phospho (ST)	0.00030030000000000000.0
U	8	IPI00473136	Tax_Id=9606 Gene_Symbol=CTNNA1 Isoform 2 of Catenin alpha-1	139	103426	3	452	1	0	1111.4828	2220.9511	2	2220.9413	0.0098	1	50.02	25	42	0.0095	R	R.SRTSVQTEDDQLIAGQSAR.A	A	2 Phospho (ST)	0.00030030000000000000.0
U	11	IPI00013297	Tax_Id=9606 Gene_Symbol=PDAP1 28 kDa heat- and acid-stable phosphoprotein	114	20618	4	441	1	1	1096.3626	2190.7106	2	2190.7039	0.0067	0	47.04	20	41	0.013	K	K.SLDSDESEDEEDDYQQK.R	R	2 Phospho (ST)	0.000300300000000000.0

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U	11	IPI00013297	Tax_Id=9606 Gene_Symbol=PDAP1 28 kDa heat- and acid-stable phosphoprotein	114	20618	4	477	1	1	1160.4184	2318.8223	2	2318.7988	0.0234	1	45.01	29	42	0.026	K	K.KSLDSDESEDEEDDYQQK.R	R	2 Phospho (ST)	0.000030030000000000.0
U	11	IPI00013297	Tax_Id=9606 Gene_Symbol=PDAP1 28 kDa heat- and acid-stable phosphoprotein	114	20618	4	482	1	1	783.2885	2346.8438	3	2346.805	0.0388	1	36.64	20	42	0.19	K	K.SLDSDESEDEEDDYQQKR.K	K	2 Phospho (ST)	0.000300300000000000.0
U	11	IPI00013297	Tax_Id=9606 Gene_Symbol=PDAP1 28 kDa heat- and acid-stable phosphoprotein	114	20618	4	481	1	1	1174.4178	2346.8211	2	2346.805	0.0162	1	56.27	26	42	0.0019	K	K.SLDSDESEDEEDDYQQKR.K	K	2 Phospho (ST)	0.000300300000000000.0
U	14	IPI00025512	Tax_Id=9606 Gene_Symbol=HSPB1 Heat shock protein beta-1	102	22826	2	134	1	1	578.2838	1154.5531	2	1154.5332	0.0199	0	60.69	37	40	0.0005	R	R.QLSSGVSEIR.H	H	Phospho (ST)	0.0030000000.0
U	15	IPI00304589	Tax_Id=9606 Gene_Symbol=TNKS1BP1 Isoform 1 of 182 kDa tankyrase 1-binding protein	102	182697	3	332	1	1	923.8592	1845.7039	2	1845.7071	-0.0032	0	71.27	36	42	6.10E-05	R	R.VPSSDEEVVEEPQSR.R	R	2 Phospho (ST)	0.003300000000000.0
U	15	IPI00855787	Tax_Id=9606 Gene_Symbol=TNKS1BP1 tankyrase 1-binding protein 1	102	182711	3	332	1	0	923.8592	1845.7039	2	1845.7071	-0.0032	0	71.27	36	42	6.10E-05	R	R.VPSSDEEVVEEPQSR.R	R	2 Phospho (ST)	0.003300000000000.0
U	16	IPI00789386	Tax_Id=9606 Gene_Symbol=PPP1R2 14 kDa protein	97	14232	2	479	1	0	1162.4014	2322.7882	2	2322.8414	-0.0532	0	94.26		41	2.80E-07	R	R.IQEQESSGEEDSDLSPEER.E	E	2 Phospho (ST)	0.0000033000000000000.0
U	16	IPI00789386	Tax_Id=9606 Gene_Symbol=PPP1R2 14 kDa protein	97	14232	2	521	1	0	860.9994	2579.9764	3	2579.9789	-0.0025	1	37.08	27	42	0.17	R	R.IQEQESSGEEDSDLSPEEREK.K	K	2 Phospho (ST)	0.00000330000000000000.0
U	16	IPI00220402	Tax_Id=9606 Gene_Symbol=PPP1R2 Protein phosphatase inhibitor 2	97	23058	2	479	1	0	1162.4014	2322.7882	2	2322.8414	-0.0532	0	94.26		41	2.80E-07	R	R.IQEQESSGEEDSDLSPEER.E	E	2 Phospho (ST)	0.0000033000000000000.0
U	16	IPI00220402	Tax_Id=9606 Gene_Symbol=PPP1R2 Protein phosphatase inhibitor 2	97	23058	2	521	1	0	860.9994	2579.9764	3	2579.9789	-0.0025	1	37.08	27	42	0.17	R	R.IQEQESSGEEDSDLSPEEREK.K	K	2 Phospho (ST)	0.00000330000000000000.0
U	16	IPI00410126	Tax_Id=9606 Gene_Symbol=PPP1R2P3 Protein phosphatase inhibitor 2-like protein 3	97	23091	2	479	1	1	1162.4014	2322.7882	2	2322.8414	-0.0532	0	94.26		41	2.80E-07	R	R.IQEQESSGEEDSDLSPEER.E	E	2 Phospho (ST)	0.0000033000000000000.0
U	16	IPI00410126	Tax_Id=9606 Gene_Symbol=PPP1R2P3 Protein phosphatase inhibitor 2-like protein 3	97	23091	2	521	1	1	860.9994	2579.9764	3	2579.9789	-0.0025	1	37.08	27	42	0.17	R	R.IQEQESSGEEDSDLSPEEREK.K	K	2 Phospho (ST)	0.00000330000000000000.0
U	17	IPI00003419	Tax_Id=9606 Gene_Symbol=C11orf58 Small acidic protein	93	20377	3	542	1	1	881.7096	2642.107	3	2642.0769	0.0301	1	39.95	19	43	0.1	R	R.SASPDDDLGSSNWEAADLGNEERK.Q	Q	Phospho (ST)	0.0030000000000000000000000.0
U	18	IPI00219368	Tax_Id=9606 Gene_Symbol=TLE3 Isoform 1 of Transducin-like enhancer protein 3	91	84162	1	329	1	0	922.3943	1842.774	2	1842.7884	-0.0144	0	91.25	29	42	6.20E-07	K	K.DAPTSPASVASSSSTPSSK.T	T	Phospho (ST)	0.0003000000000000000.0
U	18	IPI00177938	Tax_Id=9606 Gene_Symbol=TLE3 Isoform 2 of Transducin-like enhancer protein 3	91	82969	1	329	1	1	922.3943	1842.774	2	1842.7884	-0.0144	0	91.25	29	42	6.20E-07	K	K.DAPTSPASVASSSSTPSSK.T	T	Phospho (ST)	0.0003000000000000000.0
U	18	IPI00182478	Tax_Id=9606 Gene_Symbol=TLE3 Isoform 3 of Transducin-like enhancer protein 3	91	83400	1	329	1	0	922.3943	1842.774	2	1842.7884	-0.0144	0	91.25	29	42	6.20E-07	K	K.DAPTSPASVASSSSTPSSK.T	T	Phospho (ST)	0.0003000000000000000.0
U	18	IPI00221206	Tax_Id=9606 Gene_Symbol=TLE3 Isoform 4 of Transducin-like enhancer protein 3	91	84150	1	329	1	0	922.3943	1842.774	2	1842.7884	-0.0144	0	91.25	29	42	6.20E-07	K	K.DAPTSPASVASSSSTPSSK.T	T	Phospho (ST)	0.0003000000000000000.0
U	18	IPI00867718	Tax_Id=9606 Gene_Symbol=TLE3 transducin-like enhancer protein 3 isoform b	91	83861	1	329	1	0	922.3943	1842.774	2	1842.7884	-0.0144	0	91.25	29	42	6.20E-07	K	K.DAPTSPASVASSSSTPSSK.T	T	Phospho (ST)	0.0003000000000000000.0
U	20	IPI00789517	Tax_Id=9606 Gene_Symbol=- DEAH	88	34860	1	336	1	0	935.3467	1868.6789	2	1868.6965	-0.0177	0	88.24	27	41	1.20E-06	R	R.LLEDSEESSEETVSR.A	A	2 Phospho (ST)	0.000030030000000.0
U	20	IPI00297178	Tax_Id=9606 Gene_Symbol=DHX16 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	88	119816	1	336	1	1	935.3467	1868.6789	2	1868.6965	-0.0177	0	88.24	27	41	1.20E-06	R	R.LLEDSEESSEETVSR.A	A	2 Phospho (ST)	0.000030030000000.0
U	20	IPI00552073	Tax_Id=9606 Gene_Symbol=DHX16 Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	88	119874	1	336	1	0	935.3467	1868.6789	2	1868.6965	-0.0177	0	88.24	27	41	1.20E-06	R	R.LLEDSEESSEETVSR.A	A	2 Phospho (ST)	0.000030030000000.0
U	21	IPI00156793	Tax_Id=9606 Gene_Symbol=XPC DNA-repair protein complementing XP-C cells	85	106771	1	592	1	1	1016.7376	3047.1908	3	3047.1666	0.0242	0	84.92	42	43	3.30E-06	K	K.SEAAAPHTDAGGGLSSDEEEGTSSQAEAAR.I	I	2 Phospho (ST)	0.000000000000000330000000000000.0
U	25	IPI00873776	Tax_Id=9606 Gene_Symbol=MORC2 MORC family CW-type zinc finger 2	81	111454	1	344	1	0	943.8779	1885.7413	2	1885.7466	-0.0053	0	80.89	35	42	6.90E-06	R	R.SVAVSDEEEVEEEAER.R	R	Phospho (ST)	0.0000300000000000.0
U	25	IPI00455518	Tax_Id=9606 Gene_Symbol=MORC2 MORC family CW-type zinc finger protein 2	81	118548	1	344	1	1	943.8779	1885.7413	2	1885.7466	-0.0053	0	80.89	35	42	6.90E-06	R	R.SVAVSDEEEVEEEAER.R	R	Phospho (ST)	0.0000300000000000.0
U	27	IPI00479509	Tax_Id=9606 Gene_Symbol=- RcNSEP1 (Fragment)	74	35435	3	625	1	0	1113.4525	3337.3358	3	3337.3392	-0.0034	1	25.75	19	43	2.7	R	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R	R	Deamidated (NQ); Phospho (ST)	0.00000001003000000000000000000.0
U	27	IPI00031812	Tax_Id=9606 Gene_Symbol=YBX1 Nuclease-sensitive element-binding protein 1	74	35903	3	625	1	1	1113.4525	3337.3358	3	3337.3392	-0.0034	1	25.75	19	43	2.7	R	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R	R	Deamidated (NQ); Phospho (ST)	0.00000001003000000000000000000.0
U	27	IPI00643351	Tax_Id=9606 Gene_Symbol=YBX1 Protein	74	42333	3	625	1	0	1113.4525	3337.3358	3	3337.3392	-0.0034	1	25.75	19	43	2.7	R	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R	R	Deamidated (NQ); Phospho (ST)	0.00000001003000000000000000000.0
U	28	IPI00641915	Tax_Id=9606 Gene_Symbol=- 14 kDa protein	73	14355	2	612	1	1	1060.4738	3178.3994	3	3178.2614	0.138	0	64.07	30	42	0.00038	R	R.YGLLANTEDPTEMASLDSDEETVFESR.N	N	2 Phospho (ST)	0.000000000000003003000000000.0
U	28	IPI00641915	Tax_Id=9606 Gene_Symbol=- 14 kDa protein	73	14355	2	615	1	1	1065.7823	3194.3251	3	3194.2563	0.0688	0	35.56	23	43	0.28	R	R.YGLLANTEDPTEMASLDSDEETVFESR.N	N	Oxidation (M); 2 Phospho (ST)	0.000000000000203003000000000.0
U	29	IPI00867717	Tax_Id=9606 Gene_Symbol=FAM44A 55 kDa protein	71	55196	1	341	1	0	940.354	1878.6935	2	1878.6598	0.0337	0	71.45	33	42	5.80E-05	K	K.YYSDSDDELTVEQR.R	R	2 Phospho (ST)	0.00303000000000.0
U	29	IPI00797574	Tax_Id=9606 Gene_Symbol=FAM44A Protein FAM44A	71	332433	1	341	1	1	940.354	1878.6935	2	1878.6598	0.0337	0	71.45	33	42	5.80E-05	K	K.YYSDSDDELTVEQR.R	R	2 Phospho (ST)	0.00303000000000.0
U	30	IPI00029159	Tax_Id=9606 Gene_Symbol=MRE11A Isoform 1 of Double-strand break repair protein MRE11A	71	80885	1	572	1	1	932.0057	2792.9954	3	2793.015	-0.0197	1	71.22	22	42	6.10E-05	K	K.GVDFESSEDDDDDPFMNTSSLRR.N	N	2 Phospho (ST)	0.0000033000000000000000000.0
U	30	IPI00218853	Tax_Id=9606 Gene_Symbol=MRE11A Isoform 2 of Double-strand break repair protein MRE11A	71	77936	1	572	1	0	932.0057	2792.9954	3	2793.015	-0.0197	1	71.22	22	42	6.10E-05	K	K.GVDFESSEDDDDDPFMNTSSLRR.N	N	2 Phospho (ST)	0.0000033000000000000000000.0
U	33	IPI00003394	Tax_Id=9606 Gene_Symbol=LOC100133836;SMN2;SMN1;LOC100133835 Isoform SMN of Survival motor neuron protein	66	32285	2	463	1	1	1126.9649	2251.9152	2	2251.9035	0.0117	1	42.03	18	42	0.06	R	R.RGTGQSDDSDIWDDTALIK.A	A	2 Phospho (ST)	0.0000030030000000000.0
U	33	IPI00219360	Tax_Id=9606 Gene_Symbol=LOC100133836;SMN2;SMN1;LOC100133835 Isoform SMN-delta5 of Survival motor neuron protein	66	28915	2	463	1	0	1126.9649	2251.9152	2	2251.9035	0.0117	1	42.03	18	42	0.06	R	R.RGTGQSDDSDIWDDTALIK.A	A	2 Phospho (ST)	0.0000030030000000000.0
U	33	IPI00009598	Tax_Id=9606 Gene_Symbol=LOC100133836;SMN2;SMN1;LOC100133835 Isoform SMN-delta57 of Survival motor neuron protein	66	27460	2	463	1	0	1126.9649	2251.9152	2	2251.9035	0.0117	1	42.03	18	42	0.06	R	R.RGTGQSDDSDIWDDTALIK.A	A	2 Phospho (ST)	0.0000030030000000000.0
U	33	IPI00009597	Tax_Id=9606 Gene_Symbol=LOC100133836;SMN2;SMN1;LOC100133835 Isoform SMN-delta7 of Survival motor neuron protein	66	30830	2	463	1	0	1126.9649	2251.9152	2	2251.9035	0.0117	1	42.03	18	42	0.06	R	R.RGTGQSDDSDIWDDTALIK.A	A	2 Phospho (ST)	0.0000030030000000000.0
U	37	IPI00479589	Tax_Id=9606 Gene_Symbol=RBM17 RNA binding motif protein 17	63	25268	1	398	1	0	701.6154	2101.8245	3	2101.7862	0.0384	1	63.39	26	42	0.0004	R	R.RPDPDSDEDEDYERER.R	R	Phospho (ST)	0.0000030000000000.0
U	37	IPI00646846	Tax_Id=9606 Gene_Symbol=RBM17 RNA binding motif protein 17	63	27320	1	398	1	0	701.6154	2101.8245	3	2101.7862	0.0384	1	63.39	26	42	0.0004	R	R.RPDPDSDEDEDYERER.R	R	Phospho (ST)	0.0000030000000000.0
U	37	IPI00647326	Tax_Id=9606 Gene_Symbol=RBM17 RNA binding motif protein 17	63	24161	1	398	1	0	701.6154	2101.8245	3	2101.7862	0.0384	1	63.39	26	42	0.0004	R	R.RPDPDSDEDEDYERER.R	R	Phospho (ST)	0.0000030000000000.0
U	37	IPI00647772	Tax_Id=9606 Gene_Symbol=RBM17 RNA binding motif protein 17	63	25265	1	398	1	0	701.6154	2101.8245	3	2101.7862	0.0384	1	63.39	26	42	0.0004	R	R.RPDPDSDEDEDYERER.R	R	Phospho (ST)	0.0000030000000000.0
U	37	IPI00176706	Tax_Id=9606 Gene_Symbol=RBM17 Splicing factor 45	63	45162	1	398	1	1	701.6154	2101.8245	3	2101.7862	0.0384	1	63.39	26	42	0.0004	R	R.RPDPDSDEDEDYERER.R	R	Phospho (ST)	0.0000030000000000.0
U	42	IPI00022790	Tax_Id=9606 Gene_Symbol=MFAP1 Microfibrillar-associated protein 1	60	51823	1	485	1	1	1181.4871	2360.9596	2	2360.9451	0.0145	0	60.49	24	42	0.00086	K	K.IVEPEVVGESDSEVEGDAWR.M	M	2 Phospho (ST)	0.00000000030300000000.0
U	45	IPI00013881	Tax_Id=9606 Gene_Symbol=HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	57	49484	3	313	1	1	882.8627	1763.7109	2	1763.7265	-0.0156	0	53.91	22	42	0.0033	K	K.HTGPNSPDTANDGFVR.L	L	Phospho (ST)	0.0000030000000000.0
U	45	IPI00479191	Tax_Id=9606 Gene_Symbol=HNRNPH1 HNRPH1 protein	57	51482	3	313	1	0	882.8627	1763.7109	2	1763.7265	-0.0156	0	53.91	22	42	0.0033	K	K.HTGPNSPDTANDGFVR.L	L	Phospho (ST)	0.0000030000000000.0
U	47	IPI00790263	Tax_Id=9606 Gene_Symbol=NMD3 13 kDa protein	57	12924	1	353	1	1	967.3617	1932.7089	2	1932.7027	0.0062	0	56.78	29	42	0.0017	R	R.DSAIPVESDTDDEGAPR.I	I	2 Phospho (ST)	0.00000003030000000.0
U	47	IPI00797406	Tax_Id=9606 Gene_Symbol=NMD3 44 kDa protein	57	44845	1	353	1	0	967.3617	1932.7089	2	1932.7027	0.0062	0	56.78	29	42	0.0017	R	R.DSAIPVESDTDDEGAPR.I	I	2 Phospho (ST)	0.00000003030000000.0
U	47	IPI00790937	Tax_Id=9606 Gene_Symbol=NMD3 Similar to NMD3 homolog	57	61342	1	353	1	0	967.3617	1932.7089	2	1932.7027	0.0062	0	56.78	29	42	0.0017	R	R.DSAIPVESDTDDEGAPR.I	I	2 Phospho (ST)	0.00000003030000000.0
U	49	IPI00010586	Tax_Id=9606 Gene_Symbol=TMF1 TATA element modulatory factor	56	123666	2	249	1	0	780.3248	1558.635	2	1558.64	-0.005	0	56.4	23	41	0.0018	R	R.SVSEINSDDELSGK.G	G	Phospho (ST)	0.00000030000000.0
U	49	IPI00871307	Tax_Id=9606 Gene_Symbol=TMF1 TMF1 protein	56	123364	2	249	1	1	780.3248	1558.635	2	1558.64	-0.005	0	56.4	23	41	0.0018	R	R.SVSEINSDDELSGK.G	G	Phospho (ST)	0.00000030000000.0
U	54	IPI00289601	Tax_Id=9606 Gene_Symbol=HDAC2 histone deacetylase 2	53	66294	1	475	1	1	773.2621	2316.7644	3	2316.7879	-0.0235	1	52.76	19	41	0.0036	R	R.IACDEEFSDSEDEGEGGRR.N	N	2 Phospho (ST)	0.0000000303000000000.0
U	54	IPI00555868	Tax_Id=9606 Gene_Symbol=HDAC2 Histone deacetylase 2 variant (Fragment)	53	27390	1	475	1	0	773.2621	2316.7644	3	2316.7879	-0.0235	1	52.76	19	41	0.0036	R	R.IACDEEFSDSEDEGEGGRR.N	N	2 Phospho (ST)	0.0000000303000000000.0
U	56	IPI00306301	Tax_Id=9606 Gene_Symbol=PDHA1 Mitochondrial PDHA1	49	48290	5	281	1	0	558.221	1671.641	3	1671.6501	-0.0091	0	28.44	28	41	1.1	R	R.YHGHSMSDPGVSYR.T	T	Phospho (ST)	0.00000030000000.0
U	56	IPI00306301	Tax_Id=9606 Gene_Symbol=PDHA1 Mitochondrial PDHA1	49	48290	5	286	1	0	563.5512	1687.6317	3	1687.645	-0.0133	0	26.79	25	42	1.7	R	R.YHGHSMSDPGVSYR.T	T	Oxidation (M); Phospho (ST)	0.00003200000000.0
U	56	IPI00642820	Tax_Id=9606 Gene_Symbol=PDHA1 Pyruvate dehydrogenase (Lipoamide) alpha 1	49	12580	5	281	1	1	558.221	1671.641	3	1671.6501	-0.0091	0	28.44	28	41	1.1	R	R.YHGHSMSDPGVSYR.T	T	Phospho (ST)	0.00000030000000.0
U	56	IPI00642820	Tax_Id=9606 Gene_Symbol=PDHA1 Pyruvate dehydrogenase (Lipoamide) alpha 1	49	12580	5	286	1	1	563.5512	1687.6317	3	1687.645	-0.0133	0	26.79	25	42	1.7	R	R.YHGHSMSDPGVSYR.T	T	Oxidation (M); Phospho (ST)	0.00003200000000.0
U	56	IPI00024087	Tax_Id=9606 Gene_Symbol=PDHA2 Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial precursc	49	43647	5	281	1	0	558.221	1671.641	3	1671.6501	-0.0091	0	28.44	28	41	1.1	R	R.YHGHSMSDPGVSYR.T	T	Phospho (ST)	0.00000030000000.0
U	56	IPI00024087	Tax_Id=9606 Gene_Symbol=PDHA2 Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial precursc	49	43647	5	286	1	0	563.5512	1687.6317	3	1687.645	-0.0133	0	26.79	25	42	1.7	R	R.YHGHSMSDPGVSYR.T	T	Oxidation (M); Phospho (ST)	0.00003200000000.0
U	57	IPI00640924	Tax_Id=9606 Gene_Symbol=NEDD4L Isoform 1 of E3 ubiquitin-protein ligase NEDD4-like protein	48	112204	1	305	1	0	869.4402	1736.8659	2	1736.8597	0.0061	0	48.06	24	41	0.012	R	R.SLSSPTVTLSAPLEGAK.D	D	Phospho (ST)	0.00030000000000000.0
U	57	IPI00163321	Tax_Id=9606 Gene_Symbol=NEDD4L Isoform 2 of E3 ubiquitin-protein ligase NEDD4-like protein	48	105198	1	305	1	0	869.4402	1736.8659	2	1736.8597	0.0061	0	48.06	24	41	0.012	R	R.SLSSPTVTLSAPLEGAK.D	D	Phospho (ST)	0.00030000000000000.0
U	57	IPI00023287	Tax_Id=9606 Gene_Symbol=NEDD4L Isoform 4 of E3 ubiquitin-protein ligase NEDD4-like protein	48	98462	1	305	1	1	869.4402	1736.8659	2	1736.8597	0.0061	0	48.06	24	41	0.012	R	R.SLSSPTVTLSAPLEGAK.D	D	Phospho (ST)	0.00030000000000000.0
U	57	IPI00166830	Tax_Id=9606 Gene_Symbol=NEDD4L Isoform 5 of E3 ubiquitin-protein ligase NEDD4-like protein	48	110295	1	305	1	0	869.4402	1736.8659	2	1736.8597	0.0061	0	48.06	24	41	0.012	R	R.SLSSPTVTLSAPLEGAK.D	D	Phospho (ST)	0.00030000000000000.0
U	57	IPI00644256	Tax_Id=9606 Gene_Symbol=NEDD4L Isoform 6 of E3 ubiquitin-protein ligase NEDD4-like protein	48	109678	1	305	1	0	869.4402	1736.8659	2	1736.8597	0.0061	0	48.06	24	41	0.012	R	R.SLSSPTVTLSAPLEGAK.D	D	Phospho (ST)	0.00030000000000000.0
U	57	IPI00643856	Tax_Id=9606 Gene_Symbol=NEDD4L Isoform 7 of E3 ubiquitin-protein ligase NEDD4-like protein	48	111587	1	305	1	0	869.4402	1736.8659	2	1736.8597	0.0061	0	48.06	24	41	0.012	R	R.SLSSPTVTLSAPLEGAK.D	D	Phospho (ST)	0.00030000000000000.0
U	57	IPI00304945	Tax_Id=9606 Gene_Symbol=NEDD4L Isoform 8 of E3 ubiquitin-protein ligase NEDD4-like protein	48	114868	1	305	1	0	869.4402	1736.8659	2	1736.8597	0.0061	0	48.06	24	41	0.012	R	R.SLSSPTVTLSAPLEGAK.D	D	Phospho (ST)	0.00030000000000000.0
U	58	IPI00016910	Tax_Id=9606 Gene_Symbol=EIF3C Eukaryotic translation initiation factor 3 subunit C	48	105962	2	310	1	1	876.8948	1751.775	2	1751.7978	-0.0229	1	57.09		41	0.0015	K	K.QPLLLSEDEEDTKR.V	V	Phospho (ST)	0.00000300000000.0
U	58	IPI00646839	Tax_Id=9606 Gene_Symbol=EIF3CL similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 2	48	106091	2	310	1	0	876.8948	1751.775	2	1751.7978	-0.0229	1	57.09		41	0.0015	K	K.QPLLLSEDEEDTKR.V	V	Phospho (ST)	0.00000300000000.0
U	58	IPI00740719	Tax_Id=9606 Gene_Symbol=EIF3CL;EIF3C similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 5	48	90789	2	310	1	0	876.8948	1751.775	2	1751.7978	-0.0229	1	57.09		41	0.0015	K	K.QPLLLSEDEEDTKR.V	V	Phospho (ST)	0.00000300000000.0
U	63	IPI00182757	Tax_Id=9606 Gene_Symbol=KIAA1967 Isoform 1 of Protein KIAA1967	44	103465	1	613	1	1	1061.7446	3182.2121	3	3182.2263	-0.0142	1	44.42	29	42	0.034	K	K.LEDSEVRSVASNQSEMEFSSLQDMPK.E	E	3 Phospho (ST)	0.00000000300300300000000000.0
U	63	IPI00873406	Tax_Id=9606 Gene_Symbol=KIAA1967 Isoform 2 of Protein KIAA1967	44	103706	1	613	1	0	1061.7446	3182.2121	3	3182.2263	-0.0142	1	44.42	29	42	0.034	K	K.LEDSEVRSVASNQSEMEFSSLQDMPK.E	E	3 Phospho (ST)	0.00000000300300300000000000.0
U	70	IPI00329338	Tax_Id=9606 Gene_Symbol=PCYT1A Choline-phosphate cytidylyltransferase A	39	42047	1	280	1	1	836.8198	1671.625	2	1671.6301	-0.0051	1	39.15	17	41	0.094	R	R.HKAAAYDISEDEED.-	-	Phospho (ST)	0.00000000300000.0
U	71	IPI00444262	Tax_Id=9606 Gene_Symbol=NCL cDNA FLJ45706 fis, clone FEBRA2028457, highly similar to Nucleolin	39	65979	2	223	1	0	737.8689	1473.7233	2	1473.7089	0.0144	1	39.04	25	41	0.088	R	R.LELQGPRGSPNAR.S	S	Phospho (ST)	0.0000000030000.0
U	71	IPI00604620	Tax_Id=9606 Gene_Symbol=NCL Isoform 1 of Nucleolin	39	76625	2	223	1	0	737.8689	1473.7233	2	1473.7089	0.0144	1	39.04	25	41	0.088	R	R.LELQGPRGSPNAR.S	S	Phospho (ST)	0.0000000030000.0
U	71	IPI00827674	Tax_Id=9606 Gene_Symbol=NCL Isoform 2 of Nucleolin	39	74409	2	223	1	0	737.8689	1473.7233	2	1473.7089	0.0144	1	39.04	25	41	0.088	R	R.LELQGPRGSPNAR.S	S	Phospho (ST)	0.0000000030000.0
U	71	IPI00183526	Tax_Id=9606 Gene_Symbol=NCL NCL protein	39	50977	2	223	1	1	737.8689	1473.7233	2	1473.7089	0.0144	1	39.04	25	41	0.088	R	R.LELQGPRGSPNAR.S	S	Phospho (ST)	0.0000000030000.0
U	76	IPI00328753	Tax_Id=9606 Gene_Symbol=KTN1 Isoform 1 of Kinectin	37	156464	2	368	1	1	664.275	1989.8032	3	1989.8429	-0.0397	0	34.84	22	42	0.28	K	K.EIQNGNLHESDSESVPR.D	D	Phospho (ST)	0.00000000030000000.0
U	76	IPI00337736	Tax_Id=9606 Gene_Symbol=KTN1 Isoform 2 of Kinectin	37	149804	2	368	1	0	664.275	1989.8032	3	1989.8429	-0.0397	0	34.84	22	42	0.28	K	K.EIQNGNLHESDSESVPR.D	D	Phospho (ST)	0.00000000030000000.0
U	76	IPI00783726	Tax_Id=9606 Gene_Symbol=KTN1 kinectin 1 isoform b	37	150545	2	368	1	0	664.275	1989.8032	3	1989.8429	-0.0397	0	34.84	22	42	0.28	K	K.EIQNGNLHESDSESVPR.D	D	Phospho (ST)	0.00000000030000000.0
U	77	IPI00215888	Tax_Id=9606 Gene_Symbol=SRP72 Signal recognition particle 72 kDa protein	37	75130	1	580	1	1	965.8114	2894.4123	3	2894.3576	0.0547	0	36.54	19	42	0.19	K	K.TVSSPPTSPRPGSAATVSASTSNIIPPR.H	H	2 Phospho (ST)	0.0003003000000000000000000000.0
U	78	IPI00792186	Tax_Id=9606 Gene_Symbol=ABCF1 ATP-binding cassette, sub-family F (GCN20), member 1	36	96451	1	480	1	0	778.6591	2332.9554	3	2332.963	-0.0076	1	36.43	27	42	0.22	K	K.KLSVPTSDEEDEVPAPKPR.G	G	3 Phospho (ST)	0.0030033000000000000.0
U	78	IPI00873899	Tax_Id=9606 Gene_Symbol=ABCF1 Isoform 1 of ATP-binding cassette sub-family F member 1	36	96323	1	480	1	0	778.6591	2332.9554	3	2332.963	-0.0076	1	36.43	27	42	0.22	K	K.KLSVPTSDEEDEVPAPKPR.G	G	3 Phospho (ST)	0.0030033000000000000.0
U	78	IPI00013495	Tax_Id=9606 Gene_Symbol=ABCF1 Isoform 2 of ATP-binding cassette sub-family F member 1	36	92080	1	480	1	1	778.6591	2332.9554	3	2332.963	-0.0076	1	36.43	27	42	0.22	K	K.KLSVPTSDEEDEVPAPKPR.G	G	3 Phospho (ST)	0.0030033000000000000.0
U	80	IPI00883925	Tax_Id=9606 Gene_Symbol=- SRp25 nuclear protein	36	36998	1	319	1	0	892.3658	1782.7171	2	1782.7197	-0.0026	0	35.58	21	42	0.23	R	R.SAGEEEDGPVLTDEQK.S	S	Phospho (ST)	0.3000000000000000.0
U	80	IPI00873961	Tax_Id=9606 Gene_Symbol=ARL6IP4 FLJ00169 protein (Fragment)	36	46885	1	319	1	0	892.3658	1782.7171	2	1782.7197	-0.0026	0	35.58	21	42	0.23	R	R.SAGEEEDGPVLTDEQK.S	S	Phospho (ST)	0.3000000000000000.0
U	80	IPI00434965	Tax_Id=9606 Gene_Symbol=ARL6IP4 Isoform 2 of ADP-ribosylation factor-like protein 6-interacting protein 4	36	37844	1	319	1	0	892.3658	1782.7171	2	1782.7197	-0.0026	0	35.58	21	42	0.23	R	R.SAGEEEDGPVLTDEQK.S	S	Phospho (ST)	0.3000000000000000.0
U	80	IPI00877018	Tax_Id=9606 Gene_Symbol=ARL6IP4 Isoform 3 of ADP-ribosylation factor-like protein 6-interacting protein 4	36	36818	1	319	1	0	892.3658	1782.7171	2	1782.7197	-0.0026	0	35.58	21	42	0.23	R	R.SAGEEEDGPVLTDEQK.S	S	Phospho (ST)	0.3000000000000000.0
U	80	IPI00434966	Tax_Id=9606 Gene_Symbol=ARL6IP4 Isoform 4 of ADP-ribosylation factor-like protein 6-interacting protein 4	36	36417	1	319	1	0	892.3658	1782.7171	2	1782.7197	-0.0026	0	35.58	21	42	0.23	R	R.SAGEEEDGPVLTDEQK.S	S	Phospho (ST)	0.3000000000000000.0
U	80	IPI00796038	Tax_Id=9606 Gene_Symbol=ARL6IP4;OGFOD2 SRp25 nuclear protein isoform 1	36	45287	1	319	1	0	892.3658	1782.7171	2	1782.7197	-0.0026	0	35.58	21	42	0.23	R	R.SAGEEEDGPVLTDEQK.S	S	Phospho (ST)	0.3000000000000000.0
U	80	IPI00010276	Tax_Id=9606 Gene_Symbol=OGFOD2 25 kDa protein	36	24691	1	319	1	1	892.3658	1782.7171	2	1782.7197	-0.0026	0	35.58	21	42	0.23	R	R.SAGEEEDGPVLTDEQK.S	S	Phospho (ST)	0.3000000000000000.0
U	80	IPI00792543	Tax_Id=9606 Gene_Symbol=OGFOD2 26 kDa protein	36	25717	1	319	1	0	892.3658	1782.7171	2	1782.7197	-0.0026	0	35.58	21	42	0.23	R	R.SAGEEEDGPVLTDEQK.S	S	Phospho (ST)	0.3000000000000000.0
U	82	IPI00375358	Tax_Id=9606 Gene_Symbol=RFC1 Isoform 1 of Replication factor C subunit 1	35	128688	1	378	1	1	1008.4237	2014.8328	2	2014.8061	0.0267	0	34.53	18	42	0.31	R	R.IIYDSDSESEETLQVK.N	N	2 Phospho (ST)	0.0000303000000000.0
U	82	IPI00375359	Tax_Id=9606 Gene_Symbol=RFC1 Isoform 2 of Replication factor C subunit 1	35	128617	1	378	1	0	1008.4237	2014.8328	2	2014.8061	0.0267	0	34.53	18	42	0.31	R	R.IIYDSDSESEETLQVK.N	N	2 Phospho (ST)	0.0000303000000000.0
U	90	IPI00742780	Tax_Id=9606 Gene_Symbol=MYH9 FLJ00279 protein (Fragment)	30	66015	1	465	1	0	752.2943	2253.861	3	2253.891	-0.0301	1	29.8	19	42	0.97	K	K.GAGDGSDEEVDGKADGAEAKPAE.-	-	Phospho (ST)	0.00000300000000000000000.0
U	90	IPI00019502	Tax_Id=9606 Gene_Symbol=MYH9 Myosin-9	30	227646	1	465	1	1	752.2943	2253.861	3	2253.891	-0.0301	1	29.8	19	42	0.97	K	K.GAGDGSDEEVDGKADGAEAKPAE.-	-	Phospho (ST)	0.00000300000000000000000.0
U	95	IPI00031651	Tax_Id=9606 Gene_Symbol=C7orf50 Uncharacterized protein C7orf50	28	22127	1	257	1	1	795.8367	1589.6588	2	1589.661	-0.0022	0	28.04	25	41	1.2	R	R.ELDEEGSDPPLPGR.A	A	Phospho (ST)	0.00000030000000.0
U	96	IPI00061087	Tax_Id=9606 Gene_Symbol=FAM122A Protein FAM122A	28	30795	1	323	1	1	906.9294	1811.8442	2	1811.8372	0.007	1	27.94	26	42	1.3	K	K.RIDFIPVSPAPSPTR.G	G	2 Phospho (ST)	0.000000030003000.0
U	97	IPI00472044	Tax_Id=9606 Gene_Symbol=GARNL1 Isoform 1 of GTPase-activating Rap/Ran-GAP domain-like 1	28	233418	1	308	1	0	874.3915	1746.7685	2	1746.7713	-0.0028	0	27.53	26	42	1.4	R	R.SSSTSDILEPFTVER.A	A	Phospho (ST)	0.000300000000000.0
U	97	IPI00456722	Tax_Id=9606 Gene_Symbol=GARNL1 Isoform 2 of GTPase-activating Rap/Ran-GAP domain-like 1	28	236465	1	308	1	1	874.3915	1746.7685	2	1746.7713	-0.0028	0	27.53	26	42	1.4	R	R.SSSTSDILEPFTVER.A	A	Phospho (ST)	0.000300000000000.0
U	97	IPI00646904	Tax_Id=9606 Gene_Symbol=GARNL1 Isoform 3 of GTPase-activating Rap/Ran-GAP domain-like 1	28	125169	1	308	1	0	874.3915	1746.7685	2	1746.7713	-0.0028	0	27.53	26	42	1.4	R	R.SSSTSDILEPFTVER.A	A	Phospho (ST)	0.000300000000000.0
U	97	IPI00744251	Tax_Id=9606 Gene_Symbol=GARNL1 Isoform 4 of GTPase-activating Rap/Ran-GAP domain-like 1	28	223068	1	308	1	0	874.3915	1746.7685	2	1746.7713	-0.0028	0	27.53	26	42	1.4	R	R.SSSTSDILEPFTVER.A	A	Phospho (ST)	0.000300000000000.0
U	97	IPI00456723	Tax_Id=9606 Gene_Symbol=GARNL1 Isoform 5 of GTPase-activating Rap/Ran-GAP domain-like 1	28	235860	1	308	1	0	874.3915	1746.7685	2	1746.7713	-0.0028	0	27.53	26	42	1.4	R	R.SSSTSDILEPFTVER.A	A	Phospho (ST)	0.000300000000000.0