Table S1: Identified proteins following DAT$_{A\beta1-6}$ and DAT$_{A\beta17-23}$ compared to untreated cells. Herein, A1= Aβ1-6; A2= Aβ17-23; A6=No treatment. The proteins were searched for Human (*Homo sapiens*) Database.

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-Aβ$_{1-6}$ Antibody Treatment										
C9JGV6	RANBP1	5	2	40	0.004835	0.00429	1.77	A6	A1	Ran-specific GTPase-activating protein (Fragment) GN=RANBP1 PE=1 SV=8
A6NE52	WDR97	6	2	40.3	0.000492	0.000929	1.75	A6	A1	WD repeat-containing protein 97 GN=WDR97 PE=2 SV=2
Q8TDI0	CHD5	8	4	40.3	0.014943	0.010049	1.72	A1	A6	Chromodomain-helicase-DNA-binding protein 5 GN=CHD5 PE=1 SV=1
P12107	COL11A1	8	2	40.8	0.047475	0.024783	1.55	A1	A6	Collagen alpha-1(XI) chain GN=COL11A1 PE=1 SV=4
O00754	MAN2B1	9	3	40.9	0.000673	0.001156	1.65	A6	A1	Lysosomal alpha-mannosidase GN=MAN2B1 PE=1 SV=3
Q9H2C0	GAN	5	3	40.9	0.010042	0.007343	1.24	A1	A6	Gigaxonin GN=GAN PE=1 SV=1
Q9HBD1	RC3H2	8	2	41.2	0.002505	0.002715	1.47	A6	A1	Roquin-2 GN=RC3H2 PE=1 SV=2
Q15746	MYLK	7	3	41.2	0.001443	0.001893	1.55	A6	A1	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
Q9UK76	JPT1	4	4	41.2	6.14E-06	9.87E-05	4.65	A6	A1	Jupiter microtubule associated homolog 1 GN=JPT1 PE=1 SV=3
Q9Y617	PSAT1	8	2	41.4	0.002838	0.002981	1.64	A6	A1	Phosphoserine aminotransferase GN=PSAT1 PE=1 SV=2
Q02386	ZNF45	7	2	41.4	0.004895	0.004318	2.24	A6	A1	Zinc finger protein 45 GN=ZNF45 PE=1 SV=2
Q6PKC3	TXNDC11	7	2	41.4	0.002624	0.002819	1.88	A6	A1	Thioredoxin domain-containing protein 11 GN=TXNDC11 PE=1 SV=2
Q16849	PTPRN	6	2	41.4	0.001319	0.001764	1.67	A6	A1	Receptor-type tyrosine-protein phosphatase-like N GN=PTPRN PE=1 SV=1
O60486	PLXNC1	7	2	41.8	0.023179	0.014155	1.39	A6	A1	Plexin-C1 GN=PLXNC1 PE=1 SV=1
P20591	MX1	6	2	41.9	0.000517	0.000967	1.58	A1	A6	Interferon-induced GTP-binding protein Mx1 GN=MX1 PE=1 SV=4
P06744	GPI	8	2	42	7.72E-07	4.29E-05	15.6	A6	A1	Glucose-6-phosphate isomerase GN=GPI PE=1 SV=4
P46776	RPL27A	5	2	42.3	0.00637	0.005171	1.57	A6	A1	60S ribosomal protein L27a GN=RPL27A PE=1 SV=2
Q05469	LIPE	9	4	42.3	0.003463	0.003365	1.6	A1	A6	Hormone-sensitive lipase GN=LIPE PE=1 SV=4
P49458	SRP9	6	4	42.5	0.000207	0.000574	2.49	A6	A1	Signal recognition particle 9 kDa protein GN=SRP9 PE=1 SV=2
Q9UKE5	TNIK	9	2	42.6	0.003239	0.003209	1.31	A6	A1	TRAF2 and NCK-interacting protein kinase GN=TNIK PE=1 SV=1
H0Y5C6	FLNA	7	2	42.7	0.001104	0.001584	1.94	A6	A1	Filamin-A (Fragment) GN=FLNA PE=1 SV=1
P11166	SLC2A1	5	2	43.3	0.035857	0.019729	1.33	A6	A1	Solute carrier family 2_ facilitated glucose transporter member 1 GN=SLC2A1 PE=1 SV=2
P61026	RAB10	5	2	43.3	0.043846	0.023185	4.73	A6	A1	Ras-related protein Rab-10 GN=RAB10 PE=1 SV=1
Q06787	FMR1	7	2	44	0.005379	0.004586	1.39	A6	A1	Synaptic functional regulator FMR1 GN=FMR1 PE=1 SV=1
Q5JSZ5	PRRC2B	11	3	44.4	0.026689	0.015766	1.12	A6	A1	Protein PRRC2B GN=PRRC2B PE=1 SV=2
H0Y360	AMPD2	8	2	44.8	0.001818	0.002183	1.67	A6	A1	AMP deaminase 2 (Fragment) GN=AMPD2 PE=1 SV=1
P56385	ATP5ME	6	2	44.9	0.000354	0.000759	1.49	A1	A6	ATP synthase subunit e_ mitochondrial GN=ATP5I PE=1 SV=2
H0YJS3	FANCM	9	5	45	0.005893	0.004895	1.76	A6	A1	Fanconi anemia group M protein (Fragment) GN=FANCM PE=1 SV=1
A0A0A0MTQ9	TRPM1	9	4	45.1	0.007317	0.005753	1.44	A6	A1	Transient receptor potential cation channel subfamily M member 1 (Fragment) GN=TRPM1 PE=1 SV=1
Q8N1G4	LRRC47	7	4	45.4	0.00584	0.004877	2	A1	A6	Leucine-rich repeat-containing protein 47 GN=LRRC47 PE=1 SV=1
Q92994	BRF1	7	4	45.5	0.00906	0.006787	1.24	A1	A6	Transcription factor IIIB 90 kDa subunit GN=BRF1 PE=1 SV=1
P23467	PTPRB	8	3	45.6	0.000197	0.000561	1.89	A6	A1	Receptor-type tyrosine-protein phosphatase beta GN=PTPRB PE=1 SV=3
A0A1B0GV47	KIF21A	9	5	45.9	0.005118	0.004457	1.34	A6	A1	Kinesin-like protein KIF21A (Fragment) GN=KIF21A PE=1 SV=1
Q13635	PTCH1	10	3	46.1	0.008175	0.006247	1.74	A6	A1	Protein patched homolog 1 GN=PTCH1 PE=1 SV=2
P05386	RPLP1	5	2	46.3	0.016114	0.010672	1.18	A1	A6	60S acidic ribosomal protein P1 GN=RPLP1 PE=1 SV=1
O60318	MCM3AP	8	2	46.6	0.000556	0.00102	2.06	A1	A6	Germinal-center associated nuclear protein GN=MCM3AP PE=1 SV=2
Q49AJ0	FAM135B	9	4	46.6	0.024303	0.014738	1.84	A1	A6	Protein FAM135B GN=FAM135B PE=2 SV=2
Q5XKE5	KRT79	6	2	47.1	0.000358	0.000764	1.21	A6	A1	Keratin_ type II cytoskeletal 79 GN=KRT79 PE=1 SV=2
Q9BZH6	WDR11	8	4	47.1	0.010275	0.007477	1.2	A6	A1	WD repeat-containing protein 11 GN=WDR11 PE=1 SV=1
F8VWS0	RPLP0	8	2	47.3	0.031452	0.017802	1.51	A6	A1	60S acidic ribosomal protein P0 GN=RPLP0 PE=1 SV=1
P07864	LDHC	8	4	47.3	0.001474	0.001913	1.84	A1	A6	L-lactate dehydrogenase C chain GN=LDHC PE=1 SV=4
Q32Q12	NME1-NME2	7	4	48.1	4.45E-07	2.95E-05	4.73	A6	A1	Nucleoside diphosphate kinase GN=NME1-NME2 PE=1 SV=1
P29400	COL4A5	9	5	48.1	0.012006	0.008426	1.51	A1	A6	Collagen alpha-5(IV) chain GN=COL4A5 PE=1 SV=2
O95049	TJP3	6	3	48.5	0.005164	0.004477	1.45	A6	A1	Tight junction protein ZO-3 GN=TJP3 PE=1 SV=3
Q99714	HSD17B10	7	2	48.6	0.001468	0.001911	3.97	A6	A1	3-hydroxyacyl-CoA dehydrogenase type-2 GN=HSD17B10 PE=1 SV=3
Q92499	DDX1	7	2	48.6	0.003925	0.003685	1.63	A1	A6	ATP-dependent RNA helicase DDX1 GN=DDX1 PE=1 SV=2
O00468	AGRN	10	2	49.1	0.021316	0.013229	9.73	A1	A6	Agrin GN=AGRN PE=1 SV=5
Q2NL67	PARP6	7	2	49.2	0.000135	0.000442	2.32	A1	A6	Poly [ADP-ribose] polymerase 6 GN=PARP6 PE=2 SV=1
P45974	USP5	7	3	49.3	0.000348	0.000748	2.05	A1	A6	Ubiquitin carboxyl-terminal hydrolase 5 GN=USP5 PE=1 SV=2
O14497	ARID1A	12	6	49.4	0.006219	0.005089	2.14	A1	A6	AT-rich interactive domain-containing protein 1A GN=ARID1A PE=1 SV=3
O15031	PLXNB2	11	3	49.7	0.000315	0.000717	3.33	A6	A1	Plexin-B2 GN=PLXNB2 PE=1 SV=3
H0Y613	GSE1	9	4	49.7	0.000999	0.001478	10.2	A1	A6	Genetic suppressor element 1 (Fragment) GN=GSE1 PE=1 SV=1
P55196	AFDN	10	4	49.8	0.000386	0.000802	2.37	A1	A6	Afadin GN=AFDN PE=1 SV=3
P52907	CAPZA1	6	2	49.9	0.046012	0.024143	1.38	A6	A1	F-actin-capping protein subunit alpha-1 GN=CAPZA1 PE=1 SV=3
A0A087WXM3	NLRP5	9	4	49.9	0.011916	0.008382	1.35	A1	A6	NACHT_ LRR and PYD domains-containing protein 5 GN=NLRP5 PE=1 SV=1
E7EPU2	DIP2C	10	4	50.1	0.008794	0.006604	1.4	A1	A6	Disco-interacting protein 2 homolog C GN=DIP2C PE=1 SV=2
Q8TD31	CCHCR1	9	6	50.1	4.04E-06	9.38E-05	2.93	A6	A1	Coiled-coil alpha-helical rod protein 1 GN=CCHCR1 PE=1 SV=2
Q13148	TARDBP	7	3	50.2	0.001494	0.001915	1.78	A6	A1	TAR DNA-binding protein 43 GN=TARDBP PE=1 SV=1
Q86VH2	KIF27	9	4	50.6	0.020674	0.012975	3.99	A1	A6	Kinesin-like protein KIF27 GN=KIF27 PE=2 SV=1
Q9BVN2	RUSC1	9	3	50.8	0.00175	0.002114	1.66	A1	A6	RUN and SH3 domain-containing protein 1 GN=RUSC1 PE=1 SV=3
Q15459	SF3A1	7	2	51.3	0.000187	0.000544	1.86	A1	A6	Splicing factor 3A subunit 1 GN=SF3A1 PE=1 SV=1
Q8NFY4	SEMA6D	11	4	51.4	0.000217	0.000588	2.47	A1	A6	Semaphorin-6D GN=SEMA6D PE=1 SV=1
Q05209	PTPN12	8	2	51.5	0.003199	0.003203	6.29	A6	A1	Tyrosine-protein phosphatase non-receptor type 12 GN=PTPN12 PE=1 SV=3
Q86W92	PPFIBP1	11	2	52	0.001209	0.001664	3.7	A6	A1	Liprin-beta-1 GN=PPFIBP1 PE=1 SV=2
O43790	KRT86	7	2	52.5	0.019444	0.012368	4.07	A6	A1	Keratin_ type II cuticular Hb6 GN=KRT86 PE=1 SV=1

O14556	GAPDHS	8	6	52.5	0.001122	0.001598	2.16	A6	A1	Glyceraldehyde-3-phosphate dehydrogenase_ testis-specific GN=GAPDHS PE=1 SV=2
A0A0J9YVP0	HERC2	8	3	52.6	0.000212	0.000581	1.15	A1	A6	E3 ubiquitin-protein ligase HERC2 (Fragment) GN=HERC2 PE=1 SV=1
P80723	BASP1	6	4	52.8	0.000429	0.000854	2.03	A6	A1	Brain acid soluble protein 1 GN=BASP1 PE=1 SV=2
P0DN79	CBSL	10	7	52.9	0.002106	0.002388	1.57	A1	A6	Cystathionine beta-synthase-like protein GN=CBSL PE=1 SV=1
Q7Z7H5	TMED4	7	3	53	8.5E-05	0.000361	2.86	A1	A6	Transmembrane emp24 domain-containing protein 4 GN=TMED4 PE=1 SV=1
Q15700	DLG2	11	4	53.2	0.002723	0.002905	1.31	A1	A6	Disks large homolog 2 GN=DLG2 PE=1 SV=3
G3V2A4	TEP1	13	7	53.2	0.004007	0.003736	4.49	A1	A6	Telomerase protein component 1 GN=TEP1 PE=1 SV=1
P07737	PFN1	7	4	53.3	0.000171	0.000519	2.12	A1	A6	Profilin-1 GN=PFN1 PE=1 SV=2
Q9BX26	SYCP2	11	5	53.3	0.01049	0.007616	2.01	A6	A1	Synaptonemal complex protein 2 GN=SYCP2 PE=2 SV=2
A0A087WX84		9	3	53.4	0.000719	0.001209	2.06	A1	A6	A-kinase anchor protein 9 GN=AKAP9 PE=1 SV=1
Q8IYA2	CCDC144CP	9	2	53.5	0.001042	0.001528	1.49	A6	A1	Putative coiled-coil domain-containing protein 144C GN=CCDC144CP PE=5 SV=3
O00299	CLIC1	7	4	53.6	0.000265	0.000664	2.32	A6	A1	Chloride intracellular channel protein 1 GN=CLIC1 PE=1 SV=4
P30084	ECHS1	8	2	53.7	0.007975	0.006124	3.65	A6	A1	Enoyl-CoA hydratase_ mitochondrial GN=ECHS1 PE=1 SV=4
P52179	MYOM1	10	6	54	8.32E-05	0.000356	1.99	A1	A6	Myomesin-1 GN=MYOM1 PE=1 SV=2
Q15717	ELAVL1	7	3	54.4	6.41E-05	0.000331	1.94	A6	A1	ELAV-like protein 1 GN=ELAVL1 PE=1 SV=2
P00441	SOD1	7	4	54.6	0.030786	0.017506	1.27	A6	A1	Superoxide dismutase [Cu-Zn] GN=SOD1 PE=1 SV=2
P35268	RPL22	7	2	54.8	0.005189	0.004487	1.95	A6	A1	60S ribosomal protein L22 GN=RPL22 PE=1 SV=2
Q96PC5	MIA2	11	5	54.8	0.026695	0.015766	1.12	A1	A6	Melanoma inhibitory activity protein 2 GN=MIA2 PE=1 SV=4
O15075	DCLK1	9	2	54.9	0.007842	0.006037	1.57	A6	A1	Serine/threonine-protein kinase DCLK1 GN=DCLK1 PE=1 SV=2
Q96RG2	PASK	9	3	54.9	1.03E-07	2.1E-05	49.8	A1	A6	PAS domain-containing serine/threonine-protein kinase GN=PASK PE=1 SV=3
A0A0D9SF60	PKP4	9	2	55.6	0.007086	0.005596	5.32	A1	A6	Plakophilin-4 GN=PKP4 PE=1 SV=1
H0YMW2	AKAP13	9	3	55.6	0.002413	0.00263	2.22	A1	A6	A-kinase anchor protein 13 (Fragment) GN=AKAP13 PE=1 SV=1
P28331	NDUFS1	10	2	56.3	0.000287	0.000685	3.65	A6	A1	NADH-ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial GN=NDUFS1 PE=1 SV=3
O43237	DYNC1LI2	9	4	56.8	0.040286	0.021583	1.78	A6	A1	Cytoplasmic dynein 1 light intermediate chain 2 GN=DYNC1LI2 PE=1 SV=1
Q9UQ80	PA2G4	11	2	57.1	0.006655	0.005339	2.71	A6	A1	Proliferation-associated protein 2G4 GN=PA2G4 PE=1 SV=3
Q7Z553	MDGA2	8	3	57.1	0.001248	0.001692	1.55	A6	A1	MAM domain-containing glycosylphosphatidylinositol anchor protein 2 GN=MDGA2 PE=1 SV=2
O95153	TSPOAP1	10	4	57.1	0.001838	0.002199	1.33	A1	A6	Peripheral-type benzodiazepine receptor-associated protein 1 GN=TSPOAP1 PE=1 SV=2
P39023	RPL3	9	3	57.3	0.001602	0.00199	2.37	A6	A1	60S ribosomal protein L3 GN=RPL3 PE=1 SV=2
Q14011	CIRBP	5	3	57.6	0.003366	0.003313	2.79	A6	A1	Cold-inducible RNA-binding protein GN=CIRBP PE=1 SV=1
O95466	FMNL1	10	2	58	0.004909	0.004324	2.8	A1	A6	Formin-like protein 1 GN=FMNL1 PE=1 SV=3
Q13561	DCTN2	8	5	58.2	0.005255	0.004523	1.38	A1	A6	Dynactin subunit 2 GN=DCTN2 PE=1 SV=4
P07205	PGK2	7	2	58.4	0.00322	0.003207	1.49	A6	A1	Phosphoglycerate kinase 2 GN=PGK2 PE=1 SV=3
Q5TG12	PTPRK	10	3	59	0.020925	0.013048	2.16	A1	A6	Receptor-type tyrosine-protein phosphatase kappa GN=PTPRK PE=1 SV=1
Q96AA8	JAKMIP2	9	3	59.3	0.000671	0.001156	2.22	A1	A6	Janus kinase and microtubule-interacting protein 2 GN=JAKMIP2 PE=1 SV=1
Q96AG4	LRRC59	8	3	59.5	0.001299	0.001746	1.69	A6	A1	Leucine-rich repeat-containing protein 59 GN=LRRC59 PE=1 SV=1
B7ZW38	HNRNPCL3	8	4	59.9	0.000862	0.001362	2.38	A1	A6	Heterogeneous nuclear ribonucleoprotein C-like 3 GN=HNRNPCL3 PE=2 SV=1
P13674	P4HA1	10	4	60.3	0.017748	0.011493	1.24	A6	A1	Prolyl 4-hydroxylase subunit alpha-1 GN=P4HA1 PE=1 SV=2
A0A0A6YYL4	CORO7-PAM16	13	4	60.3	0.011634	0.00826	1.29	A6	A1	Coronin GN=CORO7-PAM16 PE=3 SV=1
Q8NEV8	EXPH5	12	4	60.5	0.027656	0.016209	1.45	A6	A1	Exophilin-5 GN=EXPH5 PE=1 SV=3
G3XAE9	TOGARAM1	10	4	63	0.017087	0.011159	1.56	A6	A1	KIAA0423_ isoform CRA_a GN=TOGARAM1 PE=1 SV=1
A0A0D9SGC1	MYO6	10	4	63.2	0.00249	0.002704	3.11	A1	A6	Unconventional myosin-VI GN=MYO6 PE=1 SV=1
P53804	TTC3	13	6	64.5	0.003026	0.003119	1.66	A6	A1	E3 ubiquitin-protein ligase TTC3 GN=TTC3 PE=1 SV=2
Q8NEZ3	WDR19	12	3	65.3	0.000713	0.001207	3.11	A1	A6	WD repeat-containing protein 19 GN=WDR19 PE=1 SV=2
P01308	INS	5	3	65.6	0.000141	0.000455	2.65	A1	A6	Insulin GN=INS PE=1 SV=1
E9PL09	RPS3	9	5	65.6	0.000335	0.000736	1.36	A6	A1	40S ribosomal protein S3 GN=RPS3 PE=1 SV=1
P51659	HSD17B4	12	7	65.7	0.035533	0.019586	1.21	A1	A6	Peroxisomal multifunctional enzyme type 2 GN=HSD17B4 PE=1 SV=3
P60866	RPS20	7	3	65.8	0.000195	0.00056	2.53	A1	A6	40S ribosomal protein S20 GN=RPS20 PE=1 SV=1
Q5SW79	CEP170	12	4	65.9	0.000904	0.001391	1.52	A6	A1	Centrosomal protein of 170 kDa GN=CEP170 PE=1 SV=1
O43852	CALU	9	4	66.1	0.001882	0.002226	3.02	A6	A1	Calumenin GN=CALU PE=1 SV=2
P23497	SP100	8	2	66.3	0.046164	0.024181	25.8	A6	A1	Nuclear autoantigen Sp-100 GN=SP100 PE=1 SV=3
P31150	GDI1	10	5	66.4	2.05E-06	7.38E-05	2.06	A6	A1	Rab GDP dissociation inhibitor alpha GN=GDI1 PE=1 SV=2
O15360	FANCA	12	5	66.4	0.000201	0.000565	1.43	A6	A1	Fanconi anemia group A protein GN=FANCA PE=1 SV=2
P23468	PTPRD	11	6	66.4	0.00051	0.000957	1.82	A1	A6	Receptor-type tyrosine-protein phosphatase delta GN=PTPRD PE=1 SV=2
A0A0D9SEP4		12	6	66.7	0.00036	0.000765	1.95	A6	A1	Neurexin-1-beta GN=NRXN1 PE=1 SV=1
O15067	PFAS	13	6	66.7	8.23E-05	0.000356	1.84	A1	A6	Phosphoribosylformylglycinamidine synthase GN=PFAS PE=1 SV=4
Q9NQC3	RTN4	12	6	66.8	0.003353	0.003312	1.4	A6	A1	Reticulon-4 GN=RTN4 PE=1 SV=2
Q92618	ZNF516	13	3	66.9	0.001911	0.002242	4.11	A6	A1	Zinc finger protein 516 GN=ZNF516 PE=1 SV=1
P62258	YWHAE	7	3	67.3	0.00038	0.000794	1.73	A1	A6	14-3-3 protein epsilon GN=YWHAE PE=1 SV=1
P42695	NCAPD3	11	4	67.5	0.03317	0.018551	1.62	A1	A6	Condensin-2 complex subunit D3 GN=NCAPD3 PE=1 SV=2
Q8ND30	PPFIBP2	14	6	67.7	0.028319	0.016499	1.18	A1	A6	Liprin-beta-2 GN=PPFIBP2 PE=1 SV=3
Q6N021	TET2	11	3	68.1	5.2E-06	9.38E-05	2.47	A1	A6	Methylcytosine dioxygenase TET2 GN=TET2 PE=1 SV=3
P68402	PAFAH1B2	10	7	68.1	0.000664	0.001147	2.6	A6	A1	Platelet-activating factor acetylhydrolase IB subunit beta GN=PAFAH1B2 PE=1 SV=1
P46777	RPL5	9	3	68.2	0.001177	0.001641	2.5	A6	A1	60S ribosomal protein L5 GN=RPL5 PE=1 SV=3
Q8NDI1	EHBP1	12	4	68.2	0.000286	0.000685	2.68	A1	A6	EH domain-binding protein 1 GN=EHBP1 PE=1 SV=3
Q9P2K5	MYEF2	12	4	68.6	0.035317	0.019502	1.32	A6	A1	Myelin expression factor 2 GN=MYEF2 PE=1 SV=3
Q96PY6	NEK1	12	5	68.6	0.049875	0.025815	1.36	A6	A1	Serine/threonine-protein kinase Nek1 GN=NEK1 PE=1 SV=2
P26641	EEF1G	11	6	68.7	0.004252	0.003879	1.28	A6	A1	Elongation factor 1-gamma GN=EEF1G PE=1 SV=3
F5H039	GPHN	12	4	69	0.003221	0.003207	6.23	A6	A1	Gephyrin GN=GPHN PE=1 SV=1
P16144	ITGB4	11	5	69	0.000902	0.001391	3.34	A6	A1	Integrin beta-4 GN=ITGB4 PE=1 SV=5
P67809	YBX1	10	4	69.2	0.001546	0.00196	2.41	A6	A1	Nuclease-sensitive element-binding protein 1 GN=YBX1 PE=1 SV=3
P49411	TUFM	12	5	69.2	0.006057	0.005003	1.87	A6	A1	Elongation factor Tu_ mitochondrial GN=TUFM PE=1 SV=2
Q9HCM1	RESF1	11	5	69.3	0.002336	0.002564	1.45	A6	A1	Uncharacterized protein KIAA1551 GN=KIAA1551 PE=1 SV=3
Q9UNA4	POLI	10	2	69.7	0.006426	0.005196	1.42	A6	A1	DNA polymerase iota GN=POLI PE=1 SV=3
Q9Y4B5	MTCL1	12	2	70.3	0.000991	0.00147	1.75	A6	A1	Microtubule cross-linking factor 1 GN=MTCL1 PE=1 SV=5
Q02878	RPL6	7	3	71.5	0.000293	0.000696	2.01	A1	A6	60S ribosomal protein L6 GN=RPL6 PE=1 SV=3
Q15424	SAFB	9	2	71.8	0.000327	0.000736	4.43	A6	A1	Scaffold attachment factor B1 GN=SAFB PE=1 SV=4
Q15019	SEPTIN2	11	7	72	3.35E-05	0.000251	2.27	A6	A1	Septin-2 GN=SEPT2 PE=1 SV=1
P62913	RPL11	9	3	72.2	0.000885	0.001376	1.29	A1	A6	60S ribosomal protein L11 GN=RPL11 PE=1 SV=2
P33991	MCM4	13	6	72.4	0.00076	0.001249	2.37	A1	A6	DNA replication licensing factor MCM4 GN=MCM4 PE=1 SV=5
P62829	RPL23	9	2	72.9	6.93E-05	0.000333	1.64	A1	A6	60S ribosomal protein L23 GN=RPL23 PE=1 SV=1

P62753	RPS6	8	2	73	0.004066	0.003783	1.82	A6	A1	40S ribosomal protein S6 GN=RPS6 PE=1 SV=1
Q00872	MYBPC1	13	3	73.4	0.003142	0.00317	5.86	A6	A1	Myosin-binding protein C_ slow-type GN=MYBPC1 PE=1 SV=2
J3KQV8	SYNJ1	15	3	73.5	0.005547	0.00471	1.72	A1	A6	Synaptojanin-1 GN=SYNJ1 PE=1 SV=1
Q13151	HNRNPA0	9	4	73.5	0.000122	0.000426	2.58	A6	A1	Heterogeneous nuclear ribonucleoprotein A0 GN=HNRNPA0 PE=1 SV=1
P08237	PFKM	12	5	74.2	0.028812	0.016673	1.29	A1	A6	ATP-dependent 6-phosphofructokinase_ muscle type GN=PFKM PE=1 SV=2
P62081	RPS7	10	7	74.8	0.021103	0.013123	1.17	A6	A1	40S ribosomal protein S7 GN=RPS7 PE=1 SV=1
Q9ULH0	KIDINS220	13	4	75.5	0.009773	0.007215	1.82	A1	A6	Kinase D-interacting substrate of 220 kDa GN=KIDINS220 PE=1 SV=3
Q8NF50	DOCK8	13	8	75.5	0.001573	0.00197	1.77	A1	A6	Dedicator of cytokinesis protein 8 GN=DOCK8 PE=1 SV=3
P53396	ACLY	12	4	75.7	0.00075	0.001243	1.8	A6	A1	ATP-citrate synthase GN=ACLY PE=1 SV=3
Q8N163	CCAR2	13	6	76.1	0.026876	0.015843	1.22	A6	A1	Cell cycle and apoptosis regulator protein 2 GN=CCAR2 PE=1 SV=2
Q9UBT2	UBA2	12	2	76.2	0.002791	0.002953	2.04	A6	A1	SUMO-activating enzyme subunit 2 GN=UBA2 PE=1 SV=2
Q92522	H1-10	9	2	76.3	0.017713	0.011482	2.39	A6	A1	Histone H1x GN=H1FX PE=1 SV=1
Q9ULV0	MYO5B	15	5	76.4	0.002294	0.002545	1.51	A6	A1	Unconventional myosin-Vb GN=MYO5B PE=1 SV=3
Q96GM5	SMARCD1	13	2	76.6	0.003137	0.00317	3.43	A1	A6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 GN=SMARCD1 PE=1 SV=2
P30040	ERP29	10	5	77.4	0.001531	0.00195	1.44	A6	A1	Endoplasmic reticulum resident protein 29 GN=ERP29 PE=1 SV=4
A0A0C4DG17	RPSA	9	5	77.6	3.29E-05	0.000251	1.59	A1	A6	40S ribosomal protein SA GN=RPSA PE=1 SV=1
Q6Y7W6	GIGYF2	13	4	77.7	0.029405	0.016941	1.24	A6	A1	GRB10-interacting GYF protein 2 GN=GIGYF2 PE=1 SV=1
P60981	DSTN	10	5	78.4	0.00177	0.002133	1.28	A6	A1	Destrin GN=DSTN PE=1 SV=3
P04792	HSPB1	8	3	78.6	0.00103	0.001514	1.92	A1	A6	Heat shock protein beta-1 GN=HSPB1 PE=1 SV=2
P07602	PSAP	14	8	78.9	0.031674	0.017911	1.38	A6	A1	Prosaposin GN=PSAP PE=1 SV=2
Q14160	SCRIB	13	4	79.2	3.44E-05	0.000251	1.83	A1	A6	Protein scribble homolog GN=SCRIB PE=1 SV=4
P83731	RPL24	9	4	79.4	0.015356	0.010225	1.22	A1	A6	60S ribosomal protein L24 GN=RPL24 PE=1 SV=1
P49006	MARCKSL1	8	4	80	0.002303	0.002547	1.41	A6	A1	MARCKS-related protein GN=MARCKSL1 PE=1 SV=2
Q99623	PHB2	10	3	80.1	7.07E-05	0.000335	3.43	A1	A6	Prohibitin-2 GN=PHB2 PE=1 SV=2
D6RER5	SEPTIN11	12	2	80.3	1.05E-05	0.000133	2.29	A1	A6	Septin-11 GN=SEPT11 PE=1 SV=1
Q96R06	SPAG5	13	4	80.9	0.01559	0.010347	2.48	A6	A1	Sperm-associated antigen 5 GN=SPAG5 PE=1 SV=2
Q86TI0	TBC1D1	14	3	81.2	0.030613	0.01744	1.57	A6	A1	TBC1 domain family member 1 GN=TBC1D1 PE=1 SV=2
Q00325	SLC25A3	11	4	81.5	0.038303	0.020794	1.1	A1	A6	Phosphate carrier protein_ mitochondrial GN=SLC25A3 PE=1 SV=2
Q9Y265	RUVBL1	16	3	81.8	0.001587	0.001984	2.07	A1	A6	RuvB-like 1 GN=RUVBL1 PE=1 SV=1
Q53SF7	COBLL1	15	6	81.9	9.51E-05	0.000369	2.92	A6	A1	Cordon-bleu protein-like 1 GN=COBLL1 PE=1 SV=2
Q08211	DHX9	16	7	82	0.030694	0.01747	1.2	A1	A6	ATP-dependent RNA helicase A GN=DHX9 PE=1 SV=4
Q9H583	HEATR1	15	8	82.3	0.020961	0.013048	1.24	A1	A6	HEAT repeat-containing protein 1 GN=HEATR1 PE=1 SV=3
I3L2J8	CEP131	14	3	83	0.002229	0.002491	1.37	A1	A6	Centrosomal protein of 131 kDa GN=CEP131 PE=1 SV=1
P24752	ACAT1	12	5	83.1	0.00107	0.001546	1.41	A6	A1	Acetyl-CoA acetyltransferase_ mitochondrial GN=ACAT1 PE=1 SV=1
P09471	GNAO1	12	3	84	0.00072	0.001209	3.06	A1	A6	Guanine nucleotide-binding protein G(o) subunit alpha GN=GNAO1 PE=1 SV=4
Q15293	RCN1	10	4	84.1	5.17E-06	9.38E-05	3.93	A6	A1	Reticulocalbin-1 GN=RCN1 PE=1 SV=1
P84103	SRSF3	9	6	84.2	0.030992	0.017574	1.24	A1	A6	Serine/arginine-rich splicing factor 3 GN=SRSF3 PE=1 SV=1
O94856	NFASC	15	6	84.8	0.001045	0.001528	2.02	A6	A1	Neurofascin GN=NFASC PE=1 SV=4
Q9Y3I0	RTCB	14	9	85	0.036448	0.019968	1.16	A1	A6	tRNA-splicing ligase RtcB homolog GN=RTCB PE=1 SV=1
Q96AY3	FKBP10	15	6	85.2	0.017146	0.011186	1.56	A1	A6	Peptidyl-prolyl cis-trans isomerase FKBP10 GN=FKBP10 PE=1 SV=1
O75150	RNF40	16	6	86	0.000627	0.001107	1.67	A1	A6	E3 ubiquitin-protein ligase BRE1B GN=RNF40 PE=1 SV=4
O00571	DDX3X	15	8	86	0.000223	0.000595	4.1	A6	A1	ATP-dependent RNA helicase DDX3X GN=DDX3X PE=1 SV=3
J3KN67	TPM3	10	2	86.8	0.01781	0.011519	1.75	A6	A1	Tropomyosin alpha-3 chain GN=TPM3 PE=1 SV=1
A0A0G2JNB1	KANSL1	15	2	87.2	0.010805	0.007812	1.48	A1	A6	KAT8 regulatory NSL complex subunit 1 GN=KANSL1 PE=1 SV=1
B1AJZ9	FHAD1	17	3	87.2	9.5E-05	0.000369	2.77	A6	A1	Forkhead-associated domain-containing protein 1 GN=FHAD1 PE=2 SV=2
H0Y7F7	CEP350	13	6	87.4	0.03429	0.019085	1.3	A1	A6	Centrosome-associated protein 350 (Fragment) GN=CEP350 PE=1 SV=1
Q5BJE1	CCDC178	15	3	88.6	0.00706	0.005585	1.29	A1	A6	Coiled-coil domain-containing protein 178 GN=CCDC178 PE=2 SV=3
Q14562	DHX8	15	6	88.8	0.014382	0.009747	1.25	A6	A1	ATP-dependent RNA helicase DHX8 GN=DHX8 PE=1 SV=1
P31942	HNRNPH3	13	6	88.9	0.046603	0.024369	1.21	A6	A1	Heterogeneous nuclear ribonucleoprotein H3 GN=HNRNPH3 PE=1 SV=2
P05455	SSB	15	7	89.1	0.030349	0.017354	1.31	A6	A1	Lupus La protein GN=SSB PE=1 SV=2
P15880	RPS2	12	5	90.1	0.035472	0.01957	1.25	A6	A1	40S ribosomal protein S2 GN=RPS2 PE=1 SV=2
P09211	GSTP1	11	7	90.6	9.66E-06	0.000133	2.88	A6	A1	Glutathione S-transferase P GN=GSTP1 PE=1 SV=2
O75334	PPFIA2	18	4	91.3	0.013129	0.009109	1.38	A6	A1	Liprin-alpha-2 GN=PPFIA2 PE=1 SV=2
P55795	HNRNPH2	11	3	91.4	0.000693	0.001183	1.6	A6	A1	Heterogeneous nuclear ribonucleoprotein H2 GN=HNRNPH2 PE=1 SV=1
Q86UW6	N4BP2	16	7	91.7	0.000333	0.000736	3.29	A1	A6	NEDD4-binding protein 2 GN=N4BP2 PE=1 SV=2
Q8IYT4	KATNAL2	16	4	93.4	0.002401	0.002621	1.32	A1	A6	Katanin p60 ATPase-containing subunit A-like 2 GN=KATNAL2 PE=1 SV=3
P08708	RPS17	10	2	94.7	0.013579	0.009348	1.39	A6	A1	40S ribosomal protein S17 GN=RPS17 PE=1 SV=2
P48047	ATP5PO	12	6	94.8	0.000437	0.000865	1.85	A6	A1	ATP synthase subunit O_ mitochondrial GN=ATP5O PE=1 SV=1
P61586	RHOA	11	3	95.2	0.001569	0.00197	1.28	A6	A1	Transforming protein RhoA GN=RHOA PE=1 SV=1
Q9H4G0	EPB41L1	15	4	95.3	0.001839	0.002199	2.02	A1	A6	Band 4.1-like protein 1 GN=EPB41L1 PE=1 SV=2
Q9C093	SPEF2	20	3	95.8	0.017421	0.011353	1.76	A1	A6	Sperm flagellar protein 2 GN=SPEF2 PE=2 SV=2
Q58FG1	HSP90AA4P	13	5	95.8	0.026732	0.015773	1.19	A1	A6	Putative heat shock protein HSP 90-alpha A4 GN=HSP90AA4P PE=5 SV=1
O00443	PIK3C2A	19	7	97.1	0.025802	0.015376	1.33	A6	A1	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha GN=PIK3C2A PE=1 SV=2
P27348	YWHAQ	11	2	97.5	0.008623	0.006524	1.47	A6	A1	14-3-3 protein theta GN=YWHAQ PE=1 SV=1
P62701	RPS4X	13	6	97.6	0.001493	0.001915	1.42	A1	A6	40S ribosomal protein S4_ X isoform GN=RPS4X PE=1 SV=2
A8K878		12	5	98	0.000129	0.000434	1.34	A6	A1	Mesencephalic astrocyte-derived neurotrophic factor GN=MANF PE=1 SV=1
Q07955	SRSF1	14	6	98.6	0.008061	0.006167	1.76	A1	A6	Serine/arginine-rich splicing factor 1 GN=SRSF1 PE=1 SV=2
P0C0S5	H2AZ1	7	2	99.3	0.001973	0.002284	1.85	A1	A6	Histone H2A.Z GN=H2AFZ PE=1 SV=2
P14866	HNRNPL	12	11	99.3	0.020794	0.013024	1.32	A1	A6	Heterogeneous nuclear ribonucleoprotein L GN=HNRNPL PE=1 SV=2
O43491	EPB41L2	16	6	100	0.001715	0.002089	1.79	A1	A6	Band 4.1-like protein 2 GN=EPB41L2 PE=1 SV=1
Q96SN8	CDK5RAP2	17	5	101	0.009964	0.007295	1.32	A1	A6	CDK5 regulatory subunit-associated protein 2 GN=CDK5RAP2 PE=1 SV=5
P26373	RPL13	13	4	102	0.025807	0.015376	1.27	A1	A6	60S ribosomal protein L13 GN=RPL13 PE=1 SV=4
Q03113	GNA12	15	4	102	8.74E-05	0.000365	2.91	A1	A6	Guanine nucleotide-binding protein subunit alpha-12 GN=GNA12 PE=1 SV=4
O94986	CEP152	19	3	103	7.83E-05	0.000355	2.42	A1	A6	Centrosomal protein of 152 kDa GN=CEP152 PE=1 SV=4
A0A1B0GVD5	CTSD	14	7	103	3.77E-05	0.000262	1.44	A6	A1	Cathepsin D GN=CTSD PE=1 SV=1
Q5JYT7	KIAA1755	17	4	104	0.006308	0.005135	1.82	A6	A1	Uncharacterized protein KIAA1755 GN=KIAA1755 PE=2 SV=2
P22234	PAICS	16	12	105	0.004073	0.003783	1.17	A6	A1	Multifunctional protein ADE2 GN=PAICS PE=1 SV=3
Q9BZ29	DOCK9	19	4	107	2.94E-05	0.000243	3.89	A1	A6	Dedicator of cytokinesis protein 9 GN=DOCK9 PE=1 SV=2
Q5TEC6	H3-2	8	2	108	0.000146	0.000457	2.81	A1	A6	Histone H3 GN=HIST2H3PS2 PE=1 SV=1
O43151	TET3	16	2	108	0.004552	0.004098	1.89	A1	A6	Methylcytosine dioxygenase TET3 GN=TET3 PE=1 SV=3
Q7Z5N4	SDK1	18	6	108	0.000146	0.000457	1.87	A1	A6	Protein sidekick-1 GN=SDK1 PE=2 SV=3
Q86YA3	ZGRF1	17	3	109	1.27E-05	0.000149	2.89	A6	A1	Protein ZGRF1 GN=ZGRF1 PE=1 SV=3
F5H4R6	NAP1L1	12	4	109	0.011718	0.008301	1.31	A1	A6	Nucleosome assembly protein 1-like 1 GN=NAP1L1 PE=1 SV=1
Q9UJZ1	STOML2	16	7	109	0.023792	0.014445	1.38	A1	A6	Stomatin-like protein 2_ mitochondrial GN=STOML2 PE=1 SV=1
Q05682	CALD1	16	5	110	0.000287	0.000685	1.94	A1	A6	Caldesmon GN=CALD1 PE=1 SV=3

P26232	CTNNA2	21	6	110	0.001906	0.002242	1.38	A1	A6	Catenin alpha-2 GN=CTNNA2 PE=1 SV=5
F5GXQ8	SYNE1	19	6	112	0.004332	0.00394	1.49	A6	A1	Nesprin-1 GN=SYNE1 PE=1 SV=1
Q99733	NAP1L4	12	3	113	0.003967	0.003708	1.4	A1	A6	Nucleosome assembly protein 1-like 4 GN=NAP1L4 PE=1 SV=1
P49588	AARS1	18	9	113	0.000124	0.000426	2	A6	A1	Alanine--tRNA ligase_ cytoplasmic GN=AARS PE=1 SV=2
P23381	WARS1	17	9	114	0.014527	0.009802	1.62	A1	A6	Tryptophan--tRNA ligase_ cytoplasmic GN=WARS PE=1 SV=2
Q9ULM3	YEATS2	22	10	115	0.006926	0.005513	1.53	A1	A6	YEATS domain-containing protein 2 GN=YEATS2 PE=1 SV=2
P00338	LDHA	15	7	118	0.034267	0.019085	1.17	A6	A1	L-lactate dehydrogenase A chain GN=LDHA PE=1 SV=2
P62917	RPL8	15	11	119	0.01352	0.009318	1.62	A1	A6	60S ribosomal protein L8 GN=RPL8 PE=1 SV=2
P42166	TMPO	18	2	120	0.002058	0.002359	1.58	A6	A1	Lamina-associated polypeptide 2_ isoform alpha GN=TMPO PE=1 SV=2
P31948	STIP1	17	4	120	0.000525	0.000979	2.05	A6	A1	Stress-induced-phosphoprotein 1 GN=STIP1 PE=1 SV=1
Q8TBY8	PMFBP1	21	4	120	0.000118	0.000421	1.95	A1	A6	Polyamine-modulated factor 1-binding protein 1 GN=PMFBP1 PE=2 SV=2
P21281	ATP6V1B2	21	7	120	0.045487	0.023949	1.36	A6	A1	V-type proton ATPase subunit B_ brain isoform GN=ATP6V1B2 PE=1 SV=3
Q96F07	CYFIP2	18	3	121	0.001478	0.001914	1.63	A1	A6	Cytoplasmic FMR1-interacting protein 2 GN=CYFIP2 PE=1 SV=2
Q96M83	CCDC7	19	5	121	4.09E-07	2.95E-05	3.16	A1	A6	Coiled-coil domain-containing protein 7 GN=CCDC7 PE=2 SV=3
H0Y8G5	HNRNPD	14	5	121	0.000936	0.001424	1.44	A6	A1	Heterogeneous nuclear ribonucleoprotein D0 (Fragment) GN=HNRNPD PE=1 SV=8
P57721	PCBP3	14	2	123	0.001231	0.001677	1.26	A6	A1	Poly(rC)-binding protein 3 GN=PCBP3 PE=2 SV=2
P50991	CCT4	16	2	125	0.000659	0.001147	1.77	A6	A1	T-complex protein 1 subunit delta GN=CCT4 PE=1 SV=4
Q14117	DPYS	17	6	125	0.001491	0.001915	1.9	A6	A1	Dihydropyrimidinase GN=DPYS PE=1 SV=1
A0A087WTP3	KHSRP	17	9	125	0.002247	0.002502	1.46	A1	A6	Far upstream element-binding protein 2 GN=KHSRP PE=1 SV=1
Q99536	VAT1	17	10	128	0.040844	0.021785	1.36	A6	A1	Synaptic vesicle membrane protein VAT-1 homolog GN=VAT1 PE=1 SV=2
Q8WX93	PALLD	19	4	129	6.22E-05	0.000331	2.78	A6	A1	Palladin GN=PALLD PE=1 SV=3
O75145	PPFIA3	21	6	129	4.69E-05	0.000295	2.14	A1	A6	Liprin-alpha-3 GN=PPFIA3 PE=1 SV=3
Q06830	PRDX1	14	7	129	0.002319	0.002554	1.25	A6	A1	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
Q13838	DDX39B	17	2	130	0.001066	0.001546	2.12	A6	A1	Spliceosome RNA helicase DDX39B GN=DDX39B PE=1 SV=1
M0R0F0	RPS5	16	5	130	0.011054	0.007959	1.26	A1	A6	40S ribosomal protein S5 (Fragment) GN=RPS5 PE=1 SV=1
Q12931	TRAP1	17	7	130	0.000473	0.000907	2.19	A1	A6	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
Q92608	DOCK2	23	8	130	0.001064	0.001546	1.51	A1	A6	Dedicator of cytokinesis protein 2 GN=DOCK2 PE=1 SV=2
Q6FI13	H2AC18; H2AC19	17	9	130	4.87E-06	9.38E-05	2.03	A1	A6	Histone H2A type 2-A GN=HIST2H2AA3 PE=1 SV=3
Q9Y2J2	EPB41L3	21	4	131	0.000128	0.000432	1.66	A1	A6	Band 4.1-like protein 3 GN=EPB41L3 PE=1 SV=2
Q96N67	DOCK7	27	6	131	0.005292	0.004543	1.83	A6	A1	Dedicator of cytokinesis protein 7 GN=DOCK7 PE=1 SV=4
B2R5W2	HNRNPC	13	7	131	0.006004	0.004967	1.33	A1	A6	Heterogeneous nuclear ribonucleoproteins C1/C2 GN=HNRNPC PE=1 SV=1
E9PCY7	HNRNPH1	12	2	132	0.00123	0.001677	1.55	A6	A1	Heterogeneous nuclear ribonucleoprotein H GN=HNRNPH1 PE=1 SV=1
P49321	NASP	16	7	132	0.000218	0.000588	1.78	A6	A1	Nuclear autoantigenic sperm protein GN=NASP PE=1 SV=2
Q99832	CCT7	22	9	132	9.84E-05	0.000371	2.39	A1	A6	T-complex protein 1 subunit eta GN=CCT7 PE=1 SV=2
Q9BWD1	ACAT2	17	3	133	0.000245	0.00063	2.59	A6	A1	Acetyl-CoA acetyltransferase_ cytosolic GN=ACAT2 PE=1 SV=2
P78344	EIF4G2	24	7	133	7.84E-06	0.000117	1.69	A1	A6	Eukaryotic translation initiation factor 4 gamma 2 GN=EIF4G2 PE=1 SV=1
P30613	PKLR	14	3	134	0.011785	0.008338	1.28	A1	A6	Pyruvate kinase PKLR GN=PKLR PE=1 SV=2
Q9H4B7	TUBB1	13	3	134	0.00526	0.004523	2.19	A1	A6	Tubulin beta-1 chain GN=TUBB1 PE=1 SV=1
Q9NSB2	KRT84	18	4	134	0.017891	0.011548	1.55	A6	A1	Keratin_ type II cuticular Hb4 GN=KRT84 PE=2 SV=2
Q99497	PARK7	14	7	134	4.59E-05	0.000295	3.1	A6	A1	Protein/nucleic acid deglycase DJ-1 GN=PARK7 PE=1 SV=2
P62805	H4C1;	11	9	134	2.32E-06	7.77E-05	3.4	A1	A6	Histone H4 GN=HIST1H4A PE=1 SV=2
Q16695	H3-4	17	5	137	9.67E-05	0.000369	3.06	A1	A6	Histone H3.1t GN=HIST3H3 PE=1 SV=3
Q9Y6M1	IGF2BP2	20	4	140	0.014199	0.009655	1.23	A1	A6	Insulin-like growth factor 2 mRNA-binding protein 2 GN=IGF2BP2 PE=1 SV=2
P32119	PRDX2	13	6	142	2.01E-06	7.38E-05	1.88	A6	A1	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
Q12906	ILF3	19	11	142	0.000104	0.000383	2.34	A6	A1	Interleukin enhancer-binding factor 3 GN=ILF3 PE=1 SV=3
Q58FF7	HSP90AB3P	17	3	143	0.010958	0.007899	1.25	A1	A6	Putative heat shock protein HSP 90-beta-3 GN=HSP90AB3P PE=5 SV=1
Q7KZF4	SND1	24	4	145	0.001298	0.001746	1.38	A6	A1	Staphylococcal nuclease domain-containing protein 1 GN=SND1 PE=1 SV=1
Q5JU85	IQSEC2	25	6	145	0.007368	0.005767	1.4	A1	A6	IQ motif and SEC7 domain-containing protein 2 GN=IQSEC2 PE=1 SV=2
O43602	DCX	20	10	145	0.012531	0.008754	1.51	A6	A1	Neuronal migration protein doublecortin GN=DCX PE=1 SV=4
P60660	MYL6	17	3	146	0.01011	0.007375	2.96	A6	A1	Myosin light polypeptide 6 GN=MYL6 PE=1 SV=2
P06748	NPM1	15	10	146	0.002983	0.00309	1.63	A1	A6	Nucleophosmin GN=NPM1 PE=1 SV=2
E9PEB5	FUBP1	23	5	148	0.005956	0.00494	1.35	A6	A1	Far upstream element-binding protein 1 GN=FUBP1 PE=1 SV=1
P17987	TCP1	20	7	151	0.003483	0.00338	1.82	A6	A1	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
Q9BYX7	POTEKP	17	4	152	0.001846	0.0022	1.66	A1	A6	Putative beta-actin-like protein 3 GN=POTEKP PE=5 SV=1
O60506	SYNCRIP	20	6	152	0.001894	0.002235	1.51	A6	A1	Heterogeneous nuclear ribonucleoprotein Q GN=SYNCRIP PE=1 SV=2
Q6PIF6	MYO7B	32	12	152	1.95E-05	0.000183	2.8	A1	A6	Unconventional myosin-VIIb GN=MYO7B PE=1 SV=2
O14531	DPYSL4	23	12	155	6.25E-05	0.000331	1.46	A6	A1	Dihydropyrimidinase-related protein 4 GN=DPYSL4 PE=1 SV=2
P05023	ATP1A1	24	7	156	0.009758	0.007215	1.61	A1	A6	Sodium/potassium-transporting ATPase subunit alpha-1 GN=ATP1A1 PE=1 SV=1
P35232	PHB	20	11	156	6.31E-05	0.000331	2.97	A1	A6	Prohibitin GN=PHB PE=1 SV=1
P04843	RPN1	21	8	157	0.023781	0.014445	1.33	A1	A6	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 GN=RPN1 PE=1 SV=1
P61604	HSPE1	16	10	157	3.44E-05	0.000251	2.37	A1	A6	10 kDa heat shock protein_ mitochondrial GN=HSPE1 PE=1 SV=2
P48735	IDH2	24	11	157	0.002063	0.002359	2.04	A6	A1	Isocitrate dehydrogenase [NADP]_ mitochondrial GN=IDH2 PE=1 SV=2
P40925	MDH1	19	8	159	0.005702	0.004789	1.67	A6	A1	Malate dehydrogenase_ cytoplasmic GN=MDH1 PE=1 SV=4
E7EPK1	SEPTIN7	19	10	160	0.011209	0.008035	1.32	A6	A1	Septin-7 GN=SEPT7 PE=1 SV=2
P38919	EIF4A3	23	8	161	0.002469	0.002685	1.61	A1	A6	Eukaryotic initiation factor 4A-III GN=EIF4A3 PE=1 SV=4
Q15366	PCBP2	19	4	164	0.000271	0.000667	2.9	A1	A6	Poly(rC)-binding protein 2 GN=PCBP2 PE=1 SV=1
P09936	UCHL1	14	8	164	0.007063	0.005585	1.32	A1	A6	Ubiquitin carboxyl-terminal hydrolase isozyme L1 GN=UCHL1 PE=1 SV=2
D6RA32	MAP1B	22	12	165	0.003399	0.003331	1.88	A6	A1	Microtubule-associated protein 1B (Fragment) GN=MAP1B PE=1 SV=2
P40227	CCT6A	20	6	166	0.014506	0.009802	1.4	A6	A1	T-complex protein 1 subunit zeta GN=CCT6A PE=1 SV=3
P13929	ENO3	18	4	168	0.014109	0.009604	1.77	A1	A6	Beta-enolase GN=ENO3 PE=1 SV=5
A0A087WVQ6	CLTC	28	12	168	0.000118	0.000421	2.42	A6	A1	Clathrin heavy chain GN=CLTC PE=1 SV=1
P17661	DES	18	3	170	0.016531	0.010901	1.25	A1	A6	Desmin GN=DES PE=1 SV=3
Q15365	PCBP1	17	6	170	0.000226	0.000602	1.52	A6	A1	Poly(rC)-binding protein 1 GN=PCBP1 PE=1 SV=2
P48643	CCT5	22	9	170	0.003436	0.003349	1.74	A6	A1	T-complex protein 1 subunit epsilon GN=CCT5 PE=1 SV=1
Q16658	FSCN1	23	9	171	0.008192	0.006252	1.55	A6	A1	Fascin GN=FSCN1 PE=1 SV=3
P07196	NEFL	22	5	173	0.008677	0.00654	1.4	A6	A1	Neurofilament light polypeptide GN=NEFL PE=1 SV=3
Q7RTP6	MICAL3	34	9	174	0.000296	0.000696	5.06	A1	A6	[F-actin]-monooxygenase MICAL3 GN=MICAL3 PE=1 SV=2
P09104	ENO2	20	8	175	0.041769	0.022183	1.11	A6	A1	Gamma-enolase GN=ENO2 PE=1 SV=3
P62937	PPIA	18	9	176	4.66E-06	9.38E-05	1.76	A1	A6	Peptidyl-prolyl cis-trans isomerase A GN=PPIA PE=1 SV=2
Q5THK1	PRR14L	32	10	176	0.012775	0.008904	1.95	A1	A6	Protein PRR14L GN=PRR14L PE=1 SV=1
P52209	PGD	19	12	178	3.55E-05	0.000255	3.07	A6	A1	6-phosphogluconate dehydrogenase_ decarboxylating GN=PGD PE=1 SV=3
P13010	XRCC5	26	12	179	2.19E-07	2.23E-05	1.93	A1	A6	X-ray repair cross-complementing protein 5 GN=XRCC5 PE=1 SV=3
P50990	CCT8	24	6	180	5.51E-05	0.000316	2.71	A6	A1	T-complex protein 1 subunit theta GN=CCT8 PE=1 SV=4
Q5VZ46	KIAA1614	26	6	183	3.62E-05	0.000255	2.55	A1	A6	Uncharacterized protein KIAA1614 GN=KIAA1614 PE=2 SV=3

Q8IWJ2	GCC2	36	12	183	0.013626	0.009368	1.2	A1	A6	GRIP and coiled-coil domain-containing protein 2 GN=GCC2 PE=1 SV=4
P07195	LDHB	18	7	185	0.004413	0.00399	1.53	A6	A1	L-lactate dehydrogenase B chain GN=LDHB PE=1 SV=2
P27824	CANX	20	8	186	0.005246	0.004523	1.21	A6	A1	Calnexin GN=CANX PE=1 SV=2
Q14974	KPNB1	26	12	186	9.09E-05	0.000366	1.61	A1	A6	Importin subunit beta-1 GN=KPNB1 PE=1 SV=2
P16949	STMN1	15	5	188	0.000551	0.001015	1.85	A6	A1	Stathmin GN=STMN1 PE=1 SV=3
P17066	HSPA6	22	7	188	0.000779	0.001276	1.56	A1	A6	Heat shock 70 kDa protein 6 GN=HSPA6 PE=1 SV=2
P04264	KRT1	19	13	188	0.000209	0.000576	4.72	A1	A6	Keratin_ type II cytoskeletal 1 GN=KRT1 PE=1 SV=6
P17844	DDX5	25	10	191	0.00023	0.000606	2.13	A1	A6	Probable ATP-dependent RNA helicase DDX5 GN=DDX5 PE=1 SV=1
P19338	NCL	22	11	192	8E-05	0.000356	1.66	A6	A1	Nucleolin GN=NCL PE=1 SV=3
P16401	H1-5	17	8	194	1.5E-05	0.000167	1.73	A1	A6	Histone H1.5 GN=HIST1H1B PE=1 SV=3
P12956	XRCC6	27	11	195	0.000536	0.000991	1.77	A1	A6	X-ray repair cross-complementing protein 6 GN=XRCC6 PE=1 SV=2
P13637	ATP1A3	30	6	196	0.006974	0.005544	1.2	A6	A1	Sodium/potassium-transporting ATPase subunit alpha-3 GN=ATP1A3 PE=1 SV=3
P23528	CFL1	18	5	198	1.88E-05	0.000183	1.72	A6	A1	Cofilin-1 GN=CFL1 PE=1 SV=3
P04075	ALDOA	20	11	200	0.041081	0.021856	1.51	A6	A1	Fructose-bisphosphate aldolase A GN=ALDOA PE=1 SV=2
P09651	HNRNPA1	20	12	209	0.038128	0.020736	1.54	A6	A1	Heterogeneous nuclear ribonucleoprotein A1 GN=HNRNPA1 PE=1 SV=5
P50454	SERPINH1	20	11	212	0.002161	0.002442	1.33	A1	A6	Serpin H1 GN=SERPINH1 PE=1 SV=2
O00425	IGF2BP3	25	6	213	0.000447	0.000881	2.08	A1	A6	Insulin-like growth factor 2 mRNA-binding protein 3 GN=IGF2BP3 PE=1 SV=2
P33176	KIF5B	32	9	214	0.000362	0.000765	2.2	A6	A1	Kinesin-1 heavy chain GN=KIF5B PE=1 SV=1
Q9Y4I1	MYO5A	36	14	215	0.00131	0.001756	1.47	A1	A6	Unconventional myosin-Va GN=MYO5A PE=1 SV=2
E7EVA0	MAP4	37	3	218	0.025751	0.015372	1.38	A1	A6	Microtubule-associated protein GN=MAP4 PE=1 SV=1
P35527	KRT9	20	17	220	0.000713	0.001207	5.12	A1	A6	Keratin_ type I cytoskeletal 9 GN=KRT9 PE=1 SV=3
Q13263	TRIM28	32	8	224	0.000395	0.000806	2.35	A1	A6	Transcription intermediary factor 1-beta GN=TRIM28 PE=1 SV=5
P08133	ANXA6	30	14	230	0.039515	0.021256	1.14	A6	A1	Annexin A6 GN=ANXA6 PE=1 SV=3
P16402	H1-3	25	9	234	0.001544	0.00196	1.84	A1	A6	Histone H1.3 GN=HIST1H1D PE=1 SV=2
P02461	COL3A1	35	14	234	5.5E-05	0.000316	6.49	A6	A1	Collagen alpha-1(III) chain GN=COL3A1 PE=1 SV=4
O60282	KIF5C	35	14	244	3.88E-06	9.38E-05	2.94	A1	A6	Kinesin heavy chain isoform 5C GN=KIF5C PE=1 SV=1
O60814	H2BC12	17	2	246	5.22E-06	9.38E-05	1.52	A1	A6	Histone H2B type 1-K GN=HIST1H2BK PE=1 SV=3
P0DMV8	HSPA1A	31	6	256	3.99E-05	0.000271	1.28	A6	A1	Heat shock 70 kDa protein 1A GN=HSPA1A PE=1 SV=1
Q5TZA2	CROCC	45	13	259	0.025627	0.015313	1.65	A1	A6	Rootletin GN=CROCC PE=1 SV=1
P07237	P4HB	30	13	263	0.003775	0.003584	1.14	A1	A6	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
P48681	NES	42	21	267	0.000216	0.000586	1.25	A1	A6	Nestin GN=NES PE=1 SV=2
P00558	PGK1	32	13	275	2.29E-05	0.000206	2.2	A6	A1	Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3
P29762	CRABP1	23	15	275	0.001506	0.001925	1.17	A1	A6	Cellular retinoic acid-binding protein 1 GN=CRABP1 PE=1 SV=2
P55072	VCP	43	15	279	0.003213	0.003207	1.78	A6	A1	Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4
P23246	SFPQ	30	15	279	0.003643	0.003496	1.82	A6	A1	Splicing factor_ proline- and glutamine-rich GN=SFPQ PE=1 SV=2
Q14980	NUMA1	52	3	282	0.04074	0.02175	1.22	A1	A6	Nuclear mitotic apparatus protein 1 GN=NUMA1 PE=1 SV=2
P20700	LMNB1	40	22	290	0.027297	0.016033	1.22	A1	A6	Lamin-B1 GN=LMNB1 PE=1 SV=2
Q9BUF5	TUBB6	24	2	298	0.021981	0.013522	1.59	A6	A1	Tubulin beta-6 chain GN=TUBB6 PE=1 SV=1
P0CG39	POTEJ	32	2	305	0.000793	0.001278	1.46	A1	A6	POTE ankyrin domain family member J GN=POTEJ PE=3 SV=1
P61978	HNRNPK	28	16	306	0.010072	0.007356	1.21	A6	A1	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
P54652	HSPA2	31	7	311	6.97E-05	0.000333	1.95	A1	A6	Heat shock-related 70 kDa protein 2 GN=HSPA2 PE=1 SV=1
Q07065	CKAP4	40	15	314	0.013768	0.009425	1.29	A1	A6	Cytoskeleton-associated protein 4 GN=CKAP4 PE=1 SV=2
P22626	HNRNPA2B1	27	14	324	0.002308	0.002547	1.91	A6	A1	Heterogeneous nuclear ribonucleoproteins A2/B1 GN=HNRNPA2B1 PE=1 SV=2
Q14194	CRMP1	34	15	326	0.000153	0.000477	1.87	A1	A6	Dihydropyrimidinase-related protein 1 GN=CRMP1 PE=1 SV=1
P07197	NEFM	40	11	331	0.04034	0.021593	1.42	A1	A6	Neurofilament medium polypeptide GN=NEFM PE=1 SV=3
P25705	ATP5F1A	33	9	342	0.000256	0.000643	1.44	A6	A1	ATP synthase subunit alpha_ mitochondrial GN=ATP5F1A PE=1 SV=1
A0A087WWY3	FLNA	54	22	352	0.000113	0.000413	1.74	A1	A6	Filamin-A GN=FLNA PE=1 SV=1
P68104	EEF1A1	32	11	353	0.020195	0.012726	1.42	A6	A1	Elongation factor 1-alpha 1 GN=EEF1A1 PE=1 SV=1
Q9Y4L1	HYOU1	48	18	362	0.000718	0.001209	1.47	A1	A6	Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1
P12277	CKB	29	15	368	0.000807	0.001294	1.84	A6	A1	Creatine kinase B-type GN=CKB PE=1 SV=1
Q00839	HNRNPU	37	4	377	0.000759	0.001249	1.33	A1	A6	Heterogeneous nuclear ribonucleoprotein U GN=HNRNPU PE=1 SV=6
Q14195	DPYSL3	36	15	382	0.000466	0.000898	1.54	A6	A1	Dihydropyrimidinase-related protein 3 GN=DPYSL3 PE=1 SV=1
P13639	EEF2	48	29	395	0.001989	0.002294	1.3	A1	A6	Elongation factor 2 GN=EEF2 PE=1 SV=4
P07900	HSP90AA1	41	18	407	7.64E-05	0.000351	1.37	A6	A1	Heat shock protein HSP 90-alpha GN=HSP90AA1 PE=1 SV=5
O43175	PHGDH	36	14	412	0.003502	0.003392	1.18	A1	A6	D-3-phosphoglycerate dehydrogenase GN=PHGDH PE=1 SV=4
P06576	ATP5F1B	37	12	413	0.000528	0.00098	1.33	A6	A1	ATP synthase subunit beta_ mitochondrial GN=ATP5F1B PE=1 SV=3
P02787	TF	45	19	417	1.4E-05	0.000159	1.96	A1	A6	Serotransferrin GN=TF PE=1 SV=3
P04406	GAPDH	36	23	426	0.000197	0.000561	1.5	A6	A1	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P35580	MYH10	73	34	451	1.64E-06	7.17E-05	1.89	A1	A6	Myosin-10 GN=MYH10 PE=1 SV=3
P11142	HSPA8	39	9	457	1E-05	0.000133	3.26	A6	A1	Heat shock cognate 71 kDa protein GN=HSPA8 PE=1 SV=1
Q9BQE3	TUBA1C	31	2	478	0.00087	0.001365	3.37	A6	A1	Tubulin alpha-1C chain GN=TUBA1C PE=1 SV=1
Q16555	DPYSL2	48	3	483	1.78E-05	0.000182	2.22	A6	A1	Dihydropyrimidinase-related protein 2 GN=DPYSL2 PE=1 SV=1
P35579	MYH9	76	24	483	8.08E-05	0.000356	4.54	A1	A6	Myosin-9 GN=MYH9 PE=1 SV=4
P08238	HSP90AB1	45	13	489	0.021309	0.013229	1.22	A6	A1	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
P14618	PKM	45	5	494	0.003061	0.003147	1.17	A1	A6	Pyruvate kinase PKM GN=PKM PE=1 SV=4
P68363	TUBA1B	32	2	496	0.013255	0.009166	1.38	A6	A1	Tubulin alpha-1B chain GN=TUBA1B PE=1 SV=1
P06733	ENO1	52	28	595	0.000235	0.000616	1.8	A1	A6	Alpha-enolase GN=ENO1 PE=1 SV=2
P14625	HSP90B1	54	23	603	0.017655	0.011476	1.18	A6	A1	Endoplasmin GN=HSP90B1 PE=1 SV=1
P11021	HSPA5	56	35	615	0.000124	0.000426	1.3	A1	A6	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P04350	TUBB4A	54	7	640	0.004803	0.004273	1.63	A6	A1	Tubulin beta-4A chain GN=TUBB4A PE=1 SV=2
P68032	ACTC1	55	12	645	0.001727	0.002099	1.27	A6	A1	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
Q13885	TUBB2A	53	2	764	0.001135	0.001607	1.15	A1	A6	Tubulin beta-2A chain GN=TUBB2A PE=1 SV=1
P52272	HNRNPM	77	49	770	0.00097	0.001457	1.32	A1	A6	Heterogeneous nuclear ribonucleoprotein M GN=HNRNPM PE=1 SV=3
P60709	ACTB	60	9	925	0.000875	0.001365	1.73	A6	A1	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1
P08670	VIM	72	27	929	5.53E-05	0.000316	1.4	A6	A1	Vimentin GN=VIM PE=1 SV=4

Anti-Aβ_{17-23} Antibody Treatment

Q8TDI	CHD5	8	4	40.3	0.004821	0.002859821	2.57	A2	A6	Chromodomain-helicase-DNA-binding protein 5 GN=CHD5 PE=1 SV=1
Q13332	PTPRS	8	2	40.6	0.001847	0.001416672	1.4	A2	A6	Receptor-type tyrosine-protein phosphatase S GN=PTPRS PE=1 SV=3
P12107	COL11A1	8	2	40.8	0.015204	0.006995237	1.94	A2	A6	Collagen alpha-1(XI) chain GN=COL11A1 PE=1 SV=4
O00754	MAN2B1	9	3	40.9	0.008048	0.004250018	1.73	A6	A2	Lysosomal alpha-mannosidase GN=MAN2B1 PE=1 SV=3
Q9HBD1	RC3H2	8	2	41.2	0.000629	0.000677967	1.76	A6	A2	Roquin-2 GN=RC3H2 PE=1 SV=2
Q15746	MYLK	7	3	41.2	0.008462	0.004398388	1.22	A6	A2	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
Q9UK76	JPT1	4	4	41.2	9.11E-06	6.51202E-05	3.31	A6	A2	Jupiter microtubule associated homolog 1 GN=JPT1 PE=1 SV=3
Q6PKC3	TXNDC11	7	2	41.4	0.023413	0.009945134	1.72	A6	A2	Thioredoxin domain-containing protein 11 GN=TXNDC11 PE=1 SV=2
Q9Y617	PSAT1	8	2	41.4	0.00044	0.000552451	2.17	A6	A2	Phosphoserine aminotransferase GN=PSAT1 PE=1 SV=2

Q02386	ZNF45	7	2	41.4	0.001191	0.001054393	7.36	A6	A2	Zinc finger protein 45 GN=ZNF45 PE=1 SV=2
Q16849	PTPRN	6	2	41.4	0.000281	0.000408079	3.34	A6	A2	Receptor-type tyrosine-protein phosphatase-like N GN=PTPRN PE=1 SV=1
A1KZ92	PXDNL	9	3	41.7	0.000973	0.000932583	1.63	A6	A2	Peroxidasin-like protein GN=PXDNL PE=1 SV=3
O60486	PLXNC1	7	2	41.8	0.010581	0.005214256	2.77	A6	A2	Plexin-C1 GN=PLXNC1 PE=1 SV=1
O00423	EML1	7	2	41.9	0.001737	0.001347883	2.89	A6	A2	Echinoderm microtubule-associated protein-like 1 GN=EML1 PE=1 SV=3
P20591	MX1	6	2	41.9	0.0082	0.004315526	1.23	A6	A2	Interferon-induced GTP-binding protein Mx1 GN=MX1 PE=1 SV=4
Q6SA08	TSSK4	5	2	42	0.004424	0.002666252	1.35	A2	A6	Testis-specific serine/threonine-protein kinase 4 GN=TSSK4 PE=1 SV=1
P06744	GPI	8	2	42	0.001749	0.001354914	8.13	A6	A2	Glucose-6-phosphate isomerase GN=GPI PE=1 SV=4
Q96EV2	RBM33	7	2	42.2	2.71E-05	0.000125809	11.8	A2	A6	RNA-binding protein 33 GN=RBM33 PE=1 SV=3
P46776	RPL27A	5	2	42.3	0.002546	0.001784159	1.21	A6	A2	60S ribosomal protein L27a GN=RPL27A PE=1 SV=2
Q05469	LIPE	9	4	42.3	0.000777	0.000799293	2.93	A2	A6	Hormone-sensitive lipase GN=LIPE PE=1 SV=4
P47914	RPL29	6	4	42.5	0.011525	0.005602303	1.99	A6	A2	60S ribosomal protein L29 GN=RPL29 PE=1 SV=2
P49458	SRP9	6	4	42.5	0.000393	0.000508872	2.82	A6	A2	Signal recognition particle 9 kDa protein GN=SRP9 PE=1 SV=2
E7EQ52	TNKS	8	5	42.5	0.020876	0.008981348	1.43	A2	A6	Poly [ADP-ribose] polymerase GN=TNKS PE=1 SV=1
H0Y5C6	FLNA	7	2	42.7	0.00016	0.000290925	4.35	A6	A2	Filamin-A (Fragment) GN=FLNA PE=1 SV=1
Q9UI17	DMGDH	7	3	42.8	0.011357	0.005531927	1.73	A2	A6	Dimethylglycine dehydrogenase_ mitochondrial GN=DMGDH PE=1 SV=2
Q9ULJ3	ZBTB21	7	4	43	0.03638	0.014254373	1.79	A2	A6	Zinc finger and BTB domain-containing protein 21 GN=ZBTB21 PE=1 SV=2
P11166	SLC2A1	5	2	43.3	0.035133	0.013835918	1.47	A6	A2	Solute carrier family 2_ facilitated glucose transporter member 1 GN=SLC2A1 PE=1 SV=2
P61026	RAB10	5	2	43.3	0.032534	0.01307792	5.48	A6	A2	Ras-related protein Rab-10 GN=RAB10 PE=1 SV=1
Q06278	AOX1	8	2	43.8	0.028338	0.011640726	2.04	A6	A2	Aldehyde oxidase GN=AOX1 PE=1 SV=2
J3KTE4	RPL19	6	3	44.2	0.00945	0.004760336	1.51	A2	A6	Ribosomal protein L19 GN=RPL19 PE=1 SV=1
Q5JSZ5	PRRC2B	11	3	44.4	0.010475	0.005167238	1.47	A2	A6	Protein PRRC2B GN=PRRC2B PE=1 SV=2
F5H7S7	IQGAP2	7	3	44.4	0.002189	0.001591563	1.91	A6	A2	Ras GTPase-activating-like protein IQGAP2 GN=IQGAP2 PE=1 SV=2
Q9UH03	SEPTIN3	7	4	44.6	0.0171	0.007685027	4.09	A6	A2	Neuronal-specific septin-3 GN=SEPT3 PE=1 SV=3
H0Y360	AMPD2	8	2	44.8	0.002205	0.001596404	2.43	A6	A2	AMP deaminase 2 (Fragment) GN=AMPD2 PE=1 SV=1
P56385	ATP5ME	6	2	44.9	1.93E-06	2.71774E-05	2.34	A2	A6	ATP synthase subunit e_ mitochondrial GN=ATP5I PE=1 SV=2
A0A0A0MTQ9	TRPM1	9	4	45.1	0.000672	0.000713339	2.64	A6	A2	Transient receptor potential cation channel subfamily M member 1 (Fragment) GN=TRPM1 PE=1 SV=1
Q9UKV0	HDAC9	10	5	45.2	0.001986	0.001505338	1.81	A2	A6	Histone deacetylase 9 GN=HDAC9 PE=1 SV=2
Q8N1G4	LRRC47	7	4	45.4	0.00227	0.00163562	3.54	A2	A6	Leucine-rich repeat-containing protein 47 GN=LRRC47 PE=1 SV=1
Q9P275	USP36	8	4	45.6	0.040141	0.015441651	1.56	A2	A6	Ubiquitin carboxyl-terminal hydrolase 36 GN=USP36 PE=1 SV=4
A0A1B0GV47	KIF21A	9	5	45.9	0.001221	0.001072805	1.5	A6	A2	Kinesin-like protein KIF21A (Fragment) GN=KIF21A PE=1 SV=1
Q13635	PTCH1	10	3	46.1	0.007628	0.004065007	1.7	A6	A2	Protein patched homolog 1 GN=PTCH1 PE=1 SV=2
O60318	MCM3AP	8	2	46.6	0.000615	0.000666766	1.98	A2	A6	Germinal-center associated nuclear protein GN=MCM3AP PE=1 SV=2
Q9BZH6	WDR11	8	4	47.1	3.19E-05	0.000134591	2.39	A6	A2	WD repeat-containing protein 11 GN=WDR11 PE=1 SV=1
Q9HAU0	PLEKHA5	9	8	47.2	0.001331	0.001128027	2.63	A6	A2	Pleckstrin homology domain-containing family A member 5 GN=PLEKHA5 PE=1 SV=1
F8VWS0	RPLP0	8	2	47.3	0.007139	0.003870823	7.26	A6	A2	60S acidic ribosomal protein P0 GN=RPLP0 PE=1 SV=1
Q86UV5	USP48	8	2	48.1	0.009382	0.004742483	1.7	A2	A6	Ubiquitin carboxyl-terminal hydrolase 48 GN=USP48 PE=1 SV=1
Q32Q12	NME1-NME2	7	4	48.1	1.92E-05	9.69471E-05	7.41	A6	A2	Nucleoside diphosphate kinase GN=NME1-NME2 PE=1 SV=1
E9PDF1	SH3TC2	9	5	48.1	0.018068	0.008004046	1.13	A2	A6	SH3 domain and tetratricopeptide repeat-containing protein 2 GN=SH3TC2 PE=1 SV=1
O94868	FCHSD2	11	4	48.2	0.020336	0.00879498	1.48	A2	A6	F-BAR and double SH3 domains protein 2 GN=FCHSD2 PE=1 SV=3
O95049	TJP3	6	3	48.5	0.002107	0.001570662	2.04	A2	A6	Tight junction protein ZO-3 GN=TJP3 PE=1 SV=3
Q99714	HSD17B10	7	2	48.6	0.004618	0.002769078	2.59	A6	A2	3-hydroxyacyl-CoA dehydrogenase type-2 GN=HSD17B10 PE=1 SV=3
P13489	RNH1	9	3	48.8	0.000817	0.000831034	1.5	A6	A2	Ribonuclease inhibitor GN=RNH1 PE=1 SV=2
O00468	AGRN	10	2	49.1	0.009723	0.004873924	22.4	A2	A6	Agrin GN=AGRN PE=1 SV=5
Q14839	CHD4	10	2	49.1	0.038577	0.014963886	1.78	A6	A2	Chromodomain-helicase-DNA-binding protein 4 GN=CHD4 PE=1 SV=2
Q2NL67	PARP6	7	2	49.2	0.004452	0.00267972	1.82	A2	A6	Poly [ADP-ribose] polymerase 6 GN=PARP6 PE=2 SV=1
Q9UL54	TAOK2	7	2	49.2	0.000122	0.000249536	1.74	A6	A2	Serine/threonine-protein kinase TAO2 GN=TAOK2 PE=1 SV=2
P45974	USP5	7	3	49.3	0.001328	0.001128027	1.92	A2	A6	Ubiquitin carboxyl-terminal hydrolase 5 GN=USP5 PE=1 SV=2
O14497	ARID1A	12	6	49.4	0.006786	0.003754239	2.09	A2	A6	AT-rich interactive domain-containing protein 1A GN=ARID1A PE=1 SV=3
O15031	PLXNB2	11	3	49.7	0.027874	0.011503706	2.98	A6	A2	Plexin-B2 GN=PLXNB2 PE=1 SV=3
H0Y613	GSE1	9	4	49.7	0.00032	0.000451346	25.5	A2	A6	Genetic suppressor element 1 (Fragment) GN=GSE1 PE=1 SV=1
P55196	AFDN	10	4	49.8	0.00114	0.00103486	1.97	A2	A6	Afadin GN=AFDN PE=1 SV=3
P52907	CAPZA1	6	2	49.9	0.001707	0.001337419	3.91	A6	A2	F-actin-capping protein subunit alpha-1 GN=CAPZA1 PE=1 SV=3
A0A087WXM3	NLRP5	9	4	49.9	0.008854	0.004541137	1.51	A2	A6	NACHT_ LRR and PYD domains-containing protein 5 GN=NLRP5 PE=1 SV=1
Q9HCE3	ZNF532	8	2	50.1	0.000149	0.000278858	35.7	A2	A6	Zinc finger protein 532 GN=ZNF532 PE=1 SV=2
E7EPU2	DIP2C	10	4	50.1	0.007102	0.003859868	1.84	A2	A6	Disco-interacting protein 2 homolog C GN=DIP2C PE=1 SV=2
E7EPB3	RPL14	8	5	50.1	0.000547	0.000621755	2.39	A2	A6	60S ribosomal protein L14 GN=RPL14 PE=1 SV=1
Q8TD31	CCHCR1	9	6	50.1	2.24E-05	0.000110343	10.8	A6	A2	Coiled-coil alpha-helical rod protein 1 GN=CCHCR1 PE=1 SV=2
Q13148	TARDBP	7	3	50.2	0.047019	0.017653259	1.33	A6	A2	TAR DNA-binding protein 43 GN=TARDBP PE=1 SV=1
O15056	SYNJ2	11	2	50.4	0.006305	0.003525942	2.75	A2	A6	Synaptojanin-2 GN=SYNJ2 PE=1 SV=3
Q86VH2	KIF27	9	4	50.6	0.016244	0.007378641	5.25	A2	A6	Kinesin-like protein KIF27 GN=KIF27 PE=2 SV=1
Q8TEK3	DOT1L	10	3	50.8	0.000144	0.000277149	4.28	A2	A6	Histone-lysine N-methyltransferase_ H3 lysine-79 specific GN=DOT1L PE=1 SV=2
Q9BVN2	RUSC1	9	3	50.8	0.033363	0.013330764	1.3	A2	A6	RUN and SH3 domain-containing protein 1 GN=RUSC1 PE=1 SV=3
Q15459	SF3A1	7	2	51.3	0.000103	0.000226368	2.28	A2	A6	Splicing factor 3A subunit 1 GN=SF3A1 PE=1 SV=1
Q8NFY4	SEMA6D	11	4	51.4	2.48E-05	0.000116594	6.07	A2	A6	Semaphorin-6D GN=SEMA6D PE=1 SV=1
Q05209	PTPN12	8	2	51.5	0.023933	0.010101446	8.74	A6	A2	Tyrosine-protein phosphatase non-receptor type 12 GN=PTPN12 PE=1 SV=3
Q86W92	PPFIBP1	11	2	52	7.44E-05	0.0001983	8.5	A6	A2	Liprin-beta-1 GN=PPFIBP1 PE=1 SV=2
O43790	KRT86	7	2	52.5	0.027185	0.01128914	10.6	A6	A2	Keratin_ type II cuticular Hb6 GN=KRT86 PE=1 SV=1
O14556	GAPDHS	8	6	52.5	0.006478	0.003605331	1.69	A6	A2	Glyceraldehyde-3-phosphate dehydrogenase_ testis-specific GN=GAPDHS PE=1 SV=2
A0A0J9YVP0	HERC2	8	3	52.6	0.003421	0.002226816	1.68	A6	A2	E3 ubiquitin-protein ligase HERC2 (Fragment) GN=HERC2 PE=1 SV=1
P80723	BASP1	6	4	52.8	4.76E-05	0.000162626	4.6	A6	A2	Brain acid soluble protein 1 GN=BASP1 PE=1 SV=2
P0DN79	CBSL	10	7	52.9	0.001011	0.000953107	2.1	A2	A6	Cystathionine beta-synthase-like protein GN=CBSL PE=1 SV=1
Q7Z7H5	TMED4	7	3	53	0.005495	0.00316568	1.63	A2	A6	Transmembrane emp24 domain-containing protein 4 GN=TMED4 PE=1 SV=1
Q15700	DLG2	11	4	53.2	0.000267	0.000391975	2.8	A2	A6	Disks large homolog 2 GN=DLG2 PE=1 SV=3
G3V2A4	TEP1	13	7	53.2	0.002492	0.001758597	5.92	A2	A6	Telomerase protein component 1 GN=TEP1 PE=1 SV=1
P07737	PFN1	7	4	53.3	0.000672	0.000713339	1.73	A2	A6	Profilin-1 GN=PFN1 PE=1 SV=2
Q9BX26	SYCP2	11	5	53.3	0.002498	0.001758597	2.67	A6	A2	Synaptonemal complex protein 2 GN=SYCP2 PE=2 SV=2
A0A087WX84	AKAP9	9	3	53.4	0.000247	0.00037831	2.45	A2	A6	A-kinase anchor protein 9 GN=AKAP9 PE=1 SV=1
Q8IYA2	CCDC144CP	9	2	53.5	0.014987	0.006929994	2.52	A6	A2	Putative coiled-coil domain-containing protein 144C GN=CCDC144CP PE=5 SV=3
O00299	CLIC1	7	4	53.6	0.012265	0.005900137	1.81	A6	A2	Chloride intracellular channel protein 1 GN=CLIC1 PE=1 SV=4

P30084	ECHS1	8	2	53.7	0.033882	0.013491654	34.7	A6	A2	Enoyl-CoA hydratase_ mitochondrial GN=ECHS1 PE=1 SV=4
Q3MJ40	CCDC144B	10	4	53.9	0.000807	0.000823157	2.97	A2	A6	Coiled-coil domain-containing protein 144B GN=CCDC144B PE=2 SV=1
P52179	MYOM1	10	6	54	5.77E-06	5.06782E-05	4.14	A2	A6	Myomesin-1 GN=MYOM1 PE=1 SV=2
O15357	INPPL1	11	2	54.4	0.016324	0.007393472	1.31	A6	A2	Phosphatidylinositol 3_4_5-trisphosphate 5-phosphatase 2 GN=INPPL1 PE=1 SV=2
Q15717	ELAVL1	7	3	54.4	0.000521	0.000605358	1.45	A6	A2	ELAV-like protein 1 GN=ELAVL1 PE=1 SV=2
P29966	MARCKS	7	4	54.4	0.03353	0.013386221	2.22	A6	A2	Myristoylated alanine-rich C-kinase substrate GN=MARCKS PE=1 SV=4
P00441	SOD1	7	4	54.6	0.000676	0.000715096	1.88	A6	A2	Superoxide dismutase [Cu-Zn] GN=SOD1 PE=1 SV=2
P35268	RPL22	7	2	54.8	0.037824	0.014730403	1.98	A6	A2	60S ribosomal protein L22 GN=RPL22 PE=1 SV=2
Q96PC5	MIA2	11	5	54.8	0.000852	0.000849908	2.89	A2	A6	Melanoma inhibitory activity protein 2 GN=MIA2 PE=1 SV=4
O15075	DCLK1	9	2	54.9	0.000518	0.000605358	6.76	A6	A2	Serine/threonine-protein kinase DCLK1 GN=DCLK1 PE=1 SV=2
Q96RG2	PASK	9	3	54.9	7.48E-07	1.39603E-05	158	A2	A6	PAS domain-containing serine/threonine-protein kinase GN=PASK PE=1 SV=3
Q15147	PLCB4	10	2	55.4	0.026716	0.011134329	2.06	A6	A2	1-phosphatidylinositol 4_5-bisphosphate phosphodiesterase beta-4 GN=PLCB4 PE=1 SV=3
A0A0D9SF60	PKP4	9	2	55.6	0.016354	0.007399921	3.78	A2	A6	Plakophilin-4 GN=PKP4 PE=1 SV=1
H0YMW2	AKAP13	9	3	55.6	0.049887	0.018472015	1.56	A6	A2	A-kinase anchor protein 13 (Fragment) GN=AKAP13 PE=1 SV=1
Q8IX03	WWC1	9	6	55.7	0.000857	0.000851162	1.94	A2	A6	Protein KIBRA GN=WWC1 PE=1 SV=1
E9PFH2	KDM5D	10	6	55.7	0.008419	0.00438582	2.33	A6	A2	Lysine-specific demethylase 5D (Fragment) GN=KDM5D PE=4 SV=1
Q96P48	ARAP1	11	3	56	8.63E-06	6.36541E-05	16.7	A2	A6	Arf-GAP with Rho-GAP domain_ ANK repeat and PH domain-containing protein 1 GN=ARAP1 PE=1 SV=3
P28331	NDUFS1	10	2	56.3	0.011565	0.005615863	2.37	A6	A2	NADH-ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial GN=NDUFS1 PE=1 SV=3
E9PFT7	APC	11	4	56.4	0.014329	0.006678482	5.09	A6	A2	Adenomatous polyposis coli protein (Fragment) GN=APC PE=1 SV=8
Q9UQ80	PA2G4	11	2	57.1	0.027135	0.011278549	2.11	A6	A2	Proliferation-associated protein 2G4 GN=PA2G4 PE=1 SV=3
Q7Z553	MDGA2	8	3	57.1	0.014547	0.006770238	1.88	A6	A2	MAM domain-containing glycosylphosphatidylinositol anchor protein 2 GN=MDGA2 PE=1 SV=2
O95153	TSPOAP1	10	4	57.1	6.94E-05	0.00018963	3.42	A2	A6	Peripheral-type benzodiazepine receptor-associated protein 1 GN=TSPOAP1 PE=1 SV=2
P39023	RPL3	9	3	57.3	0.005238	0.003046511	2.63	A6	A2	60S ribosomal protein L3 GN=RPL3 PE=1 SV=2
Q14011	CIRBP	5	3	57.6	0.000823	0.000834789	4.34	A6	A2	Cold-inducible RNA-binding protein GN=CIRBP PE=1 SV=1
O95466	FMNL1	10	2	58	0.000216	0.000356644	20.7	A2	A6	Formin-like protein 1 GN=FMNL1 PE=1 SV=3
Q13561	DCTN2	8	5	58.2	0.001267	0.001082445	1.99	A2	A6	Dynactin subunit 2 GN=DCTN2 PE=1 SV=4
P62979	RPS27A	8	3	58.3	0.003607	0.002296284	3.89	A6	A2	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
P07205	PGK2	7	2	58.4	0.001255	0.001077146	2.22	A6	A2	Phosphoglycerate kinase 2 GN=PGK2 PE=1 SV=3
O60346	PHLPP1	8	4	58.7	0.008556	0.004435094	3.66	A2	A6	PH domain leucine-rich repeat-containing protein phosphatase 1 GN=PHLPP1 PE=1 SV=3
Q9H2Y7	ZNF106	12	2	58.9	0.00606	0.003411921	2.63	A6	A2	Zinc finger protein 106 GN=ZNF106 PE=1 SV=1
Q9H8Y5	ANKZF1	10	4	59.1	0.04098	0.015673375	1.31	A6	A2	Ankyrin repeat and zinc finger domain-containing protein 1 GN=ANKZF1 PE=1 SV=1
Q96AA8	JAKMIP2	9	3	59.3	0.000234	0.00036931	3.35	A2	A6	Janus kinase and microtubule-interacting protein 2 GN=JAKMIP2 PE=1 SV=1
Q96AG4	LRRC59	8	3	59.5	1.27E-05	8.08269E-05	3.82	A6	A2	Leucine-rich repeat-containing protein 59 GN=LRRC59 PE=1 SV=1
P37108	SRP14	8	3	59.8	0.01371	0.006454867	1.55	A2	A6	Signal recognition particle 14 kDa protein GN=SRP14 PE=1 SV=2
B7ZW38	HNRNPCL3	8	4	59.9	0.001714	0.001339655	3.02	A2	A6	Heterogeneous nuclear ribonucleoprotein C-like 3 GN=HNRNPCL3 PE=2 SV=1
P13674	P4HA1	10	4	60.3	0.002305	0.001655738	1.6	A6	A2	Prolyl 4-hydroxylase subunit alpha-1 GN=P4HA1 PE=1 SV=2
Q8NHY6	ZFP28	9	2	60.4	0.011304	0.005519057	1.68	A2	A6	Zinc finger protein 28 homolog GN=ZFP28 PE=1 SV=1
Q8NEV8	EXPH5	12	4	60.5	0.000692	0.000725837	3.08	A6	A2	Exophilin-5 GN=EXPH5 PE=1 SV=3
Q9NQT8	KIF13B	10	4	61.3	0.002126	0.001575698	2.22	A6	A2	Kinesin-like protein KIF13B GN=KIF13B PE=1 SV=2
Q96JN8	NEURL4	11	2	61.8	0.002623	0.001819003	2.58	A2	A6	Neuralized-like protein 4 GN=NEURL4 PE=1 SV=2
A0A087WX34	RPGRIP1L	11	5	62.3	0.004073	0.002513836	2.69	A2	A6	Protein fantom GN=RPGRIP1L PE=1 SV=1
P02452	COL1A1	12	6	62.9	0.004162	0.002549294	1.89	A6	A2	Collagen alpha-1(I) chain GN=COL1A1 PE=1 SV=5
Q8TDM6	DLG5	12	5	63.2	0.000126	0.000255366	4.87	A6	A2	Disks large homolog 5 GN=DLG5 PE=1 SV=4
P53804	TTC3	13	6	64.5	0.002174	0.001586369	1.81	A2	A6	E3 ubiquitin-protein ligase TTC3 GN=TTC3 PE=1 SV=2
Q8NEZ3	WDR19	12	3	65.3	3.31E-05	0.000135648	10.3	A2	A6	WD repeat-containing protein 19 GN=WDR19 PE=1 SV=2
P40926	MDH2	10	5	65.5	0.03503	0.013807045	1.64	A2	A6	Malate dehydrogenase_ mitochondrial GN=MDH2 PE=1 SV=3
P01308	INS	5	3	65.6	1.6E-05	9.08085E-05	4.63	A2	A6	Insulin GN=INS PE=1 SV=1
P60866	RPS20	7	3	65.8	6.48E-06	5.19258E-05	9.17	A2	A6	40S ribosomal protein S20 GN=RPS20 PE=1 SV=1
Q5SW79	CEP170	12	4	65.9	0.006864	0.00377465	2.44	A6	A2	Centrosomal protein of 170 kDa GN=CEP170 PE=1 SV=1
O43852	CALU	9	4	66.1	0.000267	0.000391975	3.72	A6	A2	Calumenin GN=CALU PE=1 SV=2
O15360	FANCA	12	5	66.4	6.04E-05	0.000177888	2.57	A6	A2	Fanconi anemia group A protein GN=FANCA PE=1 SV=2
P31150	GDI1	10	5	66.4	0.00087	0.000858522	2.13	A6	A2	Rab GDP dissociation inhibitor alpha GN=GDI1 PE=1 SV=2
P23468	PTPRD	11	6	66.4	6.94E-05	0.00018963	3.18	A2	A6	Receptor-type tyrosine-protein phosphatase delta GN=PTPRD PE=1 SV=2
O15067	PFAS	13	6	66.7	3.12E-05	0.000134591	2.31	A2	A6	Phosphoribosylformylglycinamidine synthase GN=PFAS PE=1 SV=4
A0A0D9SEP4	NRXN1	12	6	66.7	0.000379	0.00050302	2.21	A6	A2	Neurexin-1-beta GN=NRXN1 PE=1 SV=1
Q9NQC3	RTN4	12	6	66.8	0.032518	0.01307792	1.16	A2	A6	Reticulon-4 GN=RTN4 PE=1 SV=2
Q92618	ZNF516	13	3	66.9	0.008528	0.004427683	2.22	A6	A2	Zinc finger protein 516 GN=ZNF516 PE=1 SV=1
P62258	YWHAE	7	3	67.3	0.004762	0.002835528	1.31	A2	A6	14-3-3 protein epsilon GN=YWHAE PE=1 SV=1
P42695	NCAPD3	11	4	67.5	0.001061	0.000992029	3.77	A2	A6	Condensin-2 complex subunit D3 GN=NCAPD3 PE=1 SV=2
Q8ND30	PPFIBP2	14	6	67.7	0.014218	0.006646995	1.49	A2	A6	Liprin-beta-2 GN=PPFIBP2 PE=1 SV=3
Q6N021	TET2	11	3	68.1	0.002804	0.001925971	1.73	A2	A6	Methylcytosine dioxygenase TET2 GN=TET2 PE=1 SV=3
P68402	PAFAH1B2	10	7	68.1	1.92E-05	9.69471E-05	8.5	A6	A2	Platelet-activating factor acetylhydrolase IB subunit beta GN=PAFAH1B2 PE=1 SV=1
E7EQV3	PABPC1	11	3	68.2	0.01408	0.006589179	1.67	A6	A2	Polyadenylate-binding protein GN=PABPC1 PE=1 SV=1
P46777	RPL5	9	3	68.2	0.000981	0.000933816	2.86	A6	A2	60S ribosomal protein L5 GN=RPL5 PE=1 SV=3
Q8NDI1	EHBP1	12	4	68.2	0.005131	0.002991942	2.85	A2	A6	EH domain-binding protein 1 GN=EHBP1 PE=1 SV=3
O75643	SNRNP200	14	4	68.6	0.001355	0.001141114	6.61	A2	A6	U5 small nuclear ribonucleoprotein 200 kDa helicase GN=SNRNP200 PE=1 SV=2
Q9P2K5	MYEF2	12	4	68.6	0.001256	0.001077146	2.38	A6	A2	Myelin expression factor 2 GN=MYEF2 PE=1 SV=3
Q96PY6	NEK1	12	5	68.6	0.001724	0.00134199	2.28	A6	A2	Serine/threonine-protein kinase Nek1 GN=NEK1 PE=1 SV=2
P26641	EEF1G	11	6	68.7	0.000491	0.000589142	1.48	A6	A2	Elongation factor 1-gamma GN=EEF1G PE=1 SV=3
F5H039	GPHN	12	4	69	0.005094	0.002977563	5.19	A6	A2	Gephyrin GN=GPHN PE=1 SV=1
P16144	ITGB4	11	5	69	0.000129	0.000257121	11.3	A6	A2	Integrin beta-4 GN=ITGB4 PE=1 SV=5
P67809	YBX1	10	4	69.2	0.012396	0.005938819	2.67	A6	A2	Nuclease-sensitive element-binding protein 1 GN=YBX1 PE=1 SV=3
P62263	RPS14	6	3	69.3	0.000754	0.000780082	1.91	A2	A6	40S ribosomal protein S14 GN=RPS14 PE=1 SV=3
Q12905	ILF2	10	4	69.3	0.014772	0.00685089	1.62	A6	A2	Interleukin enhancer-binding factor 2 GN=ILF2 PE=1 SV=2
Q9HCM1	RESF1	11	5	69.3	0.002156	0.001582792	2.1	A6	A2	Uncharacterized protein KIAA1551 GN=KIAA1551 PE=1 SV=3
Q9UNA4	POLI	10	2	69.7	0.018819	0.008289166	2.39	A6	A2	DNA polymerase iota GN=POLI PE=1 SV=3
A0A0A0MS86	CEP290	13	3	69.9	0.028971	0.011850912	1.66	A2	A6	Centrosomal protein of 290 kDa GN=CEP290 PE=1 SV=1
Q5JRA6	MIA3	12	3	70.8	0.000157	0.000287806	2.97	A2	A6	Transport and Golgi organization protein 1 homolog GN=MIA3 PE=1 SV=1
Q04637	EIF4G1	13	4	70.8	0.043918	0.016673885	1.34	A6	A2	Eukaryotic translation initiation factor 4 gamma 1 GN=EIF4G1 PE=1 SV=4

Q02878	RPL6	7	3	71.5	7.6E-05	0.000198918	2.97	A2	A6	60S ribosomal protein L6 GN=RPL6 PE=1 SV=3
Q15424	SAFB	9	2	71.8	0.007661	0.004074268	3.65	A6	A2	Scaffold attachment factor B1 GN=SAFB PE=1 SV=4
Q15019	SEPTIN2	11	7	72	0.004053	0.002507826	2.86	A6	A2	Septin-2 GN=SEPT2 PE=1 SV=1
P62913	RPL11	9	3	72.2	0.002421	0.001720437	1.65	A2	A6	60S ribosomal protein L11 GN=RPL11 PE=1 SV=2
Q9Y4G8	RAPGEF2	13	5	72.4	0.015204	0.006995237	2.63	A2	A6	Rap guanine nucleotide exchange factor 2 GN=RAPGEF2 PE=1 SV=1
P33991	MCM4	13	6	72.4	0.00014	0.000273811	5.31	A2	A6	DNA replication licensing factor MCM4 GN=MCM4 PE=1 SV=5
P62829	RPL23	9	2	72.9	0.000137	0.000269089	2.29	A2	A6	60S ribosomal protein L23 GN=RPL23 PE=1 SV=1
P62753	RPS6	8	2	73	0.012127	0.005845627	1.86	A6	A2	40S ribosomal protein S6 GN=RPS6 PE=1 SV=1
Q00872	MYBPC1	13	3	73.4	3.34E-07	1.0082E-05	9.68	A6	A2	Myosin-binding protein C_ slow-type GN=MYBPC1 PE=1 SV=2
J3KQV8	SYNJ1	15	3	73.5	6.08E-05	0.000177888	5.83	A2	A6	Synaptojanin-1 GN=SYNJ1 PE=1 SV=1
Q13151	HNRNPA0	9	4	73.5	0.000258	0.000386482	2.43	A6	A2	Heterogeneous nuclear ribonucleoprotein A0 GN=HNRNPA0 PE=1 SV=1
P13647	KRT5	8	5	74	0.019391	0.008476969	1.86	A2	A6	Keratin_ type II cytoskeletal 5 GN=KRT5 PE=1 SV=3
P08237	PFKM	12	5	74.2	0.000615	0.000666766	2.71	A6	A2	ATP-dependent 6-phosphofructokinase_ muscle type GN=PFKM PE=1 SV=2
Q8NF50	DOCK8	13	8	75.5	0.00869	0.004481832	1.9	A2	A6	Dedicator of cytokinesis protein 8 GN=DOCK8 PE=1 SV=3
P53396	ACLY	12	4	75.7	0.034162	0.013550738	3.35	A6	A2	ATP-citrate synthase GN=ACLY PE=1 SV=3
O00264	PGRMC1	9	2	76.2	0.000353	0.000474817	2	A6	A2	Membrane-associated progesterone receptor component 1 GN=PGRMC1 PE=1 SV=3
Q9UBT2	UBA2	12	2	76.2	0.00119	0.001054393	6.77	A6	A2	SUMO-activating enzyme subunit 2 GN=UBA2 PE=1 SV=2
Q9ULV0	MYO5B	15	5	76.4	0.000175	0.000309775	3.02	A6	A2	Unconventional myosin-Vb GN=MYO5B PE=1 SV=3
Q9UPV9	TRAK1	14	2	77.3	3.25E-05	0.000135648	6.56	A6	A2	Trafficking kinesin-binding protein 1 GN=TRAK1 PE=1 SV=1
P30040	ERP29	10	5	77.4	6.93E-05	0.00018963	6.84	A6	A2	Endoplasmic reticulum resident protein 29 GN=ERP29 PE=1 SV=4
A0A0C4DG17	RPSA	9	5	77.6	2.94E-06	3.50036E-05	2.53	A2	A6	40S ribosomal protein SA GN=RPSA PE=1 SV=1
P60981	DSTN	10	5	78.4	0.000334	0.000460765	1.48	A6	A2	Destrin GN=DSTN PE=1 SV=3
P04792	HSPB1	8	3	78.6	0.002974	0.002006602	2.54	A2	A6	Heat shock protein beta-1 GN=HSPB1 PE=1 SV=2
Q03252	LMNB2	12	2	79.2	0.000603	0.000660899	3.82	A2	A6	Lamin-B2 GN=LMNB2 PE=1 SV=4
Q14160	SCRIB	13	4	79.2	0.000606	0.000661574	1.72	A2	A6	Protein scribble homolog GN=SCRIB PE=1 SV=4
P83731	RPL24	9	4	79.4	0.000113	0.000238386	2.27	A2	A6	60S ribosomal protein L24 GN=RPL24 PE=1 SV=1
Q7L7X3	TAOK1	13	2	79.6	0.011959	0.005770681	1.33	A2	A6	Serine/threonine-protein kinase TAO1 GN=TAOK1 PE=1 SV=1
O75947	ATP5PD	7	2	79.8	0.001084	0.001001493	2.01	A2	A6	ATP synthase subunit d_ mitochondrial GN=ATP5H PE=1 SV=3
P49006	MARCKSL1	8	4	80	0.004131	0.002539159	1.57	A6	A2	MARCKS-related protein GN=MARCKSL1 PE=1 SV=2
Q99623	PHB2	10	3	80.1	0.001733	0.001346558	1.83	A2	A6	Prohibitin-2 GN=PHB2 PE=1 SV=2
P35221	CTNNA1	15	2	80.8	0.001394	0.001163368	72.5	A2	A6	Catenin alpha-1 GN=CTNNA1 PE=1 SV=1
Q00325	SLC25A3	11	4	81.5	0.00086	0.000851777	1.52	A6	A2	Phosphate carrier protein_ mitochondrial GN=SLC25A3 PE=1 SV=2
Q53SF7	COBLL1	15	6	81.9	0.000135	0.000267882	6.13	A6	A2	Cordon-bleu protein-like 1 GN=COBLL1 PE=1 SV=2
P30050	RPL12	9	6	82.9	0.029019	0.011856026	1.33	A2	A6	60S ribosomal protein L12 GN=RPL12 PE=1 SV=1
I3L2J8	CEP131	14	3	83	0.000334	0.000460765	2.07	A2	A6	Centrosomal protein of 131 kDa GN=CEP131 PE=1 SV=1
P24752	ACAT1	12	5	83.1	0.002405	0.001711561	1.33	A6	A2	Acetyl-CoA acetyltransferase_ mitochondrial GN=ACAT1 PE=1 SV=1
P12004	PCNA	14	7	83.2	0.048648	0.018129015	1.44	A6	A2	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
Q15293	RCN1	10	4	84.1	0.007594	0.004059554	2.09	A6	A2	Reticulocalbin-1 GN=RCN1 PE=1 SV=1
P84103	SRSF3	9	6	84.2	0.025334	0.010634626	1.4	A2	A6	Serine/arginine-rich splicing factor 3 GN=SRSF3 PE=1 SV=1
O94856	NFASC	15	6	84.8	0.009215	0.004674745	1.44	A2	A6	Neurofascin GN=NFASC PE=1 SV=4
Q9Y3I0	RTCB	14	9	85	0.001559	0.001260507	1.47	A2	A6	tRNA-splicing ligase RtcB homolog GN=RTCB PE=1 SV=1
E7EUS2	CCDC110	14	5	85.3	0.047396	0.017761861	1.75	A2	A6	Coiled-coil domain-containing protein 110 GN=CCDC110 PE=4 SV=1
Q58FF6	HSP90AB4P	11	3	85.5	0.046431	0.01749924	1.91	A6	A2	Putative heat shock protein HSP 90-beta 4 GN=HSP90AB4P PE=5 SV=1
O75150	RNF40	16	6	86	0.000939	0.000905263	1.71	A6	A2	E3 ubiquitin-protein ligase BRE1B GN=RNF40 PE=1 SV=4
O00571	DDX3X	15	8	86	0.005391	0.003116424	4.08	A6	A2	ATP-dependent RNA helicase DDX3X GN=DDX3X PE=1 SV=3
J3KN67	TPM3	10	2	86.8	0.005203	0.003029746	1.98	A6	A2	Tropomyosin alpha-3 chain GN=TPM3 PE=1 SV=1
A0A0G2JNB1	KANSL1	15	2	87.2	0.047745	0.017878261	1.27	A2	A6	KAT8 regulatory NSL complex subunit 1 GN=KANSL1 PE=1 SV=1
B1AJZ9	FHAD1	17	3	87.2	0.000127	0.000256259	2.8	A6	A2	Forkhead-associated domain-containing protein 1 GN=FHAD1 PE=2 SV=2
H0Y7F7	CEP350	13	6	87.4	0.003917	0.002446499	2.99	A2	A6	Centrosome-associated protein 350 (Fragment) GN=CEP350 PE=1 SV=1
Q14562	DHX8	15	6	88.8	0.030536	0.012382345	1.26	A2	A6	ATP-dependent RNA helicase DHX8 GN=DHX8 PE=1 SV=1
P05455	SSB	15	7	89.1	0.032973	0.013208941	1.31	A6	A2	Lupus La protein GN=SSB PE=1 SV=2
P09211	GSTP1	11	7	90.6	3.9E-05	0.000143801	5.18	A6	A2	Glutathione S-transferase P GN=GSTP1 PE=1 SV=2
P42167	TMPO	11	5	90.9	0.001189	0.001054393	1.73	A6	A2	Lamina-associated polypeptide 2_ isoforms beta/gamma GN=TMPO PE=1 SV=2
O75334	PPFIA2	18	4	91.3	0.016305	0.007392004	1.47	A6	A2	Liprin-alpha-2 GN=PPFIA2 PE=1 SV=2
P55795	HNRNPH2	11	3	91.4	0.00041	0.000522028	5.21	A6	A2	Heterogeneous nuclear ribonucleoprotein H2 GN=HNRNPH2 PE=1 SV=1
Q86UW6	N4BP2	16	7	91.7	0.001087	0.001001845	3.45	A2	A6	NEDD4-binding protein 2 GN=N4BP2 PE=1 SV=2
A0A0C4DFM7	TUT4	15	2	92.9	0.006224	0.00348868	2.42	A2	A6	Terminal uridylyltransferase 4 GN=ZCCHC11 PE=1 SV=1
Q8IYT4	KATNAL2	16	4	93.4	0.003796	0.002390349	1.5	A2	A6	Katanin p60 ATPase-containing subunit A-like 2 GN=KATNAL2 PE=1 SV=3
J3KN16	ECPAS	19	5	93.9	0.005416	0.003126272	2.2	A2	A6	Proteasome adapter and scaffold protein ECM29 GN=ECPAS PE=1 SV=1
Q99798	ACO2	15	6	94	0.00657	0.003643328	1.58	A6	A2	Aconitate hydratase_ mitochondrial GN=ACO2 PE=1 SV=2
P07954	FH	16	6	94.1	7.61E-06	5.79841E-05	2.55	A6	A2	Fumarate hydratase_ mitochondrial GN=FH PE=1 SV=3
Q99829	CPNE1	13	6	94.6	0.024204	0.010197106	1.25	A6	A2	Copine-1 GN=CPNE1 PE=1 SV=1
P08708	RPS17	10	2	94.7	0.000987	0.000937883	1.91	A2	A6	40S ribosomal protein S17 GN=RPS17 PE=1 SV=2
P48047	ATP5PO	12	6	94.8	0.000597	0.000657214	1.98	A6	A2	ATP synthase subunit O_ mitochondrial GN=ATP5O PE=1 SV=1
P61586	RHOA	11	3	95.2	0.000211	0.000350976	1.67	A6	A2	Transforming protein RhoA GN=RHOA PE=1 SV=1
Q9H4G0	EPB41L1	15	4	95.3	0.000583	0.000648681	3.27	A2	A6	Band 4.1-like protein 1 GN=EPB41L1 PE=1 SV=2
Q9C093	SPEF2	20	3	95.8	0.011307	0.005519057	1.7	A2	A6	Sperm flagellar protein 2 GN=SPEF2 PE=2 SV=2
Q58FG1	HSP90AA4P	13	5	95.8	0.003721	0.002352759	1.37	A2	A6	Putative heat shock protein HSP 90-alpha A4 GN=HSP90AA4P PE=5 SV=1
O00443	PIK3C2A	19	7	97.1	0.039439	0.015221825	1.32	A2	A6	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha GN=PIK3C2A PE=1 SV=2
A0A0A0MS79	NCKAP5	15	6	97.4	2.26E-05	0.000110343	2.1	A6	A2	Nck-associated protein 5 GN=NCKAP5 PE=1 SV=1
P62701	RPS4X	13	6	97.6	0.002329	0.001670358	2.03	A2	A6	40S ribosomal protein S4_ X isoform GN=RPS4X PE=1 SV=2
Q3V6T2	CCDC88A	19	7	97.6	0.005725	0.003264141	1.55	A2	A6	Girdin GN=CCDC88A PE=1 SV=2
F8W775	NRCAM	15	8	98.6	0.008706	0.004483456	1.55	A6	A2	Neuronal cell adhesion molecule GN=NRCAM PE=1 SV=2
P0C0S5	H2AZ1	7	2	99.3	0.003719	0.002352759	1.65	A2	A6	Histone H2A.Z GN=H2AFZ PE=1 SV=2
P14866	HNRNPL	12	11	99.3	0.000148	0.000278858	3.26	A2	A6	Heterogeneous nuclear ribonucleoprotein L GN=HNRNPL PE=1 SV=2
H0Y2S9	MPRIP	19	4	101	0.025546	0.010714224	1.55	A2	A6	Myosin phosphatase Rho-interacting protein (Fragment) GN=MPRIP PE=1 SV=3
P26373	RPL13	13	4	102	0.010301	0.005108911	2.06	A2	A6	60S ribosomal protein L13 GN=RPL13 PE=1 SV=4
Q03113	GNA12	15	4	102	0.002824	0.001935765	2.06	A2	A6	Guanine nucleotide-binding protein subunit alpha-12 GN=GNA12 PE=1 SV=4
O94986	CEP152	19	3	103	0.00029	0.000419134	1.8	A2	A6	Centrosomal protein of 152 kDa GN=CEP152 PE=1 SV=4
A0A1B0GVD5	CTSD	14	7	103	0.005749	0.003273031	2.26	A6	A2	Cathepsin D GN=CTSD PE=1 SV=1
P50993	ATP1A2	17	4	104	0.000507	0.000600766	1.75	A2	A6	Sodium/potassium-transporting ATPase subunit alpha-2 GN=ATP1A2 PE=1 SV=1
Q5JYT7	KIAA1755	17	4	104	9.1E-05	0.000217869	2.77	A6	A2	Uncharacterized protein KIAA1755 GN=KIAA1755 PE=2 SV=2
Q96Q89	KIF20B	21	4	104	0.002979	0.002006602	1.83	A6	A2	Kinesin-like protein KIF20B GN=KIF20B PE=1 SV=3
P22234	PAICS	16	12	105	0.000112	0.000238237	1.85	A6	A2	Multifunctional protein ADE2 GN=PAICS PE=1 SV=3
O43151	TET3	16	2	108	0.000395	0.000509567	3.43	A2	A6	Methylcytosine dioxygenase TET3 GN=TET3 PE=1 SV=3

Q5TEC6	H3-2	8	2	108	5.51E-05	0.000177888	4.24	A2	A6	Histone H3 GN=HIST2H3PS2 PE=1 SV=1
Q7Z5N4	SDK1	18	6	108	0.000336	0.000462467	2	A2	A6	Protein sidekick-1 GN=SDK1 PE=2 SV=3
Q86YA3	ZGRF1	17	3	109	3.6E-05	0.000140581	2.84	A6	A2	Protein ZGRF1 GN=ZGRF1 PE=1 SV=3
Q9UJZ1	STOML2	16	7	109	0.047382	0.017761861	1.16	A6	A2	Stomatin-like protein 2_ mitochondrial GN=STOML2 PE=1 SV=1
Q86U86	PBRM1	14	3	110	0.000345	0.00046938	2.69	A2	A6	Protein polybromo-1 GN=PBRM1 PE=1 SV=1
Q05682	CALD1	16	5	110	0.00214	0.001575698	1.48	A2	A6	Caldesmon GN=CALD1 PE=1 SV=3
P26232	CTNNA2	21	6	110	0.000135	0.000267785	2.98	A2	A6	Catenin alpha-2 GN=CTNNA2 PE=1 SV=5
F5GXQ8	SYNE1	19	6	112	0.007925	0.004194631	1.39	A6	A2	Nesprin-1 GN=SYNE1 PE=1 SV=1
P60174	TPI1	15	7	112	0.015828	0.007232314	1.37	A2	A6	Triosephosphate isomerase GN=TPI1 PE=1 SV=3
Q99733	NAP1L4	12	3	113	0.012289	0.005905613	1.52	A2	A6	Nucleosome assembly protein 1-like 4 GN=NAP1L4 PE=1 SV=1
P49588	AARS1	18	9	113	0.000993	0.000940189	1.41	A6	A2	Alanine--tRNA ligase_ cytoplasmic GN=AARS PE=1 SV=2
Q15102	PAFAH1B3	12	10	113	0.009455	0.004760336	1.54	A2	A6	Platelet-activating factor acetylhydrolase IB subunit gamma GN=PAFAH1B3 PE=1 SV=1
A0A087WUK2	HNRNPDL	11	3	114	0.02369	0.01001693	1.38	A6	A2	Heterogeneous nuclear ribonucleoprotein D-like GN=HNRNPDL PE=1 SV=1
O15061	SYNM	20	6	114	0.003385	0.002209319	1.3	A6	A2	Synemin GN=SYNM PE=1 SV=2
P23381	WARS1	17	9	114	0.000846	0.000845582	2.76	A2	A6	Tryptophan--tRNA ligase_ cytoplasmic GN=WARS PE=1 SV=2
P62241	RPS8	14	8	115	0.02939	0.011969724	1.2	A2	A6	40S ribosomal protein S8 GN=RPS8 PE=1 SV=2
Q08378	GOLGA3	19	3	116	6.45E-05	0.000182669	5.2	A6	A2	Golgin subfamily A member 3 GN=GOLGA3 PE=1 SV=2
P34932	HSPA4	20	8	117	0.010269	0.005098473	1.64	A2	A6	Heat shock 70 kDa protein 4 GN=HSPA4 PE=1 SV=4
P00338	LDHA	15	7	118	0.00696	0.00380491	1.37	A6	A2	L-lactate dehydrogenase A chain GN=LDHA PE=1 SV=2
O75874	IDH1	16	8	118	0.032379	0.013049682	1.88	A6	A2	Isocitrate dehydrogenase [NADP] cytoplasmic GN=IDH1 PE=1 SV=2
Q01518	CAP1	15	9	118	0.004238	0.002581161	3.22	A6	A2	Adenylyl cyclase-associated protein 1 GN=CAP1 PE=1 SV=5
P62917	RPL8	15	11	119	0.002979	0.002006602	2.77	A2	A6	60S ribosomal protein L8 GN=RPL8 PE=1 SV=2
P42166	TMPO	18	2	120	0.000117	0.000242251	3.08	A6	A2	Lamina-associated polypeptide 2_ isoform alpha GN=TMPO PE=1 SV=2
Q8TBY8	PMFBP1	21	4	120	0.000342	0.000466881	3	A2	A6	Polyamine-modulated factor 1-binding protein 1 GN=PMFBP1 PE=2 SV=2
P21281	ATP6V1B2	21	7	120	0.014307	0.006678199	1.9	A6	A2	V-type proton ATPase subunit B_ brain isoform GN=ATP6V1B2 PE=1 SV=3
Q96F07	CYFIP2	18	3	121	9.92E-05	0.000221581	2.53	A2	A6	Cytoplasmic FMR1-interacting protein 2 GN=CYFIP2 PE=1 SV=2
H0Y8G5	HNRNPD	14	5	121	4.7E-06	4.64634E-05	4.99	A6	A2	Heterogeneous nuclear ribonucleoprotein D0 (Fragment) GN=HNRNPD PE=1 SV=8
Q96M83	CCDC7	19	5	121	0.003562	0.002273781	1.63	A6	A2	Coiled-coil domain-containing protein 7 GN=CCDC7 PE=2 SV=3
Q07666	KHDRBS1	14	9	122	0.031642	0.012786057	1.9	A2	A6	KH domain-containing_ RNA-binding_ signal transduction-associated protein 1 GN=KHDRBS1 PE=1 SV=1
P57721	PCBP3	14	2	123	5.62E-05	0.000177888	2.84	A6	A2	Poly(rC)-binding protein 3 GN=PCBP3 PE=2 SV=2
Q14117	DPYS	17	6	125	9.67E-05	0.000221021	2.73	A6	A2	Dihydropyrimidinase GN=DPYS PE=1 SV=1
A0A087WTP3	KHSRP	17	9	125	1.89E-05	9.69471E-05	2.95	A2	A6	Far upstream element-binding protein 2 GN=KHSRP PE=1 SV=1
Q99536	VAT1	17	10	128	0.015412	0.007077137	1.77	A6	A2	Synaptic vesicle membrane protein VAT-1 homolog GN=VAT1 PE=1 SV=2
Q8WX93	PALLD	19	4	129	0.000243	0.000374404	2.59	A6	A2	Palladin GN=PALLD PE=1 SV=3
O75145	PPFIA3	21	6	129	9.77E-05	0.000221021	2.5	A2	A6	Liprin-alpha-3 GN=PPFIA3 PE=1 SV=3
Q06830	PRDX1	14	7	129	0.000238	0.000371395	2.23	A6	A2	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
Q13838	DDX39B	17	2	130	0.001119	0.001023283	2.4	A6	A2	Spliceosome RNA helicase DDX39B GN=DDX39B PE=1 SV=1
M0R0F0	RPS5	16	5	130	0.010451	0.005164457	1.5	A2	A6	40S ribosomal protein S5 (Fragment) GN=RPS5 PE=1 SV=1
Q12931	TRAP1	17	7	130	0.000214	0.00035415	2.93	A2	A6	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
Q92608	DOCK2	23	8	130	0.000256	0.000385096	1.97	A2	A6	Dedicator of cytokinesis protein 2 GN=DOCK2 PE=1 SV=2
Q6FI13	H2AC18; H2AC19	17	9	130	0.011227	0.005491781	1.4	A6	A2	Histone H2A type 2-A GN=HIST2H2AA3 PE=1 SV=3
Q96N67	DOCK7	27	6	131	0.008892	0.004555741	1.75	A6	A2	Dedicator of cytokinesis protein 7 GN=DOCK7 PE=1 SV=4
B2R5W2	HNRNPC	13	7	131	0.000542	0.000621755	1.87	A2	A6	Heterogeneous nuclear ribonucleoproteins C1/C2 GN=HNRNPC PE=1 SV=1
E9PCY7	HNRNPH1	12	2	132	0.000501	0.000596375	4.81	A6	A2	Heterogeneous nuclear ribonucleoprotein H GN=HNRNPH1 PE=1 SV=1
P49321	NASP	16	7	132	0.014934	0.006918954	1.19	A6	A2	Nuclear autoantigenic sperm protein GN=NASP PE=1 SV=2
Q9BWD1	ACAT2	17	3	133	0.000224	0.000363362	3.17	A6	A2	Acetyl-CoA acetyltransferase_ cytosolic GN=ACAT2 PE=1 SV=2
P78344	EIF4G2	24	7	133	9.82E-05	0.000221021	1.48	A2	A6	Eukaryotic translation initiation factor 4 gamma 2 GN=EIF4G2 PE=1 SV=1
P30613	PKLR	14	3	134	0.017588	0.007851356	1.93	A2	A6	Pyruvate kinase PKLR GN=PKLR PE=1 SV=2
Q9H4B7	TUBB1	13	3	134	0.028357	0.011640726	2.17	A2	A6	Tubulin beta-1 chain GN=TUBB1 PE=1 SV=1
Q9NSB2	KRT84	18	4	134	0.000166	0.000297312	2.4	A6	A2	Keratin_ type II cuticular Hb4 GN=KRT84 PE=2 SV=2
Q99497	PARK7	14	7	134	0.000203	0.000342537	3.84	A6	A2	Protein/nucleic acid deglycase DJ-1 GN=PARK7 PE=1 SV=2
P62805	H4C1	11	9	134	9.54E-05	0.000221021	3.85	A6	A2	Histone H4 GN=HIST1H4A PE=1 SV=2
Q16695	H3-4	17	5	137	6.09E-05	0.000177888	4.07	A2	A6	Histone H3.1t GN=HIST3H3 PE=1 SV=3
Q9Y6M1	IGF2BP2	20	4	140	0.000302	0.000432564	1.87	A2	A6	Insulin-like growth factor 2 mRNA-binding protein 2 GN=IGF2BP2 PE=1 SV=2
P32119	PRDX2	13	6	142	3.79E-05	0.000142365	4.19	A6	A2	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
Q12906	ILF3	19	11	142	0.000504	0.000598935	2.32	A6	A2	Interleukin enhancer-binding factor 3 GN=ILF3 PE=1 SV=3
Q58FF7	HSP90AB3P	17	3	143	0.00076	0.000782589	1.5	A2	A6	Putative heat shock protein HSP 90-beta-3 GN=HSP90AB3P PE=5 SV=1
Q5JU85	IQSEC2	25	6	145	0.005083	0.002976066	1.61	A2	A6	IQ motif and SEC7 domain-containing protein 2 GN=IQSEC2 PE=1 SV=2
P60660	MYL6	17	3	146	0.012318	0.005913567	7.02	A6	A2	Myosin light polypeptide 6 GN=MYL6 PE=1 SV=2
P06748	NPM1	15	10	146	7.39E-05	0.0001983	4.28	A2	A6	Nucleophosmin GN=NPM1 PE=1 SV=2
E9PEB5	FUBP1	23	5	148	0.01969	0.008583197	1.24	A6	A2	Far upstream element-binding protein 1 GN=FUBP1 PE=1 SV=1
P17987	TCP1	20	7	151	0.004738	0.002830257	1.74	A6	A2	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
Q9BYX7	POTEKP	17	4	152	0.002203	0.001596404	4.17	A6	A2	Putative beta-actin-like protein 3 GN=POTEKP PE=5 SV=1
Q6PIF6	MYO7B	32	12	152	1.41E-05	8.40608E-05	7.53	A2	A6	Unconventional myosin-VIIb GN=MYO7B PE=1 SV=2
O14531	DPYSL4	23	12	155	2.45E-05	0.000116027	1.6	A6	A2	Dihydropyrimidinase-related protein 4 GN=DPYSL4 PE=1 SV=2
P05023	ATP1A1	24	7	156	0.001424	0.00117548	2.58	A2	A6	Sodium/potassium-transporting ATPase subunit alpha-1 GN=ATP1A1 PE=1 SV=1
P35232	PHB	20	11	156	0.000546	0.000621755	1.86	A2	A6	Prohibitin GN=PHB PE=1 SV=1
P61604	HSPE1	16	10	157	0.019012	0.00834242	1.54	A6	A2	10 kDa heat shock protein_ mitochondrial GN=HSPE1 PE=1 SV=2
P48735	IDH2	24	11	157	0.001469	0.001205774	4.18	A6	A2	Isocitrate dehydrogenase [NADP]_ mitochondrial GN=IDH2 PE=1 SV=2
P49368	CCT3	21	12	158	0.034622	0.013669237	1.96	A2	A6	T-complex protein 1 subunit gamma GN=CCT3 PE=1 SV=4
P40925	MDH1	19	8	159	0.009492	0.004773724	1.89	A6	A2	Malate dehydrogenase_ cytoplasmic GN=MDH1 PE=1 SV=4
Q15366	PCBP2	19	4	164	0.000115	0.000240785	31	A2	A6	Poly(rC)-binding protein 2 GN=PCBP2 PE=1 SV=1
P09936	UCHL1	14	8	164	0.003125	0.002071299	1.65	A6	A2	Ubiquitin carboxyl-terminal hydrolase isozyme L1 GN=UCHL1 PE=1 SV=2
D6RA32	MAP1B	22	12	165	0.001645	0.001302553	3.28	A6	A2	Microtubule-associated protein 1B (Fragment) GN=MAP1B PE=1 SV=2
P40227	CCT6A	20	6	166	0.008618	0.004454938	1.88	A6	A2	T-complex protein 1 subunit zeta GN=CCT6A PE=1 SV=3
P13929	ENO3	18	4	168	0.01534	0.007050882	2.26	A2	A6	Beta-enolase GN=ENO3 PE=1 SV=5
A0A087WVQ6	CLTC	28	12	168	6.38E-05	0.000181968	3.73	A6	A2	Clathrin heavy chain GN=CLTC PE=1 SV=1
P17661	DES	18	3	170	0.000282	0.000408079	2.07	A2	A6	Desmin GN=DES PE=1 SV=3
Q15365	PCBP1	17	6	170	0.002041	0.001537299	1.36	A6	A2	Poly(rC)-binding protein 1 GN=PCBP1 PE=1 SV=2
P48643	CCT5	22	9	170	0.000113	0.000238527	1.73	A6	A2	T-complex protein 1 subunit epsilon GN=CCT5 PE=1 SV=1
Q16658	FSCN1	23	9	171	0.002114	0.001571973	2.59	A6	A2	Fascin GN=FSCN1 PE=1 SV=3
Q7RTP6	MICAL3	34	9	174	2.43E-05	0.000116027	23.1	A2	A6	[F-actin]-monooxygenase MICAL3 GN=MICAL3 PE=1 SV=2
P09104	ENO2	20	8	175	0.006809	0.003762112	1.29	A6	A2	Gamma-enolase GN=ENO2 PE=1 SV=3

Q7L576	CYFIP1	26	9	175	0.000315	0.000447888	2.38	A2	A6	Cytoplasmic FMR1-interacting protein 1 GN=CYFIP1 PE=1 SV=1
P62937	PPIA	18	9	176	0.00123	0.001073226	1.43	A2	A6	Peptidyl-prolyl cis-trans isomerase A GN=PPIA PE=1 SV=2
Q5THK1	PRR14L	32	10	176	0.032553	0.01307792	2.28	A2	A6	Protein PRR14L GN=PRR14L PE=1 SV=1
O43390	HNRNPR	26	8	178	0.001075	0.001000849	1.33	A6	A2	Heterogeneous nuclear ribonucleoprotein R GN=HNRNPR PE=1 SV=1
P52209	PGD	19	12	178	5.05E-05	0.000167671	3.44	A6	A2	6-phosphogluconate dehydrogenase_ decarboxylating GN=PGD PE=1 SV=3
P50990	CCT8	24	6	180	8.77E-05	0.000212972	3.62	A6	A2	T-complex protein 1 subunit theta GN=CCT8 PE=1 SV=4
Q5VZ46	KIAA1614	26	6	183	0.00069	0.000725837	1.9	A2	A6	Uncharacterized protein KIAA1614 GN=KIAA1614 PE=2 SV=3
Q8IWJ2	GCC2	36	12	183	0.001461	0.001201373	1.55	A2	A6	GRIP and coiled-coil domain-containing protein 2 GN=GCC2 PE=1 SV=4
P07195	LDHB	18	7	185	0.001517	0.001241354	1.94	A6	A2	L-lactate dehydrogenase B chain GN=LDHB PE=1 SV=2
P31939	ATIC	27	12	185	0.001235	0.001074146	5.83	A2	A6	Bifunctional purine biosynthesis protein PURH GN=ATIC PE=1 SV=3
P27824	CANX	20	8	186	6.79E-05	0.000189061	4.89	A6	A2	Calnexin GN=CANX PE=1 SV=2
P16949	STMN1	15	5	188	0.000155	0.000287203	2.35	A6	A2	Stathmin GN=STMN1 PE=1 SV=3
P17066	HSPA6	22	7	188	0.000456	0.000565564	2.01	A2	A6	Heat shock 70 kDa protein 6 GN=HSPA6 PE=1 SV=2
P04264	KRT1	19	13	188	0.017718	0.00789413	1.55	A2	A6	Keratin_ type II cytoskeletal 1 GN=KRT1 PE=1 SV=6
P17844	DDX5	25	10	191	1.47E-05	8.42091E-05	4.6	A2	A6	Probable ATP-dependent RNA helicase DDX5 GN=DDX5 PE=1 SV=1
Q15084	PDIA6	20	13	191	3.9E-06	4.02765E-05	4.97	A6	A2	Protein disulfide-isomerase A6 GN=PDIA6 PE=1 SV=1
P19338	NCL	22	11	192	1.29E-05	8.08269E-05	3.23	A6	A2	Nucleolin GN=NCL PE=1 SV=3
P16401	H1-5	17	8	194	0.006065	0.003411921	1.29	A6	A2	Histone H1.5 GN=HIST1H1B PE=1 SV=3
P41219	PRPH	19	2	195	0.033031	0.013218551	1.21	A2	A6	Peripherin GN=PRPH PE=1 SV=2
P36578	RPL4	25	10	196	0.00059	0.000654482	1.64	A2	A6	60S ribosomal protein L4 GN=RPL4 PE=1 SV=5
H0Y6I0	GOLGA4	33	13	196	0.048909	0.018196866	1.34	A2	A6	Golgin subfamily A member 4 (Fragment) GN=GOLGA4 PE=1 SV=1
P23528	CFL1	18	5	198	3.67E-05	0.000142107	1.96	A6	A2	Cofilin-1 GN=CFL1 PE=1 SV=3
P04075	ALDOA	20	11	200	0.001535	0.001249236	1.6	A6	A2	Fructose-bisphosphate aldolase A GN=ALDOA PE=1 SV=2
O00425	IGF2BP3	25	6	213	0.000243	0.000374404	6.58	A2	A6	Insulin-like growth factor 2 mRNA-binding protein 3 GN=IGF2BP3 PE=1 SV=2
P33176	KIF5B	32	9	214	0.000449	0.000560898	3.04	A6	A2	Kinesin-1 heavy chain GN=KIF5B PE=1 SV=1
Q9Y4I1	MYO5A	36	14	215	0.002832	0.001937955	1.5	A6	A2	Unconventional myosin-Va GN=MYO5A PE=1 SV=2
P12036	NEFH	28	7	217	0.026035	0.010880087	1.49	A2	A6	Neurofilament heavy polypeptide GN=NEFH PE=1 SV=4
P27797	CALR	25	13	223	0.000796	0.000814747	2.29	A6	A2	Calreticulin GN=CALR PE=1 SV=1
Q13263	TRIM28	32	8	224	3.17E-05	0.000134591	6.99	A2	A6	Transcription intermediary factor 1-beta GN=TRIM28 PE=1 SV=5
P08133	ANXA6	30	14	230	5.09E-06	4.92609E-05	4.45	A6	A2	Annexin A6 GN=ANXA6 PE=1 SV=3
P16402	H1-3	25	9	234	0.041972	0.015987307	1.25	A2	A6	Histone H1.3 GN=HIST1H1D PE=1 SV=2
P02461	COL3A1	35	14	234	0.000183	0.000318432	6.15	A6	A2	Collagen alpha-1(III) chain GN=COL3A1 PE=1 SV=4
Q14697	GANAB	28	13	243	0.006382	0.003564362	1.5	A6	A2	Neutral alpha-glucosidase AB GN=GANAB PE=1 SV=3
Q15233	NONO	28	20	243	0.001555	0.001260507	1.6	A2	A6	Non-POU domain-containing octamer-binding protein GN=NONO PE=1 SV=4
O60282	KIF5C	35	14	244	0.015132	0.006979496	1.58	A2	A6	Kinesin heavy chain isoform 5C GN=KIF5C PE=1 SV=1
Q8N7X0	ADGB	45	12	247	0.002878	0.001960742	3.24	A2	A6	Androglobin GN=ADGB PE=2 SV=3
P0DMV8	HSPA1A	31	6	256	0.003463	0.00223943	1.75	A6	A2	Heat shock 70 kDa protein 1A GN=HSPA1A PE=1 SV=1
Q5TZA2	CROCC	45	13	259	0.002705	0.001867591	4.27	A2	A6	Rootletin GN=CROCC PE=1 SV=1
P07237	P4HB	30	13	263	0.001259	0.001077432	1.85	A6	A2	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
P48681	NES	42	21	267	1.76E-07	6.81318E-06	2.21	A2	A6	Nestin GN=NES PE=1 SV=2
A0A0R4J2E8	MATR3	28	11	271	0.009943	0.00496288	1.35	A2	A6	Matrin-3 GN=MATR3 PE=1 SV=1
P78371	CCT2	35	20	272	0.000553	0.000625691	1.43	A6	A2	T-complex protein 1 subunit beta GN=CCT2 PE=1 SV=4
P00558	PGK1	32	13	275	1.84E-05	9.68446E-05	4.77	A6	A2	Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3
P23246	SFPQ	30	15	279	0.017381	0.007773854	1.43	A6	A2	Splicing factor_ proline- and glutamine-rich GN=SFPQ PE=1 SV=2
P55072	VCP	43	15	279	0.040781	0.015623108	1.5	A6	A2	Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4
Q14980	NUMA1	52	3	282	0.014956	0.006922526	2.07	A2	A6	Nuclear mitotic apparatus protein 1 GN=NUMA1 PE=1 SV=2
P20700	LMNB1	40	22	290	0.000499	0.000596045	2.13	A2	A6	Lamin-B1 GN=LMNB1 PE=1 SV=2
Q9BUF5	TUBB6	24	2	298	0.002101	0.001570192	2.48	A6	A2	Tubulin beta-6 chain GN=TUBB6 PE=1 SV=1
P61978	HNRNPK	28	16	306	0.000307	0.000438819	1.97	A6	A2	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
P54652	HSPA2	31	7	311	3.33E-05	0.000135648	4.61	A2	A6	Heat shock-related 70 kDa protein 2 GN=HSPA2 PE=1 SV=1
P02768	ALB	43	11	324	0.03394	0.013491654	1.72	A6	A2	Serum albumin GN=ALB PE=1 SV=2
Q14194	CRMP1	34	15	326	1.14E-05	7.55574E-05	2.58	A6	A2	Dihydropyrimidinase-related protein 1 GN=CRMP1 PE=1 SV=1
P07197	NEFM	40	11	331	0.000265	0.000391975	1.18	A2	A6	Neurofilament medium polypeptide GN=NEFM PE=1 SV=3
P13667	PDIA4	37	17	337	0.014555	0.006770238	1.36	A6	A2	Protein disulfide-isomerase A4 GN=PDIA4 PE=1 SV=2
P25705	ATP5F1A	33	9	342	0.000163	0.000293667	1.93	A6	A2	ATP synthase subunit alpha_ mitochondrial GN=ATP5F1A PE=1 SV=1
A0A087WWY3	FLNA	54	22	352	4.88E-05	0.00016549	1.73	A2	A6	Filamin-A GN=FLNA PE=1 SV=1
P38646	HSPA9	36	21	366	0.011344	0.005531378	1.69	A2	A6	Stress-70 protein_ mitochondrial GN=HSPA9 PE=1 SV=2
P12277	CKB	29	15	368	0.002139	0.001575698	1.75	A6	A2	Creatine kinase B-type GN=CKB PE=1 SV=1
Q00839	HNRNPU	37	4	377	4.12E-06	4.15825E-05	5.25	A2	A6	Heterogeneous nuclear ribonucleoprotein U GN=HNRNPU PE=1 SV=6
Q14195	DPYSL3	36	15	382	0.001615	0.001283289	1.81	A6	A2	Dihydropyrimidinase-related protein 3 GN=DPYSL3 PE=1 SV=1
P11137	MAP2	59	28	393	0.000142	0.000276521	1.78	A2	A6	Microtubule-associated protein 2 GN=MAP2 PE=1 SV=4
P13639	EEF2	48	29	395	0.007856	0.004165509	1.23	A2	A6	Elongation factor 2 GN=EEF2 PE=1 SV=4
P07900	HSP90AA1	41	18	407	1.22E-06	2.10267E-05	2.99	A6	A2	Heat shock protein HSP 90-alpha GN=HSP90AA1 PE=1 SV=5
O43175	PHGDH	36	14	412	0.003874	0.002427643	1.39	A2	A6	D-3-phosphoglycerate dehydrogenase GN=PHGDH PE=1 SV=4
P06576	ATP5F1B	37	12	413	8.8E-05	0.000212972	3.1	A6	A2	ATP synthase subunit beta_ mitochondrial GN=ATP5F1B PE=1 SV=3
P04406	GAPDH	36	23	426	9.46E-05	0.000221021	2.69	A6	A2	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P35580	MYH10	73	34	451	0.004352	0.00263306	1.45	A2	A6	Myosin-10 GN=MYH10 PE=1 SV=3
P11142	HSPA8	39	9	457	0.000101	0.000224958	3.41	A6	A2	Heat shock cognate 71 kDa protein GN=HSPA8 PE=1 SV=1
P22314	UBA1	52	28	472	0.001066	0.00099507	1.68	A6	A2	Ubiquitin-like modifier-activating enzyme 1 GN=UBA1 PE=1 SV=3
Q9BQE3	TUBA1C	31	2	478	0.004136	0.002539159	2.38	A6	A2	Tubulin alpha-1C chain GN=TUBA1C PE=1 SV=1
Q16555	DPYSL2	48	3	483	3.55E-05	0.000139677	4.77	A6	A2	Dihydropyrimidinase-related protein 2 GN=DPYSL2 PE=1 SV=1
P35579	MYH9	76	24	483	2.31E-05	0.000111662	11	A2	A6	Myosin-9 GN=MYH9 PE=1 SV=4
P08238	HSP90AB1	45	13	489	0.004357	0.00263306	2.05	A6	A2	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
P30101	PDIA3	40	18	493	4.75E-05	0.000162626	3.17	A6	A2	Protein disulfide-isomerase A3 GN=PDIA3 PE=1 SV=4
P68363	TUBA1B	32	2	496	0.000166	0.000297387	3.1	A6	A2	Tubulin alpha-1B chain GN=TUBA1B PE=1 SV=1
P06733	ENO1	52	28	595	0.000162	0.000293667	1.72	A2	A6	Alpha-enolase GN=ENO1 PE=1 SV=2
P14625	HSP90B1	54	23	603	9.62E-05	0.000221021	3.99	A6	A2	Endoplasmin GN=HSP90B1 PE=1 SV=1
P11021	HSPA5	56	35	615	7.56E-05	0.000198918	1.64	A6	A2	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
Q13509	TUBB3	54	16	619	0.04568	0.017286127	1.17	A6	A2	Tubulin beta-3 chain GN=TUBB3 PE=1 SV=2
P04350	TUBB4A	54	7	640	0.000211	0.000350976	4.64	A6	A2	Tubulin beta-4A chain GN=TUBB4A PE=1 SV=2
P68032	ACTC1	55	12	645	0.001333	0.001128027	1.82	A6	A2	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
P52272	HNRNPM	77	49	770	1.26E-05	8.08269E-05	4.9	A2	A6	Heterogeneous nuclear ribonucleoprotein M GN=HNRNPM PE=1 SV=3
P10809	HSPD1	68	37	798	0.001241	0.001076006	1.8	A2	A6	60 kDa heat shock protein_ mitochondrial GN=HSPD1 PE=1 SV=2
P07437	TUBB	58	5	858	0.028417	0.011655162	1.2	A6	A2	Tubulin beta chain GN=TUBB PE=1 SV=2
P60709	ACTB	60	9	925	3.11E-05	0.000134591	7.34	A6	A2	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1
P08670	VIM	72	27	929	0.000182	0.000317962	2.27	A6	A2	Vimentin GN=VIM PE=1 SV=4

Table S2: Identified allergy-related proteins following DAT$_{A\beta 1\text{-}6}$ and DAT$_{A\beta 17\text{-}23}$ compared to untreated cells. Herein, A1= Aβ1-6; A2= Aβ17-23; A6=No treatment. The proteins were searched for Human (*Homo sapiens*) database.

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-A$\beta_{1\text{-}6}$ Antibody Treatment										
Q9Y617	PSAT1	8	2	41.4	0.002838	0.002981	1.64	A6	A1	Phosphoserine aminotransferase
Q16849	PTPRN	6	2	41.4	0.001319	0.001764	1.67	A6	A1	Receptor-type tyrosine-protein phosphatase-like N
P61586	RHOA	11	3	95.2	0.001569	0.00197	1.28	A6	A1	Transforming protein RhoA
Q15746	MYLK	7	3	41.2	0.001443	0.001893	1.55	A6	A1	Myosin light chain kinase_ smooth muscle
P04792	HSPB1	8	3	78.6	0.00103	0.001514	1.92	A1	A6	Heat shock protein beta 1
A0A1B0GVD5	CTSD	14	7	103	3.77E-05	0.000262	1.44	A6	A1	Cathepsin D
O00443	PIK3C2A	19	7	97.1	0.025802	0.015376	1.33	A6	A1	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha
Q99497	PARK7	14	7	134	4.59E-05	0.000295	3.1	A6	A1	Protein/nucleic acid deglycase DJ-1
Q06830	PRDX1	14	7	129	0.002319	0.002554	1.25	A6	A1	Peroxiredoxin-1
P09211	GSTP1	11	7	90.6	9.66E-06	0.000133	2.88	A6	A1	Glutathione S-transferase P
P00338	LDHA	15	7	118	0.034267	0.019085	1.17	A6	A1	L-lactate dehydrogenase A chain
Q92608	DOCK2	23	8	130	0.001064	0.001546	1.51	A1	A6	Dedicator of cytokinesis protein 2
Q8NF50	DOCK8	13	8	75.5	0.001573	0.00197	1.77	A1	A6	Dedicator of cytokinesis protein 8
P62937	PPIA	18	9	176	4.66E-06	9.38E-05	1.76	A1	A6	Peptidyl-prolyl cis-trans isomerase A
P68104	EEF1A1	32	11	353	0.020195	0.012726	1.42	A6	A1	Elongation factor 1-alpha 1
P35232	PHB	20	11	156	6.31E-05	0.000331	2.97	A1	A6	Prohibitin
P00558	PGK1	32	13	275	2.29E-05	0.000206	2.2	A6	A1	Phosphoglycerate kinase 1
P02787	TF	45	19	417	1.40E-05	0.000159	1.96	A1	A6	Serotransferrin
P14625	HSP90B1	54	23	603	0.017655	0.011476	1.18	A6	A1	Endoplasmin
P08670	VIM	72	27	929	5.53E-05	0.000316	1.4	A6	A1	Vimentin
Anti-A$\beta_{17\text{-}23}$ Antibody Treatment										
O00443	PIK3C2A	19	7	97.1	0.039439	0.015222	1.32	A2	A6	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha
P04792	HSPB1	8	3	78.6	0.002974	0.002007	2.54	A2	A6	Heat shock protein beta-1
P10809	HSPD1	68	37	798	0.001241	0.001076	1.8	A2	A6	60 kDa heat shock protein_ mitochondrial
P34932	HSPA4	20	8	117	0.010269	0.005098	1.64	A2	A6	Heat shock 70 kDa protein 4
P35232	PHB	20	11	156	0.000546	0.000622	1.86	A2	A6	Prohibitin
P62937	PPIA	18	9	176	0.00123	0.001073	1.43	A2	A6	Peptidyl-prolyl cis-trans isomerase A
Q8NF50	DOCK8	13	8	75.5	0.00869	0.004482	1.9	A2	A6	Dedicator of cytokinesis protein 8
Q92608	DOCK2	23	8	130	0.000256	0.000385	1.97	A2	A6	Dedicator of cytokinesis protein 2
A0A1B0GVD5	CTSD	14	7	103	0.005749	0.003273	2.26	A6	A2	Cathepsin D
P00338	LDHA	15	7	118	0.00696	0.003805	1.37	A6	A2	L-lactate dehydrogenase A chain
P00558	PGK1	32	13	275	1.84E-05	9.68E-05	4.77	A6	A2	Phosphoglycerate kinase 1
P08670	VIM	72	27	929	0.000182	0.000318	2.27	A6	A2	Vimentin
P09211	GSTP1	11	7	90.6	3.9E-05	0.000144	5.18	A6	A2	Glutathione S-transferase P
P12004	PCNA	14	7	83.2	0.048648	0.018129	1.44	A6	A2	Proliferating cell nuclear antigen
P14625	HSP90B1	54	23	603	9.62E-05	0.000221	3.99	A6	A2	Endoplasmin
P30101	PDIA3	40	18	493	4.75E-05	0.000163	3.17	A6	A2	Protein disulfide-isomerase A3
P61586	RHOA	11	3	95.2	0.000211	0.000351	1.67	A6	A2	Transforming protein RhoA
Q9Y617	PSAT1	8	2	41.4	0.00044	0.000552	2.17	A6	A2	Phosphoserine aminotransferase
Q06830	PRDX1	14	7	129	0.000238	0.000371	2.23	A6	A2	Peroxiredoxin-1
Q15746	MYLK	7	3	41.2	0.008462	0.004398	1.22	A6	A2	Myosin light chain kinase_ smooth muscle
Q16849	PTPRN	6	2	41.4	0.000281	0.000408	3.34	A6	A2	Receptor-type tyrosine-protein phosphatase-like N
Q99497	PARK7	14	7	134	0.000203	0.000343	3.84	A6	A2	Protein/nucleic acid deglycase DJ-1

Table S3: Statistical overrepresentation test of the identified allergy related proteins following $\text{DAT}_{\text{A}\beta 1\text{-}6}$ and $\text{DAT}_{\text{A}\beta 17\text{-}23}$ by PANTHER. Herein, FDR indicates false discovery rate. Displaying only results for FDR $P < 0.05$.

Reactome pathways	Fold Enrichment	raw P value	FDR
Anti-$\text{A}\beta_{1\text{-}6}$ Antibody Treatment			
Chaperone Mediated Autophagy	> 100	2.07E-06	5.15E-03
Neutrophil degranulation	12.33	6.46E-06	8.05E-03
Innate Immune System	6.20	7.87E-05	3.93E-02
Anti-$\text{A}\beta_{17\text{-}23}$ Antibody Treatment			
Unclassified	.09	1.18E-05	2.95E-02

Table S4: Gene enriched term and their associated genes for the identified allergy-related genes following ${}_{\text{Allg}}\text{DAT}_{\text{A}\beta 1\text{-}6}$ and ${}_{\text{Allg}}\text{DAT}_{\text{A}\beta 17\text{-}23}$. Herein, GO= Biological Processes; R-HAS= Reactome Gene Sets; M14= Canonical Pathways; WP= WikiPathways; and has= KEGG Pathway.

<table>
<tr><th>GO</th><th>Description</th><th>Hits</th><th>LogP</th><th>Log(q-value)</th></tr>
<tr><td>GO:0001895</td><td>retina homeostasis</td><td>HSPB1|PRDX1|TF</td><td>-4.70485</td><td>-2.242216085</td></tr>
<tr><td>R-HSA-9613829</td><td>Chaperone Mediated Autophagy</td><td>EEF1A1|VIM|PARK7</td><td>-6.42136</td><td>-3.153854646</td></tr>
<tr><td>hsa04530</td><td>Tight junction</td><td>RHOA|HSPA4|PCNA</td><td>-3.61102</td><td>-1.590670877</td></tr>
<tr><td>WP4290</td><td>Metabolic reprogramming in colon cancer</td><td>LDHA|PGK1|PSAT1</td><td>-5.63522</td><td>-2.750936924</td></tr>
<tr><td>GO:1901222</td><td>regulation of NIK/NF-kappaB signaling</td><td>RHOA|PRDX1|PHB1</td><td>-4.43383</td><td>-2.108333645</td></tr>
<tr><td>GO:2000147</td><td>positive regulation of cell motility</td><td>RHOA|HSPB1|MYLK|PIK3C2A|TF|DOCK8</td><td>-5.80545</td><td>-2.810578363</td></tr>
<tr><td>M14</td><td>PID AURORA B PATHWAY</td><td>RHOA|MYLK|VIM</td><td>-5.79554</td><td>-2.810578363</td></tr>
<tr><td>R-HSA-6798695</td><td>Neutrophil degranulation</td><td>RHOA|CTSD|DOCK2|EEF1A1|GSTP1|PPIA</td><td>-6.30077</td><td>-3.094681683</td></tr>
<tr><td>GO:0000302</td><td>response to reactive oxygen species</td><td>GSTP1|PRDX1|PCNA|PTPRN|PARK7</td><td>-6.87467</td><td>-3.153854646</td></tr>
<tr><td>GO:0001775</td><td>cell activation</td><td>RHOA|DOCK2|HSPB1|HSPD1|PRDX1|PHB1|PPIA|DOCK8</td><td>-8.04089</td><td>-3.694204795</td></tr>
<tr><td>R-HSA-109582</td><td>Hemostasis</td><td>RHOA|DOCK2|PPIA|TF|DOCK8</td><td>-4.36308</td><td>-2.085728254</td></tr>
<tr><td>GO:0044283</td><td>small molecule biosynthetic process</td><td>GSTP1|PGK1|PARK7|PSAT1</td><td>-4.00332</td><td>-1.849322049</td></tr>
<tr><td>GO:0006457</td><td>protein folding</td><td>PDIA3|HSPB1|HSPD1|PPIA|HSP90B1</td><td>-6.48354</td><td>-3.153854646</td></tr>
<tr><td>R-HSA-2262752</td><td>Cellular responses to stress</td><td>EEF1A1|GSTP1|HSPA4|PRDX1|HSP90B1</td><td>-3.55458</td><td>-1.118149096</td></tr>
<tr><td>R-HSA-449147</td><td>Signaling by Interleukins</td><td>PPIA|HSP90B1|VIM</td><td>-2.61193</td><td>-0.838117174</td></tr>
</table>

Table S5: Identified apoptosis-related proteins following DAT$_{A\beta 1\text{-}6}$ and DAT$_{A\beta 17\text{-}23}$ compared to untreated cells. Herein, A1= Aβ1-6; A2= Aβ17-23; A6=No treatment. The proteins were searched for Human (*Homo sapiens*) database.

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-A$\beta_{1\text{-}6}$ Antibody Treatment										
P06744	GPI	8	2	42	7.72E-07	4.29E-05	15.6	A6	A1	Glucose-6-phosphate isomerase GN=GPI PE=1 SV=4
Q9BX26	SYCP2	11	5	53.3	0.01049	0.007616	2.01	A6	A1	Synaptonemal complex protein 2 GN=SYCP2 PE=2 SV=2
P00441	SOD1	7	4	54.6	0.030786	0.017506	1.27	A6	A1	Superoxide dismutase [Cu-Zn] GN=SOD1 PE=1 SV=2
E9PL09	RPS3	9	5	65.6	0.000335	0.000736	1.36	A6	A1	40S ribosomal protein S3 GN=RPS3 PE=1 SV=1
P23497	SP100	8	2	66.3	0.046164	0.024181	25.8	A6	A1	Nuclear autoantigen Sp-100 GN=SP100 PE=1 SV=3
Q9NQC3	RTN4	12	6	66.8	0.003353	0.003312	1.4	A6	A1	Reticulon-4 GN=RTN4 PE=1 SV=2
P62258	YWHAE	7	3	67.3	0.00038	0.000794	1.73	A1	A6	14-3-3 protein epsilon GN=YWHAE PE=1 SV=1
P62753	RPS6	8	2	73	0.004066	0.003783	1.82	A6	A1	40S ribosomal protein S6 GN=RPS6 PE=1 SV=1
Q8NF50	DOCK8	13	8	75.5	0.001573	0.00197	1.77	A1	A6	Dedicator of cytokinesis protein 8 GN=DOCK8 PE=1 SV=3
Q8N163	CCAR2	13	6	76.1	0.026876	0.015843	1.22	A6	A1	Cell cycle and apoptosis regulator protein 2 GN=CCAR2 PE=1 SV=2
P30040	ERP29	10	5	77.4	0.001531	0.00195	1.44	A6	A1	Endoplasmic reticulum resident protein 29 GN=ERP29 PE=1 SV=4
P04792	HSPB1	8	3	78.6	0.00103	0.001514	1.92	A1	A6	Heat shock protein beta-1 GN=HSPB1 PE=1 SV=2
Q14160	SCRIB	13	4	79.2	3.44E-05	0.000251	1.83	A1	A6	Protein scribble homolog GN=SCRIB PE=1 SV=4
O00571	DDX3X	15	8	86	0.000223	0.000595	4.1	A6	A1	ATP-dependent RNA helicase DDX3X GN=DDX3X PE=1 SV=3
P09211	GSTP1	11	7	90.6	9.66E-06	0.000133	2.88	A6	A1	Glutathione S-transferase P GN=GSTP1 PE=1 SV=2
P27348	YWHAQ	11	2	97.5	0.008623	0.006524	1.47	A6	A1	14-3-3 protein theta GN=YWHAQ PE=1 SV=1
P49588	AARS1	18	9	113	0.000124	0.000426	2	A6	A1	Alanine--tRNA ligase_ cytoplasmic GN=AARS PE=1 SV=2
P00338	LDHA	15	7	118	0.034267	0.019085	1.17	A6	A1	L-lactate dehydrogenase A chain GN=LDHA PE=1 SV=2
Q12931	TRAP1	17	7	130	0.000473	0.000907	2.19	A1	A6	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
Q99497	PARK7	14	7	134	4.59E-05	0.000295	3.1	A6	A1	Protein/nucleic acid deglycase DJ-1 GN=PARK7 PE=1 SV=2
P32119	PRDX2	13	6	142	2.01E-06	7.38E-05	1.88	A6	A1	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
P06748	NPM1	15	10	146	0.002983	0.00309	1.63	A1	A6	Nucleophosmin GN=NPM1 PE=1 SV=2
P17987	TCP1	20	7	151	0.003483	0.00338	1.82	A6	A1	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
P35232	PHB	20	11	156	6.31E-05	0.000331	2.97	A1	A6	Prohibitin GN=PHB PE=1 SV=1
P07196	NEFL	22	5	173	0.008677	0.00654	1.4	A6	A1	Neurofilament light polypeptide GN=NEFL PE=1 SV=3
P17844	DDX5	25	10	191	0.00023	0.000606	2.13	A1	A6	Probable ATP-dependent RNA helicase DDX5 GN=DDX5 PE=1 SV=1
P23528	CFL1	18	5	198	1.88E-05	0.000183	1.72	A6	A1	Cofilin-1 GN=CFL1 PE=1 SV=3
P08133	ANXA6	30	14	230	0.039515	0.021256	1.14	A6	A1	Annexin A6 GN=ANXA6 PE=1 SV=3
P0DMV8	HSPA1A	31	6	256	3.99E-05	0.000271	1.28	A6	A1	Heat shock 70 kDa protein 1A GN=HSPA1A PE=1 SV=1
P07237	P4HB	30	13	263	0.003775	0.003584	1.14	A1	A6	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
P48681	NES	42	21	267	0.000216	0.000586	1.25	A1	A6	Nestin GN=NES PE=1 SV=2
P55072	VCP	43	15	279	0.003213	0.003207	1.78	A6	A1	Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4
P23246	SFPQ	30	15	279	0.003643	0.003496	1.82	A6	A1	Splicing factor_ proline- and glutamine-rich GN=SFPQ PE=1 SV=2
P61978	HNRNPK	28	16	306	0.010072	0.007356	1.21	A6	A1	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
Q9Y4L1	HYOU1	48	18	362	0.000718	0.001209	1.47	A1	A6	Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1
P04406	GAPDH	36	23	426	0.000197	0.000561	1.5	A6	A1	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P08238	HSP90AB1	45	13	489	0.021309	0.013229	1.22	A6	A1	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
P14625	HSP90B1	54	23	603	0.017655	0.011476	1.18	A6	A1	Endoplasmin GN=HSP90B1 PE=1 SV=1
P11021	HSPA5	56	35	615	0.000124	0.000426	1.3	A1	A6	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P68032	ACTC1	55	12	645	0.001727	0.002099	1.27	A6	A1	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
Anti-A$\beta_{1\text{-}6}$ Antibody Treatment										
P06744	GPI	8	2	42	0.001749	0.001355	8.13	A6	A2	Glucose-6-phosphate isomerase GN=GPI PE=1 SV=4
Q9P275	USP36	8	4	45.6	0.040141	0.015442	1.56	A2	A6	Ubiquitin carboxyl-terminal hydrolase 36 GN=USP36 PE=1 SV=4
Q9BX26	SYCP2	11	5	53.3	0.002498	0.001759	2.67	A6	A2	Synaptonemal complex protein 2 GN=SYCP2 PE=2 SV=2
P00441	SOD1	7	4	54.6	0.000676	0.000715	1.88	A6	A2	Superoxide dismutase [Cu-Zn] GN=SOD1 PE=1 SV=2
E9PFT7	APC	11	4	56.4	0.014329	0.006678	5.09	A6	A2	Adenomatous polyposis coli protein (Fragment) GN=APC PE=1 SV=8
Q9UQ80	PA2G4	11	2	57.1	0.027135	0.011279	2.11	A6	A2	Proliferation-associated protein 2G4 GN=PA2G4 PE=1 SV=3
P62979	RPS27A	8	3	58.3	0.003607	0.002296	3.89	A6	A2	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
O60346	PHLPP1	8	4	58.7	0.008556	0.004435	3.66	A2	A6	PH domain leucine-rich repeat-containing protein phosphatase 1 GN=PHLPP1 PE=1 SV=3
Q8TDM6	DLG5	12	5	63.2	0.000126	0.000255	4.87	A6	A2	Disks large homolog 5 GN=DLG5 PE=1 SV=4
Q9NQC3	RTN4	12	6	66.8	0.032518	0.013078	1.16	A2	A6	Reticulon-4 GN=RTN4 PE=1 SV=2
P62258	YWHAE	7	3	67.3	0.004762	0.002836	1.31	A2	A6	14-3-3 protein epsilon GN=YWHAE PE=1 SV=1
Q9Y4G8	RAPGEF2	13	5	72.4	0.015204	0.006995	2.63	A2	A6	Rap guanine nucleotide exchange factor 2 GN=RAPGEF2 PE=1 SV=1
P62753	RPS6	8	2	73	0.012127	0.005846	1.86	A6	A2	40S ribosomal protein S6 GN=RPS6 PE=1 SV=1
Q8NF50	DOCK8	13	8	75.5	0.00869	0.004482	1.9	A2	A6	Dedicator of cytokinesis protein 8 GN=DOCK8 PE=1 SV=3
P30040	ERP29	10	5	77.4	6.93E-05	0.00019	6.84	A6	A2	Endoplasmic reticulum resident protein 29 GN=ERP29 PE=1 SV=4
P04792	HSPB1	8	3	78.6	0.002974	0.002007	2.54	A2	A6	Heat shock protein beta-1 GN=HSPB1 PE=1 SV=2
Q14160	SCRIB	13	4	79.2	0.000606	0.000662	1.72	A2	A6	Protein scribble homolog GN=SCRIB PE=1 SV=4
P35221	CTNNA1	15	2	80.8	0.001394	0.001163	72.5	A2	A6	Catenin alpha-1 GN=CTNNA1 PE=1 SV=1
O00571	DDX3X	15	8	86	0.005391	0.003116	4.08	A6	A2	ATP-dependent RNA helicase DDX3X GN=DDX3X PE=1 SV=3
P09211	GSTP1	11	7	90.6	3.9E-05	0.000144	5.18	A6	A2	Glutathione S-transferase P GN=GSTP1 PE=1 SV=2
P49588	AARS1	18	9	113	0.000993	0.00094	1.41	A6	A2	Alanine--tRNA ligase_ cytoplasmic GN=AARS PE=1 SV=2
P00338	LDHA	15	7	118	0.00696	0.003805	1.37	A6	A2	L-lactate dehydrogenase A chain GN=LDHA PE=1 SV=2
Q12931	TRAP1	17	7	130	0.000214	0.000354	2.93	A2	A6	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
Q99497	PARK7	14	7	134	0.000203	0.000343	3.84	A6	A2	Protein/nucleic acid deglycase DJ-1 GN=PARK7 PE=1 SV=2
P32119	PRDX2	13	6	142	3.79E-05	0.000142	4.19	A6	A2	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
P06748	NPM1	15	10	146	7.39E-05	0.000198	4.28	A2	A6	Nucleophosmin GN=NPM1 PE=1 SV=2
P17987	TCP1	20	7	151	0.004738	0.00283	1.74	A6	A2	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
P35232	PHB	20	11	156	0.000546	0.000622	1.86	A2	A6	Prohibitin GN=PHB PE=1 SV=1

P17844	DDX5	25	10	191	1.47E-05	8.42E-05	4.6	A2	A6	Probable ATP-dependent RNA helicase DDX5 GN=DDX5 PE=1 SV=1
P23528	CFL1	18	5	198	3.67E-05	0.000142	1.96	A6	A2	Cofilin-1 GN=CFL1 PE=1 SV=3
P27797	CALR	25	13	223	0.000796	0.000815	2.29	A6	A2	Calreticulin GN=CALR PE=1 SV=1
P08133	ANXA6	30	14	230	5.09E-06	4.93E-05	4.45	A6	A2	Annexin A6 GN=ANXA6 PE=1 SV=3
Q15233	NONO	28	20	243	0.001555	0.001261	1.6	A2	A6	Non-POU domain-containing octamer-binding protein GN=NONO PE=1 SV=4
P0DMV8	HSPA1A	31	6	256	0.003463	0.002239	1.75	A6	A2	Heat shock 70 kDa protein 1A GN=HSPA1A PE=1 SV=1
P07237	P4HB	30	13	263	0.001259	0.001077	1.85	A6	A2	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
P48681	NES	42	21	267	1.76E-07	6.81E-06	2.21	A2	A6	Nestin GN=NES PE=1 SV=2
P23246	SFPQ	30	15	279	0.017381	0.007774	1.43	A6	A2	Splicing factor_ proline- and glutamine-rich GN=SFPQ PE=1 SV=2
P55072	VCP	43	15	279	0.040781	0.015623	1.5	A6	A2	Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4
P61978	HNRNPK	28	16	306	0.000307	0.000439	1.97	A6	A2	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
P38646	HSPA9	36	21	366	0.011344	0.005531	1.69	A2	A6	Stress-70 protein_ mitochondrial GN=HSPA9 PE=1 SV=2
P04406	GAPDH	36	23	426	9.46E-05	0.000221	2.69	A6	A2	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P08238	HSP90AB1	45	13	489	0.004357	0.002633	2.05	A6	A2	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
P30101	PDIA3	40	18	493	4.75E-05	0.000163	3.17	A6	A2	Protein disulfide-isomerase A3 GN=PDIA3 PE=1 SV=4
P14625	HSP90B1	54	23	603	9.62E-05	0.000221	3.99	A6	A2	Endoplasmin GN=HSP90B1 PE=1 SV=1
P11021	HSPA5	56	35	615	7.56E-05	0.000199	1.64	A6	A2	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P68032	ACTC1	55	12	645	0.001333	0.001128	1.82	A6	A2	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
P10809	HSPD1	68	37	798	0.001241	0.001076	1.8	A2	A6	60 kDa heat shock protein_ mitochondrial GN=HSPD1 PE=1 SV=2

Table S6: Identified allergy and apoptosis-related gene lists following DAT, DMT, and DMAT.

Treatment	**Total protein *P* value only**	**Unique≥2 confidence≥40**	**No. of Allergenic proteins**	**Upregulated**	**Downregulated**	**Common allergenic protein following Aβ1-6 and Aβ17-23 treatment**
DAT/Aβ1-6/HSC	1182	389	20	6	14	PSAT1, PTPRN, RHOA, MYLK, HSPB1, CTSD, PIK3C2A, PARK7, PRDX1, GSTP1, LDHA, DOCK2, DOCK8, PPIA, PHB, PGK1, HSP90B1, VIM
DAT/ Aβ17-23/HSC	1255	422	22	8	14	
DMT_/Aβ1-6 /HSC	1124	340	18	9	9	TYK2, PCNA, CTSD, ANXA1, MYLK, DSG1, PPARD, PIK3C2A, PRDX1, PGK1, ALB, EEF1A1, HSP90B1, ACTB
DMT_/Aβ17-23/HSC	1061	315	16	8	8	
DMAT_/Aβ1-6 /HSC	861	271	16	6	10	MYLK, PCNA, ACTB
DMAT_/Aβ17-23/HSC	740	232	5	2	3	
Treatment	**Total protein P value only**	**Unique≥2 confidence≥40**	**No. of Apoptotic proteins**	**Upregulated**	**Downregulated**	**Common apoptotic protein following Aβ1-6 and Aβ17-23 treatment**
DAT/Aβ1-6/HSC	1182	389	40	12	28	GPI, SYCP2, SOD1, RTN4, YWHAE, RPS6, DOCK8, ERP29, HSPB1, SCRIB, DDX3X, GSTP1, AARS1, LDHA, RAP1, PARK7, PRDX2, NPM1, TCP1, PHB, DDX5, CFL1, ANXA6, HSPA1A, P4HB, NES, VCP, SFPQ, HNRNPK, GAPDH, HSP90AB1, HSP90B1, HSPA5, ACTC1
DAT/ Aβ17-23/HSC	1255	422	46	17	29	
DMT_/Aβ1-6 /HSC	1124	340	31	16	15	CCAR2, TIAM2, YWHAQ, RPS27A, RPS6, ANXA1, PPARD, NPM1, NEFL, PRDX2, ANXA6, TRAP1, VCP, CFL1, P4HB, HNRNPK, HYOU1, HSPA9, ALB, HSP90AB1, HSPA5, HSP90B1, ACTC1
DMT_/Aβ17-23/HSC	1061	315	27	15	12	
DMAT_/Aβ1-6 /HSC	861	271	29	13	16	HINT1, RPS27A, RBM5, INS, TCP1, NPM1, PRDX2, ANXA6, NES, CFL1, ITSN1, GAPDH, HSP90AB1, ACTC1
DMAT_/Aβ17-23/HSC	740	232	19	9	10	

Table S7: Statistical overrepresentation test of the identified apoptosis related proteins following DAT$_{A\beta 1\text{-}6}$ and DAT$_{A\beta 17\text{-}23}$ by PANTHER. Herein, FDR indicates false discovery rate. Displaying only results for FDR $P < 0.05$.

Reactome pathways	Fold Enrichment	Raw P value	FDR
Anti-A$\beta_{1\text{-}6}$ Antibody Treatment			
HSF1 activation	> 100	3.51E-06	1.25E-03
Cellular response to heat stress	33.42	3.50E-08	2.91E-05
Cellular responses to stress	9.56	9.32E-11	2.32E-07
ATF6 (ATF6-alpha) activates chaperone genes	> 100	2.20E-04	2.61E-02
ATF6 (ATF6-alpha) activates chaperones	89.13	3.11E-04	3.37E-02
Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	75.42	4.18E-04	4.01E-02
Attenuation phase	70.03	4.77E-04	4.40E-02
Activation of BAD and translocation to mitochondria	65.36	5.40E-04	4.81E-02
Detoxification of Reactive Oxygen Species	56.02	1.16E-06	5.78E-04
Cellular response to chemical stress	12.73	2.95E-04	3.35E-02
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	39.75	7.35E-05	1.08E-02
Interleukin-12 signaling	42.63	3.19E-06	1.33E-03
Interleukin-12 family signaling	35.02	6.66E-06	2.08E-03
SUMOylation of transcription cofactors	35.02	1.05E-04	1.38E-02
SUMO E3 ligases SUMOylate target proteins	15.61	1.89E-05	4.28E-03
SUMOylation	15.04	2.25E-05	4.67E-03
Regulation of HSF1-mediated heat shock response	28.84	1.38E-05	3.82E-03
TP53 Regulates Metabolic Genes	23.62	2.92E-05	5.60E-03
Neutrophil degranulation	6.17	4.10E-04	4.08E-02
Signaling by Rho GTPases	5.85	5.73E-05	1.02E-02
Signaling by Rho GTPases, Miro GTPases and RHOBTB3	5.73	6.68E-05	1.11E-02
Infectious disease	4.93	6.92E-05	1.08E-02
Anti-A$\beta_{17\text{-}23}$ Antibody Treatment			
TFAP2A acts as a transcriptional repressor during retinoic acid induced cell differentiation	> 100	1.15E-04	1.10E-02
ATF6 (ATF6-alpha) activates chaperone genes	> 100	2.73E-06	6.18E-04
ATF6 (ATF6-alpha) activates chaperones	> 100	4.49E-06	8.62E-04
Cellular responses to stress	8.19	9.41E-10	2.35E-06
HSF1 activation	> 100	5.61E-06	9.99E-04
Cellular response to heat stress	28.65	9.07E-08	5.65E-05
Josephin domain DUBs	70.03	4.93E-04	3.32E-02
Post-translational protein modification	3.31	3.72E-04	2.73E-02
Attenuation phase	60.03	6.49E-04	3.85E-02
Chaperone Mediated Autophagy	57.30	2.79E-05	3.86E-03
Sema3A PAK dependent Axon repulsion	52.52	8.25E-04	4.47E-02
Calnexin/calreticulin cycle	48.48	4.40E-05	4.99E-03
N-glycan trimming in the ER and Calnexin/Calreticulin cycle	48.02	2.17E-06	6.76E-04
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	48.48	4.40E-05	4.77E-03
Detoxification of Reactive Oxygen Species	48.02	2.17E-06	6.01E-04
Cellular response to chemical stress	13.64	3.70E-05	4.61E-03
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	45.43	2.66E-06	6.64E-04

Interleukin-12 signaling	45.67	1.32E-07	6.60E-05
Interleukin-12 family signaling	37.52	3.29E-07	1.37E-04
Signaling by Interleukins	6.57	9.33E-05	9.69E-03
Ovarian tumor domain proteases	32.32	1.35E-04	1.25E-02
SUMOylation of transcription cofactors	30.01	1.66E-04	1.43E-02
SUMO E3 ligases SUMOylate target proteins	10.71	5.75E-04	3.50E-02
SUMOylation	10.31	6.60E-04	3.83E-02
Aggrephagy	28.65	1.89E-04	1.57E-02
SARS-CoV-1 Infection	25.21	2.71E-04	2.11E-02
SARS-CoV Infections	10.91	5.36E-04	3.43E-02
Infectious disease	4.69	4.33E-05	5.14E-03
Regulation of HSF1-mediated heat shock response	24.72	2.56E-05	4.26E-03
AUF1 (hnRNP D0) binds and destabilizes mRNA	23.78	3.19E-04	2.41E-02
Hedgehog ligand biogenesis	19.70	5.41E-04	3.37E-02
SARS-CoV-2 Infection	17.75	7.24E-04	4.01E-02
Influenza Infection	10.99	5.23E-04	3.43E-02
Neutrophil degranulation	6.17	1.37E-04	1.22E-02
Innate Immune System	3.80	2.47E-04	1.98E-02
Diseases of signal transduction by growth factor receptors and second messengers	6.03	4.81E-04	3.42E-02
RHO GTPase cycle	5.63	6.88E-04	3.90E-02
Signaling by Rho GTPases	5.64	2.71E-05	3.97E-03
Signaling by Rho GTPases, Miro GTPases and RHOBTB3	5.52	3.21E-05	4.22E-03

Table S8: Gene enriched term and their associated genes for the identified apoptosis-related genes following ${}_{\mathrm{Apop}}\mathrm{DAT}_{\mathrm{A}\beta 1\text{-}6}$ and ${}_{\mathrm{Apop}}\mathrm{DAT}_{\mathrm{A}\beta 17\text{-}23}$.

Description	Hits	LogP	Log(q-value)
regulation of apoptotic signaling pathway	CTNNA1|DDX3X|PDIA3|GSTP1|HNRNPK|HSPA1A|HSPB1|NONO|P4HB|RPS3|SFPQ|SOD1|SP100|PRDX2|TRAP1|HYOU1|ERP29|PARK7|CCAR2	-22.68478937	-18.3381
protein folding	CALR|PDIA3|HSPA1A|HSPA5|HSPA9|HSPB1|HSP90AB1|HSPD1|P4HB|TCP1|HSP90B1|TRAP1|ERP29	-17.29614609	-13.4266
Cellular responses to stress	CALR|GSTP1|HSPA1A|HSPA5|HSPA9|HSP90AB1|P4HB|RPS3|RPS6|RPS27A|SOD1|PRDX2|HSP90B1|VCP|YWHAE|HYOU1|CCAR2	-14.15135422	-10.5036
protein stabilization	CALR|GAPDH|HSPA1A|HSP90AB1|HSPD1|PHB1|TCP1|PARK7|RTN4|USP36	-12.46832643	-9.20082
Protein processing in endoplasmic reticulum	CALR|PDIA3|HSPA1A|HSPA5|HSP90AB1|P4HB|HSP90B1|VCP|HYOU1|ERP29	-12.38819645	-8.99575
positive regulation of cell death	APC|CTNNA1|DDX3X|PDIA3|HSPD1|PHB1|RPS3|RPS6|SFPQ|SOD1|RAPGEF2|PARK7|SCRIB|CCAR2	-11.78287554	-8.47758
negative regulation of neuron apoptotic process	AARS1|GPI|HSP90AB1|NEFL|NONO|SOD1|HYOU1|NES|PARK7	-11.40967132	-8.15903
VEGFA-VEGFR2 signaling pathway	CALR|CFL1|CTNNA1|GAPDH|HSPA1A|HSPB1|LDHA|P4HB|RPS6|PRDX2|YWHAE|HYOU1	-10.92486801	-7.83346
cellular response to organic cyclic compound	CALR|CTNNA1|DDX5|HSPA1A|HSPA5|HSP90AB1|NPM1|PHB1|SOD1|HSP90B1|RAPGEF2	-9.596439409	-6.79382
regulation of extrinsic apoptotic signaling pathway	CTNNA1|DDX3X|PDIA3|GSTP1|HSPA1A|SP100|PRDX2|PARK7	-9.580137718	-6.62846
regulation of protein kinase activity	APC|DDX3X|GSTP1|HSPB1|HSP90AB1|NPM1|PHB1|RPS3|SOD1|RAPGEF2|ERP29|PARK7	-9.012124281	-6.0968
positive regulation of cytokine production	DDX3X|GAPDH|HSPA1A|HSPB1|HSPD1|PHB1|RPS3|SOD1|PARK7|SCRIB	-8.048203045	-5.25782
positive regulation of protein modification by small protein conjugation or removal	DDX3X|HSPA5|VCP	-3.280170505	-1.81885
Interleukin-12 signaling	CFL1|HSPA9|P4HB|SOD1|TCP1	-7.971029739	-5.45685
snRNP-free U1A (SF-A) complex	DDX5|NONO|SFPQ	-7.850798674	-5.35537
regulation of cellular amide metabolic process	AARS1|CALR|DDX3X|GAPDH|HSPB1|NPM1|PA2G4|RPS3|TRAP1|RTN4	-7.622444168	-4.87782
positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	SFPQ|SOD1|PARK7	-7.585282488	-5.11941
response to heat	HSPA1A|HSP90AB1|SOD1|VCP|YWHAE	-7.168498475	-4.7856
H2AX complex I	CALR|HSPA5|NPM1	-6.910214571	-4.58884
response to inorganic substance	CALR|GPI|HSPA5|NEFL|RPS3|SOD1|PRDX2|VCP|PARK7	-6.602358646	-3.97995

Table S9: Identified proteins following DMT$_{A\beta1\text{-}6}$ and DMT$_{A\beta17\text{-}23}$ compared to untreated cells. Herein, CuK1= Aβ1-6; Cuk2= Aβ17-23; CuK3=NoT The proteins were searched for Human (*Homo sapiens*) Database.

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-A$\beta_{1\text{-}6}$ Antibody Treatment										
Q96L93	KIF16B	9	5	40	6.95E-06	4.18E-05	4.38	cuk1	cuk3	Kinesin-like protein KIF16B GN=KIF16B PE=1 SV=2
Q15700	DLG2	7	4	40.1	2.39E-05	6.70E-05	70.3	cuk1	cuk3	Disks large homolog 2 GN=DLG2 PE=1 SV=3
P40926	MDH2	6	2	40.3	7.82E-06	4.31E-05	3.91	cuk3	cuk1	Malate dehydrogenase_ mitochondrial GN=MDH2 PE=1 SV=3
Q96GQ7	DDX27	8	3	40.6	0.023766	0.007276	2.45	cuk1	cuk3	Probable ATP-dependent RNA helicase DDX27 GN=DDX27 PE=1 SV=2
Q8TF32	ZNF431	6	2	40.9	0.026229	0.007888	1.98	cuk3	cuk1	Zinc finger protein 431 GN=ZNF431 PE=2 SV=2
O75362	ZNF217	8	2	41.1	9.26E-05	0.000141	3.18	cuk3	cuk1	Zinc finger protein 217 GN=ZNF217 PE=1 SV=1
Q86VH2	KIF27	7	5	41.3	0.002021	0.001106	2	cuk1	cuk3	Kinesin-like protein KIF27 GN=KIF27 PE=2 SV=1
B7ZM99	MTHFD1L	8	2	41.4	0.005636	0.002342	2.56	cuk3	cuk1	MTHFD1L protein GN=MTHFD1L PE=1 SV=1
Q8NDQ6	ZNF540	7	2	41.5	0.000574	0.00048	1.55	cuk1	cuk3	Zinc finger protein 540 GN=ZNF540 PE=1 SV=1
E7EX29	YWHAZ	5	3	41.6	0.0028	0.001403	1.49	cuk1	cuk3	14-3-3 protein zeta/delta (Fragment) GN=YWHAZ PE=1 SV=1
Q8N163	CCAR2	8	4	41.6	0.004323	0.001929	2.36	cuk3	cuk1	Cell cycle and apoptosis regulator protein 2 GN=CCAR2 PE=1 SV=2
H0Y5C6	FLNA	6	5	41.6	0.001036	0.00069	2.18	cuk1	cuk3	Filamin-A (Fragment) GN=FLNA PE=1 SV=1
Q05BV3	EML5	8	2	41.7	0.001071	0.00071	2.99	cuk3	cuk1	Echinoderm microtubule-associated protein-like 5 GN=EML5 PE=2 SV=3
A0A087WY36	AKAP13	7	4	41.7	0.000976	0.000657	2.23	cuk3	cuk1	A-kinase anchor protein 13 (Fragment) GN=AKAP13 PE=1 SV=1
B4E1Z4	Not Available	8	2	41.9	0.000292	0.000302	5.37	cuk3	cuk1	cDNA FLJ55673_ highly similar to Complement factor B (EC 3.4.21.47) PE=1 SV=1
Q38SD2	LRRK1	8	2	42	9.24E-05	0.000141	3.79	cuk1	cuk3	Leucine-rich repeat serine/threonine-protein kinase 1 GN=LRRK1 PE=1 SV=3
E9PCN5	CNOT10	6	3	42	0.016461	0.005337	2	cuk1	cuk3	CCR4-NOT transcription complex subunit 10 GN=CNOT10 PE=1 SV=1
A0A087X2I1	PSMC6	6	4	42	0.011333	0.003986	1.29	cuk1	cuk3	26S proteasome regulatory subunit 10B GN=PSMC6 PE=1 SV=1
P29597	TYK2	8	2	42.1	0.042145	0.011808	1.58	cuk1	cuk3	Non-receptor tyrosine-protein kinase TYK2 GN=TYK2 PE=1 SV=3
Q8IWY7	TTBK2	6	3	42.1	6.42E-06	4.02E-05	41.7	cuk1	cuk3	Tau-tubulin kinase GN=TTBK2 PE=1 SV=1
F8VUX9	WDR90	6	4	42.6	0.003733	0.001734	1.51	cuk3	cuk1	WD repeat-containing protein 90 GN=WDR90 PE=1 SV=1
O60237	PPP1R12B	8	4	42.6	0.001167	0.000748	1.45	cuk1	cuk3	Protein phosphatase 1 regulatory subunit 12B GN=PPP1R12B PE=1 SV=2
A8MZ36	EVPLL	6	3	42.7	0.011503	0.004023	1.72	cuk1	cuk3	Envoplakin-like protein GN=EVPLL PE=2 SV=1
Q2M1P5	KIF7	8	3	42.7	0.000507	0.000438	1.49	cuk3	cuk1	Kinesin-like protein KIF7 GN=KIF7 PE=1 SV=2
Q8NFY4	SEMA6D	9	4	42.7	0.000274	0.000291	1.5	cuk1	cuk3	Semaphorin-6D GN=SEMA6D PE=1 SV=1
P26373	RPL13	6	2	42.8	0.000515	0.000443	1.85	cuk3	cuk1	60S ribosomal protein L13 GN=RPL13 PE=1 SV=4
Q569K6	CCDC157	7	4	42.8	3.48E-05	8.03E-05	4.39	cuk3	cuk1	Coiled-coil domain-containing protein 157 GN=CCDC157 PE=2 SV=3
Q969P6	TOP1MT	8	4	42.8	0.003349	0.001604	1.51	cuk1	cuk3	DNA topoisomerase I_ mitochondrial GN=TOP1MT PE=1 SV=1
O60343	TBC1D4	7	2	43	0.00189	0.001053	1.77	cuk3	cuk1	TBC1 domain family member 4 GN=TBC1D4 PE=1 SV=2
Q6P4R8	NFRKB	8	3	43.3	0.000462	0.000408	4.54	cuk3	cuk1	Nuclear factor related to kappa-B-binding protein GN=NFRKB PE=1 SV=2
Q9Y536	PPIAL4A	7	3	43.3	0.003221	0.001548	1.3	cuk1	cuk3	Peptidyl-prolyl cis-trans isomerase A-like 4A GN=PPIAL4A PE=2 SV=1
P33993	MCM7	6	4	43.5	0.006442	0.002589	1.68	cuk3	cuk1	DNA replication licensing factor MCM7 GN=MCM7 PE=1 SV=4
Q8IVF5	TIAM2	10	3	43.9	0.002479	0.001277	3.49	cuk1	cuk3	T-lymphoma invasion and metastasis-inducing protein 2 GN=TIAM2 PE=2 SV=4
Q96SN8	CDK5RAP2	9	3	43.9	0.044066	0.012256	1.37	cuk3	cuk1	CDK5 regulatory subunit-associated protein 2 GN=CDK5RAP2 PE=1 SV=5
P52948	NUP98	8	3	44	0.002743	0.001381	1.35	cuk1	cuk3	Nuclear pore complex protein Nup98-Nup96 GN=NUP98 PE=1 SV=4
C9JZR2	CTNND1	8	3	44.1	0.011628	0.004053	2.88	cuk3	cuk1	Catenin delta-1 GN=CTNND1 PE=1 SV=2
Q05209	PTPN12	9	5	44.2	9.48E-05	0.000143	3.83	cuk1	cuk3	Tyrosine-protein phosphatase non-receptor type 12 GN=PTPN12 PE=1 SV=3
G3V2A4	TEP1	7	4	44.6	0.005794	0.002387	1.54	cuk3	cuk1	Telomerase protein component 1 GN=TEP1 PE=1 SV=1
P49773	HINT1	4	2	44.7	0.000726	0.000554	2.74	cuk1	cuk3	Histidine triad nucleotide-binding protein 1 GN=HINT1 PE=1 SV=2
P46776	RPL27A	6	2	44.8	0.002123	0.001146	1.41	cuk3	cuk1	60S ribosomal protein L27a GN=RPL27A PE=1 SV=2
Q9UN70	PCDHGC3	8	3	44.8	0.016847	0.005455	1.45	cuk3	cuk1	Protocadherin gamma-C3 GN=PCDHGC3 PE=1 SV=1
P12004	PCNA	6	4	44.8	0.012169	0.004175	1.9	cuk3	cuk1	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
P27348	YWHAQ	6	3	45	0.000901	0.000623	6.87	cuk3	cuk1	14-3-3 protein theta GN=YWHAQ PE=1 SV=1
Q8N1G1	REXO1	6	3	45	9.29E-05	0.000141	2.8	cuk1	cuk3	RNA exonuclease 1 homolog GN=REXO1 PE=1 SV=3
P46940	IQGAP1	9	3	45	0.000318	0.000322	2.56	cuk3	cuk1	Ras GTPase-activating-like protein IQGAP1 GN=IQGAP1 PE=1 SV=1
P53804	TTC3	8	3	45	0.002509	0.001291	2.15	cuk1	cuk3	E3 ubiquitin-protein ligase TTC3 GN=TTC3 PE=1 SV=2
Q9HCE3	ZNF532	8	3	45	0.004531	0.001993	2.02	cuk1	cuk3	Zinc finger protein 532 GN=ZNF532 PE=1 SV=2
I6L899	GOLGA8R	7	2	45.3	0.000265	0.000288	17.2	cuk1	cuk3	Golgin subfamily A member 8R GN=GOLGA8R PE=3 SV=1
H3BQN4	ALDOA	6	2	46	5.17E-06	3.75E-05	46.3	cuk1	cuk3	Fructose-bisphosphate aldolase GN=ALDOA PE=1 SV=1
P07195	LDHB	7	3	46	0.02805	0.008332	1.27	cuk3	cuk1	L-lactate dehydrogenase B chain GN=LDHB PE=1 SV=2
Q8N3U4	STAG2	7	2	46.5	0.005711	0.00236	2.4	cuk1	cuk3	Cohesin subunit SA-2 GN=STAG2 PE=1 SV=3
Q9H1A4	ANAPC1	8	2	46.6	0.007309	0.002808	1.22	cuk3	cuk1	Anaphase-promoting complex subunit 1 GN=ANAPC1 PE=1 SV=1
P62979	RPS27A	6	3	46.9	0.000223	0.000255	10.5	cuk3	cuk1	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
Q17RC7	EXOC3L4	8	5	47.1	0.001176	0.000753	1.52	cuk3	cuk1	Exocyst complex component 3-like protein 4 GN=EXOC3L4 PE=1 SV=2
Q8TET4	GANC	7	3	47.3	0.011257	0.003964	1.68	cuk1	cuk3	Neutral alpha-glucosidase C GN=GANC PE=2 SV=3
Q9NSY1	BMP2K	8	4	47.4	0.030037	0.008792	1.35	cuk3	cuk1	BMP-2-inducible protein kinase GN=BMP2K PE=1 SV=2
P02461	COL3A1	8	2	47.5	0.00021	0.000243	2.74	cuk3	cuk1	Collagen alpha-1(III) chain GN=COL3A1 PE=1 SV=4
Q9UBZ9	REV1	6	2	47.6	8.56E-06	4.31E-05	2.19	cuk3	cuk1	DNA repair protein REV1 GN=REV1 PE=1 SV=1
Q9P0M6	MACROH2A2	6	4	48.2	0.013414	0.004506	1.27	cuk1	cuk3	Core histone macro-H2A.2 GN=H2AFY2 PE=1 SV=3
P62829	RPL23	6	4	48.3	1.68E-05	5.54E-05	3.21	cuk3	cuk1	60S ribosomal protein L23 GN=RPL23 PE=1 SV=1
Q96NG3	ODAD4	8	2	48.5	0.011024	0.003918	1.6	cuk1	cuk3	Tetratricopeptide repeat protein 25 GN=TTC25 PE=1 SV=2
Q12873	CHD3	9	2	48.5	0.020839	0.006477	1.32	cuk1	cuk3	Chromodomain-helicase-DNA-binding protein 3 GN=CHD3 PE=1 SV=3
A0A1B0GV23	CTSD	9	6	48.6	0.003074	0.001487	1.98	cuk3	cuk1	Cathepsin D GN=CTSD PE=1 SV=1
Q8WVV9	HNRNPLL	8	4	48.7	0.041359	0.01163	1.27	cuk1	cuk3	Heterogeneous nuclear ribonucleoprotein L-like GN=HNRNPLL PE=1 SV=1
A2RUB1	MEIOC	7	2	48.9	2.70E-05	7.03E-05	5.35	cuk1	cuk3	Meiosis-specific coiled-coil domain-containing protein MEIOC GN=MEIOC PE=2 SV=3
P10586	PTPRF	10	4	48.9	0.000861	0.000609	2.72	cuk1	cuk3	Receptor-type tyrosine-protein phosphatase F GN=PTPRF PE=1 SV=2
Q9UQ16	DNM3	10	4	49.2	0.001226	0.000775	3.07	cuk3	cuk1	Dynamin-3 GN=DNM3 PE=1 SV=4

Q8TCU6	PREX1	10	6	49.2	0.000892	0.00062	2.12	cuk1	cuk3	Phosphatidylinositol 3_4_5-trisphosphate-dependent Rac exchanger 1 protein GN=PREX1 PE=1 SV=3
P07384	CAPN1	7	3	49.4	9.21E-05	0.000141	10	cuk3	cuk1	Calpain-1 catalytic subunit GN=CAPN1 PE=1 SV=1
Q96QP1	ALPK1	9	4	49.6	4.50E-05	9.27E-05	2.52	cuk3	cuk1	Alpha-protein kinase 1 GN=ALPK1 PE=2 SV=3
P52597	HNRNPF	7	5	49.6	0.00042	0.000382	1.99	cuk1	cuk3	Heterogeneous nuclear ribonucleoprotein F GN=HNRNPF PE=1 SV=3
Q8NA03	FSIP1	8	4	49.7	0.001251	0.000787	1.81	cuk3	cuk1	Fibrous sheath-interacting protein 1 GN=FSIP1 PE=2 SV=1
P13647	KRT5	6	2	49.8	0.000918	0.000631	1.53	cuk1	cuk3	Keratin_ type II cytoskeletal 5 GN=KRT5 PE=1 SV=3
Q96N67	DOCK7	10	2	49.9	0.000296	0.000303	2.81	cuk3	cuk1	Dedicator of cytokinesis protein 7 GN=DOCK7 PE=1 SV=4
P04899	GNAI2	8	6	50.4	0.046148	0.012732	1.2	cuk3	cuk1	Guanine nucleotide-binding protein G(i) subunit alpha-2 GN=GNAI2 PE=1 SV=3
P0DP91	ERCC6	8	2	50.5	0.005457	0.002297	2.81	cuk1	cuk3	Chimeric ERCC6-PGBD3 protein GN=CSB-PGBD3 PE=1 SV=1
Q9BY66	KDM5D	10	6	50.5	0.027747	0.008265	1.52	cuk3	cuk1	Lysine-specific demethylase 5D GN=KDM5D PE=1 SV=2
Q9H792	PEAK1	10	5	50.6	0.000339	0.000338	1.74	cuk1	cuk3	Pseudopodium-enriched atypical kinase 1 GN=PEAK1 PE=1 SV=4
P04004	VTN	7	5	50.6	0.000122	0.000169	1.57	cuk3	cuk1	Vitronectin GN=VTN PE=1 SV=1
Q14117	DPYS	7	2	50.7	7.34E-05	0.000125	1.79	cuk1	cuk3	Dihydropyrimidinase GN=DPYS PE=1 SV=1
Q92878	RAD50	11	3	51	3.70E-05	8.29E-05	9.3	cuk1	cuk3	DNA repair protein RAD50 GN=RAD50 PE=1 SV=1
O43683	BUB1	9	4	51.3	1.27E-05	5.21E-05	4.23	cuk1	cuk3	Mitotic checkpoint serine/threonine-protein kinase BUB1 GN=BUB1 PE=1 SV=1
A0A0A0M QX1	MYO10	8	5	51.3	0.017807	0.005695	1.67	cuk1	cuk3	Unconventional myosin-X GN=MYO10 PE=1 SV=1
A0A0C4DF M7	TUT4	10	3	51.5	1.48E-05	5.22E-05	6.89	cuk1	cuk3	Terminal uridylyltransferase 4 GN=ZCCHC11 PE=1 SV=1
P62753	RPS6	8	4	51.5	0.004989	0.002134	1.92	cuk3	cuk1	40S ribosomal protein S6 GN=RPS6 PE=1 SV=1
Q7Z4S6	KIF21A	9	5	51.6	0.008385	0.003132	1.63	cuk1	cuk3	Kinesin-like protein KIF21A GN=KIF21A PE=1 SV=2
Q6ZNG0	ZNF620	8	3	52.1	1.99E-05	6.23E-05	4.28	cuk1	cuk3	Zinc finger protein 620 GN=ZNF620 PE=2 SV=1
Q12906	ILF3	9	3	52.1	0.015296	0.005045	1.75	cuk1	cuk3	Interleukin enhancer-binding factor 3 GN=ILF3 PE=1 SV=3
Q8N4C6	NIN	11	2	52.3	1.90E-06	2.17E-05	26.1	cuk3	cuk1	Ninein GN=NIN PE=1 SV=4
O60282	KIF5C	8	2	52.3	0.010257	0.003718	2.98	cuk3	cuk1	Kinesin heavy chain isoform 5C GN=KIF5C PE=1 SV=1
Q96RY7	IFT140	7	2	52.4	0.01063	0.003831	1.64	cuk3	cuk1	Intraflagellar transport protein 140 homolog GN=IFT140 PE=1 SV=1
O60610	DIAPH1	10	6	52.5	2.56E-05	6.96E-05	1.91	cuk1	cuk3	Protein diaphanous homolog 1 GN=DIAPH1 PE=1 SV=2
A0A0A0M S86	CEP290	7	3	52.6	0.000156	0.000196	14.5	cuk1	cuk3	Centrosomal protein of 290 kDa GN=CEP290 PE=1 SV=1
P35527	KRT9	10	7	52.7	0.001561	0.000918	1.54	cuk1	cuk3	Keratin_ type I cytoskeletal 9 GN=KRT9 PE=1 SV=3
Q5TB80	CEP162	10	2	52.8	0.001733	0.000995	6.76	cuk1	cuk3	Centrosomal protein of 162 kDa GN=CEP162 PE=1 SV=2
P80723	BASP1	7	6	53.2	0.008384	0.003132	3.72	cuk1	cuk3	Brain acid soluble protein 1 GN=BASP1 PE=1 SV=2
K7EM46	KIAA1328	8	2	53.3	0.009608	0.003512	1.54	cuk3	cuk1	Protein hinderin (Fragment) GN=KIAA1328 PE=1 SV=1
Q9P2E9	RRBP1	8	4	53.6	0.041135	0.011588	1.52	cuk1	cuk3	Ribosome-binding protein 1 GN=RRBP1 PE=1 SV=5
O43896	KIF1C	9	2	53.8	3.65E-05	8.25E-05	6.85	cuk1	cuk3	Kinesin-like protein KIF1C GN=KIF1C PE=1 SV=3
P60866	RPS20	6	3	53.9	0.001553	0.000917	1.9	cuk3	cuk1	40S ribosomal protein S20 GN=RPS20 PE=1 SV=1
P62917	RPL8	7	4	53.9	0.004346	0.001937	1.43	cuk1	cuk3	60S ribosomal protein L8 GN=RPL8 PE=1 SV=2
Q9H9B1	EHMT1	8	3	54.5	0.000129	0.000176	1.62	cuk1	cuk3	Histone-lysine N-methyltransferase EHMT1 GN=EHMT1 PE=1 SV=4
Q12888	TP53BP1	11	5	54.6	0.000577	0.00048	1.94	cuk1	cuk3	TP53-binding protein 1 GN=TP53BP1 PE=1 SV=2
P04083	ANXA1	9	3	54.8	0.000105	0.000153	2.69	cuk3	cuk1	Annexin A1 GN=ANXA1 PE=1 SV=2
F6RFD5	DSTN	7	2	55.1	0.011243	0.003963	2.81	cuk1	cuk3	Destrin GN=DSTN PE=1 SV=1
P48047	ATP5PO	8	5	55.7	0.007179	0.002791	1.3	cuk3	cuk1	ATP synthase subunit O_ mitochondrial GN=ATP5O PE=1 SV=1
O14715	RGPD8	9	4	56.4	0.043114	0.012035	1.18	cuk1	cuk3	RANBP2-like and GRIP domain-containing protein 8 GN=RGPD8 PE=1 SV=2
Q5R372	RABGAP1L	10	3	56.5	0.000226	0.000256	2.01	cuk1	cuk3	Rab GTPase-activating protein 1-like GN=RABGAP1L PE=1 SV=1
Q9NVE5	USP40	8	4	56.5	0.008346	0.00313	1.53	cuk1	cuk3	Ubiquitin carboxyl-terminal hydrolase 40 GN=USP40 PE=1 SV=3
H7BYL6	AKAP9	11	5	56.8	0.000255	0.00028	2.76	cuk1	cuk3	A-kinase anchor protein 9 (Fragment) GN=AKAP9 PE=1 SV=1
P62263	RPS14	6	3	57.6	0.010968	0.003907	1.39	cuk3	cuk1	40S ribosomal protein S14 GN=RPS14 PE=1 SV=3
Q15029	EFTUD2	9	6	57.8	5.01E-05	9.92E-05	1.42	cuk3	cuk1	116 kDa U5 small nuclear ribonucleoprotein component GN=EFTUD2 PE=1 SV=1
O43432	EIF4G3	10	4	58	2.45E-05	6.78E-05	5.92	cuk1	cuk3	Eukaryotic translation initiation factor 4 gamma 3 GN=EIF4G3 PE=1 SV=2
O75335	PPFIA4	9	4	58.4	6.14E-05	0.000111	2.97	cuk1	cuk3	Liprin-alpha-4 GN=PPFIA4 PE=2 SV=3
Q8N653	LZTR1	11	4	58.7	0.003385	0.001617	1.86	cuk1	cuk3	Leucine-zipper-like transcriptional regulator 1 GN=LZTR1 PE=1 SV=2
A0A087W UK2	HNRNPDL	7	2	58.8	0.000116	0.000166	1.83	cuk1	cuk3	Heterogeneous nuclear ribonucleoprotein D-like GN=HNRNPDL PE=1 SV=1
Q17RG1	KCTD19	8	3	59.3	0.002583	0.001318	4.69	cuk1	cuk3	BTB/POZ domain-containing protein KCTD19 GN=KCTD19 PE=2 SV=1
Q13332	PTPRS	12	4	60.3	0.005989	0.002455	1.73	cuk1	cuk3	Receptor-type tyrosine-protein phosphatase S GN=PTPRS PE=1 SV=3
Q9BPU6	DPYSL5	9	4	60.4	1.14E-05	5.10E-05	3.34	cuk3	cuk1	Dihydropyrimidinase-related protein 5 GN=DPYSL5 PE=1 SV=1
P33991	MCM4	12	7	60.4	2.24E-06	2.37E-05	10	cuk1	cuk3	DNA replication licensing factor MCM4 GN=MCM4 PE=1 SV=5
J3KP97	CCDC18	10	3	60.7	0.000157	0.000197	4.66	cuk1	cuk3	Coiled-coil domain-containing protein 18 (Fragment) GN=CCDC18 PE=1 SV=1
Q9NYU2	UGGT1	13	3	61	0.007063	0.002763	1.82	cuk1	cuk3	UDP-glucose:glycoprotein glucosyltransferase 1 GN=UGGT1 PE=1 SV=3
P11137	MAP2	10	6	61.2	0.000362	0.00035	1.83	cuk1	cuk3	Microtubule-associated protein 2 GN=MAP2 PE=1 SV=4
Q1KMD3	HNRNPUL2	9	2	61.4	0.020982	0.006508	1.84	cuk1	cuk3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 GN=HNRNPUL2 PE=1 SV=1
P12035	KRT3	8	3	61.6	0.015387	0.005069	1.89	cuk1	cuk3	Keratin_ type II cytoskeletal 3 GN=KRT3 PE=1 SV=3
Q6SA08	TSSK4	9	4	62.2	0.003717	0.001731	3.74	cuk1	cuk3	Testis-specific serine/threonine-protein kinase 4 GN=TSSK4 PE=1 SV=1
Q6ZU80	CEP128	13	5	62.2	0.000749	0.000555	2.33	cuk1	cuk3	Centrosomal protein of 128 kDa GN=CEP128 PE=1 SV=2
Q9C0F0	ASXL3	11	6	62.6	0.001585	0.000931	1.76	cuk1	cuk3	Putative Polycomb group protein ASXL3 GN=ASXL3 PE=2 SV=3
Q6P280	ZNF529	9	2	62.8	0.011828	0.004081	5.12	cuk3	cuk1	Zinc finger protein 529 GN=ZNF529 PE=1 SV=2
Q6PIF6	MYO7B	10	3	63	0.00041	0.000381	2.96	cuk1	cuk3	Unconventional myosin-VIIb GN=MYO7B PE=1 SV=2
O14994	SYN3	9	3	63.1	0.001141	0.000737	1.74	cuk1	cuk3	Synapsin-3 GN=SYN3 PE=1 SV=2
B7Z645	SYNCRIP	11	3	63.4	0.003011	0.001484	2.6	cuk3	cuk1	Heterogeneous nuclear ribonucleoprotein Q GN=SYNCRIP PE=1 SV=1
E7EPS8	PTPRM	11	6	63.5	0.000108	0.000157	3.06	cuk3	cuk1	Receptor-type tyrosine-protein phosphatase mu GN=PTPRM PE=1 SV=2
Q7L014	DDX46	12	7	63.5	0.011779	0.004076	1.53	cuk1	cuk3	Probable ATP-dependent RNA helicase DDX46 GN=DDX46 PE=1 SV=2
Q9P2M7	CGN	12	5	63.7	0.024627	0.00748	1.52	cuk1	cuk3	Cingulin GN=CGN PE=1 SV=2
Q8NEZ3	WDR19	11	2	64	0.03211	0.009346	1.59	cuk1	cuk3	WD repeat-containing protein 19 GN=WDR19 PE=1 SV=2
Q8ND30	PPFIBP2	10	5	64.2	0.001314	0.000814	2.55	cuk1	cuk3	Liprin-beta-2 GN=PPFIBP2 PE=1 SV=3
O95153	TSPOAP1	10	4	64.5	6.85E-05	0.000119	4.64	cuk1	cuk3	Peripheral-type benzodiazepine receptor-associated protein 1 GN=TSPOAP1 PE=1 SV=2
Q8NI27	THOC2	11	5	64.5	0.010736	0.003856	1.55	cuk1	cuk3	THO complex subunit 2 GN=THOC2 PE=1 SV=2
P31930	UQCRC1	10	3	64.6	0.004277	0.001915	1.77	cuk1	cuk3	Cytochrome b-c1 complex subunit 1_ mitochondrial GN=UQCRC1 PE=1 SV=3
Q9HCJ0	TNRC6C	13	7	64.6	2.17E-05	6.47E-05	3.22	cuk1	cuk3	Trinucleotide repeat-containing gene 6C protein GN=TNRC6C PE=1 SV=3
Q8WUI4	HDAC7	11	2	64.7	0.040905	0.011534	1.12	cuk3	cuk1	Histone deacetylase 7 GN=HDAC7 PE=1 SV=2
Q15746	MYLK	10	6	64.8	0.002075	0.001128	2.14	cuk1	cuk3	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
Q92805	GOLGA1	11	5	66.3	0.001273	0.000794	1.98	cuk1	cuk3	Golgin subfamily A member 1 GN=GOLGA1 PE=1 SV=3
Q02413	DSG1	8	3	66.4	0.00033	0.000333	3	cuk1	cuk3	Desmoglein-1 GN=DSG1 PE=1 SV=2
Q13838	DDX39B	8	2	66.6	0.006288	0.002549	2.06	cuk1	cuk3	Spliceosome RNA helicase DDX39B GN=DDX39B PE=1 SV=1
Q99460	PSMD1	11	3	66.7	2.28E-05	6.63E-05	3.43	cuk1	cuk3	26S proteasome non-ATPase regulatory subunit 1 GN=PSMD1 PE=1 SV=2
Q96QT6	PHF12	9	4	66.7	0.004896	0.002112	2.06	cuk1	cuk3	PHD finger protein 12 GN=PHF12 PE=1 SV=2
Q03181	PPARD	7	2	67.2	0.002091	0.001131	1.99	cuk1	cuk3	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1

O75947	ATP5PD	8	3	67.4	0.00182	0.001026	1.48	cuk3	cuk1	ATP synthase subunit d_ mitochondrial GN=ATP5H PE=1 SV=3
Q03252	LMNB2	9	3	67.5	1.33E-05	5.22E-05	8.84	cuk1	cuk3	Lamin-B2 GN=LMNB2 PE=1 SV=4
P17987	TCP1	10	4	67.5	0.00026	0.000283	1.59	cuk3	cuk1	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
Q03112	MECOM	13	7	67.9	0.008047	0.003036	1.35	cuk1	cuk3	MDS1 and EVI1 complex locus protein GN=MECOM PE=1 SV=3
P53814	SMTN	10	3	68	0.002405	0.00125	5.18	cuk3	cuk1	Smoothelin GN=SMTN PE=1 SV=7
O43166	SIPA1L1	12	3	68.6	5.21E-05	9.96E-05	5.61	cuk1	cuk3	Signal-induced proliferation-associated 1-like protein 1 GN=SIPA1L1 PE=1 SV=4
F5H2F4	MTHFD1	10	2	69.5	0.000738	0.000554	1.94	cuk3	cuk1	C-1-tetrahydrofolate synthase_ cytoplasmic GN=MTHFD1 PE=1 SV=1
P39023	RPL3	9	5	69.6	0.000227	0.000256	2.7	cuk3	cuk1	60S ribosomal protein L3 GN=RPL3 PE=1 SV=2
P46782	RPS5	8	6	69.7	0.000399	0.000374	1.68	cuk3	cuk1	40S ribosomal protein S5 GN=RPS5 PE=1 SV=4
P84103	SRSF3	9	5	70.5	1.46E-05	5.22E-05	2.04	cuk3	cuk1	Serine/arginine-rich splicing factor 3 GN=SRSF3 PE=1 SV=1
Q8WWZ7	ABCA5	10	2	70.6	0.000198	0.000233	1.48	cuk3	cuk1	ATP-binding cassette sub-family A member 5 GN=ABCA5 PE=2 SV=2
Q96SE7	ZNF347	9	3	71.1	0.034485	0.009915	1.5	cuk3	cuk1	Zinc finger protein 347 GN=ZNF347 PE=1 SV=2
O94885	SASH1	13	3	71.2	0.000484	0.000425	2.51	cuk1	cuk3	SAM and SH3 domain-containing protein 1 GN=SASH1 PE=1 SV=3
H0YKD8	RPL28	10	7	71.2	0.002896	0.001434	1.25	cuk1	cuk3	60S ribosomal protein L28 GN=RPL28 PE=1 SV=1
O14513	NCKAP5	12	3	71.4	0.048129	0.013172	1.35	cuk3	cuk1	Nck-associated protein 5 GN=NCKAP5 PE=1 SV=2
Q12840	KIF5A	11	4	71.4	0.002849	0.001423	3.31	cuk1	cuk3	Kinesin heavy chain isoform 5A GN=KIF5A PE=1 SV=2
Q66GS9	CEP135	14	5	71.4	0.000152	0.000193	2.56	cuk1	cuk3	Centrosomal protein of 135 kDa GN=CEP135 PE=1 SV=2
O15075	DCLK1	11	2	73.9	0.03315	0.009585	1.45	cuk1	cuk3	Serine/threonine-protein kinase DCLK1 GN=DCLK1 PE=1 SV=2
P05023	ATP1A1	10	2	74.3	0.003066	0.001487	1.46	cuk1	cuk3	Sodium/potassium-transporting ATPase subunit alpha-1 GN=ATP1A1 PE=1 SV=1
A6NC98	CCDC88B	13	4	74.8	0.013378	0.004504	1.73	cuk1	cuk3	Coiled-coil domain-containing protein 88B GN=CCDC88B PE=1 SV=1
D3DQV9	EIF4G2	14	5	75.1	0.003016	0.001484	1.2	cuk1	cuk3	Eukaryotic translation initiation factor 4 gamma 2 (Fragment) GN=EIF4G2 PE=1 SV=1
A0A0G2JPF8	HNRNPCL4	9	2	75.3	0.000202	0.000236	1.95	cuk1	cuk3	Heterogeneous nuclear ribonucleoprotein C-like 4 PE=4 SV=1
P23396	RPS3	11	4	75.3	0.000241	0.000268	5.99	cuk3	cuk1	40S ribosomal protein S3 GN=RPS3 PE=1 SV=2
Q03468	ERCC6	13	4	75.3	0.00289	0.001434	2.66	cuk1	cuk3	DNA excision repair protein ERCC-6 GN=ERCC6 PE=1 SV=1
Q96JM4	LRRIQ1	16	6	76.6	0.036835	0.010512	2.11	cuk3	cuk1	Leucine-rich repeat and IQ domain-containing protein 1 GN=LRRIQ1 PE=2 SV=3
P62241	RPS8	7	6	76.9	0.000448	0.000401	1.76	cuk1	cuk3	40S ribosomal protein S8 GN=RPS8 PE=1 SV=2
O00299	CLIC1	11	6	77.6	0.000751	0.000556	1.24	cuk1	cuk3	Chloride intracellular channel protein 1 GN=CLIC1 PE=1 SV=4
Q9Y4F4	TOGARAM1	15	10	77.6	0.000836	0.000605	2.36	cuk1	cuk3	TOG array regulator of axonemal microtubules protein 1 GN=TOGARAM1 PE=1 SV=4
P12036	NEFH	10	2	78.5	0.005577	0.00233	3.51	cuk1	cuk3	Neurofilament heavy polypeptide GN=NEFH PE=1 SV=4
P22234	PAICS	12	4	79.9	0.024077	0.007363	1.4	cuk1	cuk3	Multifunctional protein ADE2 GN=PAICS PE=1 SV=3
B7ZAR1	CCT5	12	6	80.1	0.000604	0.000495	2.27	cuk3	cuk1	T-complex protein 1 subunit epsilon GN=CCT5 PE=1 SV=1
P50914	RPL14	10	5	81.6	3.94E-06	3.36E-05	3.93	cuk3	cuk1	60S ribosomal protein L14 GN=RPL14 PE=1 SV=4
A0A0G2JNB1	KANSL1	13	4	81.7	0.005677	0.002355	1.76	cuk1	cuk3	KAT8 regulatory NSL complex subunit 1 GN=KANSL1 PE=1 SV=1
Q8WVM7	STAG1	13	6	81.9	0.000138	0.000182	2.7	cuk1	cuk3	Cohesin subunit SA-1 GN=STAG1 PE=1 SV=3
Q15643	TRIP11	12	4	82.7	0.000119	0.000168	3.11	cuk1	cuk3	Thyroid receptor-interacting protein 11 GN=TRIP11 PE=1 SV=3
Q9Y6M1	IGF2BP2	12	4	84.8	1.21E-05	5.10E-05	1.61	cuk1	cuk3	Insulin-like growth factor 2 mRNA-binding protein 2 GN=IGF2BP2 PE=1 SV=2
P09211	GSTP1	8	3	85.1	8.82E-05	0.000139	2.87	cuk3	cuk1	Glutathione S-transferase P GN=GSTP1 PE=1 SV=2
Q9H0X9	OSBPL5	13	4	85.4	0.007217	0.002795	1.42	cuk1	cuk3	Oxysterol-binding protein-related protein 5 GN=OSBPL5 PE=1 SV=1
P50991	CCT4	14	7	85.5	0.040088	0.011324	1.32	cuk3	cuk1	T-complex protein 1 subunit delta GN=CCT4 PE=1 SV=4
O75122	CLASP2	13	5	85.6	0.034245	0.009873	1.23	cuk1	cuk3	CLIP-associating protein 2 GN=CLASP2 PE=1 SV=2
Q9UG01	IFT172	16	6	85.7	5.22E-05	9.96E-05	6.31	cuk1	cuk3	Intraflagellar transport protein 172 homolog GN=IFT172 PE=1 SV=2
Q9BY12	SCAPER	16	9	86.2	8.73E-06	4.31E-05	2.92	cuk1	cuk3	S phase cyclin A-associated protein in the endoplasmic reticulum GN=SCAPER PE=1 SV=2
P61247	RPS3A	11	5	86.8	3.98E-05	8.55E-05	2.93	cuk3	cuk1	40S ribosomal protein S3a GN=RPS3A PE=1 SV=2
Q14679	TTLL4	16	7	87.1	9.54E-05	0.000143	7.13	cuk1	cuk3	Tubulin polyglutamylase TTLL4 GN=TTLL4 PE=1 SV=2
Q15276	RABEP1	15	4	87.3	0.000593	0.000488	2.98	cuk3	cuk1	Rab GTPase-binding effector protein 1 GN=RABEP1 PE=1 SV=2
O43491	EPB41L2	16	3	87.5	4.51E-06	3.60E-05	14.1	cuk1	cuk3	Band 4.1-like protein 2 GN=EPB41L2 PE=1 SV=1
O43390	HNRNPR	13	3	87.5	0.003053	0.001485	1.38	cuk3	cuk1	Heterogeneous nuclear ribonucleoprotein R GN=HNRNPR PE=1 SV=1
P62913	RPL11	8	3	87.6	0.004223	0.001899	1.28	cuk3	cuk1	60S ribosomal protein L11 GN=RPL11 PE=1 SV=2
Q6WCQ1	MPRIP	15	5	88	8.21E-05	0.000136	1.71	cuk1	cuk3	Myosin phosphatase Rho-interacting protein GN=MPRIP PE=1 SV=3
Q8NDI1	EHBP1	15	7	88.7	0.000147	0.000189	2.02	cuk1	cuk3	EH domain-binding protein 1 GN=EHBP1 PE=1 SV=3
E7EPK1	SEPTIN7	14	5	88.8	0.012746	0.004342	2.69	cuk1	cuk3	Septin-7 GN=SEPT7 PE=1 SV=2
Q8NI35	PATJ	15	3	89.3	4.39E-05	9.11E-05	2.87	cuk1	cuk3	InaD-like protein GN=PATJ PE=1 SV=3
O00443	PIK3C2A	14	4	90.7	0.001509	0.000896	4.48	cuk3	cuk1	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha GN=PIK3C2A PE=1 SV=2
Q8N960	CEP120	14	2	91.1	0.003056	0.001485	3.98	cuk1	cuk3	Centrosomal protein of 120 kDa GN=CEP120 PE=1 SV=2
Q9UKX3	MYH13	15	6	91.3	0.002399	0.00125	1.78	cuk1	cuk3	Myosin-13 GN=MYH13 PE=2 SV=2
P08729	KRT7	9	4	91.4	0.011117	0.003944	1.16	cuk1	cuk3	Keratin_ type II cytoskeletal 7 GN=KRT7 PE=1 SV=5
P48735	IDH2	14	6	91.4	0.000341	0.000338	1.96	cuk1	cuk3	Isocitrate dehydrogenase [NADP]_ mitochondrial GN=IDH2 PE=1 SV=2
Q92598	HSPH1	14	6	91.4	0.002406	0.00125	1.64	cuk1	cuk3	Heat shock protein 105 kDa GN=HSPH1 PE=1 SV=1
P34897	SHMT2	15	10	93.2	0.000119	0.000168	2.03	cuk1	cuk3	Serine hydroxymethyltransferase_ mitochondrial GN=SHMT2 PE=1 SV=3
F8W1R7	MYL6	12	7	93.4	0.000382	0.000363	1.96	cuk3	cuk1	Myosin light polypeptide 6 GN=MYL6 PE=1 SV=1
Q5JU85	IQSEC2	16	9	94.9	0.000322	0.000325	1.38	cuk1	cuk3	IQ motif and SEC7 domain-containing protein 2 GN=IQSEC2 PE=1 SV=2
P62424	RPL7A	15	8	95	0.000267	0.000288	4.66	cuk3	cuk1	60S ribosomal protein L7a GN=RPL7A PE=1 SV=2
Q7L576	CYFIP1	15	3	95.4	0.003032	0.001485	1.79	cuk1	cuk3	Cytoplasmic FMR1-interacting protein 1 GN=CYFIP1 PE=1 SV=1
P38919	EIF4A3	13	6	97.1	0.000686	0.000536	2.63	cuk3	cuk1	Eukaryotic initiation factor 4A-III GN=EIF4A3 PE=1 SV=4
E7EVA0	MAP4	17	6	97.2	0.0041	0.001857	1.31	cuk1	cuk3	Microtubule-associated protein GN=MAP4 PE=1 SV=1
P35232	PHB	15	9	97.2	0.002467	0.001273	1.32	cuk3	cuk1	Prohibitin GN=PHB PE=1 SV=1
P16949	STMN1	12	5	97.6	0.00064	0.000514	1.45	cuk1	cuk3	Stathmin GN=STMN1 PE=1 SV=3
Q14103	HNRNPD	13	4	98.7	0.02082	0.006477	1.18	cuk3	cuk1	Heterogeneous nuclear ribonucleoprotein D0 GN=HNRNPD PE=1 SV=1
P50990	CCT8	14	4	99.9	0.018614	0.005911	1.84	cuk3	cuk1	T-complex protein 1 subunit theta GN=CCT8 PE=1 SV=4
P78371	CCT2	15	7	100	0.010311	0.003734	2.16	cuk1	cuk3	T-complex protein 1 subunit beta GN=CCT2 PE=1 SV=4
Q9HCM1	RESF1	19	6	101	0.000248	0.000273	5.81	cuk1	cuk3	Uncharacterized protein KIAA1551 GN=KIAA1551 PE=1 SV=3
O00425	IGF2BP3	14	6	101	0.000593	0.000488	2.44	cuk3	cuk1	Insulin-like growth factor 2 mRNA-binding protein 3 GN=IGF2BP3 PE=1 SV=2
P06748	NPM1	9	4	102	4.29E-05	8.98E-05	3.16	cuk3	cuk1	Nucleophosmin GN=NPM1 PE=1 SV=2
O14529	CUX2	17	5	102	0.000494	0.000428	2.64	cuk1	cuk3	Homeobox protein cut-like 2 GN=CUX2 PE=1 SV=4
Q06830	PRDX1	13	6	102	0.000567	0.000478	2.01	cuk1	cuk3	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
P49368	CCT3	14	8	102	0.007992	0.003018	1.4	cuk3	cuk1	T-complex protein 1 subunit gamma GN=CCT3 PE=1 SV=4
Q86U86	PBRM1	18	5	103	0.019128	0.006055	1.15	cuk1	cuk3	Protein polybromo-1 GN=PBRM1 PE=1 SV=1
P11940	PABPC1	16	5	104	0.000409	0.000381	1.62	cuk3	cuk1	Polyadenylate-binding protein 1 GN=PABPC1 PE=1 SV=2
Q99623	PHB2	16	7	104	0.000237	0.000266	3.44	cuk1	cuk3	Prohibitin-2 GN=PHB2 PE=1 SV=2
Q14974	KPNB1	14	7	106	2.99E-05	7.53E-05	13.4	cuk1	cuk3	Importin subunit beta-1 GN=KPNB1 PE=1 SV=2
O75128	COBL	19	8	106	0.010242	0.003717	1.56	cuk3	cuk1	Protein cordon-bleu GN=COBL PE=1 SV=2
Q15084	PDIA6	13	8	106	0.006275	0.002549	1.24	cuk3	cuk1	Protein disulfide-isomerase A6 GN=PDIA6 PE=1 SV=1
Q9C0D4	ZNF518B	17	6	107	0.003057	0.001485	1.37	cuk1	cuk3	Zinc finger protein 518B GN=ZNF518B PE=1 SV=2
O14974	PPP1R12A	18	7	107	0.002396	0.00125	1.75	cuk1	cuk3	Protein phosphatase 1 regulatory subunit 12A GN=PPP1R12A PE=1 SV=1

P57721	PCBP3	12	3	108	0.01961	0.00617	2.08	cuk1	cuk3	Poly(rC)-binding protein 3 GN=PCBP3 PE=2 SV=2
Q15233	NONO	17	7	108	0.022259	0.006849	1.24	cuk1	cuk3	Non-POU domain-containing octamer-binding protein GN=NONO PE=1 SV=4
P07737	PFN1	11	9	108	1.14E-05	5.10E-05	9.43	cuk1	cuk3	Profilin-1 GN=PFN1 PE=1 SV=2
Q3MJ40	CCDC144B	19	2	111	8.79E-05	0.000139	2.84	cuk1	cuk3	Coiled-coil domain-containing protein 144B GN=CCDC144B PE=2 SV=1
P02765	AHSG	13	9	112	5.45E-06	3.81E-05	3.3	cuk1	cuk3	Alpha-2-HS-glycoprotein GN=AHSG PE=1 SV=1
P07196	NEFL	15	3	113	0.019655	0.006177	1.86	cuk3	cuk1	Neurofilament light polypeptide GN=NEFL PE=1 SV=3
Q86YA3	ZGRF1	20	5	113	0.009068	0.003351	2.03	cuk1	cuk3	Protein ZGRF1 GN=ZGRF1 PE=1 SV=3
Q9UHF7	TRPS1	21	7	113	0.000899	0.000623	4.04	cuk1	cuk3	Zinc finger transcription factor Trps1 GN=TRPS1 PE=1 SV=2
Q6ZN16	MAP3K15	16	5	114	2.72E-05	7.03E-05	2.56	cuk1	cuk3	Mitogen-activated protein kinase kinase kinase 15 GN=MAP3K15 PE=1 SV=2
P32119	PRDX2	10	5	114	9.30E-05	0.000141	2.4	cuk1	cuk3	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
Q99832	CCT7	20	12	114	3.74E-05	8.32E-05	2.21	cuk3	cuk1	T-complex protein 1 subunit eta GN=CCT7 PE=1 SV=2
Q8N7X0	ADGB	18	4	115	0.01928	0.006091	1.59	cuk1	cuk3	Androglobin GN=ADGB PE=2 SV=3
P27824	CANX	14	7	115	0.000695	0.000539	2.1	cuk3	cuk1	Calnexin GN=CANX PE=1 SV=2
Q5JSZ5	PRRC2B	18	6	116	6.29E-05	0.000112	2.08	cuk1	cuk3	Protein PRRC2B GN=PRRC2B PE=1 SV=2
A6QL64	ANKRD36	21	8	117	2.14E-05	6.47E-05	5.06	cuk1	cuk3	Ankyrin repeat domain-containing protein 36A GN=ANKRD36 PE=2 SV=3
Q8N1I0	DOCK4	20	8	118	0.00448	0.001985	1.62	cuk1	cuk3	Dedicator of cytokinesis protein 4 GN=DOCK4 PE=1 SV=3
O60292	SIPA1L3	21	12	120	8.54E-05	0.000138	2.62	cuk1	cuk3	Signal-induced proliferation-associated 1-like protein 3 GN=SIPA1L3 PE=1 SV=3
P48741	HSPA7	14	3	121	0.000105	0.000153	3.81	cuk1	cuk3	Putative heat shock 70 kDa protein 7 GN=HSPA7 PE=5 SV=2
Q5VZ46	KIAA1614	19	8	121	0.011643	0.004053	1.17	cuk1	cuk3	Uncharacterized protein KIAA1614 GN=KIAA1614 PE=2 SV=3
P04264	KRT1	17	6	122	9.19E-07	1.57E-05	2.29	cuk1	cuk3	Keratin_ type II cytoskeletal 1 GN=KRT1 PE=1 SV=6
Q7RTP6	MICAL3	23	6	123	0.001115	0.00073	1.78	cuk1	cuk3	[F-actin]-monooxygenase MICAL3 GN=MICAL3 PE=1 SV=2
A0A1B0GWD1	DCX	16	7	123	0.001367	0.00084	2.62	cuk3	cuk1	Neuronal migration protein doublecortin GN=DCX PE=1 SV=1
Q9UDT6	CLIP2	23	9	126	0.021958	0.006776	1.63	cuk3	cuk1	CAP-Gly domain-containing linker protein 2 GN=CLIP2 PE=1 SV=1
Q16821	PPP1R3A	21	12	128	8.58E-06	4.31E-05	5.73	cuk1	cuk3	Protein phosphatase 1 regulatory subunit 3A GN=PPP1R3A PE=1 SV=3
P07910	HNRNPC	15	5	132	0.00093	0.000635	2.53	cuk3	cuk1	Heterogeneous nuclear ribonucleoproteins C1/C2 GN=HNRNPC PE=1 SV=4
O75145	PPFIA3	22	11	133	0.000191	0.000227	2.58	cuk1	cuk3	Liprin-alpha-3 GN=PPFIA3 PE=1 SV=3
C9J7T7	NCOR2	24	7	134	0.000146	0.000189	2.03	cuk1	cuk3	Nuclear receptor corepressor 2 GN=NCOR2 PE=1 SV=3
Q9UPN4	CEP131	21	7	134	0.00101	0.000676	1.91	cuk1	cuk3	Centrosomal protein of 131 kDa GN=CEP131 PE=1 SV=3
P08133	ANXA6	18	7	134	0.023401	0.007171	1.47	cuk1	cuk3	Annexin A6 GN=ANXA6 PE=1 SV=3
P36578	RPL4	18	8	134	3.42E-05	7.95E-05	3.13	cuk3	cuk1	60S ribosomal protein L4 GN=RPL4 PE=1 SV=5
P62701	RPS4X	16	6	137	0.000434	0.000391	1.62	cuk3	cuk1	40S ribosomal protein S4_ X isoform GN=RPS4X PE=1 SV=2
Q8IWJ2	GCC2	27	11	137	0.034419	0.009905	1.27	cuk1	cuk3	GRIP and coiled-coil domain-containing protein 2 GN=GCC2 PE=1 SV=4
P52209	PGD	18	13	139	0.004297	0.00192	1.29	cuk3	cuk1	6-phosphogluconate dehydrogenase_ decarboxylating GN=PGD PE=1 SV=3
A2RUR9	CCDC144A	22	2	141	8.59E-05	0.000138	2.91	cuk1	cuk3	Coiled-coil domain-containing protein 144A GN=CCDC144A PE=2 SV=1
Q8NB25	FAM184A	23	7	141	0.008604	0.003202	1.26	cuk1	cuk3	Protein FAM184A GN=FAM184A PE=2 SV=3
Q9BZ29	DOCK9	22	10	142	0.0115	0.004023	1.17	cuk1	cuk3	Dedicator of cytokinesis protein 9 GN=DOCK9 PE=1 SV=2
Q12931	TRAP1	18	8	143	4.30E-05	8.98E-05	2.11	cuk1	cuk3	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
Q14240	EIF4A2	19	8	144	0.033125	0.009585	1.17	cuk1	cuk3	Eukaryotic initiation factor 4A-II GN=EIF4A2 PE=1 SV=2
P12277	CKB	18	12	145	0.000373	0.000356	1.47	cuk3	cuk1	Creatine kinase B-type GN=CKB PE=1 SV=1
Q16695	H3-4	18	4	147	0.02452	0.007462	1.51	cuk3	cuk1	Histone H3.1t GN=HIST3H3 PE=1 SV=3
Q9NQT8	KIF13B	22	13	147	1.14E-05	5.10E-05	6	cuk1	cuk3	Kinesin-like protein KIF13B GN=KIF13B PE=1 SV=2
P00558	PGK1	20	9	150	0.005587	0.002331	1.48	cuk1	cuk3	Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3
P60842	EIF4A1	19	6	152	0.000368	0.000353	2.46	cuk1	cuk3	Eukaryotic initiation factor 4A-I GN=EIF4A1 PE=1 SV=1
Q86UP2	KTN1	27	11	153	0.00436	0.00194	1.34	cuk1	cuk3	Kinectin GN=KTN1 PE=1 SV=1
P16401	H1-5	13	5	154	0.04582	0.012669	1.17	cuk3	cuk1	Histone H1.5 GN=HIST1H1B PE=1 SV=3
Q6FI13	H2AC18; H2AC19	17	6	154	0.002665	0.001351	1.6	cuk3	cuk1	Histone H2A type 2-A GN=HIST2H2AA3 PE=1 SV=3
P35579	MYH9	25	10	154	0.000699	0.000539	2.23	cuk1	cuk3	Myosin-9 GN=MYH9 PE=1 SV=4
P04843	RPN1	23	12	155	8.01E-06	4.31E-05	5.16	cuk1	cuk3	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 GN=RPN1 PE=1 SV=1
P55072	VCP	22	7	157	0.046573	0.012791	1.14	cuk3	cuk1	Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4
Q5THK1	PRR14L	26	9	158	0.000232	0.00026	1.91	cuk1	cuk3	Protein PRR14L GN=PRR14L PE=1 SV=1
Q05682	CALD1	25	7	162	0.011776	0.004076	1.47	cuk1	cuk3	Caldesmon GN=CALD1 PE=1 SV=3
E9PK25	CFL1	15	4	163	0.001982	0.001087	1.24	cuk1	cuk3	Cofilin-1 GN=CFL1 PE=1 SV=1
P50454	SERPINH1	20	7	164	0.00178	0.001014	1.21	cuk3	cuk1	Serpin H1 GN=SERPINH1 PE=1 SV=2
Q9HC77	CENPJ	26	9	166	0.017647	0.005666	1.3	cuk3	cuk1	Centromere protein J GN=CENPJ PE=1 SV=2
Q8TBY8	PMFBP1	26	12	166	0.000649	0.000519	1.87	cuk1	cuk3	Polyamine-modulated factor 1-binding protein 1 GN=PMFBP1 PE=2 SV=2
P34931	HSPA1L	21	4	168	0.011817	0.004081	1.58	cuk1	cuk3	Heat shock 70 kDa protein 1-like GN=HSPA1L PE=1 SV=2
A6NHL2	TUBAL3	18	5	169	0.022761	0.006996	1.52	cuk1	cuk3	Tubulin alpha chain-like 3 GN=TUBAL3 PE=1 SV=2
Q15365	PCBP1	22	13	171	8.95E-05	0.000139	2.19	cuk1	cuk3	Poly(rC)-binding protein 1 GN=PCBP1 PE=1 SV=2
Q15811	ITSN1	28	6	174	3.09E-05	7.62E-05	9.38	cuk1	cuk3	Intersectin-1 GN=ITSN1 PE=1 SV=3
P15880	RPS2	22	12	175	0.028976	0.008547	1.55	cuk1	cuk3	40S ribosomal protein S2 GN=RPS2 PE=1 SV=2
A0A0G2JIW1	HSPA1B	21	5	178	0.00034	0.000338	3.22	cuk1	cuk3	Heat shock 70 kDa protein 1B GN=HSPA1B PE=1 SV=1
Q9P219	CCDC88C	28	5	179	0.000211	0.000243	3.93	cuk1	cuk3	Protein Daple GN=CCDC88C PE=1 SV=3
P31943	HNRNPH1	20	5	183	0.022167	0.006827	1.27	cuk1	cuk3	Heterogeneous nuclear ribonucleoprotein H GN=HNRNPH1 PE=1 SV=4
P17661	DES	20	5	185	0.003031	0.001485	1.3	cuk1	cuk3	Desmin GN=DES PE=1 SV=3
Q9NZI8	IGF2BP1	22	15	185	0.001456	0.000876	2.17	cuk3	cuk1	Insulin-like growth factor 2 mRNA-binding protein 1 GN=IGF2BP1 PE=1 SV=2
P07237	P4HB	23	9	201	0.004832	0.002096	1.41	cuk1	cuk3	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
Q05639	EEF1A2	17	2	202	0.004611	0.00202	1.64	cuk3	cuk1	Elongation factor 1-alpha 2 GN=EEF1A2 PE=1 SV=1
O43175	PHGDH	22	3	206	0.001719	0.00099	2.05	cuk3	cuk1	D-3-phosphoglycerate dehydrogenase GN=PHGDH PE=1 SV=4
Q16778	H2BC21	21	4	207	0.036248	0.010354	1.36	cuk3	cuk1	Histone H2B type 2-E GN=HIST2H2BE PE=1 SV=3
Q15366	PCBP2	21	6	207	3.88E-06	3.36E-05	2.91	cuk3	cuk1	Poly(rC)-binding protein 2 GN=PCBP2 PE=1 SV=1
P55196	AFDN	32	9	208	0.000663	0.000526	3.39	cuk1	cuk3	Afadin GN=AFDN PE=1 SV=3
Q14194	CRMP1	29	11	215	0.000138	0.000182	3.62	cuk1	cuk3	Dihydropyrimidinase-related protein 1 GN=CRMP1 PE=1 SV=1
P22626	HNRNPA2B1	24	11	215	0.017005	0.005496	1.19	cuk1	cuk3	Heterogeneous nuclear ribonucleoproteins A2/B1 GN=HNRNPA2B1 PE=1 SV=2
Q14980	NUMA1	38	14	221	2.19E-06	2.37E-05	2.8	cuk1	cuk3	Nuclear mitotic apparatus protein 1 GN=NUMA1 PE=1 SV=2
P41219	PRPH	24	6	226	0.000394	0.000373	2.26	cuk1	cuk3	Peripherin GN=PRPH PE=1 SV=2
P13667	PDIA4	29	15	229	0.00391	0.001781	1.41	cuk3	cuk1	Protein disulfide-isomerase A4 GN=PDIA4 PE=1 SV=2
P61978	HNRNPK	30	4	248	3.84E-05	8.36E-05	2.7	cuk1	cuk3	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
A0A087WWY3	FLNA	41	20	250	2.40E-05	6.70E-05	1.27	cuk1	cuk3	Filamin-A GN=FLNA PE=1 SV=1
A0A0R4J2E8	MATR3	32	3	263	0.001501	0.000895	1.67	cuk3	cuk1	Matrin-3 GN=MATR3 PE=1 SV=1
P35580	MYH10	42	19	266	2.71E-05	7.03E-05	2.34	cuk1	cuk3	Myosin-10 GN=MYH10 PE=1 SV=3

Q00610	CLTC	44	18	290	0.000347	0.00034	2.12	cuk1	cuk3	Clathrin heavy chain 1 GN=CLTC PE=1 SV=5
Q9Y4L1	HYOU1	39	18	290	0.027309	0.008181	1.57	cuk1	cuk3	Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1
P25705	ATP5F1A	28	15	293	0.01076	0.00386	1.37	cuk1	cuk3	ATP synthase subunit alpha_ mitochondrial GN=ATP5F1A PE=1 SV=1
Q07065	CKAP4	36	16	309	0.036903	0.010521	1.07	cuk1	cuk3	Cytoskeleton-associated protein 4 GN=CKAP4 PE=1 SV=2
P38646	HSPA9	40	21	309	0.000642	0.000515	1.58	cuk1	cuk3	Stress-70 protein_ mitochondrial GN=HSPA9 PE=1 SV=2
Q9BUF5	TUBB6	26	3	314	0.001499	0.000895	2.13	cuk1	cuk3	Tubulin beta-6 chain GN=TUBB6 PE=1 SV=1
P11142	HSPA8	31	18	319	0.005102	0.00217	1.57	cuk3	cuk1	Heat shock cognate 71 kDa protein GN=HSPA8 PE=1 SV=1
P02768	ALB	35	24	319	0.002915	0.001439	1.88	cuk1	cuk3	Serum albumin GN=ALB PE=1 SV=2
P07900	HSP90AA1	35	8	324	0.004867	0.002104	1.37	cuk1	cuk3	Heat shock protein HSP 90-alpha GN=HSP90AA1 PE=1 SV=5
P04406	GAPDH	33	5	334	0.048566	0.013267	1.21	cuk3	cuk1	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P68104	EEF1A1	32	4	335	0.000273	0.000291	2.14	cuk3	cuk1	Elongation factor 1-alpha 1 GN=EEF1A1 PE=1 SV=1
A0A1C7CYX9	DPYSL2	34	3	351	0.000772	0.000568	1.64	cuk1	cuk3	Dihydropyrimidinase-related protein 2 GN=DPYSL2 PE=1 SV=1
Q5TZA2	CROCC	59	18	354	9.48E-05	0.000143	3.91	cuk1	cuk3	Rootletin GN=CROCC PE=1 SV=1
P08238	HSP90AB1	38	12	379	3.10E-05	7.62E-05	5.49	cuk1	cuk3	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
H0Y6I0	GOLGA4	58	26	382	0.001648	0.00096	1.26	cuk1	cuk3	Golgin subfamily A member 4 (Fragment) GN=GOLGA4 PE=1 SV=1
P13639	EEF2	51	27	415	0.000576	0.00048	1.37	cuk1	cuk3	Elongation factor 2 GN=EEF2 PE=1 SV=4
P11021	HSPA5	43	25	466	0.000628	0.000509	1.65	cuk1	cuk3	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P52272	HNRNPM	50	28	488	0.000241	0.000268	1.51	cuk3	cuk1	Heterogeneous nuclear ribonucleoprotein M GN=HNRNPM PE=1 SV=3
P14625	HSP90B1	52	26	564	0.000455	0.000404	1.23	cuk3	cuk1	Endoplasmin GN=HSP90B1 PE=1 SV=1
P04350	TUBB4A	47	6	599	0.028059	0.008332	1.35	cuk3	cuk1	Tubulin beta-4A chain GN=TUBB4A PE=1 SV=2
Q13509	TUBB3	54	10	613	0.000341	0.000338	2.01	cuk3	cuk1	Tubulin beta-3 chain GN=TUBB3 PE=1 SV=2
Q9BQE3	TUBA1C	46	6	617	0.000708	0.000545	2.85	cuk3	cuk1	Tubulin alpha-1C chain GN=TUBA1C PE=1 SV=1
P02787	TF	62	25	655	1.46E-05	5.22E-05	2.5	cuk1	cuk3	Serotransferrin GN=TF PE=1 SV=3
P68032	ACTC1	54	11	688	1.35E-06	1.97E-05	3.89	cuk3	cuk1	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
Q13885	TUBB2A	50	2	735	0.001004	0.000674	1.75	cuk3	cuk1	Tubulin beta-2A chain GN=TUBB2A PE=1 SV=1
P07437	TUBB	58	7	847	0.000161	0.000201	2.03	cuk3	cuk1	Tubulin beta chain GN=TUBB PE=1 SV=2
P60709	ACTB	66	15	1.01E+03	8.69E-06	4.31E-05	2.44	cuk3	cuk1	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1
Anti-Aβ$_{17-23}$ Antibody Treatment										
Q96L93	KIF16B	9	5	40	7.42E-05	0.000152	2.31	cuk2	cuk3	Kinesin-like protein KIF16B GN=KIF16B PE=1 SV=2
Q15700	DLG2	7	4	40.1	0.006642	0.002739	10.9	cuk2	cuk3	Disks large homolog 2 GN=DLG2 PE=1 SV=3
P40926	MDH2	6	2	40.3	8.26E-06	4.58E-05	1.85	cuk3	cuk2	Malate dehydrogenase_ mitochondrial GN=MDH2 PE=1 SV=3
O14531	DPYSL4	7	3	40.3	0.048123	0.012932	1.13	cuk2	cuk3	Dihydropyrimidinase-related protein 4 GN=DPYSL4 PE=1 SV=2
Q8TF32	ZNF431	6	2	40.9	0.021777	0.006811	1.41	cuk2	cuk3	Zinc finger protein 431 GN=ZNF431 PE=2 SV=2
O75362	ZNF217	8	2	41.1	0.014227	0.004882	1.54	cuk3	cuk2	Zinc finger protein 217 GN=ZNF217 PE=1 SV=1
Q86VH2	KIF27	7	5	41.3	0.003813	0.001792	1.39	cuk2	cuk3	Kinesin-like protein KIF27 GN=KIF27 PE=2 SV=1
Q8NDQ6	ZNF540	7	2	41.5	0.003115	0.00157	1.7	cuk2	cuk3	Zinc finger protein 540 GN=ZNF540 PE=1 SV=1
E7EX29	YWHAZ	5	3	41.6	0.00091	0.000641	1.21	cuk3	cuk2	14-3-3 protein zeta/delta (Fragment) GN=YWHAZ PE=1 SV=1
Q8N163	CCAR2	8	4	41.6	0.000296	0.00032	2.76	cuk3	cuk2	Cell cycle and apoptosis regulator protein 2 GN=CCAR2 PE=1 SV=2
Q05BV3	EML5	8	2	41.7	0.00137	0.000867	1.58	cuk3	cuk2	Echinoderm microtubule-associated protein-like 5 GN=EML5 PE=2 SV=3
A0A087WY36	AKAP13	7	4	41.7	0.023962	0.00738	1.22	cuk3	cuk2	A-kinase anchor protein 13 (Fragment) GN=AKAP13 PE=1 SV=1
Q38SD2	LRRK1	8	2	42	1.64E-05	6.7E-05	3.39	cuk3	cuk2	Leucine-rich repeat serine/threonine-protein kinase 1 GN=LRRK1 PE=1 SV=3
E9PCN5	CNOT10	6	3	42	0.004677	0.002087	1.35	cuk3	cuk2	CCR4-NOT transcription complex subunit 10 GN=CNOT10 PE=1 SV=1
P29597	TYK2	8	2	42.1	0.02816	0.008425	1.49	cuk2	cuk3	Non-receptor tyrosine-protein kinase TYK2 GN=TYK2 PE=1 SV=3
Q8IWY7	TTBK2	6	3	42.1	0.000655	0.000508	2.12	cuk2	cuk3	Tau-tubulin kinase GN=TTBK2 PE=1 SV=1
Q9Y5Y9	SCN10A	7	3	42.5	0.003758	0.001772	1.95	cuk2	cuk3	Sodium channel protein type 10 subunit alpha GN=SCN10A PE=1 SV=2
A0A087WTP3	KHSRP	7	2	42.6	0.010528	0.003877	1.27	cuk2	cuk3	Far upstream element-binding protein 2 GN=KHSRP PE=1 SV=1
F8VUX9	WDR90	6	4	42.6	2.5E-05	8.39E-05	2.95	cuk3	cuk2	WD repeat-containing protein 90 GN=WDR90 PE=1 SV=1
O60237	PPP1R12B	8	4	42.6	0.000319	0.000332	1.78	cuk2	cuk3	Protein phosphatase 1 regulatory subunit 12B GN=PPP1R12B PE=1 SV=2
P23381	WARS1	6	2	42.7	0.000318	0.000332	1.44	cuk3	cuk2	Tryptophan--tRNA ligase_ cytoplasmic GN=WARS PE=1 SV=2
A8MZ36	EVPLL	6	3	42.7	0.004796	0.00212	2.35	cuk3	cuk2	Envoplakin-like protein GN=EVPLL PE=2 SV=1
Q8NFY4	SEMA6D	9	4	42.7	0.002162	0.001212	1.45	cuk3	cuk2	Semaphorin-6D GN=SEMA6D PE=1 SV=1
P26373	RPL13	6	2	42.8	0.006674	0.002744	1.31	cuk3	cuk2	60S ribosomal protein L13 GN=RPL13 PE=1 SV=4
Q969P6	TOP1MT	8	4	42.8	0.004768	0.002116	1.15	cuk3	cuk2	DNA topoisomerase I_ mitochondrial GN=TOP1MT PE=1 SV=1
Q9NWH9	SLTM	8	2	43.1	0.008131	0.003185	1.24	cuk2	cuk3	SAFB-like transcription modulator GN=SLTM PE=1 SV=2
Q9Y536	PPIAL4A	7	3	43.3	0.000478	0.00043	1.76	cuk2	cuk3	Peptidyl-prolyl cis-trans isomerase A-like 4A GN=PPIAL4A PE=2 SV=1
Q6P4R8	NFRKB	8	3	43.3	0.046284	0.012526	1.23	cuk3	cuk2	Nuclear factor related to kappa-B-binding protein GN=NFRKB PE=1 SV=2
P42166	TMPO	7	3	43.4	0.000126	0.000199	1.92	cuk2	cuk3	Lamina-associated polypeptide 2_ isoform alpha GN=TMPO PE=1 SV=2
P33993	MCM7	6	4	43.5	0.000729	0.000547	1.48	cuk2	cuk3	DNA replication licensing factor MCM7 GN=MCM7 PE=1 SV=4
Q8IVF5	TIAM2	10	3	43.9	0.002187	0.001215	2.9	cuk2	cuk3	T-lymphoma invasion and metastasis-inducing protein 2 GN=TIAM2 PE=2 SV=4
P52948	NUP98	8	3	44	0.004929	0.002162	1.3	cuk2	cuk3	Nuclear pore complex protein Nup98-Nup96 GN=NUP98 PE=1 SV=4
Q8IYT4	KATNAL2	7	5	44	9.37E-05	0.000172	1.69	cuk3	cuk2	Katanin p60 ATPase-containing subunit A-like 2 GN=KATNAL2 PE=1 SV=3
C9JZR2	CTNND1	8	3	44.1	0.000572	0.000477	3.92	cuk3	cuk2	Catenin delta-1 GN=CTNND1 PE=1 SV=2
Q05209	PTPN12	9	5	44.2	0.016948	0.005627	1.65	cuk2	cuk3	Tyrosine-protein phosphatase non-receptor type 12 GN=PTPN12 PE=1 SV=3
Q9UN70	PCDHGC3	8	3	44.8	0.003194	0.001587	1.47	cuk3	cuk2	Protocadherin gamma-C3 GN=PCDHGC3 PE=1 SV=1
P12004	PCNA	6	4	44.8	0.039943	0.011214	1.18	cuk2	cuk3	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
A0A0D9SF53	DDX3X	5	3	44.9	0.021173	0.006659	1.35	cuk2	cuk3	ATP-dependent RNA helicase DDX3X GN=DDX3X PE=1 SV=1
Q08495	DMTN	6	3	44.9	0.031757	0.009295	1.23	cuk2	cuk3	Dematin GN=DMTN PE=1 SV=3
Q8N1G1	REXO1	6	3	45	0.000258	0.000293	1.78	cuk2	cuk3	RNA exonuclease 1 homolog GN=REXO1 PE=1 SV=3
P46940	IQGAP1	9	3	45	0.00127	0.000827	1.73	cuk3	cuk2	Ras GTPase-activating-like protein IQGAP1 GN=IQGAP1 PE=1 SV=1
Q9HCE3	ZNF532	8	3	45	0.016033	0.005397	1.45	cuk2	cuk3	Zinc finger protein 532 GN=ZNF532 PE=1 SV=2
P27348	YWHAQ	6	3	45	0.009973	0.003726	1.34	cuk2	cuk3	14-3-3 protein theta GN=YWHAQ PE=1 SV=1
P53804	TTC3	8	3	45	0.042754	0.011791	1.24	cuk2	cuk3	E3 ubiquitin-protein ligase TTC3 GN=TTC3 PE=1 SV=2
I6L899	GOLGA8R	7	2	45.3	0.027111	0.008172	1.49	cuk2	cuk3	Golgin subfamily A member 8R GN=GOLGA8R PE=3 SV=1
Q13247	SRSF6	5	4	45.3	0.002185	0.001215	1.45	cuk2	cuk3	Serine/arginine-rich splicing factor 6 GN=SRSF6 PE=1 SV=2
Q5SW79	CEP170	9	3	45.5	0.003369	0.001644	2.22	cuk2	cuk3	Centrosomal protein of 170 kDa GN=CEP170 PE=1 SV=1
H3BQN4	ALDOA	6	2	46	0.002746	0.001424	1.96	cuk2	cuk3	Fructose-bisphosphate aldolase GN=ALDOA PE=1 SV=1
P07195	LDHB	7	3	46	0.000862	0.000624	1.29	cuk3	cuk2	L-lactate dehydrogenase B chain GN=LDHB PE=1 SV=2
O43663	PRC1	8	2	46.3	5.89E-05	0.000137	1.96	cuk3	cuk2	Protein regulator of cytokinesis 1 GN=PRC1 PE=1 SV=2
Q8N3U4	STAG2	7	2	46.5	0.022321	0.006966	2.54	cuk3	cuk2	Cohesin subunit SA-2 GN=STAG2 PE=1 SV=3
Q9H1A4	ANAPC1	8	2	46.6	1.13E-05	5.39E-05	2.78	cuk2	cuk3	Anaphase-promoting complex subunit 1 GN=ANAPC1 PE=1 SV=1

Q07666	KHDRBS1	5	3	46.8	0.047877	0.012879	1.27	cuk2	cuk3	KH domain-containing_ RNA-binding_ signal transduction-associated protein 1 GN=KHDRBS1 PE=1 SV=1
P62979	RPS27A	6	3	46.9	0.001275	0.000827	1.82	cuk2	cuk3	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
Q17RC7	EXOC3L4	8	5	47.1	0.028474	0.008501	1.17	cuk2	cuk3	Exocyst complex component 3-like protein 4 GN=EXOC3L4 PE=1 SV=2
Q9NSY1	BMP2K	8	4	47.4	0.000965	0.000668	1.53	cuk3	cuk2	BMP-2-inducible protein kinase GN=BMP2K PE=1 SV=2
Q9UBZ9	REV1	6	2	47.6	1.17E-05	5.4E-05	2.24	cuk2	cuk3	DNA repair protein REV1 GN=REV1 PE=1 SV=1
Q9P0M6	MACROH2A2	6	4	48.2	0.000457	0.000417	1.55	cuk2	cuk3	Core histone macro-H2A.2 GN=H2AFY2 PE=1 SV=3
Q12873	CHD3	9	2	48.5	2.49E-09	4.17E-07	4.19	cuk3	cuk2	Chromodomain-helicase-DNA-binding protein 3 GN=CHD3 PE=1 SV=3
Q96NG3	ODAD4	8	2	48.5	0.000492	0.000434	1.86	cuk2	cuk3	Tetratricopeptide repeat protein 25 GN=TTC25 PE=1 SV=2
A0A1B0GV23	CTSD	9	6	48.6	0.019826	0.006322	1.19	cuk3	cuk2	Cathepsin D GN=CTSD PE=1 SV=1
P10586	PTPRF	10	4	48.9	1.44E-05	6.35E-05	2.05	cuk3	cuk2	Receptor-type tyrosine-protein phosphatase F GN=PTPRF PE=1 SV=2
Q8TCU6	PREX1	10	6	49.2	0.001142	0.000762	1.68	cuk2	cuk3	Phosphatidylinositol 3_4_5-trisphosphate-dependent Rac exchanger 1 protein GN=PREX1 PE=1 SV=3
Q96QP1	ALPK1	9	4	49.6	0.004153	0.00192	1.38	cuk3	cuk2	Alpha-protein kinase 1 GN=ALPK1 PE=2 SV=3
P52597	HNRNPF	7	5	49.6	9.23E-05	0.000172	1.35	cuk3	cuk2	Heterogeneous nuclear ribonucleoprotein F GN=HNRNPF PE=1 SV=3
Q8NA03	FSIP1	8	4	49.7	0.004247	0.00195	1.53	cuk3	cuk2	Fibrous sheath-interacting protein 1 GN=FSIP1 PE=2 SV=1
P13647	KRT5	6	2	49.8	3.66E-05	0.000104	2.08	cuk3	cuk2	Keratin_ type II cytoskeletal 5 GN=KRT5 PE=1 SV=3
Q96N67	DOCK7	10	2	49.9	0.000543	0.000464	2.23	cuk3	cuk2	Dedicator of cytokinesis protein 7 GN=DOCK7 PE=1 SV=4
P04899	GNAI2	8	6	50.4	0.006981	0.002845	1.28	cuk2	cuk3	Guanine nucleotide-binding protein G(i) subunit alpha-2 GN=GNAI2 PE=1 SV=3
Q9BY66	KDM5D	10	6	50.5	0.00058	0.000478	1.78	cuk2	cuk3	Lysine-specific demethylase 5D GN=KDM5D PE=1 SV=2
P04004	VTN	7	5	50.6	0.016497	0.005508	1.11	cuk2	cuk3	Vitronectin GN=VTN PE=1 SV=1
Q14117	DPYS	7	2	50.7	0.001906	0.001101	1.26	cuk2	cuk3	Dihydropyrimidinase GN=DPYS PE=1 SV=1
A0A0A0MRP0	MAP7D3	6	2	51	0.017129	0.005656	1.12	cuk3	cuk2	MAP7 domain-containing protein 3 (Fragment) GN=MAP7D3 PE=1 SV=1
O43683	BUB1	9	4	51.3	0.007195	0.002911	1.27	cuk2	cuk3	Mitotic checkpoint serine/threonine-protein kinase BUB1 GN=BUB1 PE=1 SV=1
A0A0A0MQX1	MYO10	8	5	51.3	0.003457	0.001672	1.48	cuk3	cuk2	Unconventional myosin-X GN=MYO10 PE=1 SV=1
P62753	RPS6	8	4	51.5	0.008689	0.003343	1.61	cuk3	cuk2	40S ribosomal protein S6 GN=RPS6 PE=1 SV=1
Q7Z4S6	KIF21A	9	5	51.6	2.42E-06	2.07E-05	2.33	cuk2	cuk3	Kinesin-like protein KIF21A GN=KIF21A PE=1 SV=2
Q6ZNG0	ZNF620	8	3	52.1	0.000138	0.000212	2.56	cuk2	cuk3	Zinc finger protein 620 GN=ZNF620 PE=2 SV=1
O60282	KIF5C	8	2	52.3	0.0006	0.000485	2.42	cuk3	cuk2	Kinesin heavy chain isoform 5C GN=KIF5C PE=1 SV=1
Q96RY7	IFT140	7	2	52.4	0.001538	0.000942	1.53	cuk2	cuk3	Intraflagellar transport protein 140 homolog GN=IFT140 PE=1 SV=1
A0A0D9SF60	PKP4	9	2	52.4	0.0046	0.002062	1.44	cuk2	cuk3	Plakophilin-4 GN=PKP4 PE=1 SV=1
O60610	DIAPH1	10	6	52.5	0.009243	0.003509	1.15	cuk2	cuk3	Protein diaphanous homolog 1 GN=DIAPH1 PE=1 SV=2
A0A0A0MS86	CEP290	7	3	52.6	0.000799	0.000589	2.69	cuk2	cuk3	Centrosomal protein of 290 kDa GN=CEP290 PE=1 SV=1
Q86V48	LUZP1	9	2	52.7	0.014453	0.004954	1.32	cuk2	cuk3	Leucine zipper protein 1 GN=LUZP1 PE=1 SV=2
P35527	KRT9	10	7	52.7	8.81E-05	0.000168	1.89	cuk3	cuk2	Keratin_ type I cytoskeletal 9 GN=KRT9 PE=1 SV=3
Q5TB80	CEP162	10	2	52.8	0.002396	0.001284	4.75	cuk2	cuk3	Centrosomal protein of 162 kDa GN=CEP162 PE=1 SV=2
Q9NYF8	BCLAF1	10	5	52.8	0.002255	0.001234	1.55	cuk2	cuk3	Bcl-2-associated transcription factor 1 GN=BCLAF1 PE=1 SV=2
K7EM46	KIAA1328	8	2	53.3	0.001504	0.000924	1.32	cuk3	cuk2	Protein hinderin (Fragment) GN=KIAA1328 PE=1 SV=1
Q9P2E9	RRBP1	8	4	53.6	0.003619	0.001728	1.53	cuk3	cuk2	Ribosome-binding protein 1 GN=RRBP1 PE=1 SV=5
P60866	RPS20	6	3	53.9	0.001695	0.001004	1.73	cuk2	cuk3	40S ribosomal protein S20 GN=RPS20 PE=1 SV=1
P62917	RPL8	7	4	53.9	0.007634	0.00305	1.44	cuk2	cuk3	60S ribosomal protein L8 GN=RPL8 PE=1 SV=2
Q9H9B1	EHMT1	8	3	54.5	0.00735	0.002966	1.3	cuk2	cuk3	Histone-lysine N-methyltransferase EHMT1 GN=EHMT1 PE=1 SV=4
Q12888	TP53BP1	11	5	54.6	0.000638	0.000501	2.1	cuk2	cuk3	TP53-binding protein 1 GN=TP53BP1 PE=1 SV=2
P04083	ANXA1	9	3	54.8	5.13E-06	3.09E-05	1.94	cuk3	cuk2	Annexin A1 GN=ANXA1 PE=1 SV=2
Q5R372	RABGAP1L	10	3	56.5	0.00056	0.00047	1.45	cuk3	cuk2	Rab GTPase-activating protein 1-like GN=RABGAP1L PE=1 SV=1
Q9P107	GMIP	9	2	56.8	0.001983	0.001138	1.52	cuk3	cuk2	GEM-interacting protein GN=GMIP PE=1 SV=2
E7EPM6	ACSL1	9	3	56.8	0.018642	0.006018	1.41	cuk3	cuk2	Long-chain-fatty-acid--CoA ligase 1 GN=ACSL1 PE=1 SV=1
H7BYL6	AKAP9	11	5	56.8	0.000698	0.000531	2.19	cuk2	cuk3	A-kinase anchor protein 9 (Fragment) GN=AKAP9 PE=1 SV=1
P62263	RPS14	6	3	57.6	0.00183	0.001061	1.44	cuk2	cuk3	40S ribosomal protein S14 GN=RPS14 PE=1 SV=3
Q15029	EFTUD2	9	6	57.8	0.001685	0.001	1.35	cuk2	cuk3	116 kDa U5 small nuclear ribonucleoprotein component GN=EFTUD2 PE=1 SV=1
O75335	PPFIA4	9	4	58.4	0.000607	0.000487	1.2	cuk2	cuk3	Liprin-alpha-4 GN=PPFIA4 PE=2 SV=3
Q9BXT6	MOV10L1	10	2	58.8	4.45E-06	2.79E-05	2.05	cuk2	cuk3	RNA helicase Mov10l1 GN=MOV10L1 PE=2 SV=1
A0A087WUK2	HNRNPDL	7	2	58.8	0.000259	0.000293	1.45	cuk2	cuk3	Heterogeneous nuclear ribonucleoprotein D-like GN=HNRNPDL PE=1 SV=1
Q6P0N0	MIS18BP1	11	2	59.1	0.002456	0.001306	1.4	cuk3	cuk2	Mis18-binding protein 1 GN=MIS18BP1 PE=1 SV=1
Q13332	PTPRS	12	4	60.3	0.001727	0.001016	1.69	cuk2	cuk3	Receptor-type tyrosine-protein phosphatase S GN=PTPRS PE=1 SV=3
J3KP97	CCDC18	10	3	60.7	0.001713	0.001011	1.35	cuk2	cuk3	Coiled-coil domain-containing protein 18 (Fragment) GN=CCDC18 PE=1 SV=1
Q9NYU2	UGGT1	13	3	61	0.030411	0.008985	1.14	cuk2	cuk3	UDP-glucose:glycoprotein glucosyltransferase 1 GN=UGGT1 PE=1 SV=3
Q1KMD3	HNRNPUL2	9	2	61.4	0.012961	0.004542	1.61	cuk3	cuk2	Heterogeneous nuclear ribonucleoprotein U-like protein 2 GN=HNRNPUL2 PE=1 SV=1
Q6ZU80	CEP128	13	5	62.2	4.36E-05	0.000117	1.56	cuk2	cuk3	Centrosomal protein of 128 kDa GN=CEP128 PE=1 SV=2
O94910	ADGRL1	10	4	62.3	0.003891	0.001822	1.23	cuk2	cuk3	Adhesion G protein-coupled receptor L1 GN=ADGRL1 PE=1 SV=1
P29400	COL4A5	11	4	62.5	0.026938	0.008137	1.12	cuk3	cuk2	Collagen alpha-5(IV) chain GN=COL4A5 PE=1 SV=2
Q6P280	ZNF529	9	2	62.8	0.038676	0.010935	1.28	cuk2	cuk3	Zinc finger protein 529 GN=ZNF529 PE=1 SV=2
Q6PIF6	MYO7B	10	3	63	0.007294	0.002947	1.27	cuk3	cuk2	Unconventional myosin-VIIb GN=MYO7B PE=1 SV=2
A0A0G2JP87	CCHCR1	10	5	63	0.000399	0.000387	2.09	cuk2	cuk3	Coiled-coil alpha-helical rod protein 1 GN=CCHCR1 PE=1 SV=1
O14994	SYN3	9	3	63.1	0.00012	0.000195	5.84	cuk3	cuk2	Synapsin-3 GN=SYN3 PE=1 SV=2
Q9P275	USP36	11	6	63.4	0.048302	0.012962	1.2	cuk3	cuk2	Ubiquitin carboxyl-terminal hydrolase 36 GN=USP36 PE=1 SV=4
P08865	RPSA	9	4	63.5	0.001748	0.001022	1.26	cuk3	cuk2	40S ribosomal protein SA GN=RPSA PE=1 SV=4
E7EPS8	PTPRM	11	6	63.5	1.53E-05	6.46E-05	3.24	cuk3	cuk2	Receptor-type tyrosine-protein phosphatase mu GN=PTPRM PE=1 SV=2
Q9P2M7	CGN	12	5	63.7	0.034352	0.00987	1.14	cuk3	cuk2	Cingulin GN=CGN PE=1 SV=2
Q8NEZ3	WDR19	11	2	64	0.007428	0.002984	2.49	cuk2	cuk3	WD repeat-containing protein 19 GN=WDR19 PE=1 SV=2
Q8ND30	PPFIBP2	10	5	64.2	0.011082	0.004039	1.37	cuk3	cuk2	Liprin-beta-2 GN=PPFIBP2 PE=1 SV=3
O95153	TSPOAP1	10	4	64.5	0.00094	0.000657	2.27	cuk3	cuk2	Peripheral-type benzodiazepine receptor-associated protein 1 GN=TSPOAP1 PE=1 SV=2
Q8NI27	THOC2	11	5	64.5	8.98E-06	4.7E-05	4.46	cuk3	cuk2	THO complex subunit 2 GN=THOC2 PE=1 SV=2
P31930	UQCRC1	10	3	64.6	0.003035	0.001539	1.38	cuk3	cuk2	Cytochrome b-c1 complex subunit 1_ mitochondrial GN=UQCRC1 PE=1 SV=3
Q15746	MYLK	10	6	64.8	0.00026	0.000293	1.45	cuk3	cuk2	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
O75970	MPDZ	12	2	65.3	0.005706	0.002442	1.63	cuk2	cuk3	Multiple PDZ domain protein GN=MPDZ PE=1 SV=2
P35908	KRT2	10	4	65.7	0.00026	0.000293	1.55	cuk3	cuk2	Keratin_ type II cytoskeletal 2 epidermal GN=KRT2 PE=1 SV=2
Q02413	DSG1	8	3	66.4	0.038582	0.010923	1.17	cuk2	cuk3	Desmoglein-1 GN=DSG1 PE=1 SV=2
Q13838	DDX39B	8	2	66.6	0.012309	0.004379	1.65	cuk2	cuk3	Spliceosome RNA helicase DDX39B GN=DDX39B PE=1 SV=1
Q99460	PSMD1	11	3	66.7	3.36E-05	9.99E-05	2.83	cuk2	cuk3	26S proteasome non-ATPase regulatory subunit 1 GN=PSMD1 PE=1 SV=2

Q96QT6	PHF12	9	4	66.7	0.000183	0.000245	1.56	cuk2	cuk3	PHD finger protein 12 GN=PHF12 PE=1 SV=2
Q03181	PPARD	7	2	67.2	0.037875	0.01074	1.21	cuk2	cuk3	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1
Q03252	LMNB2	9	3	67.5	8.71E-07	1.45E-05	12.5	cuk2	cuk3	Lamin-B2 GN=LMNB2 PE=1 SV=4
Q03112	MECOM	13	7	67.9	0.000121	0.000196	1.52	cuk2	cuk3	MDS1 and EVI1 complex locus protein GN=MECOM PE=1 SV=3
P53814	SMTN	10	3	68	0.001714	0.001011	1.27	cuk2	cuk3	Smoothelin GN=SMTN PE=1 SV=7
O43166	SIPA1L1	12	3	68.6	0.000227	0.000277	3.77	cuk3	cuk2	Signal-induced proliferation-associated 1-like protein 1 GN=SIPA1L1 PE=1 SV=4
P13637	ATP1A3	9	2	69.4	0.002297	0.00125	1.6	cuk3	cuk2	Sodium/potassium-transporting ATPase subunit alpha-3 GN=ATP1A3 PE=1 SV=3
F5H2F4	MTHFD1	10	2	69.5	0.003775	0.001777	1.6	cuk2	cuk3	C-1-tetrahydrofolate synthase_ cytoplasmic GN=MTHFD1 PE=1 SV=1
P39023	RPL3	9	5	69.6	0.040131	0.011245	1.39	cuk3	cuk2	60S ribosomal protein L3 GN=RPL3 PE=1 SV=2
Q8WWZ7	ABCA5	10	2	70.6	0.000216	0.00027	1.78	cuk3	cuk2	ATP-binding cassette sub-family A member 5 GN=ABCA5 PE=2 SV=2
H0YKD8	RPL28	10	7	71.2	0.000286	0.000312	2.08	cuk2	cuk3	60S ribosomal protein L28 GN=RPL28 PE=1 SV=1
O14513	NCKAP5	12	3	71.4	0.038937	0.010977	1.13	cuk2	cuk3	Nck-associated protein 5 GN=NCKAP5 PE=1 SV=2
Q12840	KIF5A	11	4	71.4	0.001427	0.00089	1.45	cuk3	cuk2	Kinesin heavy chain isoform 5A GN=KIF5A PE=1 SV=2
Q96F07	CYFIP2	10	2	72.2	2.56E-05	8.47E-05	5.91	cuk2	cuk3	Cytoplasmic FMR1-interacting protein 2 GN=CYFIP2 PE=1 SV=2
P62280	RPS11	9	3	72.7	0.012446	0.004411	1.18	cuk3	cuk2	40S ribosomal protein S11 GN=RPS11 PE=1 SV=3
P13010	XRCC5	11	9	73.3	0.025934	0.007885	1.68	cuk3	cuk2	X-ray repair cross-complementing protein 5 GN=XRCC5 PE=1 SV=3
P49321	NASP	12	6	74.1	0.016238	0.005436	1.69	cuk3	cuk2	Nuclear autoantigenic sperm protein GN=NASP PE=1 SV=2
D3DQV9	EIF4G2	14	5	75.1	0.002828	0.001451	1.35	cuk3	cuk2	Eukaryotic translation initiation factor 4 gamma 2 (Fragment) GN=EIF4G2 PE=1 SV=1
A0A0G2JP F8	HNRNPCL4	9	2	75.3	0.012522	0.004432	1.17	cuk3	cuk2	Heterogeneous nuclear ribonucleoprotein C-like 4 PE=4 SV=1
Q9NTJ3	SMC4	13	7	75.9	0.033421	0.009662	1.18	cuk3	cuk2	Structural maintenance of chromosomes protein 4 GN=SMC4 PE=1 SV=2
Q96JM4	LRRIQ1	16	6	76.6	0.000735	0.000551	2.03	cuk3	cuk2	Leucine-rich repeat and IQ domain-containing protein 1 GN=LRRIQ1 PE=2 SV=3
P62241	RPS8	7	6	76.9	0.000567	0.000475	1.26	cuk2	cuk3	40S ribosomal protein S8 GN=RPS8 PE=1 SV=2
Q9C093	SPEF2	13	3	77.4	0.005954	0.002517	1.29	cuk2	cuk3	Sperm flagellar protein 2 GN=SPEF2 PE=2 SV=2
O00299	CLIC1	11	6	77.6	1.51E-05	6.46E-05	2.43	cuk3	cuk2	Chloride intracellular channel protein 1 GN=CLIC1 PE=1 SV=4
Q9Y4F4	TOGARAM1	15	10	77.6	1.25E-05	5.71E-05	2.47	cuk2	cuk3	TOG array regulator of axonemal microtubules protein 1 GN=TOGARAM1 PE=1 SV=4
O00264	PGRMC1	10	6	79.3	0.008082	0.003179	1.16	cuk2	cuk3	Membrane-associated progesterone receptor component 1 GN=PGRMC1 PE=1 SV=3
A7E2Y1	MYH7B	16	6	79.6	0.0046	0.002062	1.37	cuk3	cuk2	Myosin-7B GN=MYH7B PE=1 SV=4
P26641	EEF1G	11	7	80.1	0.015593	0.005281	1.29	cuk2	cuk3	Elongation factor 1-gamma GN=EEF1G PE=1 SV=3
P50914	RPL14	10	5	81.6	0.020704	0.006546	1.22	cuk3	cuk2	60S ribosomal protein L14 GN=RPL14 PE=1 SV=4
A0A0G2JN B1	KANSL1	13	4	81.7	0.000395	0.000387	1.56	cuk3	cuk2	KAT8 regulatory NSL complex subunit 1 GN=KANSL1 PE=1 SV=1
Q8WVM7	STAG1	13	6	81.9	0.007652	0.003052	1.41	cuk2	cuk3	Cohesin subunit SA-1 GN=STAG1 PE=1 SV=3
Q15643	TRIP11	12	4	82.7	0.000139	0.000213	1.63	cuk2	cuk3	Thyroid receptor-interacting protein 11 GN=TRIP11 PE=1 SV=3
Q9UNA4	POLI	13	7	83.9	0.03736	0.010637	1.47	cuk3	cuk2	DNA polymerase iota GN=POLI PE=1 SV=3
Q9Y6M1	IGF2BP2	12	4	84.8	0.042689	0.011791	1.11	cuk3	cuk2	Insulin-like growth factor 2 mRNA-binding protein 2 GN=IGF2BP2 PE=1 SV=2
Q99536	VAT1	11	7	84.8	0.017078	0.005654	1.44	cuk2	cuk3	Synaptic vesicle membrane protein VAT-1 homolog GN=VAT1 PE=1 SV=2
P09211	GSTP1	8	3	85.1	0.00242	0.001294	1.23	cuk3	cuk2	Glutathione S-transferase P GN=GSTP1 PE=1 SV=2
Q9H0X9	OSBPL5	13	4	85.4	0.007662	0.003052	1.26	cuk2	cuk3	Oxysterol-binding protein-related protein 5 GN=OSBPL5 PE=1 SV=1
P50991	CCT4	14	7	85.5	0.003144	0.00158	1.4	cuk2	cuk3	T-complex protein 1 subunit delta GN=CCT4 PE=1 SV=4
O75122	CLASP2	13	5	85.6	0.000205	0.000263	1.84	cuk3	cuk2	CLIP-associating protein 2 GN=CLASP2 PE=1 SV=2
Q9UG01	IFT172	16	6	85.7	1.43E-05	6.35E-05	5.69	cuk2	cuk3	Intraflagellar transport protein 172 homolog GN=IFT172 PE=1 SV=2
Q9BY12	SCAPER	16	9	86.2	6.68E-05	0.000143	2.33	cuk2	cuk3	S phase cyclin A-associated protein in the endoplasmic reticulum GN=SCAPER PE=1 SV=2
Q15276	RABEP1	15	4	87.3	0.000615	0.000492	1.93	cuk3	cuk2	Rab GTPase-binding effector protein 1 GN=RABEP1 PE=1 SV=2
O43491	EPB41L2	16	3	87.5	3.22E-06	2.43E-05	2.71	cuk2	cuk3	Band 4.1-like protein 2 GN=EPB41L2 PE=1 SV=1
P62913	RPL11	8	3	87.6	0.000301	0.000321	1.41	cuk2	cuk3	60S ribosomal protein L11 GN=RPL11 PE=1 SV=2
Q6WCQ1	MPRIP	15	5	88	0.008787	0.003367	1.29	cuk2	cuk3	Myosin phosphatase Rho-interacting protein GN=MPRIP PE=1 SV=3
Q96M83	CCDC7	14	6	88.5	0.01592	0.005366	1.25	cuk2	cuk3	Coiled-coil domain-containing protein 7 GN=CCDC7 PE=2 SV=3
E7EPK1	SEPTIN7	14	5	88.8	0.038816	0.010963	1.08	cuk3	cuk2	Septin-7 GN=SEPT7 PE=1 SV=2
Q8NI35	PATJ	15	3	89.3	0.001601	0.000964	1.48	cuk2	cuk3	InaD-like protein GN=PATJ PE=1 SV=3
O00443	PIK3C2A	14	4	90.7	3.5E-05	0.000102	6.2	cuk2	cuk3	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha GN=PIK3C2A PE=1 SV=2
P08729	KRT7	9	4	91.4	0.022449	0.006998	1.22	cuk2	cuk3	Keratin_ type II cytoskeletal 7 GN=KRT7 PE=1 SV=5
P48735	IDH2	14	6	91.4	0.000358	0.000358	1.63	cuk2	cuk3	Isocitrate dehydrogenase [NADP]_ mitochondrial GN=IDH2 PE=1 SV=2
P34897	SHMT2	15	10	93.2	0.000492	0.000434	1.27	cuk3	cuk2	Serine hydroxymethyltransferase_ mitochondrial GN=SHMT2 PE=1 SV=3
F8W1R7	MYL6	12	7	93.4	0.00016	0.000232	1.79	cuk3	cuk2	Myosin light polypeptide 6 GN=MYL6 PE=1 SV=1
Q3V6T2	CCDC88A	17	7	94.6	2.63E-05	8.47E-05	2.35	cuk2	cuk3	Girdin GN=CCDC88A PE=1 SV=2
Q5JU85	IQSEC2	16	9	94.9	0.001042	0.000713	1.96	cuk3	cuk2	IQ motif and SEC7 domain-containing protein 2 GN=IQSEC2 PE=1 SV=2
Q7L576	CYFIP1	15	3	95.4	0.000676	0.000521	2.8	cuk3	cuk2	Cytoplasmic FMR1-interacting protein 1 GN=CYFIP1 PE=1 SV=1
P38919	EIF4A3	13	6	97.1	0.001441	0.000894	2.6	cuk3	cuk2	Eukaryotic initiation factor 4A-III GN=EIF4A3 PE=1 SV=4
E7EVA0	MAP4	17	6	97.2	0.004243	0.00195	1.75	cuk2	cuk3	Microtubule-associated protein GN=MAP4 PE=1 SV=1
P16949	STMN1	12	5	97.6	0.001418	0.000887	1.25	cuk3	cuk2	Stathmin GN=STMN1 PE=1 SV=3
Q14103	HNRNPD	13	4	98.7	0.001598	0.000964	1.41	cuk2	cuk3	Heterogeneous nuclear ribonucleoprotein D0 GN=HNRNPD PE=1 SV=1
P50990	CCT8	14	4	99.9	9.42E-05	0.000172	1.98	cuk3	cuk2	T-complex protein 1 subunit theta GN=CCT8 PE=1 SV=4
P78371	CCT2	15	7	100	0.03971	0.01116	1.28	cuk2	cuk3	T-complex protein 1 subunit beta GN=CCT2 PE=1 SV=4
D6RE83	UCHL1	10	5	101	0.033381	0.00966	1.13	cuk2	cuk3	Ubiquitin carboxyl-terminal hydrolase GN=UCHL1 PE=1 SV=1
Q9HCM1	RESF1	19	6	101	0.01836	0.00596	1.49	cuk2	cuk3	Uncharacterized protein KIAA1551 GN=KIAA1551 PE=1 SV=3
Q08211	DHX9	18	12	101	0.000412	0.000396	1.32	cuk3	cuk2	ATP-dependent RNA helicase A GN=DHX9 PE=1 SV=4
P06748	NPM1	9	4	102	0.005529	0.002384	1.16	cuk3	cuk2	Nucleophosmin GN=NPM1 PE=1 SV=2
O14529	CUX2	17	5	102	0.000802	0.000589	2.33	cuk2	cuk3	Homeobox protein cut-like 2 GN=CUX2 PE=1 SV=4
Q06830	PRDX1	13	6	102	0.004353	0.001989	1.15	cuk3	cuk2	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
Q86U86	PBRM1	18	5	103	0.004366	0.001992	1.49	cuk2	cuk3	Protein polybromo-1 GN=PBRM1 PE=1 SV=1
Q99623	PHB2	16	7	104	1.02E-07	3.14E-06	2.29	cuk2	cuk3	Prohibitin-2 GN=PHB2 PE=1 SV=2
Q14974	KPNB1	14	7	106	2E-06	1.94E-05	11.8	cuk2	cuk3	Importin subunit beta-1 GN=KPNB1 PE=1 SV=2
O75128	COBL	19	8	106	0.000576	0.000478	2.32	cuk3	cuk2	Protein cordon-bleu GN=COBL PE=1 SV=2
Q15084	PDIA6	13	8	106	2.61E-05	8.47E-05	2.31	cuk3	cuk2	Protein disulfide-isomerase A6 GN=PDIA6 PE=1 SV=1
Q76FK4	NOL8	16	6	107	1.71E-06	1.8E-05	1.91	cuk2	cuk3	Nucleolar protein 8 GN=NOL8 PE=1 SV=1
Q9C0D4	ZNF518B	17	6	107	0.038944	0.010977	1.26	cuk2	cuk3	Zinc finger protein 518B GN=ZNF518B PE=1 SV=2
O14974	PPP1R12A	18	7	107	0.020669	0.006545	1.08	cuk2	cuk3	Protein phosphatase 1 regulatory subunit 12A GN=PPP1R12A PE=1 SV=1
P07737	PFN1	11	9	108	9.26E-06	4.76E-05	8.65	cuk2	cuk3	Profilin-1 GN=PFN1 PE=1 SV=2
Q13263	TRIM28	17	6	109	0.002451	0.001306	1.29	cuk3	cuk2	Transcription intermediary factor 1-beta GN=TRIM28 PE=1 SV=5
Q3MJ40	CCDC144B	19	2	111	1.78E-06	1.8E-05	6.93	cuk3	cuk2	Coiled-coil domain-containing protein 144B GN=CCDC144B PE=2 SV=1
P02765	AHSG	13	9	112	0.002238	0.001228	1.46	cuk2	cuk3	Alpha-2-HS-glycoprotein GN=AHSG PE=1 SV=1
P07196	NEFL	15	3	113	0.000186	0.000245	2.45	cuk3	cuk2	Neurofilament light polypeptide GN=NEFL PE=1 SV=3
Q86YA3	ZGRF1	20	5	113	0.000427	0.000402	4.07	cuk2	cuk3	Protein ZGRF1 GN=ZGRF1 PE=1 SV=3
Q9UHF7	TRPS1	21	7	113	0.001383	0.000873	1.6	cuk2	cuk3	Zinc finger transcription factor Trps1 GN=TRPS1 PE=1 SV=2
Q9C0C2	TNKS1BP1	19	9	113	0.006671	0.002744	1.37	cuk2	cuk3	182 kDa tankyrase-1-binding protein GN=TNKS1BP1 PE=1 SV=4

P32119	PRDX2	10	5	114	0.010567	0.003885	1.29	cuk3	cuk2	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
Q6ZN16	MAP3K15	16	5	114	0.00383	0.001797	1.26	cuk2	cuk3	Mitogen-activated protein kinase kinase kinase 15 GN=MAP3K15 PE=1 SV=2
Q58FF3	HSP90B2P	16	6	114	0.011485	0.004148	1.17	cuk3	cuk2	Putative endoplasmin-like protein GN=HSP90B2P PE=5 SV=1
Q99832	CCT7	20	12	114	5.3E-05	0.000131	2.52	cuk3	cuk2	T-complex protein 1 subunit eta GN=CCT7 PE=1 SV=2
Q8N7X0	ADGB	18	4	115	0.007399	0.002979	1.41	cuk2	cuk3	Androglobin GN=ADGB PE=2 SV=3
P27824	CANX	14	7	115	0.033256	0.009634	1.18	cuk3	cuk2	Calnexin GN=CANX PE=1 SV=2
Q5JSZ5	PRRC2B	18	6	116	0.002368	0.001274	1.34	cuk2	cuk3	Protein PRRC2B GN=PRRC2B PE=1 SV=2
Q9Y4I1	MYO5A	22	6	117	0.001392	0.000876	1.5	cuk2	cuk3	Unconventional myosin-Va GN=MYO5A PE=1 SV=2
A6QL64	ANKRD36	21	8	117	0.019072	0.006135	1.13	cuk3	cuk2	Ankyrin repeat domain-containing protein 36A GN=ANKRD36 PE=2 SV=3
Q8N1I0	DOCK4	20	8	118	0.013821	0.004788	1.41	cuk2	cuk3	Dedicator of cytokinesis protein 4 GN=DOCK4 PE=1 SV=3
Q9H4B7	TUBB1	10	2	119	0.000303	0.000322	1.53	cuk2	cuk3	Tubulin beta-1 chain GN=TUBB1 PE=1 SV=1
O60292	SIPA1L3	21	12	120	6.92E-05	0.000146	2.52	cuk3	cuk2	Signal-induced proliferation-associated 1-like protein 3 GN=SIPA1L3 PE=1 SV=3
P48741	HSPA7	14	3	121	0.000841	0.000613	1.74	cuk2	cuk3	Putative heat shock 70 kDa protein 7 GN=HSPA7 PE=5 SV=2
Q16658	FSCN1	16	9	121	0.028147	0.008425	1.2	cuk3	cuk2	Fascin GN=FSCN1 PE=1 SV=3
P04264	KRT1	17	6	122	4.61E-05	0.000121	1.89	cuk3	cuk2	Keratin_ type II cytoskeletal 1 GN=KRT1 PE=1 SV=6
P62805	H4C1	10	6	123	0.000422	0.0004	1.42	cuk3	cuk2	Histone H4 GN=HIST1H4A PE=1 SV=2
P17844	DDX5	18	7	123	0.000458	0.000417	1.71	cuk2	cuk3	Probable ATP-dependent RNA helicase DDX5 GN=DDX5 PE=1 SV=1
P55795	HNRNPH2	18	4	125	0.001249	0.000815	1.57	cuk3	cuk2	Heterogeneous nuclear ribonucleoprotein H2 GN=HNRNPH2 PE=1 SV=1
Q9UDT6	CLIP2	23	9	126	0.008955	0.003418	1.15	cuk2	cuk3	CAP-Gly domain-containing linker protein 2 GN=CLIP2 PE=1 SV=1
P07910	HNRNPC	15	5	132	0.000989	0.000681	1.42	cuk3	cuk2	Heterogeneous nuclear ribonucleoproteins C1/C2 GN=HNRNPC PE=1 SV=4
Q9NSB2	KRT84	20	8	132	0.047266	0.012739	1.15	cuk2	cuk3	Keratin_ type II cuticular Hb4 GN=KRT84 PE=2 SV=2
O75145	PPFIA3	22	11	133	0.013459	0.004681	1.25	cuk2	cuk3	Liprin-alpha-3 GN=PPFIA3 PE=1 SV=3
P08133	ANXA6	18	7	134	0.002085	0.001177	1.77	cuk3	cuk2	Annexin A6 GN=ANXA6 PE=1 SV=3
C9J7T7	NCOR2	24	7	134	0.00252	0.00133	1.68	cuk2	cuk3	Nuclear receptor corepressor 2 GN=NCOR2 PE=1 SV=3
Q9UPN4	CEP131	21	7	134	0.014868	0.005066	1.23	cuk2	cuk3	Centrosomal protein of 131 kDa GN=CEP131 PE=1 SV=3
P36578	RPL4	18	8	134	0.000324	0.000334	1.2	cuk3	cuk2	60S ribosomal protein L4 GN=RPL4 PE=1 SV=5
P62701	RPS4X	16	6	137	0.008302	0.003221	1.3	cuk3	cuk2	40S ribosomal protein S4_ X isoform GN=RPS4X PE=1 SV=2
Q8IWJ2	GCC2	27	11	137	0.000963	0.000668	1.98	cuk3	cuk2	GRIP and coiled-coil domain-containing protein 2 GN=GCC2 PE=1 SV=4
A2RUR9	CCDC144A	22	2	141	2.64E-05	8.47E-05	3.64	cuk3	cuk2	Coiled-coil domain-containing protein 144A GN=CCDC144A PE=2 SV=1
Q8NB25	FAM184A	23	7	141	0.000483	0.000432	1.25	cuk2	cuk3	Protein FAM184A GN=FAM184A PE=2 SV=3
Q9BZ29	DOCK9	22	10	142	0.000195	0.000255	1.31	cuk3	cuk2	Dedicator of cytokinesis protein 9 GN=DOCK9 PE=1 SV=2
Q12931	TRAP1	18	8	143	0.011339	0.004101	1.32	cuk2	cuk3	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
Q14240	EIF4A2	19	8	144	2.48E-05	8.39E-05	1.91	cuk2	cuk3	Eukaryotic initiation factor 4A-II GN=EIF4A2 PE=1 SV=2
K7ELL7	PRKCSH	18	10	145	0.001138	0.000762	1.64	cuk3	cuk2	Glucosidase 2 subunit beta GN=PRKCSH PE=1 SV=1
P12277	CKB	18	12	145	0.00038	0.000376	1.36	cuk3	cuk2	Creatine kinase B-type GN=CKB PE=1 SV=1
Q16695	H3-4	18	4	147	0.001285	0.000827	1.2	cuk3	cuk2	Histone H3.1t GN=HIST3H3 PE=1 SV=3
Q9NQT8	KIF13B	22	13	147	8.13E-05	0.000158	1.7	cuk2	cuk3	Kinesin-like protein KIF13B GN=KIF13B PE=1 SV=2
P00558	PGK1	20	9	150	0.002585	0.00136	1.32	cuk2	cuk3	Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3
Q86UP2	KTN1	27	11	153	0.000222	0.000276	1.49	cuk2	cuk3	Kinectin GN=KTN1 PE=1 SV=1
P16401	H1-5	13	5	154	0.004823	0.002127	1.19	cuk2	cuk3	Histone H1.5 GN=HIST1H1B PE=1 SV=3
Q6FI13	H2AC18; H2AC19	17	6	154	0.000172	0.000237	1.71	cuk3	cuk2	Histone H2A type 2-A GN=HIST2H2AA3 PE=1 SV=3
P35579	MYH9	25	10	154	0.000398	0.000387	1.6	cuk2	cuk3	Myosin-9 GN=MYH9 PE=1 SV=4
P04843	RPN1	23	12	155	0.002881	0.001471	1.23	cuk3	cuk2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 GN=RPN1 PE=1 SV=1
P05787	KRT8	19	8	156	0.014572	0.004983	1.35	cuk2	cuk3	Keratin_ type II cytoskeletal 8 GN=KRT8 PE=1 SV=7
P55072	VCP	22	7	157	0.008122	0.003185	1.13	cuk2	cuk3	Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4
Q5THK1	PRR14L	26	9	158	0.000537	0.000459	1.58	cuk2	cuk3	Protein PRR14L GN=PRR14L PE=1 SV=1
Q05682	CALD1	25	7	162	0.000625	0.000495	2	cuk3	cuk2	Caldesmon GN=CALD1 PE=1 SV=3
E9PK25	CFL1	15	4	163	0.000172	0.000237	1.43	cuk3	cuk2	Cofilin-1 GN=CFL1 PE=1 SV=1
P62937	PPIA	17	8	163	0.006841	0.0028	1.24	cuk2	cuk3	Peptidyl-prolyl cis-trans isomerase A GN=PPIA PE=1 SV=2
H7C5E8	TF	17	2	166	0.027186	0.008177	1.52	cuk2	cuk3	Serotransferrin (Fragment) GN=TF PE=1 SV=1
Q9HC77	CENPJ	26	9	166	0.001155	0.000767	1.43	cuk3	cuk2	Centromere protein J GN=CENPJ PE=1 SV=2
Q8TBY8	PMFBP1	26	12	166	0.009629	0.003621	1.42	cuk3	cuk2	Polyamine-modulated factor 1-binding protein 1 GN=PMFBP1 PE=2 SV=2
P34931	HSPA1L	21	4	168	0.000164	0.000232	1.54	cuk3	cuk2	Heat shock 70 kDa protein 1-like GN=HSPA1L PE=1 SV=2
Q15365	PCBP1	22	13	171	0.000162	0.000232	2.11	cuk3	cuk2	Poly(rC)-binding protein 1 GN=PCBP1 PE=1 SV=2
P16402	H1-3	14	3	173	0.00283	0.001451	1.25	cuk2	cuk3	Histone H1.3 GN=HIST1H1D PE=1 SV=2
P15880	RPS2	22	12	175	7.16E-05	0.000149	1.64	cuk2	cuk3	40S ribosomal protein S2 GN=RPS2 PE=1 SV=2
Q8WX93	PALLD	28	15	183	0.013981	0.004812	1.4	cuk3	cuk2	Palladin GN=PALLD PE=1 SV=3
Q86UW6	N4BP2	27	11	189	0.001072	0.000726	1.23	cuk3	cuk2	NEDD4-binding protein 2 GN=N4BP2 PE=1 SV=2
P07237	P4HB	23	9	201	0.00565	0.002425	2.47	cuk3	cuk2	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
H7BZ55	CROCC2	37	12	201	0.002302	0.00125	1.33	cuk2	cuk3	Putative ciliary rootlet coiled-coil protein 2 GN=CROCC2 PE=5 SV=3
P54652	HSPA2	20	4	202	0.00015	0.000221	1.22	cuk3	cuk2	Heat shock-related 70 kDa protein 2 GN=HSPA2 PE=1 SV=1
O43175	PHGDH	22	3	206	0.003369	0.001644	1.46	cuk2	cuk3	D-3-phosphoglycerate dehydrogenase GN=PHGDH PE=1 SV=4
Q15366	PCBP2	21	6	207	0.000301	0.000321	1.49	cuk3	cuk2	Poly(rC)-binding protein 2 GN=PCBP2 PE=1 SV=1
P55196	AFDN	32	9	208	0.018	0.005864	1.44	cuk2	cuk3	Afadin GN=AFDN PE=1 SV=3
P06733	ENO1	28	12	213	0.016955	0.005627	1.21	cuk2	cuk3	Alpha-enolase GN=ENO1 PE=1 SV=2
P20700	LMNB1	26	11	214	0.001664	0.000992	1.6	cuk2	cuk3	Lamin-B1 GN=LMNB1 PE=1 SV=2
Q14194	CRMP1	29	11	215	4.55E-07	9.89E-06	1.75	cuk2	cuk3	Dihydropyrimidinase-related protein 1 GN=CRMP1 PE=1 SV=1
Q14980	NUMA1	38	14	221	1.87E-05	7.07E-05	2.03	cuk2	cuk3	Nuclear mitotic apparatus protein 1 GN=NUMA1 PE=1 SV=2
P41219	PRPH	24	6	226	0.000152	0.000224	2.03	cuk2	cuk3	Peripherin GN=PRPH PE=1 SV=2
P61978	HNRNPK	30	4	248	0.000165	0.000232	2.41	cuk2	cuk3	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
P35580	MYH10	42	19	266	8.78E-06	4.68E-05	1.48	cuk2	cuk3	Myosin-10 GN=MYH10 PE=1 SV=3
Q14195	DPYSL3	28	14	269	0.003564	0.001712	1.32	cuk3	cuk2	Dihydropyrimidinase-related protein 3 GN=DPYSL3 PE=1 SV=1
Q9Y4L1	HYOU1	39	18	290	3.31E-05	9.99E-05	2.33	cuk2	cuk3	Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1
Q00610	CLTC	44	18	290	3.78E-05	0.000107	1.96	cuk2	cuk3	Clathrin heavy chain 1 GN=CLTC PE=1 SV=5
P25705	ATP5F1A	28	15	293	0.004988	0.002181	1.21	cuk3	cuk2	ATP synthase subunit alpha_ mitochondrial GN=ATP5F1A PE=1 SV=1
P07197	NEFM	41	14	302	0.000399	0.000387	1.37	cuk3	cuk2	Neurofilament medium polypeptide GN=NEFM PE=1 SV=3
Q07065	CKAP4	36	16	309	0.035556	0.010175	1.08	cuk2	cuk3	Cytoskeleton-associated protein 4 GN=CKAP4 PE=1 SV=2
P38646	HSPA9	40	21	309	0.002201	0.001215	1.47	cuk2	cuk3	Stress-70 protein_ mitochondrial GN=HSPA9 PE=1 SV=2
Q9BUF5	TUBB6	26	3	314	3.61E-06	2.55E-05	1.78	cuk3	cuk2	Tubulin beta-6 chain GN=TUBB6 PE=1 SV=1
P06576	ATP5F1B	34	27	317	0.003294	0.001621	1.2	cuk3	cuk2	ATP synthase subunit beta_ mitochondrial GN=ATP5F1B PE=1 SV=3
P02768	ALB	35	24	319	0.000256	0.000293	1.43	cuk3	cuk2	Serum albumin GN=ALB PE=1 SV=2
P07900	HSP90AA1	35	8	324	1.67E-06	1.8E-05	2.35	cuk3	cuk2	Heat shock protein HSP 90-alpha GN=HSP90AA1 PE=1 SV=5
P68104	EEF1A1	32	4	335	0.025289	0.00773	1.09	cuk3	cuk2	Elongation factor 1-alpha 1 GN=EEF1A1 PE=1 SV=1
A0A1C7C YX9	DPYSL2	34	3	351	0.000256	0.000293	1.98	cuk3	cuk2	Dihydropyrimidinase-related protein 2 GN=DPYSL2 PE=1 SV=1

Q00839	HNRNPU	43	6	360	0.017414	0.005726	1.14	cuk3	cuk2	Heterogeneous nuclear ribonucleoprotein U GN=HNRNPU PE=1 SV=6
Q6PEY2	TUBA3E	28	2	369	0.00033	0.000339	9.73	cuk3	cuk2	Tubulin alpha-3E chain GN=TUBA3E PE=1 SV=2
P08238	HSP90AB1	38	12	379	0.003283	0.001618	1.23	cuk3	cuk2	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
H0Y6I0	GOLGA4	58	26	382	4.26E-06	2.79E-05	1.49	cuk3	cuk2	Golgin subfamily A member 4 (Fragment) GN=GOLGA4 PE=1 SV=1
P14618	PKM	33	6	386	0.000338	0.000343	1.25	cuk3	cuk2	Pyruvate kinase PKM GN=PKM PE=1 SV=4
P22314	UBA1	54	18	408	0.008585	0.00331	1.27	cuk2	cuk3	Ubiquitin-like modifier-activating enzyme 1 GN=UBA1 PE=1 SV=3
P13639	EEF2	51	27	415	6.13E-06	3.53E-05	1.73	cuk3	cuk2	Elongation factor 2 GN=EEF2 PE=1 SV=4
P11021	HSPA5	43	25	466	0.025384	0.007751	1.25	cuk2	cuk3	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P52272	HNRNPM	50	28	488	0.00024	0.000285	1.45	cuk2	cuk3	Heterogeneous nuclear ribonucleoprotein M GN=HNRNPM PE=1 SV=3
P14625	HSP90B1	52	26	564	0.047453	0.012777	1.1	cuk2	cuk3	Endoplasmin GN=HSP90B1 PE=1 SV=1
A0A0B4J269	Not Found	43	3	572	0.038597	0.010923	1.2	cuk2	cuk3	Uncharacterized protein PE=1 SV=1
P02787	TF	62	25	655	0.000226	0.000277	1.44	cuk2	cuk3	Serotransferrin GN=TF PE=1 SV=3
P08670	VIM	52	22	676	0.001112	0.00075	1.27	cuk3	cuk2	Vimentin GN=VIM PE=1 SV=4
P68032	ACTC1	54	11	688	8.02E-05	0.000158	1.68	cuk3	cuk2	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
Q13885	TUBB2A	50	2	735	0.007946	0.003138	1.11	cuk2	cuk3	Tubulin beta-2A chain GN=TUBB2A PE=1 SV=1
P07437	TUBB	58	7	847	0.0118	0.004235	1.19	cuk3	cuk2	Tubulin beta chain GN=TUBB PE=1 SV=2
P60709	ACTB	66	15	1010	0.001635	0.000981	1.48	cuk3	cuk2	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1

Table S10: Identified allergy-related proteins following DMT$_{A\beta 1\text{-}6}$, DMT$_{A\beta 17\text{-}23}$ compared to untreated cells. Herein, CuK1= Aβ1-6; Cuk2= Aβ17-23; CuK3=NoT

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-Aβ_{1-6} Antibody Treatment										
P29597	TYK2	8	2	42.1	0.042145	0.011808	1.58	cuk1	cuk3	Non-receptor tyrosine-protein kinase TYK2 GN=TYK2 PE=1 SV=3
O60343	TBC1D4	7	2	43	0.00189	0.001053	1.77	cuk3	cuk1	TBC1 domain family member 4 GN=TBC1D4 PE=1 SV=2
P12004	PCNA	6	4	44.8	0.012169	0.004175	1.9	cuk3	cuk1	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
A0A1B0GV23	CTSD	9	6	48.6	0.003074	0.001487	1.98	cuk3	cuk1	Cathepsin D GN=CTSD PE=1 SV=1
Q92878	RAD50	11	3	51	3.7E-05	8.29E-05	9.3	cuk1	cuk3	DNA repair protein RAD50 GN=RAD50 PE=1 SV=1
P04083	ANXA1	9	3	54.8	0.000105	0.000153	2.69	cuk3	cuk1	Annexin A1 GN=ANXA1 PE=1 SV=2
Q15746	MYLK	10	6	64.8	0.002075	0.001128	2.14	cuk1	cuk3	Myosin light chain kinase_ smooth muscleGN=MYLK PE=1 SV=4
Q02413	DSG1	8	3	66.4	0.00033	0.000333	3	cuk1	cuk3	Desmoglein-1 GN=DSG1 PE=1 SV=2
Q03181	PPARD	7	2	67.2	0.002091	0.001131	1.99	cuk1	cuk3	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1
O00443	PIK3C2A	14	4	90.7	0.001509	0.000896	4.48	cuk3	cuk1	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha GN=PIK3C2A PE=1 SV=2
P35232	PHB	15	9	97.2	0.002467	0.001273	1.32	cuk3	cuk1	Prohibitin GN=PHB PE=1 SV=1
Q06830	PRDX1	13	6	102	0.000567	0.000478	2.01	cuk1	cuk3	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
P00558	PGK1	20	9	150	0.005587	0.002331	1.48	cuk1	cuk3	Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3
P02768	ALB	35	24	319	0.002915	0.001439	1.88	cuk1	cuk3	Serum albumin GN=ALB PE=1 SV=2
P68104	EEF1A1	32	4	335	0.000273	0.000291	2.14	cuk3	cuk1	Elongation factor 1-alpha 1 GN=EEF1A1 PE=1 SV=1
P14625	HSP90B1	52	26	564	0.000455	0.000404	1.23	cuk3	cuk1	Endoplasmin GN=HSP90B1 PE=1 SV=1
P02787	TF	62	25	655	1.46E-05	5.22E-05	2.5	cuk1	cuk3	Serotransferrin GN=TF PE=1 SV=3
P60709	ACTB	66	15	1010	8.69E-06	4.31E-05	2.44	cuk3	cuk1	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1
Anti-Aβ_{1-6} Antibody Treatment										
P29597	TYK2	8	2	42.1	0.02816	0.008425	1.49	cuk2	cuk3	Non-receptor tyrosine-protein kinase TYK2 GN=TYK2 PE=1 SV=3
P12004	PCNA	6	4	44.8	0.039943	0.011214	1.18	cuk2	cuk3	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
A0A1B0GV23	CTSD	9	6	48.6	0.019826	0.006322	1.19	cuk3	cuk2	Cathepsin D GN=CTSD PE=1 SV=1
P04083	ANXA1	9	3	54.8	5.13E-06	3.09E-05	1.94	cuk3	cuk2	Annexin A1 GN=ANXA1 PE=1 SV=2
Q15746	MYLK	10	6	64.8	0.00026	0.000293	1.45	cuk3	cuk2	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
Q02413	DSG1	8	3	66.4	0.038582	0.010923	1.17	cuk2	cuk3	Desmoglein-1 GN=DSG1 PE=1 SV=2
Q03181	PPARD	7	2	67.2	0.037875	0.01074	1.21	cuk2	cuk3	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1
O00443	PIK3C2A	14	4	90.7	3.5E-05	0.000102	6.2	cuk2	cuk3	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha GN=PIK3C2A PE=1 SV=2
Q06830	PRDX1	13	6	102	0.004353	0.001989	1.15	cuk3	cuk2	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
P00558	PGK1	20	9	150	0.002585	0.00136	1.32	cuk2	cuk3	Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3
P62937	PPIA	17	8	163	0.006841	0.0028	1.24	cuk2	cuk3	Peptidyl-prolyl cis-trans isomerase A GN=PPIA PE=1 SV=2
P02768	ALB	35	24	319	0.000256	0.000293	1.43	cuk3	cuk2	Serum albumin GN=ALB PE=1 SV=2
P68104	EEF1A1	32	4	335	0.025289	0.00773	1.09	cuk3	cuk2	Elongation factor 1-alpha 1 GN=EEF1A1 PE=1 SV=1
P14625	HSP90B1	52	26	564	0.047453	0.012777	1.1	cuk2	cuk3	Endoplasmin GN=HSP90B1 PE=1 SV=1
P08670	VIM	52	22	676	0.001112	0.00075	1.27	cuk3	cuk2	Vimentin GN=VIM PE=1 SV=4
P60709	ACTB	66	15	1010	0.001635	0.000981	1.48	cuk3	cuk2	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1

Table S11: Statistical overrepresentation test of the identified allergy related proteins following $DMT_{A\beta 1\text{-}6}$ and $DMT_{A\beta 17\text{-}23}$ by PANTHER. Herein, FDR indicates false discovery rate. Displaying only results for FDR $P < 0.05$.

Reactome pathways	**Fold Enrichment**	**Raw P value**	**FDR**
Anti-A$\beta_{1\text{-}6}$ Antibody Treatment			
Unclassified	< 0.01	2.06E-06	5.13E-03
Anti-A$\beta_{17\text{-}23}$ Antibody Treatment			
Interleukin-4 and Interleukin-13 signaling	43.64	2.07E-06	5.16E-03
Signaling by Interleukins	13.52	2.50E-05	1.56E-02

Table S12: Gene enriched term and their associated genes for the identified allergy related genes following ${}_{Allg}DMT_{A\beta 1\text{-}6}$ and ${}_{Allg}DMT_{A\beta 17\text{-}23}$.

Description	Hits	LogP	Log(q-value)
response to hormone	ANXA1|DSG1|PCNA|PHB1|PIK3C2A|PPARD|TBC1D4	-6.88025	-2.87477
retina homeostasis	ACTB|ALB|PRDX1|TF	-6.8678	-2.87477
cellular response to chemical stress	ANXA1|MYLK|PRDX1|PCNA|PPIA	-6.74433	-2.87477
Interleukin-4 and Interleukin-13 signaling	ANXA1|HSP90B1|TYK2|VIM	-6.56557	-2.82094
Vesicle-mediated transport	ACTB|ALB|PIK3C2A|TF|HSP90B1|TBC1D4	-5.7531	-2.18456
DNA biosynthetic process	PCNA|PHB1|RAD50	-4.69472	-1.70907
Cellular responses to stress	ALB|EEF1A1|PRDX1|HSP90B1|RAD50	-4.19601	-1.40296
Neutrophil degranulation	CTSD|DSG1|EEF1A1|PPIA	-4.00691	-1.29369
regulation of kinase activity	ACTB|EEF1A1|PHB1|PPIA|RAD50	-3.94041	-1.03487
Muscle contraction	ANXA1|MYLK|VIM	-3.84272	-1.18623
cell-cell adhesion	ACTB|ANXA1|DSG1|PPIA	-3.83179	-1.18408
epithelial cell differentiation	ANXA1|PCNA|PGK1|VIM	-3.78249	-1.15181
response to hypoxia	PGK1|PPARD|HSP90B1	-3.60305	-1.02818
positive regulation of hydrolase activity	CTSD|PCNA|PHB1|TBC1D4	-3.48727	-0.97943
Signaling by Rho GTPases	ACTB|DSG1|MYLK|VIM	-3.36404	-0.93541
regulation of protein stability	DSG1|PHB1|TF	-3.14981	-0.79435
Metabolism of lipids	ALB|PIK3C2A|PPARD	-2.35781	-0.21252

Table S13: Identified apoptosis-related proteins following DMT$_{A\beta1\text{-}6}$, DMT$_{A\beta17\text{-}23}$ compared to untreated cells. Herein, CuK1= Aβ1-6; Cuk2= Aβ17-23; CuK3=NoT

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-Aβ_{1-6} Antibody Treatment										
Q8N163	CCAR2	8	4	41.6	0.004323	0.001929	2.36	cuk3	cuk1	Cell cycle and apoptosis regulator protein 2 GN=CCAR2 PE=1 SV=2
Q8IVF5	TIAM2	10	3	43.9	0.002479	0.001277	3.49	cuk1	cuk3	T-lymphoma invasion and metastasis-inducing protein 2 GN=TIAM2 PE=2 SV=4
P49773	HINT1	4	2	44.7	0.000726	0.000554	2.74	cuk1	cuk3	Histidine triad nucleotide-binding protein 1 GN=HINT1 PE=1 SV=2
P27348	YWHAQ	6	3	45	0.000901	0.000623	6.87	cuk3	cuk1	14-3-3 protein theta GN=YWHAQ PE=1 SV=1
P62979	RPS27A	6	3	46.9	0.000223	0.000255	10.5	cuk3	cuk1	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
P62753	RPS6	8	4	51.5	0.004989	0.002134	1.92	cuk3	cuk1	40S ribosomal protein S6 GN=RPS6 PE=1 SV=1
P04083	ANXA1	9	3	54.8	0.000105	0.000153	2.69	cuk3	cuk1	Annexin A1 GN=ANXA1 PE=1 SV=2
Q03181	PPARD	7	2	67.2	0.002091	0.001131	1.99	cuk1	cuk3	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1
P17987	TCP1	10	4	67.5	0.00026	0.000283	1.59	cuk3	cuk1	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
P61247	RPS3A	11	5	86.8	3.98E-05	8.55E-05	2.93	cuk3	cuk1	40S ribosomal protein S3a GN=RPS3A PE=1 SV=2
P35232	PHB	15	9	97.2	0.002467	0.001273	1.32	cuk3	cuk1	Prohibitin GN=PHB PE=1 SV=1
P06748	NPM1	9	4	102	4.29E-05	8.98E-05	3.16	cuk3	cuk1	Nucleophosmin GN=NPM1 PE=1 SV=2
Q15233	NONO	17	7	108	0.022259	0.006849	1.24	cuk1	cuk3	Non-POU domain-containing octamer-binding protein GN=NONO PE=1 SV=4
P07196	NEFL	15	3	113	0.019655	0.006177	1.86	cuk3	cuk1	Neurofilament light polypeptide GN=NEFL PE=1 SV=3
P32119	PRDX2	10	5	114	9.3E-05	0.000141	2.4	cuk1	cuk3	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
P08133	ANXA6	18	7	134	0.023401	0.007171	1.47	cuk1	cuk3	Annexin A6 GN=ANXA6 PE=1 SV=3
Q12931	TRAP1	18	8	143	4.3E-05	8.98E-05	2.11	cuk1	cuk3	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
P55072	VCP	22	7	157	0.046573	0.012791	1.14	cuk3	cuk1	Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4
E9PK25	CFL1	15	4	163	0.001982	0.001087	1.24	cuk1	cuk3	Cofilin-1 GN=CFL1 PE=1 SV=1
Q15811	ITSN1	28	6	174	3.09E-05	7.62E-05	9.38	cuk1	cuk3	Intersectin-1 GN=ITSN1 PE=1 SV=3
P07237	P4HB	23	9	201	0.004832	0.002096	1.41	cuk1	cuk3	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
Q05639	EEF1A2	17	2	202	0.004611	0.00202	1.64	cuk3	cuk1	Elongation factor 1-alpha 2 GN=EEF1A2 PE=1 SV=1
P61978	HNRNPK	30	4	248	3.84E-05	8.36E-05	2.7	cuk1	cuk3	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
Q9Y4L1	HYOU1	39	18	290	0.027309	0.008181	1.57	cuk1	cuk3	Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1
P38646	HSPA9	40	21	309	0.000642	0.000515	1.58	cuk1	cuk3	Stress-70 protein_ mitochondrial GN=HSPA9 PE=1 SV=2
P02768	ALB	35	24	319	0.002915	0.001439	1.88	cuk1	cuk3	Serum albumin GN=ALB PE=1 SV=2
P04406	GAPDH	33	5	334	0.048566	0.013267	1.21	cuk3	cuk1	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P08238	HSP90AB1	38	12	379	3.1E-05	7.62E-05	5.49	cuk1	cuk3	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
P11021	HSPA5	43	25	466	0.000628	0.000509	1.65	cuk1	cuk3	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P14625	HSP90B1	52	26	564	0.000455	0.000404	1.23	cuk3	cuk1	Endoplasmin GN=HSP90B1 PE=1 SV=1
P68032	ACTC1	54	11	688	1.35E-06	1.97E-05	3.89	cuk3	cuk1	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
Anti-Aβ_{17-23} Antibody Treatment										
Q8N163	CCAR2	8	4	41.6	0.000296	0.00032	2.76	cuk3	cuk2	Cell cycle and apoptosis regulator protein 2 GN=CCAR2 PE=1 SV=2
Q8IVF5	TIAM2	10	3	43.9	0.002187	0.001215	2.9	cuk2	cuk3	T-lymphoma invasion and metastasis-inducing protein 2 GN=TIAM2 PE=2 SV=4
P27348	YWHAQ	6	3	45	0.009973	0.003726	1.34	cuk2	cuk3	14-3-3 protein theta GN=YWHAQ PE=1 SV=1
Q13247	SRSF6	5	4	45.3	0.002185	0.001215	1.45	cuk2	cuk3	Serine/arginine-rich splicing factor 6 GN=SRSF6 PE=1 SV=2
P62979	RPS27A	6	3	46.9	0.001275	0.000827	1.82	cuk2	cuk3	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
P62753	RPS6	8	4	51.5	0.008689	0.003343	1.61	cuk3	cuk2	40S ribosomal protein S6 GN=RPS6 PE=1 SV=1
Q9NYF8	BCLAF1	10	5	52.8	0.002255	0.001234	1.55	cuk2	cuk3	Bcl-2-associated transcription factor 1 GN=BCLAF1 PE=1 SV=2
P04083	ANXA1	9	3	54.8	5.13E-06	3.09E-05	1.94	cuk3	cuk2	Annexin A1 GN=ANXA1 PE=1 SV=2
Q03181	PPARD	7	2	67.2	0.037875	0.01074	1.21	cuk2	cuk3	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1
P06748	NPM1	9	4	102	0.005529	0.002384	1.16	cuk3	cuk2	Nucleophosmin GN=NPM1 PE=1 SV=2
P07196	NEFL	15	3	113	0.000186	0.000245	2.45	cuk3	cuk2	Neurofilament light polypeptide GN=NEFL PE=1 SV=3
P32119	PRDX2	10	5	114	0.010567	0.003885	1.29	cuk3	cuk2	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
P17844	DDX5	18	7	123	0.000458	0.000417	1.71	cuk2	cuk3	Probable ATP-dependent RNA helicase DDX5 GN=DDX5 PE=1 SV=1
P08133	ANXA6	18	7	134	0.002085	0.001177	1.77	cuk3	cuk2	Annexin A6 GN=ANXA6 PE=1 SV=3
Q12931	TRAP1	18	8	143	0.011339	0.004101	1.32	cuk2	cuk3	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
P05787	KRT8	19	8	156	0.014572	0.004983	1.35	cuk2	cuk3	Keratin_ type II cytoskeletal 8 GN=KRT8 PE=1 SV=7
P55072	VCP	22	7	157	0.008122	0.003185	1.13	cuk2	cuk3	Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4
E9PK25	CFL1	15	4	163	0.000172	0.000237	1.43	cuk3	cuk2	Cofilin-1 GN=CFL1 PE=1 SV=1
P07237	P4HB	23	9	201	0.00565	0.002425	2.47	cuk3	cuk2	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
P61978	HNRNPK	30	4	248	0.000165	0.000232	2.41	cuk2	cuk3	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
Q9Y4L1	HYOU1	39	18	290	3.31E-05	9.99E-05	2.33	cuk2	cuk3	Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1
P38646	HSPA9	40	21	309	0.002201	0.001215	1.47	cuk2	cuk3	Stress-70 protein_ mitochondrial GN=HSPA9 PE=1 SV=2
P02768	ALB	35	24	319	0.000256	0.000293	1.43	cuk3	cuk2	Serum albumin GN=ALB PE=1 SV=2
P08238	HSP90AB1	38	12	379	0.003283	0.001618	1.23	cuk3	cuk2	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
P11021	HSPA5	43	25	466	0.025384	0.007751	1.25	cuk2	cuk3	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P14625	HSP90B1	52	26	564	0.047453	0.012777	1.1	cuk2	cuk3	Endoplasmin GN=HSP90B1 PE=1 SV=1
P68032	ACTC1	54	11	688	8.02E-05	0.000158	1.68	cuk3	cuk2	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1

Table S14: Statistical overrepresentation test of the identified apoptosis related proteins following DMT$_{A\beta 1\text{-}6}$ and DMT$_{A\beta 17\text{-}23}$ by PANTHER. Herein, FDR indicates false discovery rate. Displaying only results for FDR $P < 0.05$.

Reactome pathways	**Fold Enrichment**	**Raw P value**	**FDR**
Anti-Aβ$_{1\text{-}6}$ Antibody Treatment			
ATF6 (ATF6-alpha) activates chaperone genes	> 100	1.44E-04	1.99E-02
ATF6 (ATF6-alpha) activates chaperones	> 100	2.03E-04	2.31E-02
Unfolded Protein Response (UPR)	19.96	4.95E-04	3.74E-02
Cellular responses to stress	10.96	5.85E-11	1.46E-07
Josephin domain DUBs	> 100	2.37E-04	2.46E-02
HSF1 activation	> 100	2.37E-04	2.36E-02
Cellular response to heat stress	34.41	4.20E-07	3.49E-04
Sema3A PAK dependent Axon repulsion	75.69	3.97E-04	3.41E-02
Axon guidance	6.62	2.62E-04	2.51E-02
Nervous system development	6.33	3.31E-04	2.95E-02
Nuclear events stimulated by ALK signaling in cancer	67.28	4.92E-04	3.83E-02
Diseases of signal transduction by growth factor receptors and second messengers	7.24	6.04E-04	3.77E-02
Translesion Synthesis by POLH	63.74	5.43E-04	3.76E-02
Chaperone Mediated Autophagy	55.05	7.12E-04	4.03E-02
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	49.10	3.88E-05	9.67E-03
Interleukin-12 signaling	52.66	1.34E-06	8.37E-04
Interleukin-12 family signaling	43.25	2.81E-06	1.40E-03
Signaling by Interleukins	9.46	7.80E-06	2.78E-03
Cytokine Signaling in Immune system	6.08	1.26E-04	2.25E-02
Formation of the ternary complex, and subsequently, the 43S complex	35.62	9.59E-05	2.17E-02
Cap-dependent Translation Initiation	15.27	1.06E-03	4.97E-02
Eukaryotic Translation Initiation	15.27	1.06E-03	4.88E-02
Ribosomal scanning and start codon recognition	31.32	1.38E-04	2.15E-02
Translation initiation complex formation	31.32	1.38E-04	2.02E-02
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	30.79	1.45E-04	1.90E-02
Hedgehog ligand biogenesis	28.39	1.82E-04	2.17E-02
Regulation of HSF1-mediated heat shock response	26.72	2.17E-04	2.35E-02
Cell death signalling via NRAGE, NRIF and NADE	23.90	2.97E-04	2.74E-02
p75 NTR receptor-mediated signalling	18.73	5.93E-04	3.79E-02
Peptide chain elongation	20.41	4.65E-04	3.86E-02
Eukaryotic Translation Elongation	25.77	1.99E-05	5.52E-03
Viral mRNA Translation	20.41	4.65E-04	3.74E-02
Infectious disease	4.74	5.71E-04	3.75E-02
Eukaryotic Translation Termination	19.53	5.27E-04	3.86E-02
Selenocysteine synthesis	19.53	5.27E-04	3.75E-02
Selenoamino acid metabolism	15.66	9.84E-04	4.72E-02
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	19.12	5.60E-04	3.77E-02
Nonsense-Mediated Decay (NMD)	15.80	9.60E-04	4.69E-02
Formation of a pool of free 40S subunits	17.99	6.65E-04	4.05E-02
Response of EIF2AK4 (GCN2) to amino acid deficiency	17.99	6.65E-04	3.95E-02
Binding and Uptake of Ligands by Scavenger Receptors	17.81	6.84E-04	3.97E-02

Post-translational protein phosphorylation	16.98	7.83E-04	4.34E-02
L13a-mediated translational silencing of Ceruloplasmin expression	16.37	8.69E-04	4.61E-02
GTP hydrolysis and joining of the 60S ribosomal subunit	16.22	8.91E-04	4.63E-02
SRP-dependent cotranslational protein targeting to membrane	16.22	8.91E-04	4.53E-02
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	15.80	9.60E-04	4.79E-02
Cellular response to chemical stress	15.73	1.29E-04	2.14E-02
RHO GTPase cycle	6.76	8.23E-04	4.46E-02
Signaling by Rho GTPases	6.33	9.89E-05	2.05E-02
Signaling by Rho GTPases, Miro GTPases and RHOBTB3	6.19	1.13E-04	2.17E-02
Anti-Aβ_{17-23} Antibody Treatment			
ATF6 (ATF6-alpha) activates chaperone genes	> 100	1.12E-04	2.32E-02
ATF6 (ATF6-alpha) activates chaperones	> 100	1.58E-04	2.63E-02
Unfolded Protein Response (UPR)	22.63	3.41E-04	4.04E-02
Cellular responses to stress	11.47	1.71E-10	4.26E-07
Josephin domain DUBs	> 100	1.84E-04	2.70E-02
HSF1 activation	> 100	1.84E-04	2.55E-02
Cellular response to heat stress	38.99	2.18E-07	1.81E-04
Sema3A PAK dependent Axon repulsion	85.79	3.09E-04	3.85E-02
Nuclear events stimulated by ALK signaling in cancer	76.26	3.83E-04	4.15E-02
Translesion Synthesis by POLH	72.24	4.22E-04	4.21E-02
Chaperone Mediated Autophagy	62.39	5.54E-04	4.76E-02
Interleukin-12 signaling	44.76	4.89E-05	1.74E-02
Interleukin-12 family signaling	36.77	8.55E-05	1.94E-02
Signaling by Interleukins	9.19	4.18E-05	1.74E-02
Cytokine Signaling in Immune system	5.91	4.53E-04	4.35E-02
SARS-CoV-1 Infection	41.18	6.20E-05	1.93E-02
SARS-CoV Infections	17.83	7.79E-05	1.94E-02
Infectious disease	5.37	2.52E-04	3.31E-02
Hedgehog ligand biogenesis	32.17	1.25E-04	2.40E-02
Regulation of HSF1-mediated heat shock response	30.28	1.49E-04	2.65E-02
SARS-CoV-2 Infection	29.00	1.68E-04	2.62E-02
Binding and Uptake of Ligands by Scavenger Receptors	20.19	4.71E-04	4.35E-02
Post-translational protein phosphorylation	19.24	5.40E-04	4.81E-02
Cellular response to chemical stress	17.83	7.79E-05	2.16E-02
Signaling by Rho GTPases	6.15	3.68E-04	4.17E-02
Signaling by Rho GTPases, Miro GTPases and RHOBTB3	6.01	4.14E-04	4.30E-02

Table S15: Gene enriched term and their associated genes for the identified apoptosis related genes following ${}_{Apop}DMT_{A\beta 1\text{-}6}$ and ${}_{Apop}DMT_{A\beta 17\text{-}23}$.

Description	**Hits**	**LogP**	**Log(q-value)**
Cellular responses to stress	ALB|HSPA5|HSPA9|HSP90AB1|P4HB|RPS6|RPS27A|PRDX2|HSP90B1|VCP|HYOU1|CCAR2	-13.2289	-9.089159876
regulation of intrinsic apoptotic signaling pathway	HNRNPK|NONO|P4HB|BCLAF1|TRAP1|HYOU1|CCAR2	-9.01412	-5.144553328
protein folding	HSPA5|HSPA9|HSP90AB1|P4HB|TCP1|HSP90B1|TRAP1	-8.86357	-5.361985575
VEGFA-VEGFR2 signaling pathway	ALB|ANXA1|CFL1|GAPDH|P4HB|RPS6|PRDX2|HYOU1	-7.95938	-4.758822079
cellular response to organic cyclic compound	ANXA1|DDX5|HSPA5|HSP90AB1|NPM1|PHB1|PPARD|HSP90B1	-7.04606	-3.699378837
Interleukin-12 signaling	CFL1|HSPA9|P4HB|TCP1	-6.80458	-3.879181608
Eukaryotic Translation Elongation	EEF1A2|RPS3A|RPS6|RPS27A	-5.60484	-2.881401405
Binding and Uptake of Ligands by Scavenger Receptors	ALB|HSP90B1|HYOU1	-5.36255	-2.723436681
biological process involved in symbiotic interaction	CFL1|GAPDH|HSP90AB1|PHB1|TCP1	-5.34336	-2.712681465
Signaling by Rho GTPases	ACTC1|CFL1|HSP90AB1|ITSN1|VCP|YWHAQ|TIAM2	-5.22075	-2.608931297
Cellular response to chemical stress	ALB|P4HB|RPS27A|PRDX2	-5.20743	-2.608931297
reproductive structure development	ANXA1|HSPA5|HSP90AB1|PPARD|RPS6	-4.86261	-2.3909823
negative regulation of neuron apoptotic process	HSP90AB1|NEFL|NONO|HYOU1	-4.83919	-2.378992065
Regulation of HSF1-mediated heat shock response	HSPA5|HSPA9|CCAR2	-4.70903	-2.27260467
homeostasis of number of cells	ANXA1|HSPA9|RPS6|PRDX2	-4.54358	-2.163276002
supramolecular fiber organization	ACTC1|CFL1|HSP90AB1|NEFL|HSP90B1	-4.40563	-2.084246903
regulation of protein catabolic process	EEF1A2|HSP90AB1|PHB1|VCP|CCAR2	-4.32022	-2.026612428
positive regulation of cell death	ANXA1|EEF1A2|PHB1|RPS6|BCLAF1|CCAR2	-4.20953	-1.525602978
regulation of response to DNA damage stimulus	DDX5|HNRNPK|BCLAF1|CCAR2	-4.18725	-1.958260042
Platelet degranulation	ALB|CFL1|HSPA5	-3.8978	-1.780560531

Table S16: Identified proteins following DMAT$_{A\beta 1\text{-}6}$, DMAT$_{A\beta 17\text{-}23}$ compared to untreated cells. Herein, Cuk4=Aβ1-6; Cuk5=Aβ17-23; Cuk6= NoT.

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-A$\beta_{1\text{-}6}$ Antibody Treatment										
O14531	DPYSL4	7	3	40.3	0.000101	0.000563	1.85	cuk6	cuk4	Dihydropyrimidinase-related protein 4 GN=DPYSL4 PE=1 SV=2
Q96GQ7	DDX27	8	3	40.6	0.036395	0.021534	2.08	cuk6	cuk4	Probable ATP-dependent RNA helicase DDX27 GN=DDX27 PE=1 SV=2
Q99733	NAP1L4	7	2	40.7	0.006038	0.005947	1.39	cuk4	cuk6	Nucleosome assembly protein 1-like 4 GN=NAP1L4 PE=1 SV=1
Q86YW9	MED12L	7	5	40.9	0.027357	0.017524	1.46	cuk6	cuk4	Mediator of RNA polymerase II transcription subunit 12-like protein GN=MED12L PE=1 SV=2
Q86VH2	KIF27	7	5	41.3	0.001879	0.00279	1.33	cuk4	cuk6	Kinesin-like protein KIF27 GN=KIF27 PE=2 SV=1
E7EX29	YWHAZ	5	3	41.6	0.000625	0.00137	1.42	cuk4	cuk6	14-3-3 protein zeta/delta (Fragment) GN=YWHAZ PE=1 SV=1
Q8N163	CCAR2	8	4	41.6	0.006093	0.005976	2.09	cuk6	cuk4	Cell cycle and apoptosis regulator protein 2 GN=CCAR2 PE=1 SV=2
A0A087WY36	AKAP13	7	4	41.7	7.42E-05	0.000508	2.72	cuk6	cuk4	A-kinase anchor protein 13 (Fragment) GN=AKAP13 PE=1 SV=1
E9PCN5	CNOT10	6	3	42	0.021583	0.014681	1.62	cuk6	cuk4	CCR4-NOT transcription complex subunit 10 GN=CNOT10 PE=1 SV=1
A0A087X2I1	PSMC6	6	4	42	1.32E-05	0.000206	2.45	cuk4	cuk6	26S proteasome regulatory subunit 10B GN=PSMC6 PE=1 SV=1
P29597	TYK2	8	2	42.1	0.000571	0.001291	2.23	cuk4	cuk6	Non-receptor tyrosine-protein kinase TYK2 GN=TYK2 PE=1 SV=3
Q8IWY7	TTBK2	6	3	42.1	0.014222	0.010689	1.39	cuk6	cuk4	Tau-tubulin kinase GN=TTBK2 PE=1 SV=1
Q9Y5Y9	SCN10A	7	3	42.5	0.003581	0.004222	1.53	cuk4	cuk6	Sodium channel protein type 10 subunit alpha GN=SCN10A PE=1 SV=2
O60237	PPP1R12B	8	4	42.6	0.01306	0.010056	1.39	cuk4	cuk6	Protein phosphatase 1 regulatory subunit 12B GN=PPP1R12B PE=1 SV=2
P23381	WARS1	6	2	42.7	0.003651	0.004251	1.35	cuk6	cuk4	Tryptophan--tRNA ligase_ cytoplasmic GN=WARS PE=1 SV=2
A8MZ36	EVPLL	6	3	42.7	0.048117	0.026699	1.2	cuk6	cuk4	Envoplakin-like protein GN=EVPLL PE=2 SV=1
Q8NFY4	SEMA6D	9	4	42.7	0.00016	0.000653	1.35	cuk4	cuk6	Semaphorin-6D GN=SEMA6D PE=1 SV=1
P26373	RPL13	6	2	42.8	0.00032	0.000909	2.12	cuk4	cuk6	60S ribosomal protein L13 GN=RPL13 PE=1 SV=4
Q569K6	CCDC157	7	4	42.8	0.020065	0.013868	1.3	cuk4	cuk6	Coiled-coil domain-containing protein 157 GN=CCDC157 PE=2 SV=3
O60343	TBC1D4	7	2	43	0.01107	0.008916	1.44	cuk6	cuk4	TBC1 domain family member 4 GN=TBC1D4 PE=1 SV=2
Q9Y536	PPIAL4A	7	3	43.3	0.000558	0.001273	1.72	cuk4	cuk6	Peptidyl-prolyl cis-trans isomerase A-like 4A GN=PPIAL4A PE=2 SV=1
P42166	TMPO	7	3	43.4	0.002718	0.00351	1.82	cuk4	cuk6	Lamina-associated polypeptide 2_ isoform alpha GN=TMPO PE=1 SV=2
P33993	MCM7	6	4	43.5	0.043627	0.024909	1.19	cuk6	cuk4	DNA replication licensing factor MCM7 GN=MCM7 PE=1 SV=4
Q8IVF5	TIAM2	10	3	43.9	0.000421	0.001063	1.94	cuk4	cuk6	T-lymphoma invasion and metastasis-inducing protein 2 GN=TIAM2 PE=2 SV=4
Q96SN8	CDK5RAP2	9	3	43.9	0.006921	0.006403	1.54	cuk4	cuk6	CDK5 regulatory subunit-associated protein 2 GN=CDK5RAP2 PE=1 SV=5
P52948	NUP98	8	3	44	4.58E-06	0.000127	8.47	cuk6	cuk4	Nuclear pore complex protein Nup98-Nup96 GN=NUP98 PE=1 SV=4
Q8IYT4	KATNAL2	7	5	44	0.000342	0.000946	1.65	cuk6	cuk4	Katanin p60 ATPase-containing subunit A-like 2 GN=KATNAL2 PE=1 SV=3
G3V2A4	TEP1	7	4	44.6	8.38E-05	0.000535	2.69	cuk4	cuk6	Telomerase protein component 1 GN=TEP1 PE=1 SV=1
P49773	HINT1	4	2	44.7	0.002123	0.003023	1.82	cuk6	cuk4	Histidine triad nucleotide-binding protein 1 GN=HINT1 PE=1 SV=2
P46776	RPL27A	6	2	44.8	0.000704	0.001452	1.47	cuk6	cuk4	60S ribosomal protein L27a GN=RPL27A PE=1 SV=2
P12004	PCNA	6	4	44.8	0.019921	0.013809	1.35	cuk4	cuk6	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
A0A0D9SF53	DDX3X	5	3	44.9	0.013218	0.010128	1.4	cuk6	cuk4	ATP-dependent RNA helicase DDX3X GN=DDX3X PE=1 SV=1
P53804	TTC3	8	3	45	0.009572	0.008055	1.46	cuk6	cuk4	E3 ubiquitin-protein ligase TTC3 GN=TTC3 PE=1 SV=2
Q8N1G1	REXO1	6	3	45	0.005751	0.005756	1.4	cuk4	cuk6	RNA exonuclease 1 homolog GN=REXO1 PE=1 SV=3
Q9ULE3	DENND2A	7	3	45.1	0.044022	0.025068	1.43	cuk4	cuk6	DENN domain-containing protein 2A GN=DENND2A PE=2 SV=4
Q5SW79	CEP170	9	3	45.5	0.001127	0.001975	1.46	cuk4	cuk6	Centrosomal protein of 170 kDa GN=CEP170 PE=1 SV=1
P07195	LDHB	7	3	46	0.006755	0.006299	1.42	cuk6	cuk4	L-lactate dehydrogenase B chain GN=LDHB PE=1 SV=2
Q8N3U4	STAG2	7	2	46.5	0.000668	0.001419	2.74	cuk6	cuk4	Cohesin subunit SA-2 GN=STAG2 PE=1 SV=3
Q9H1A4	ANAPC1	8	2	46.6	0.00515	0.00527	1.38	cuk4	cuk6	Anaphase-promoting complex subunit 1 GN=ANAPC1 PE=1 SV=1
P62979	RPS27A	6	3	46.9	0.022204	0.014975	2.3	cuk4	cuk6	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
Q9NSY1	BMP2K	8	4	47.4	0.035667	0.021317	1.35	cuk6	cuk4	BMP-2-inducible protein kinase GN=BMP2K PE=1 SV=2
P02461	COL3A1	8	2	47.5	0.001096	0.00195	2.26	cuk4	cuk6	Collagen alpha-1(III) chain GN=COL3A1 PE=1 SV=4
A0A087X0A8	COL12A1	8	4	47.5	0.000299	0.000909	2.29	cuk6	cuk4	Collagen alpha-1(XII) chain GN=COL12A1 PE=1 SV=1
Q9UBZ9	REV1	6	2	47.6	0.049784	0.027371	1.3	cuk4	cuk6	DNA repair protein REV1 GN=REV1 PE=1 SV=1
Q9P0M6	MACROH2A2	6	4	48.2	0.028874	0.018235	1.23	cuk6	cuk4	Core histone macro-H2A.2 GN=H2AFY2 PE=1 SV=3
P62829	RPL23	6	4	48.3	0.007387	0.006716	1.14	cuk6	cuk4	60S ribosomal protein L23 GN=RPL23 PE=1 SV=1
Q96NG3	ODAD4	8	2	48.5	0.000262	0.000838	1.46	cuk4	cuk6	Tetratricopeptide repeat protein 25 GN=TTC25 PE=1 SV=2
A0A1B0GV23	CTSD	9	6	48.6	0.008586	0.007434	1.42	cuk6	cuk4	Cathepsin D GN=CTSD PE=1 SV=1
A2RUB1	MEIOC	7	2	48.9	0.002553	0.00339	1.77	cuk6	cuk4	Meiosis-specific coiled-coil domain-containing protein MEIOC GN=MEIOC PE=2 SV=3
P10586	PTPRF	10	4	48.9	0.003949	0.004446	1.55	cuk6	cuk4	Receptor-type tyrosine-protein phosphatase F GN=PTPRF PE=1 SV=2
P16144	ITGB4	7	5	49	0.001351	0.002235	1.54	cuk4	cuk6	Integrin beta-4 GN=ITGB4 PE=1 SV=5
Q9UQ16	DNM3	10	4	49.2	0.03818	0.022394	1.38	cuk6	cuk4	Dynamin-3 GN=DNM3 PE=1 SV=4
Q8TCU6	PREX1	10	6	49.2	0.004505	0.004819	1.52	cuk4	cuk6	Phosphatidylinositol 3_4_5-trisphosphate-dependent Rac exchanger 1 protein GN=PREX1 PE=1 SV=3
P07384	CAPN1	7	3	49.4	0.009872	0.008188	1.12	cuk6	cuk4	Calpain-1 catalytic subunit GN=CAPN1 PE=1 SV=1
Q96QP1	ALPK1	9	4	49.6	0.002929	0.003693	2.15	cuk4	cuk6	Alpha-protein kinase 1 GN=ALPK1 PE=2 SV=3
P52597	HNRNPF	7	5	49.6	0.048229	0.02673	1.11	cuk4	cuk6	Heterogeneous nuclear ribonucleoprotein F GN=HNRNPF PE=1 SV=3
P13647	KRT5	6	2	49.8	0.002446	0.003285	1.47	cuk6	cuk4	Keratin_ type II cytoskeletal 5 GN=KRT5 PE=1 SV=3
Q96N67	DOCK7	10	2	49.9	6.73E-07	4.16E-05	3.3	cuk6	cuk4	Dedicator of cytokinesis protein 7 GN=DOCK7 PE=1 SV=4
P52756	RBM5	7	3	50.1	0.028247	0.017949	1.17	cuk6	cuk4	RNA-binding protein 5 GN=RBM5 PE=1 SV=2
Q9BY66	KDM5D	10	6	50.5	0.006806	0.006309	2	cuk4	cuk6	Lysine-specific demethylase 5D GN=KDM5D PE=1 SV=2
Q9H792	PEAK1	10	5	50.6	0.002833	0.003629	1.31	cuk6	cuk4	Pseudopodium-enriched atypical kinase 1 GN=PEAK1 PE=1 SV=4
P04004	VTN	7	5	50.6	0.001805	0.002709	1.29	cuk6	cuk4	Vitronectin GN=VTN PE=1 SV=1
Q14117	DPYS	7	2	50.7	0.005764	0.005756	1.22	cuk6	cuk4	Dihydropyrimidinase GN=DPYS PE=1 SV=1
J3KSB5	NF1	10	7	51.1	0.024678	0.016159	1.11	cuk4	cuk6	Neurofibromin (Fragment) GN=NF1 PE=1 SV=1
O43683	BUB1	9	4	51.3	0.045449	0.025635	1.27	cuk4	cuk6	Mitotic checkpoint serine/threonine-protein kinase BUB1 GN=BUB1 PE=1 SV=1
P01308	INS	5	3	51.6	0.000351	0.000964	1.82	cuk6	cuk4	Insulin GN=INS PE=1 SV=1
Q7Z4S6	KIF21A	9	5	51.6	9.75E-06	0.000178	2.36	cuk4	cuk6	Kinesin-like protein KIF21A GN=KIF21A PE=1 SV=2
A0A087WTQ6	SDK1	8	3	51.9	0.001577	0.002465	1.62	cuk6	cuk4	Protein sidekick-1 GN=SDK1 PE=1 SV=1

O60282	KIF5C	8	2	52.3	0.002244	0.00313	1.32	cuk6	cuk4	Kinesin heavy chain isoform 5C GN=KIF5C PE=1 SV=1
Q96RY7	IFT140	7	2	52.4	0.002082	0.002982	1.42	cuk4	cuk6	Intraflagellar transport protein 140 homolog GN=IFT140 PE=1 SV=1
A0A0D9SF60	PKP4	9	2	52.4	0.031057	0.019319	1.19	cuk6	cuk4	Plakophilin-4 GN=PKP4 PE=1 SV=1
Q13136	PPFIA1	9	5	52.5	0.003265	0.003924	1.82	cuk6	cuk4	Liprin-alpha-1 GN=PPFIA1 PE=1 SV=1
A0A0A0MS86	CEP290	7	3	52.6	0.000462	0.001137	1.91	cuk4	cuk6	Centrosomal protein of 290 kDa GN=CEP290 PE=1 SV=1
P35527	KRT9	10	7	52.7	2.61E-06	9.48E-05	4.63	cuk6	cuk4	Keratin_ type I cytoskeletal 9 GN=KRT9 PE=1 SV=3
Q5TB80	CEP162	10	2	52.8	0.006614	0.006228	5.53	cuk6	cuk4	Centrosomal protein of 162 kDa GN=CEP162 PE=1 SV=2
P62917	RPL8	7	4	53.9	0.046899	0.026207	1.1	cuk4	cuk6	60S ribosomal protein L8 GN=RPL8 PE=1 SV=2
Q9H9B1	EHMT1	8	3	54.5	0.002527	0.003365	1.33	cuk6	cuk4	Histone-lysine N-methyltransferase EHMT1 GN=EHMT1 PE=1 SV=4
Q12888	TP53BP1	11	5	54.6	0.000217	0.00077	2.74	cuk4	cuk6	TP53-binding protein 1 GN=TP53BP1 PE=1 SV=2
P04083	ANXA1	9	3	54.8	0.000135	0.000622	2.02	cuk6	cuk4	Annexin A1 GN=ANXA1 PE=1 SV=2
O14715	RGPD8	9	4	56.4	0.000157	0.000653	1.71	cuk6	cuk4	RANBP2-like and GRIP domain-containing protein 8 GN=RGPD8 PE=1 SV=2
E7EPM6	ACSL1	9	3	56.8	0.0023	0.003171	1.62	cuk4	cuk6	Long-chain-fatty-acid--CoA ligase 1 GN=ACSL1 PE=1 SV=1
H7BYL6	AKAP9	11	5	56.8	0.016047	0.011689	1.37	cuk4	cuk6	A-kinase anchor protein 9 (Fragment) GN=AKAP9 PE=1 SV=1
E5RGX5	STMN2	8	3	57.1	0.027563	0.017609	1.25	cuk6	cuk4	Stathmin GN=STMN2 PE=1 SV=1
Q15029	EFTUD2	9	6	57.8	0.003647	0.004251	1.4	cuk4	cuk6	116 kDa U5 small nuclear ribonucleoprotein component GN=EFTUD2 PE=1 SV=1
O75335	PPFIA4	9	4	58.4	0.011559	0.009153	1.26	cuk6	cuk4	Liprin-alpha-4 GN=PPFIA4 PE=2 SV=3
Q8N653	LZTR1	11	4	58.7	0.00064	0.001382	2.61	cuk4	cuk6	Leucine-zipper-like transcriptional regulator 1 GN=LZTR1 PE=1 SV=2
Q9BXT6	MOV10L1	10	2	58.8	0.007261	0.006639	1.55	cuk4	cuk6	RNA helicase Mov10l1 GN=MOV10L1 PE=2 SV=1
A0A087WUK2	HNRNPDL	7	2	58.8	0.004762	0.004991	1.24	cuk6	cuk4	Heterogeneous nuclear ribonucleoprotein D-like GN=HNRNPDL PE=1 SV=1
P09104	ENO2	9	2	59.2	0.045495	0.025635	1.63	cuk4	cuk6	Gamma-enolase GN=ENO2 PE=1 SV=3
Q9BPU6	DPYSL5	9	4	60.4	0.006164	0.005997	1.73	cuk4	cuk6	Dihydropyrimidinase-related protein 5 GN=DPYSL5 PE=1 SV=1
P33991	MCM4	12	7	60.4	3E-06	9.9E-05	2.89	cuk6	cuk4	DNA replication licensing factor MCM4 GN=MCM4 PE=1 SV=5
Q1KMD3	HNRNPUL2	9	2	61.4	0.02361	0.01564	1.34	cuk6	cuk4	Heterogeneous nuclear ribonucleoprotein U-like protein 2 GN=HNRNPUL2 PE=1 SV=1
P12035	KRT3	8	3	61.6	0.007702	0.006851	1.19	cuk6	cuk4	Keratin_ type II cytoskeletal 3 GN=KRT3 PE=1 SV=3
Q6ZU80	CEP128	13	5	62.2	5.34E-05	0.000436	1.63	cuk4	cuk6	Centrosomal protein of 128 kDa GN=CEP128 PE=1 SV=2
P29400	COL4A5	11	4	62.5	6.6E-05	0.000484	1.48	cuk4	cuk6	Collagen alpha-5(IV) chain GN=COL4A5 PE=1 SV=2
Q6P280	ZNF529	9	2	62.8	0.013855	0.01048	1.61	cuk4	cuk6	Zinc finger protein 529 GN=ZNF529 PE=1 SV=2
Q6PIF6	MYO7B	10	3	63	0.023486	0.015616	1.31	cuk6	cuk4	Unconventional myosin-VIIb GN=MYO7B PE=1 SV=2
Q9P275	USP36	11	6	63.4	0.000725	0.001484	1.69	cuk4	cuk6	Ubiquitin carboxyl-terminal hydrolase 36 GN=USP36 PE=1 SV=4
P08865	RPSA	9	4	63.5	0.003357	0.003998	1.67	cuk6	cuk4	40S ribosomal protein SA GN=RPSA PE=1 SV=4
E7EPS8	PTPRM	11	6	63.5	0.007628	0.00684	1.5	cuk6	cuk4	Receptor-type tyrosine-protein phosphatase mu GN=PTPRM PE=1 SV=2
Q7L014	DDX46	12	7	63.5	0.010016	0.008263	1.85	cuk6	cuk4	Probable ATP-dependent RNA helicase DDX46 GN=DDX46 PE=1 SV=2
Q9P2M7	CGN	12	5	63.7	0.008184	0.007164	1.27	cuk6	cuk4	Cingulin GN=CGN PE=1 SV=2
Q8ND30	PPFIBP2	10	5	64.2	0.030128	0.018831	1.16	cuk6	cuk4	Liprin-beta-2 GN=PPFIBP2 PE=1 SV=3
O95153	TSPOAP1	10	4	64.5	0.000159	0.000653	2.36	cuk6	cuk4	Peripheral-type benzodiazepine receptor-associated protein 1 GN=TSPOAP1 PE=1 SV=2
Q8NI27	THOC2	11	5	64.5	0.00223	0.003128	1.88	cuk6	cuk4	THO complex subunit 2 GN=THOC2 PE=1 SV=2
P31930	UQCRC1	10	3	64.6	0.005047	0.005209	1.53	cuk6	cuk4	Cytochrome b-c1 complex subunit 1_ mitochondrial GN=UQCRC1 PE=1 SV=3
Q15746	MYLK	10	6	64.8	5.01E-05	0.000431	1.77	cuk6	cuk4	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
O75970	MPDZ	12	2	65.3	0.032752	0.020161	1.27	cuk6	cuk4	Multiple PDZ domain protein GN=MPDZ PE=1 SV=2
Q92805	GOLGA1	11	5	66.3	9.78E-06	0.000178	1.63	cuk6	cuk4	Golgin subfamily A member 1 GN=GOLGA1 PE=1 SV=3
Q99460	PSMD1	11	3	66.7	8.67E-07	4.16E-05	2.14	cuk4	cuk6	26S proteasome non-ATPase regulatory subunit 1 GN=PSMD1 PE=1 SV=2
Q96QT6	PHF12	9	4	66.7	0.000268	0.00085	1.72	cuk4	cuk6	PHD finger protein 12 GN=PHF12 PE=1 SV=2
Q03252	LMNB2	9	3	67.5	3.13E-05	0.000308	4.64	cuk4	cuk6	Lamin-B2 GN=LMNB2 PE=1 SV=4
P17987	TCP1	10	4	67.5	0.001525	0.002411	1.44	cuk6	cuk4	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
O43166	SIPA1L1	12	3	68.6	1.83E-05	0.000247	4.07	cuk6	cuk4	Signal-induced proliferation-associated 1-like protein 1 GN=SIPA1L1 PE=1 SV=4
P13637	ATP1A3	9	2	69.4	3.39E-05	0.000321	1.54	cuk4	cuk6	Sodium/potassium-transporting ATPase subunit alpha-3 GN=ATP1A3 PE=1 SV=3
F5H2F4	MTHFD1	10	2	69.5	0.006591	0.006222	1.54	cuk4	cuk6	C-1-tetrahydrofolate synthase_ cytoplasmic GN=MTHFD1 PE=1 SV=1
P46782	RPS5	8	6	69.7	0.036318	0.021516	1.17	cuk6	cuk4	40S ribosomal protein S5 GN=RPS5 PE=1 SV=4
P84103	SRSF3	9	5	70.5	1.15E-05	0.000193	1.72	cuk6	cuk4	Serine/arginine-rich splicing factor 3 GN=SRSF3 PE=1 SV=1
Q96SE7	ZNF347	9	3	71.1	0.006493	0.006187	1.8	cuk6	cuk4	Zinc finger protein 347 GN=ZNF347 PE=1 SV=2
O94885	SASH1	13	3	71.2	0.007596	0.00684	1.34	cuk6	cuk4	SAM and SH3 domain-containing protein 1 GN=SASH1 PE=1 SV=3
O14513	NCKAP5	12	3	71.4	0.01743	0.012485	1.42	cuk4	cuk6	Nck-associated protein 5 GN=NCKAP5 PE=1 SV=2
Q12840	KIF5A	11	4	71.4	0.002051	0.002966	1.6	cuk6	cuk4	Kinesin heavy chain isoform 5A GN=KIF5A PE=1 SV=2
Q66GS9	CEP135	14	5	71.4	0.001898	0.002804	1.41	cuk6	cuk4	Centrosomal protein of 135 kDa GN=CEP135 PE=1 SV=2
Q96F07	CYFIP2	10	2	72.2	0.014784	0.011006	1.26	cuk4	cuk6	Cytoplasmic FMR1-interacting protein 2 GN=CYFIP2 PE=1 SV=2
P62280	RPS11	9	3	72.7	0.00084	0.001642	1.5	cuk4	cuk6	40S ribosomal protein S11 GN=RPS11 PE=1 SV=3
O15075	DCLK1	11	2	73.9	0.025057	0.016339	1.1	cuk6	cuk4	Serine/threonine-protein kinase DCLK1 GN=DCLK1 PE=1 SV=2
P49321	NASP	12	6	74.1	0.000122	0.000581	2.29	cuk6	cuk4	Nuclear autoantigenic sperm protein GN=NASP PE=1 SV=2
P05023	ATP1A1	10	2	74.3	0.035184	0.021108	1.13	cuk4	cuk6	Sodium/potassium-transporting ATPase subunit alpha-1 GN=ATP1A1 PE=1 SV=1
A6NC98	CCDC88B	13	4	74.8	0.001506	0.002393	1.33	cuk4	cuk6	Coiled-coil domain-containing protein 88B GN=CCDC88B PE=1 SV=1
D3DQV9	EIF4G2	14	5	75.1	0.000873	0.001692	1.39	cuk4	cuk6	Eukaryotic translation initiation factor 4 gamma 2 (Fragment) GN=EIF4G2 PE=1 SV=1
Q03468	ERCC6	13	4	75.3	0.039195	0.022933	1.69	cuk4	cuk6	DNA excision repair protein ERCC-6 GN=ERCC6 PE=1 SV=1
P23396	RPS3	11	4	75.3	0.048532	0.026835	1.51	cuk4	cuk6	40S ribosomal protein S3 GN=RPS3 PE=1 SV=2
O00299	CLIC1	11	6	77.6	0.000221	0.000774	1.72	cuk6	cuk4	Chloride intracellular channel protein 1 GN=CLIC1 PE=1 SV=4
Q9Y4F4	TOGARAM1	15	10	77.6	2.14E-05	0.000266	3.29	cuk6	cuk4	TOG array regulator of axonemal microtubules protein 1 GN=TOGARAM1 PE=1 SV=4
O00264	PGRMC1	10	6	79.3	0.004901	0.005106	1.44	cuk4	cuk6	Membrane-associated progesterone receptor component 1 GN=PGRMC1 PE=1 SV=3
P22234	PAICS	12	4	79.9	0.004611	0.004887	1.21	cuk6	cuk4	Multifunctional protein ADE2 GN=PAICS PE=1 SV=3
P53396	ACLY	13	5	81.6	0.000112	0.000574	2.12	cuk4	cuk6	ATP-citrate synthase GN=ACLY PE=1 SV=3
P50914	RPL14	10	5	81.6	0.007643	0.00684	1.31	cuk4	cuk6	60S ribosomal protein L14 GN=RPL14 PE=1 SV=4
A0A0G2JNB1	KANSL1	13	4	81.7	0.0348	0.020931	1.24	cuk4	cuk6	KAT8 regulatory NSL complex subunit 1 GN=KANSL1 PE=1 SV=1
Q8WVM7	STAG1	13	6	81.9	0.000372	0.000988	1.86	cuk4	cuk6	Cohesin subunit SA-1 GN=STAG1 PE=1 SV=3
Q99536	VAT1	11	7	84.8	0.041466	0.023936	1.11	cuk6	cuk4	Synaptic vesicle membrane protein VAT-1 homolog GN=VAT1 PE=1 SV=2
Q9H0X9	OSBPL5	13	4	85.4	6.42E-07	4.16E-05	5.47	cuk6	cuk4	Oxysterol-binding protein-related protein 5 GN=OSBPL5 PE=1 SV=1
O75122	CLASP2	13	5	85.6	0.035146	0.021108	1.31	cuk6	cuk4	CLIP-associating protein 2 GN=CLASP2 PE=1 SV=2
Q9UG01	IFT172	16	6	85.7	0.008875	0.007615	2.04	cuk4	cuk6	Intraflagellar transport 172 homolog GN=IFT172 PE=1 SV=2
Q9BY12	SCAPER	16	9	86.2	0.000232	0.000776	2.32	cuk4	cuk6	S phase cyclin A-associated protein in the endoplasmic reticulum GN=SCAPER PE=1 SV=2
Q15276	RABEP1	15	4	87.3	3.62E-05	0.000329	2.3	cuk6	cuk4	Rab GTPase-binding effector protein 1 GN=RABEP1 PE=1 SV=2
O43491	EPB41L2	16	3	87.5	0.000175	0.000702	1.75	cuk6	cuk4	Band 4.1-like protein 2 GN=EPB41L2 PE=1 SV=1
P62913	RPL11	8	3	87.6	2.45E-05	0.000286	2.47	cuk4	cuk6	60S ribosomal protein L11 GN=RPL11 PE=1 SV=2
Q6WCQ1	MPRIP	15	5	88	0.002165	0.003046	1.54	cuk6	cuk4	Myosin phosphatase Rho-interacting protein GN=MPRIP PE=1 SV=3
Q8NI35	PATJ	15	3	89.3	0.00375	0.004284	1.42	cuk4	cuk6	InaD-like protein GN=PATJ PE=1 SV=3

Q8N960	CEP120	14	2	91.1	0.000574	0.001291	2.04	cuk4	cuk6	Centrosomal protein of 120 kDa GN=CEP120 PE=1 SV=2
Q92598	HSPH1	14	6	91.4	0.009575	0.008055	1.26	cuk6	cuk4	Heat shock protein 105 kDa GN=HSPH1 PE=1 SV=1
P34897	SHMT2	15	10	93.2	0.003765	0.004289	1.37	cuk6	cuk4	Serine hydroxymethyltransferase_ mitochondrial GN=SHMT2 PE=1 SV=3
Q3V6T2	CCDC88A	17	7	94.6	0.003523	0.004164	1.37	cuk4	cuk6	Girdin GN=CCDC88A PE=1 SV=2
Q5JU85	IQSEC2	16	9	94.9	0.014082	0.010618	1.73	cuk6	cuk4	IQ motif and SEC7 domain-containing protein 2 GN=IQSEC2 PE=1 SV=2
P62424	RPL7A	15	8	95	0.003954	0.004446	1.52	cuk4	cuk6	60S ribosomal protein L7a GN=RPL7A PE=1 SV=2
Q7L576	CYFIP1	15	3	95.4	0.001669	0.002562	1.75	cuk6	cuk4	Cytoplasmic FMR1-interacting protein 1 GN=CYFIP1 PE=1 SV=1
Q92841	DDX17	15	6	95.6	0.019836	0.01379	1.13	cuk6	cuk4	Probable ATP-dependent RNA helicase DDX17 GN=DDX17 PE=1 SV=2
E7EVA0	MAP4	17	6	97.2	0.025116	0.016355	1.18	cuk4	cuk6	Microtubule-associated protein GN=MAP4 PE=1 SV=1
Q14103	HNRNPD	13	4	98.7	0.01399	0.010565	1.5	cuk6	cuk4	Heterogeneous nuclear ribonucleoprotein D0 GN=HNRNPD PE=1 SV=1
Q9HCM1	RESF1	19	6	101	0.03327	0.020269	1.2	cuk4	cuk6	Uncharacterized protein KIAA1551 GN=KIAA1551 PE=1 SV=3
Q08211	DHX9	18	12	101	0.032936	0.020169	1.1	cuk4	cuk6	ATP-dependent RNA helicase A GN=DHX9 PE=1 SV=4
P06748	NPM1	9	4	102	0.022784	0.015234	1.32	cuk6	cuk4	Nucleophosmin GN=NPM1 PE=1 SV=2
O14529	CUX2	17	5	102	0.009942	0.008217	1.53	cuk4	cuk6	Homeobox protein cut-like 2 GN=CUX2 PE=1 SV=4
Q06830	PRDX1	13	6	102	0.010672	0.008698	1.15	cuk6	cuk4	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
Q86U86	PBRM1	18	5	103	0.000676	0.001426	1.56	cuk6	cuk4	Protein polybromo-1 GN=PBRM1 PE=1 SV=1
Q99623	PHB2	16	7	104	0.011483	0.009123	1.27	cuk4	cuk6	Prohibitin-2 GN=PHB2 PE=1 SV=2
Q14974	KPNB1	14	7	106	0.000301	0.000909	2.92	cuk4	cuk6	Importin subunit beta-1 GN=KPNB1 PE=1 SV=2
Q15084	PDIA6	13	8	106	0.002581	0.003418	1.33	cuk6	cuk4	Protein disulfide-isomerase A6 GN=PDIA6 PE=1 SV=1
Q9C0D4	ZNF518B	17	6	107	0.049536	0.027294	1.18	cuk6	cuk4	Zinc finger protein 518B GN=ZNF518B PE=1 SV=2
P07737	PFN1	11	9	108	9.96E-05	0.000563	2.46	cuk4	cuk6	Profilin-1 GN=PFN1 PE=1 SV=2
Q13263	TRIM28	17	6	109	0.006234	0.006027	1.41	cuk6	cuk4	Transcription intermediary factor 1-beta GN=TRIM28 PE=1 SV=5
Q3MJ40	CCDC144B	19	2	111	0.002116	0.003022	1.42	cuk6	cuk4	Coiled-coil domain-containing protein 144B GN=CCDC144B PE=2 SV=1
P27635	RPL10	13	6	111	0.041121	0.023824	1.11	cuk4	cuk6	60S ribosomal protein L10 GN=RPL10 PE=1 SV=4
P02765	AHSG	13	9	112	0.038059	0.022351	1.18	cuk6	cuk4	Alpha-2-HS-glycoprotein GN=AHSG PE=1 SV=1
P07196	NEFL	15	3	113	0.006072	0.005968	1.95	cuk6	cuk4	Neurofilament light polypeptide GN=NEFL PE=1 SV=3
Q9UHF7	TRPS1	21	7	113	0.040054	0.02332	1.25	cuk6	cuk4	Zinc finger transcription factor Trps1 GN=TRPS1 PE=1 SV=2
P32119	PRDX2	10	5	114	0.000697	0.001446	1.29	cuk6	cuk4	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
Q6ZN16	MAP3K15	16	5	114	0.00229	0.003165	1.26	cuk4	cuk6	Mitogen-activated protein kinase kinase kinase 15 GN=MAP3K15 PE=1 SV=2
Q58FF3	HSP90B2P	16	6	114	0.007709	0.006851	1.4	cuk4	cuk6	Putative endoplasmin-like protein GN=HSP90B2P PE=5 SV=1
Q8N7X0	ADGB	18	4	115	0.018232	0.012884	1.41	cuk6	cuk4	Androglobin GN=ADGB PE=2 SV=3
P27824	CANX	14	7	115	0.004011	0.004466	1.31	cuk6	cuk4	Calnexin GN=CANX PE=1 SV=2
Q5JSZ5	PRRC2B	18	6	116	0.000696	0.001446	1.27	cuk4	cuk6	Protein PRRC2B GN=PRRC2B PE=1 SV=2
A6QL64	ANKRD36	21	8	117	0.000376	0.000988	1.73	cuk6	cuk4	Ankyrin repeat domain-containing protein 36A GN=ANKRD36 PE=2 SV=3
Q8N1I0	DOCK4	20	8	118	0.001557	0.002453	1.43	cuk4	cuk6	Dedicator of cytokinesis protein 4 GN=DOCK4 PE=1 SV=3
Q9H4B7	TUBB1	10	2	119	0.001374	0.002255	1.51	cuk4	cuk6	Tubulin beta-1 chain GN=TUBB1 PE=1 SV=1
O60292	SIPA1L3	21	12	120	0.002496	0.003333	1.23	cuk6	cuk4	Signal-induced proliferation-associated 1-like protein 3 GN=SIPA1L3 PE=1 SV=3
P48741	HSPA7	14	3	121	0.004647	0.004893	1.45	cuk6	cuk4	Putative heat shock 70 kDa protein 7 GN=HSPA7 PE=5 SV=2
Q16658	FSCN1	16	9	121	8.12E-07	4.16E-05	2.04	cuk6	cuk4	Fascin GN=FSCN1 PE=1 SV=3
P04264	KRT1	17	6	122	5.66E-05	0.000439	1.94	cuk6	cuk4	Keratin_ type II cytoskeletal 1 GN=KRT1 PE=1 SV=6
P62805	H4C1	10	6	123	8.86E-05	0.000546	2.27	cuk6	cuk4	Histone H4 GN=HIST1H4A PE=1 SV=2
Q7RTP6	MICAL3	23	6	123	0.006556	0.006211	1.3	cuk4	cuk6	[F-actin]-monooxygenase MICAL3 GN=MICAL3 PE=1 SV=2
P55795	HNRNPH2	18	4	125	0.000203	0.000748	1.28	cuk6	cuk4	Heterogeneous nuclear ribonucleoprotein H2 GN=HNRNPH2 PE=1 SV=1
Q6W2J9	BCOR	21	8	125	0.009098	0.007759	1.3	cuk4	cuk6	BCL-6 corepressor GN=BCOR PE=1 SV=1
Q9UDT6	CLIP2	23	9	126	0.001097	0.00195	1.8	cuk4	cuk6	CAP-Gly domain-containing linker protein 2 GN=CLIP2 PE=1 SV=1
P07910	HNRNPC	15	5	132	0.000185	0.000718	2.16	cuk6	cuk4	Heterogeneous nuclear ribonucleoproteins C1/C2 GN=HNRNPC PE=1 SV=4
O75145	PPFIA3	22	11	133	0.001194	0.002053	1.8	cuk6	cuk4	Liprin-alpha-3 GN=PPFIA3 PE=1 SV=3
Q9UPN4	CEP131	21	7	134	0.025822	0.016736	1.23	cuk6	cuk4	Centrosomal protein of 131 kDa GN=CEP131 PE=1 SV=3
P08133	ANXA6	18	7	134	0.004933	0.005114	1.19	cuk6	cuk4	Annexin A6 GN=ANXA6 PE=1 SV=3
C9J7T7	NCOR2	24	7	134	0.02282	0.015234	1.18	cuk6	cuk4	Nuclear receptor corepressor 2 GN=NCOR2 PE=1 SV=3
P36578	RPL4	18	8	134	0.000492	0.001179	1.4	cuk4	cuk6	60S ribosomal protein L4 GN=RPL4 PE=1 SV=5
P62701	RPS4X	16	6	137	0.019864	0.01379	1.08	cuk6	cuk4	40S ribosomal protein S4_ X isoform GN=RPS4X PE=1 SV=2
Q8IWJ2	GCC2	27	11	137	0.000315	0.000909	1.7	cuk6	cuk4	GRIP and coiled-coil domain-containing protein 2 GN=GCC2 PE=1 SV=4
A2RUR9	CCDC144A	22	2	141	0.000321	0.000909	1.62	cuk6	cuk4	Coiled-coil domain-containing protein 144A GN=CCDC144A PE=2 SV=1
Q8NB25	FAM184A	23	7	141	0.007844	0.006925	1.3	cuk4	cuk6	Protein FAM184A GN=FAM184A PE=2 SV=3
Q9BZ29	DOCK9	22	10	142	0.00669	0.006251	1.38	cuk4	cuk6	Dedicator of cytokinesis protein 9 GN=DOCK9 PE=1 SV=2
Q12931	TRAP1	18	8	143	0.00585	0.005786	1.3	cuk6	cuk4	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
Q14240	EIF4A2	19	8	144	0.012932	0.009973	1.33	cuk4	cuk6	Eukaryotic initiation factor 4A-II GN=EIF4A2 PE=1 SV=2
K7ELL7	PRKCSH	18	10	145	0.034748	0.020927	1.15	cuk4	cuk6	Glucosidase 2 subunit beta GN=PRKCSH PE=1 SV=1
P12277	CKB	18	12	145	0.001876	0.00279	1.34	cuk6	cuk4	Creatine kinase B-type GN=CKB PE=1 SV=1
Q16695	H3-4	18	4	147	0.000229	0.000774	2.11	cuk6	cuk4	Histone H3.1t GN=HIST3H3 PE=1 SV=3
Q9NQT8	KIF13B	22	13	147	0.006436	0.006166	1.29	cuk6	cuk4	Kinesin-like protein KIF13B GN=KIF13B PE=1 SV=2
P48681	NES	24	9	150	0.0002	0.000748	1.6	cuk4	cuk6	Nestin GN=NES PE=1 SV=2
P00558	PGK1	20	9	150	0.004034	0.004466	1.47	cuk4	cuk6	Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3
Q86UP2	KTN1	27	11	153	0.013647	0.01039	1.18	cuk4	cuk6	Kinectin GN=KTN1 PE=1 SV=1
P16401	H1-5	13	5	154	0.041237	0.023862	1.12	cuk4	cuk6	Histone H1.5 GN=HIST1H1B PE=1 SV=3
Q6FI13	H2AC18	17	6	154	9.86E-05	0.000563	2.29	cuk6	cuk4	Histone H2A type 2-A GN=HIST2H2AA3 PE=1 SV=3
P04843	RPN1	23	12	155	0.000108	0.000563	1.95	cuk6	cuk4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 GN=RPN1 PE=1 SV=1
P05787	KRT8	19	8	156	0.007764	0.00688	1.39	cuk4	cuk6	Keratin_ type II cytoskeletal 8 GN=KRT8 PE=1 SV=7
Q5THK1	PRR14L	26	9	158	0.000211	0.000763	1.61	cuk4	cuk6	Protein PRR14L GN=PRR14L PE=1 SV=1
Q05682	CALD1	25	7	162	0.009917	0.008211	1.36	cuk6	cuk4	Caldesmon GN=CALD1 PE=1 SV=3
E9PK25	CFL1	15	4	163	0.024237	0.015964	1.1	cuk6	cuk4	Cofilin-1 GN=CFL1 PE=1 SV=1
P62937	PPIA	17	8	163	0.000441	0.001097	1.67	cuk6	cuk4	Peptidyl-prolyl cis-trans isomerase A GN=PPIA PE=1 SV=2
Q8TBY8	PMFBP1	26	12	166	0.000332	0.000924	2.05	cuk6	cuk4	Polyamine-modulated factor 1-binding protein 1 GN=PMFBP1 PE=2 SV=2
P34931	HSPA1L	21	4	168	0.019095	0.013374	1.47	cuk6	cuk4	Heat shock 70 kDa protein 1-like GN=HSPA1L PE=1 SV=2
A6NHL2	TUBAL3	18	5	169	0.001036	0.001885	1.97	cuk4	cuk6	Tubulin alpha chain-like 3 GN=TUBAL3 PE=1 SV=2
Q15365	PCBP1	22	13	171	0.009109	0.007759	1.15	cuk6	cuk4	Poly(rC)-binding protein 1 GN=PCBP1 PE=1 SV=2
P16402	H1-3	14	3	173	0.011859	0.009344	1.39	cuk4	cuk6	Histone H1.3 GN=HIST1H1D PE=1 SV=2
Q15811	ITSN1	28	6	174	0.015478	0.011362	1.7	cuk6	cuk4	Intersectin-1 GN=ITSN1 PE=1 SV=3
P15880	RPS2	22	12	175	0.000985	0.001834	1.6	cuk4	cuk6	40S ribosomal protein S2 GN=RPS2 PE=1 SV=2
A0A0G2JIW1	HSPA1B	21	5	178	0.000411	0.001057	1.72	cuk6	cuk4	Heat shock 70 kDa protein 1B GN=HSPA1B PE=1 SV=1
P31943	HNRNPH1	20	5	183	0.003606	0.00423	1.19	cuk4	cuk6	Heterogeneous nuclear ribonucleoprotein H GN=HNRNPH1 PE=1 SV=4
Q8WX93	PALLD	28	15	183	0.018847	0.013259	1.11	cuk4	cuk6	Palladin GN=PALLD PE=1 SV=3
F8W6I7	HNRNPA1	21	10	190	0.011475	0.009123	1.13	cuk6	cuk4	Heterogeneous nuclear ribonucleoprotein A1 GN=HNRNPA1 PE=1 SV=2
Q05639	EEF1A2	17	2	202	0.029425	0.018498	1.14	cuk6	cuk4	Elongation factor 1-alpha 2 GN=EEF1A2 PE=1 SV=1
Q16778	H2BC21	21	4	207	0.000275	0.000865	2.27	cuk6	cuk4	Histone H2B type 2-E GN=HIST2H2BE PE=1 SV=3

Q15366	PCBP2	21	6	207	0.025794	0.016736	1.09	cuk4	cuk6	Poly(rC)-binding protein 2 GN=PCBP2 PE=1 SV=1
P06733	ENO1	28	12	213	0.001243	0.002107	1.49	cuk4	cuk6	Alpha-enolase GN=ENO1 PE=1 SV=2
P20700	LMNB1	26	11	214	0.004271	0.004649	1.52	cuk4	cuk6	Lamin-B1 GN=LMNB1 PE=1 SV=2
P22626	HNRNPA2B1	24	11	215	5.64E-06	0.00014	2.73	cuk6	cuk4	Heterogeneous nuclear ribonucleoproteins A2/B1 GN=HNRNPA2B1 PE=1 SV=2
Q14194	CRMP1	29	11	215	0.001366	0.002251	1.58	cuk6	cuk4	Dihydropyrimidinase-related protein 1 GN=CRMP1 PE=1 SV=1
Q14980	NUMA1	38	14	221	0.000224	0.000774	1.22	cuk4	cuk6	Nuclear mitotic apparatus protein 1 GN=NUMA1 PE=1 SV=2
P41219	PRPH	24	6	226	0.01012	0.008335	1.15	cuk6	cuk4	Peripherin GN=PRPH PE=1 SV=2
P29762	CRABP1	21	13	246	0.00668	0.006251	1.23	cuk6	cuk4	Cellular retinoic acid-binding protein 1 GN=CRABP1 PE=1 SV=2
P61978	HNRNPK	30	4	248	0.004001	0.004466	1.43	cuk4	cuk6	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
A0A087WWY3	FLNA	41	20	250	0.004395	0.004722	1.26	cuk6	cuk4	Filamin-A GN=FLNA PE=1 SV=1
Q14195	DPYSL3	28	14	269	0.00164	0.002542	1.69	cuk4	cuk6	Dihydropyrimidinase-related protein 3 GN=DPYSL3 PE=1 SV=1
Q9Y4L1	HYOU1	39	18	290	0.000318	0.000909	1.92	cuk4	cuk6	Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1
Q00610	CLTC	44	18	290	0.004757	0.004991	1.32	cuk4	cuk6	Clathrin heavy chain 1 GN=CLTC PE=1 SV=5
P07197	NEFM	41	14	302	0.000382	0.000999	1.35	cuk6	cuk4	Neurofilament medium polypeptide GN=NEFM PE=1 SV=3
Q9BUF5	TUBB6	26	3	314	0.000992	0.001839	2.11	cuk6	cuk4	Tubulin beta-6 chain GN=TUBB6 PE=1 SV=1
P11142	HSPA8	31	18	319	0.005597	0.005629	1.43	cuk6	cuk4	Heat shock cognate 71 kDa protein GN=HSPA8 PE=1 SV=1
P07900	HSP90AA1	35	8	324	0.000262	0.000838	1.57	cuk6	cuk4	Heat shock protein HSP 90-alpha GN=HSP90AA1 PE=1 SV=5
P04406	GAPDH	33	5	334	0.001352	0.002235	1.91	cuk4	cuk6	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P68104	EEF1A1	32	4	335	0.002743	0.003524	1.23	cuk6	cuk4	Elongation factor 1-alpha 1 GN=EEF1A1 PE=1 SV=1
Q5TZA2	CROCC	59	18	354	0.000796	0.001574	1.66	cuk6	cuk4	Rootletin GN=CROCC PE=1 SV=1
P08238	HSP90AB1	38	12	379	0.015276	0.011267	1.24	cuk4	cuk6	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
H0Y6I0	GOLGA4	58	26	382	0.002687	0.003503	1.27	cuk6	cuk4	Golgin subfamily A member 4 (Fragment) GN=GOLGA4 PE=1 SV=1
P13639	EEF2	51	27	415	0.000196	0.000741	1.28	cuk6	cuk4	Elongation factor 2 GN=EEF2 PE=1 SV=4
P11021	HSPA5	43	25	466	0.008819	0.007601	1.47	cuk4	cuk6	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P52272	HNRNPM	50	28	488	0.018118	0.012842	1.18	cuk6	cuk4	Heterogeneous nuclear ribonucleoprotein M GN=HNRNPM PE=1 SV=3
P10809	HSPD1	44	19	497	0.026764	0.017191	1.14	cuk4	cuk6	60 kDa heat shock protein_ mitochondrial GN=HSPD1 PE=1 SV=2
P14625	HSP90B1	52	26	564	0.000312	0.000909	1.81	cuk6	cuk4	Endoplasmin GN=HSP90B1 PE=1 SV=1
P04350	TUBB4A	47	6	599	0.002633	0.003458	1.67	cuk6	cuk4	Tubulin beta-4A chain GN=TUBB4A PE=1 SV=2
Q9BQE3	TUBA1C	46	6	617	0.039572	0.023096	1.77	cuk6	cuk4	Tubulin alpha-1C chain GN=TUBA1C PE=1 SV=1
P02787	TF	62	25	655	0.002431	0.003274	1.2	cuk4	cuk6	Serotransferrin GN=TF PE=1 SV=3
P08670	VIM	52	22	676	0.000206	0.00075	1.38	cuk6	cuk4	Vimentin GN=VIM PE=1 SV=4
P68032	ACTC1	54	11	688	0.032896	0.020169	1.19	cuk6	cuk4	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
Q13885	TUBB2A	50	2	735	0.025993	0.01681	1.23	cuk6	cuk4	Tubulin beta-2A chain GN=TUBB2A PE=1 SV=1
P07437	TUBB	58	7	847	0.002082	0.002982	1.47	cuk6	cuk4	Tubulin beta chain GN=TUBB PE=1 SV=2
P60709	ACTB	66	15	1010	0.001344	0.002235	1.3	cuk6	cuk4	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1
Anti-Aβ$_{17-23}$ Antibody Treatment										
Q96L93	KIF16B	9	5	40	0.001535	0.003071	1.86	cuk6	cuk5	Kinesin-like protein KIF16B GN=KIF16B PE=1 SV=2
Q15700	DLG2	7	4	40.1	0.020914	0.017656	2.55	cuk6	cuk5	Disks large homolog 2 GN=DLG2 PE=1 SV=3
O14531	DPYSL4	7	3	40.3	0.003774	0.005422	1.67	cuk6	cuk5	Dihydropyrimidinase-related protein 4 GN=DPYSL4 PE=1 SV=2
Q99733	NAP1L4	7	2	40.7	0.000716	0.002117	1.61	cuk6	cuk5	Nucleosome assembly protein 1-like 4 GN=NAP1L4 PE=1 SV=1
Q8TF32	ZNF431	6	2	40.9	0.037443	0.026855	1.54	cuk5	cuk6	Zinc finger protein 431 GN=ZNF431 PE=2 SV=2
O75362	ZNF217	8	2	41.1	0.012218	0.011909	1.33	cuk5	cuk6	Zinc finger protein 217 GN=ZNF217 PE=1 SV=1
B7ZM99	MTHFD1L	8	2	41.4	0.046183	0.031327	1.94	cuk5	cuk6	MTHFD1L protein GN=MTHFD1L PE=1 SV=1
E7EX29	YWHAZ	5	3	41.6	0.001726	0.003337	1.38	cuk5	cuk6	14-3-3 protein zeta/delta (Fragment) GN=YWHAZ PE=1 SV=1
Q05BV3	EML5	8	2	41.7	0.012278	0.011944	1.45	cuk5	cuk6	Echinoderm microtubule-associated protein-like 5 GN=EML5 PE=2 SV=3
B4E1Z4		8	2	41.9	0.003575	0.005227	1.7	cuk5	cuk6	cDNA FLJ55673_ highly similar to Complement factor B (EC 3.4.21.47) PE=1 SV=1
Q38SD2	LRRK1	8	2	42	0.004326	0.005988	1.73	cuk6	cuk5	Leucine-rich repeat serine/threonine-protein kinase 1 GN=LRRK1 PE=1 SV=3
A0A087X2I1	PSMC6	6	4	42	0.010167	0.010393	1.13	cuk5	cuk6	26S proteasome regulatory subunit 10B GN=PSMC6 PE=1 SV=1
Q8IWY7	TTBK2	6	3	42.1	0.000728	0.002118	2.02	cuk6	cuk5	Tau-tubulin kinase GN=TTBK2 PE=1 SV=1
A0A087WTP3	KHSRP	7	2	42.6	0.003266	0.00492	1.43	cuk6	cuk5	Far upstream element-binding protein 2 GN=KHSRP PE=1 SV=1
F8VUX9	WDR90	6	4	42.6	0.01491	0.013849	1.32	cuk5	cuk6	WD repeat-containing protein 90 GN=WDR90 PE=1 SV=1
P23381	WARS1	6	2	42.7	0.002577	0.004361	1.18	cuk6	cuk5	Tryptophan--tRNA ligase_ cytoplasmic GN=WARS PE=1 SV=2
A8MZ36	EVPLL	6	3	42.7	0.000941	0.0025	1.69	cuk6	cuk5	Envoplakin-like protein GN=EVPLL PE=2 SV=1
P26373	RPL13	6	2	42.8	0.001476	0.003013	1.59	cuk5	cuk6	60S ribosomal protein L13 GN=RPL13 PE=1 SV=4
Q969P6	TOP1MT	8	4	42.8	0.000667	0.002025	1.33	cuk6	cuk5	DNA topoisomerase I_ mitochondrial GN=TOP1MT PE=1 SV=1
Q9NWH9	SLTM	8	2	43.1	0.029945	0.022765	1.23	cuk6	cuk5	SAFB-like transcription modulator GN=SLTM PE=1 SV=2
P42166	TMPO	7	3	43.4	0.003061	0.004772	1.67	cuk5	cuk6	Lamina-associated polypeptide 2_ isoform alpha GN=TMPO PE=1 SV=2
P33993	MCM7	6	4	43.5	0.038129	0.027071	1.24	cuk5	cuk6	DNA replication licensing factor MCM7 GN=MCM7 PE=1 SV=4
P52948	NUP98	8	3	44	0.001914	0.003569	2.07	cuk6	cuk5	Nuclear pore complex protein Nup98-Nup96 GN=NUP98 PE=1 SV=4
Q8IYT4	KATNAL2	7	5	44	4.6E-05	0.000652	2.5	cuk6	cuk5	Katanin p60 ATPase-containing subunit A-like 2 GN=KATNAL2 PE=1 SV=3
G3V2A4	TEP1	7	4	44.6	0.000367	0.001531	1.87	cuk5	cuk6	Telomerase protein component 1 GN=TEP1 PE=1 SV=1
P49773	HINT1	4	2	44.7	0.000369	0.001531	2.22	cuk6	cuk5	Histidine triad nucleotide-binding protein 1 GN=HINT1 PE=1 SV=2
P12004	PCNA	6	4	44.8	0.047014	0.031657	1.24	cuk5	cuk6	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
P53804	TTC3	8	3	45	0.001936	0.003586	1.75	cuk6	cuk5	E3 ubiquitin-protein ligase TTC3 GN=TTC3 PE=1 SV=2
P46940	IQGAP1	9	3	45	0.002593	0.004372	1.67	cuk5	cuk6	Ras GTPase-activating-like protein IQGAP1 GN=IQGAP1 PE=1 SV=1
I6L899	GOLGA8R	7	2	45.3	0.006587	0.007824	1.37	cuk6	cuk5	Golgin subfamily A member 8R GN=GOLGA8R PE=3 SV=1
Q13247	SRSF6	5	4	45.3	0.008277	0.009151	1.47	cuk5	cuk6	Serine/arginine-rich splicing factor 6 GN=SRSF6 PE=1 SV=2
Q8N3U4	STAG2	7	2	46.5	0.009982	0.010298	2.03	cuk6	cuk5	Cohesin subunit SA-2 GN=STAG2 PE=1 SV=3
Q9H1A4	ANAPC1	8	2	46.6	0.010624	0.010714	1.32	cuk5	cuk6	Anaphase-promoting complex subunit 1 GN=ANAPC1 PE=1 SV=1
P62979	RPS27A	6	3	46.9	0.022825	0.018798	2.24	cuk5	cuk6	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
Q17RC7	EXOC3L4	8	5	47.1	0.027415	0.021641	1.17	cuk5	cuk6	Exocyst complex component 3-like protein 4 GN=EXOC3L4 PE=1 SV=2
Q8TET4	GANC	7	3	47.3	0.025577	0.020609	1.14	cuk6	cuk5	Neutral alpha-glucosidase C GN=GANC PE=2 SV=3
P02461	COL3A1	8	2	47.5	0.01484	0.013845	1.57	cuk5	cuk6	Collagen alpha-1(III) chain GN=COL3A1 PE=1 SV=4
A0A087X0A8	COL12A1	8	4	47.5	0.00325	0.00492	1.69	cuk6	cuk5	Collagen alpha-1(XII) chain GN=COL12A1 PE=1 SV=1
P62829	RPL23	6	4	48.3	0.024237	0.019797	1.33	cuk5	cuk6	60S ribosomal protein L23 GN=RPL23 PE=1 SV=1
Q12873	CHD3	9	2	48.5	0.000436	0.001667	1.77	cuk6	cuk5	Chromodomain-helicase-DNA-binding protein 3 GN=CHD3 PE=1 SV=3
Q8WVV9	HNRNPLL	8	4	48.7	0.030829	0.023294	1.19	cuk6	cuk5	Heterogeneous nuclear ribonucleoprotein L-like GN=HNRNPLL PE=1 SV=1
A2RUB1	MEIOC	7	2	48.9	0.000549	0.00187	3.34	cuk6	cuk5	Meiosis-specific coiled-coil domain-containing protein MEIOC GN=MEIOC PE=2 SV=3
P10586	PTPRF	10	4	48.9	0.01145	0.011385	1.26	cuk6	cuk5	Receptor-type tyrosine-protein phosphatase F GN=PTPRF PE=1 SV=2
Q96QP1	ALPK1	9	4	49.6	0.003662	0.005318	1.76	cuk5	cuk6	Alpha-protein kinase 1 GN=ALPK1 PE=2 SV=3
P52597	HNRNPF	7	5	49.6	0.000455	0.001691	1.41	cuk6	cuk5	Heterogeneous nuclear ribonucleoprotein F GN=HNRNPF PE=1 SV=3
P13647	KRT5	6	2	49.8	0.001729	0.003337	1.57	cuk6	cuk5	Keratin_ type II cytoskeletal 5 GN=KRT5 PE=1 SV=3

Q96N67	DOCK7	10	2	49.9	0.004886	0.006508	1.41	cuk5	cuk6	Dedicator of cytokinesis protein 7 GN=DOCK7 PE=1 SV=4
P52756	RBM5	7	3	50.1	0.025648	0.020609	1.26	cuk6	cuk5	RNA-binding protein 5 GN=RBM5 PE=1 SV=2
Q13200	PSMD2	8	6	50.1	0.005194	0.006755	1.35	cuk6	cuk5	26S proteasome non-ATPase regulatory subunit 2 GN=PSMD2 PE=1 SV=3
O43683	BUB1	9	4	51.3	0.029125	0.022279	1.29	cuk6	cuk5	Mitotic checkpoint serine/threonine-protein kinase BUB1 GN=BUB1 PE=1 SV=1
A0A0C4DFM7	TUT4	10	3	51.5	0.003681	0.005318	1.39	cuk6	cuk5	Terminal uridylyltransferase 4 GN=ZCCHC11 PE=1 SV=1
P01308	INS	5	3	51.6	0.000214	0.001222	1.37	cuk5	cuk6	Insulin GN=INS PE=1 SV=1
Q7Z4S6	KIF21A	9	5	51.6	0.000828	0.002285	1.26	cuk5	cuk6	Kinesin-like protein KIF21A GN=KIF21A PE=1 SV=2
Q12906	ILF3	9	3	52.1	0.000514	0.001829	1.76	cuk6	cuk5	Interleukin enhancer-binding factor 3 GN=ILF3 PE=1 SV=3
Q6ZNG0	ZNF620	8	3	52.1	0.019961	0.017095	1.29	cuk6	cuk5	Zinc finger protein 620 GN=ZNF620 PE=2 SV=1
P35527	KRT9	10	7	52.7	0.000961	0.002525	1.45	cuk6	cuk5	Keratin_ type I cytoskeletal 9 GN=KRT9 PE=1 SV=3
Q5TB80	CEP162	10	2	52.8	0.011207	0.01121	3.15	cuk6	cuk5	Centrosomal protein of 162 kDa GN=CEP162 PE=1 SV=2
P80723	BASP1	7	6	53.2	0.008646	0.009268	2.15	cuk6	cuk5	Brain acid soluble protein 1 GN=BASP1 PE=1 SV=2
O43896	KIF1C	9	2	53.8	0.01244	0.012053	1.33	cuk6	cuk5	Kinesin-like protein KIF1C GN=KIF1C PE=1 SV=3
Q9H9B1	EHMT1	8	3	54.5	0.01603	0.014588	1.19	cuk6	cuk5	Histone-lysine N-methyltransferase EHMT1 GN=EHMT1 PE=1 SV=4
Q12888	TP53BP1	11	5	54.6	0.016465	0.014929	1.48	cuk5	cuk6	TP53-binding protein 1 GN=TP53BP1 PE=1 SV=2
P48047	ATP5PO	8	5	55.7	0.010526	0.010637	1.2	cuk5	cuk6	ATP synthase subunit O_ mitochondrial GN=ATP5O PE=1 SV=1
O14715	RGPD8	9	4	56.4	0.009515	0.009881	1.18	cuk6	cuk5	RANBP2-like and GRIP domain-containing protein 8 GN=RGPD8 PE=1 SV=2
Q9P107	GMIP	9	2	56.8	0.006676	0.007911	1.51	cuk6	cuk5	GEM-interacting protein GN=GMIP PE=1 SV=2
E7EPM6	ACSL1	9	3	56.8	0.000553	0.00187	2.43	cuk5	cuk6	Long-chain-fatty-acid--CoA ligase 1 GN=ACSL1 PE=1 SV=1
P62263	RPS14	6	3	57.6	0.039226	0.027534	1.22	cuk5	cuk6	40S ribosomal protein S14 GN=RPS14 PE=1 SV=3
Q15029	EFTUD2	9	6	57.8	0.001525	0.003063	1.54	cuk5	cuk6	116 kDa U5 small nuclear ribonucleoprotein component GN=EFTUD2 PE=1 SV=1
O43432	EIF4G3	10	4	58	0.002937	0.004652	1.35	cuk6	cuk5	Eukaryotic translation initiation factor 4 gamma 3 GN=EIF4G3 PE=1 SV=2
Q9BXT6	MOV10L1	10	2	58.8	0.003392	0.005049	1.26	cuk5	cuk6	RNA helicase Mov10l1 GN=MOV10L1 PE=2 SV=1
Q13332	PTPRS	12	4	60.3	0.001205	0.002743	1.46	cuk6	cuk5	Receptor-type tyrosine-protein phosphatase S GN=PTPRS PE=1 SV=3
Q9BPU6	DPYSL5	9	4	60.4	0.002818	0.004612	1.82	cuk5	cuk6	Dihydropyrimidinase-related protein 5 GN=DPYSL5 PE=1 SV=1
P33991	MCM4	12	7	60.4	2.07E-05	0.000487	1.94	cuk6	cuk5	DNA replication licensing factor MCM4 GN=MCM4 PE=1 SV=5
J3KP97	CCDC18	10	3	60.7	0.037941	0.026985	1.28	cuk5	cuk6	Coiled-coil domain-containing protein 18 (Fragment) GN=CCDC18 PE=1 SV=1
P12035	KRT3	8	3	61.6	8.24E-06	0.000371	1.89	cuk6	cuk5	Keratin_ type II cytoskeletal 3 GN=KRT3 PE=1 SV=3
Q6ZU80	CEP128	13	5	62.2	0.000714	0.002117	1.76	cuk6	cuk5	Centrosomal protein of 128 kDa GN=CEP128 PE=1 SV=2
O94910	ADGRL1	10	4	62.3	0.004416	0.00608	1.62	cuk5	cuk6	Adhesion G protein-coupled receptor L1 GN=ADGRL1 PE=1 SV=1
Q6PIF6	MYO7B	10	3	63	0.005704	0.007129	1.68	cuk6	cuk5	Unconventional myosin-VIIb GN=MYO7B PE=1 SV=2
A0A0G2JP87	CCHCR1	10	5	63	0.001886	0.003568	1.59	cuk6	cuk5	Coiled-coil alpha-helical rod protein 1 GN=CCHCR1 PE=1 SV=1
O14994	SYN3	9	3	63.1	0.000231	0.001222	1.71	cuk6	cuk5	Synapsin-3 GN=SYN3 PE=1 SV=2
Q9P275	USP36	11	6	63.4	0.001323	0.002862	1.4	cuk5	cuk6	Ubiquitin carboxyl-terminal hydrolase 36 GN=USP36 PE=1 SV=4
P08865	RPSA	9	4	63.5	0.001664	0.003268	1.4	cuk6	cuk5	40S ribosomal protein SA GN=RPSA PE=1 SV=4
E7EPS8	PTPRM	11	6	63.5	0.035808	0.026091	1.27	cuk6	cuk5	Receptor-type tyrosine-protein phosphatase mu GN=PTPRM PE=1 SV=2
Q7L014	DDX46	12	7	63.5	0.002543	0.004319	2.3	cuk6	cuk5	Probable ATP-dependent RNA helicase DDX46 GN=DDX46 PE=1 SV=2
O95153	TSPOAP1	10	4	64.5	0.0054	0.006923	1.54	cuk6	cuk5	Peripheral-type benzodiazepine receptor-associated protein 1 GN=TSPOAP1 PE=1 SV=2
P31930	UQCRC1	10	3	64.6	0.006009	0.007278	1.44	cuk6	cuk5	Cytochrome b-c1 complex subunit 1_ mitochondrial GN=UQCRC1 PE=1 SV=3
Q15746	MYLK	10	6	64.8	0.002662	0.004452	1.17	cuk6	cuk5	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
Q02413	DSG1	8	3	66.4	0.001401	0.002916	1.92	cuk6	cuk5	Desmoglein-1 GN=DSG1 PE=1 SV=2
Q13838	DDX39B	8	2	66.6	0.017074	0.015326	1.34	cuk6	cuk5	Spliceosome RNA helicase DDX39B GN=DDX39B PE=1 SV=1
Q99460	PSMD1	11	3	66.7	0.002226	0.003973	1.22	cuk5	cuk6	26S proteasome non-ATPase regulatory subunit 1 GN=PSMD1 PE=1 SV=2
Q03181	PPARD	7	2	67.2	0.003216	0.00492	1.43	cuk6	cuk5	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1
P17987	TCP1	10	4	67.5	0.028958	0.02222	1.23	cuk6	cuk5	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
P49748	ACADVL	10	2	68	0.005713	0.007129	2.39	cuk5	cuk6	Very long-chain specific acyl-CoA dehydrogenase_ mitochondrial GN=ACADVL PE=1 SV=1
O43166	SIPA1L1	12	3	68.6	0.001212	0.002747	1.51	cuk6	cuk5	Signal-induced proliferation-associated 1-like protein 1 GN=SIPA1L1 PE=1 SV=4
P13637	ATP1A3	9	2	69.4	0.02867	0.022067	1.14	cuk5	cuk6	Sodium/potassium-transporting ATPase subunit alpha-3 GN=ATP1A3 PE=1 SV=3
F5H2F4	MTHFD1	10	2	69.5	0.00107	0.002604	1.69	cuk5	cuk6	C-1-tetrahydrofolate synthase_ cytoplasmic GN=MTHFD1 PE=1 SV=1
P84103	SRSF3	9	5	70.5	0.000824	0.002285	1.15	cuk5	cuk6	Serine/arginine-rich splicing factor 3 GN=SRSF3 PE=1 SV=1
O94885	SASH1	13	3	71.2	0.0416	0.028671	1.17	cuk6	cuk5	SAM and SH3 domain-containing protein 1 GN=SASH1 PE=1 SV=3
H0YKD8	RPL28	10	7	71.2	0.025977	0.020838	1.28	cuk5	cuk6	60S ribosomal protein L28 GN=RPL28 PE=1 SV=1
O14513	NCKAP5	12	3	71.4	0.044163	0.03031	1.19	cuk5	cuk6	Nck-associated protein 5 GN=NCKAP5 PE=1 SV=2
Q12840	KIF5A	11	4	71.4	0.004185	0.005875	1.45	cuk6	cuk5	Kinesin heavy chain isoform 5A GN=KIF5A PE=1 SV=2
Q66GS9	CEP135	14	5	71.4	0.000649	0.00202	1.73	cuk6	cuk5	Centrosomal protein of 135 kDa GN=CEP135 PE=1 SV=2
Q96F07	CYFIP2	10	2	72.2	0.008556	0.009223	1.33	cuk5	cuk6	Cytoplasmic FMR1-interacting protein 2 GN=CYFIP2 PE=1 SV=2
P62280	RPS11	9	3	72.7	6.79E-05	0.000671	2.03	cuk5	cuk6	40S ribosomal protein S11 GN=RPS11 PE=1 SV=3
P13010	XRCC5	11	9	73.3	0.044666	0.030613	1.29	cuk6	cuk5	X-ray repair cross-complementing protein 5 GN=XRCC5 PE=1 SV=3
O15075	DCLK1	11	2	73.9	9.89E-05	0.000795	1.44	cuk6	cuk5	Serine/threonine-protein kinase DCLK1 GN=DCLK1 PE=1 SV=2
D3DQV9	EIF4G2	14	5	75.1	0.021826	0.018143	1.09	cuk6	cuk5	Eukaryotic translation initiation factor 4 gamma 2 (Fragment) GN=EIF4G2 PE=1 SV=1
P23396	RPS3	11	4	75.3	0.007451	0.008482	2.05	cuk5	cuk6	40S ribosomal protein S3 GN=RPS3 PE=1 SV=2
Q96JM4	LRRIQ1	16	6	76.6	0.032861	0.024455	1.34	cuk6	cuk5	Leucine-rich repeat and IQ domain-containing protein 1 GN=LRRIQ1 PE=2 SV=3
P62241	RPS8	7	6	76.9	0.000586	0.001942	1.35	cuk6	cuk5	40S ribosomal protein S8 GN=RPS8 PE=1 SV=2
Q9Y4F4	TOGARAM1	15	10	77.6	1.39E-05	0.000457	1.75	cuk6	cuk5	TOG array regulator of axonemal microtubules protein 1 GN=TOGARAM1 PE=1 SV=4
P30622	CLIP1	14	3	78.4	0.001062	0.002604	1.6	cuk6	cuk5	CAP-Gly domain-containing linker protein 1 GN=CLIP1 PE=1 SV=2
B7ZAR1	CCT5	12	6	80.1	0.025642	0.020609	1.35	cuk5	cuk6	T-complex protein 1 subunit epsilon GN=CCT5 PE=1 SV=1
P50914	RPL14	10	5	81.6	0.000801	0.00225	1.57	cuk5	cuk6	60S ribosomal protein L14 GN=RPL14 PE=1 SV=4
P53396	ACLY	13	5	81.6	0.036693	0.026489	1.1	cuk6	cuk5	ATP-citrate synthase GN=ACLY PE=1 SV=3
A0A0G2JNB1	KANSL1	13	4	81.7	0.033889	0.024995	1.26	cuk6	cuk5	KAT8 regulatory NSL complex subunit 1 GN=KANSL1 PE=1 SV=1
Q8WVM7	STAG1	13	6	81.9	0.013146	0.012445	1.34	cuk5	cuk6	Cohesin subunit SA-1 GN=STAG1 PE=1 SV=3
Q99536	VAT1	11	7	84.8	0.001386	0.002901	1.16	cuk6	cuk5	Synaptic vesicle membrane protein VAT-1 homolog GN=VAT1 PE=1 SV=2
Q9H0X9	OSBPL5	13	4	85.4	1.52E-06	0.000277	3.18	cuk6	cuk5	Oxysterol-binding protein-related protein 5 GN=OSBPL5 PE=1 SV=1
P61247	RPS3A	11	5	86.8	0.010061	0.010336	1.37	cuk5	cuk6	40S ribosomal protein S3a GN=RPS3A PE=1 SV=2
Q15276	RABEP1	15	4	87.3	8.76E-05	0.000746	2.14	cuk6	cuk5	Rab GTPase-binding effector protein 1 GN=RABEP1 PE=1 SV=2
O43491	EPB41L2	16	3	87.5	3.39E-05	0.0006	2.96	cuk6	cuk5	Band 4.1-like protein 2 GN=EPB41L2 PE=1 SV=1
O43390	HNRNPR	13	3	87.5	0.002394	0.004195	1.77	cuk5	cuk6	Heterogeneous nuclear ribonucleoprotein R GN=HNRNPR PE=1 SV=1
P62913	RPL11	8	3	87.6	5.53E-05	0.000652	1.25	cuk5	cuk6	60S ribosomal protein L11 GN=RPL11 PE=1 SV=2
Q6WCQ1	MPRIP	15	5	88	0.000195	0.001146	2.25	cuk6	cuk5	Myosin phosphatase Rho-interacting protein GN=MPRIP PE=1 SV=3
Q96M83	CCDC7	14	6	88.5	0.003467	0.005129	1.61	cuk5	cuk6	Coiled-coil domain-containing protein 7 GN=CCDC7 PE=2 SV=3
E7EPK1	SEPTIN7	14	5	88.8	0.031456	0.023675	1.25	cuk6	cuk5	Septin-7 GN=SEPT7 PE=1 SV=2
Q8N960	CEP120	14	2	91.1	0.004169	0.005869	2.7	cuk5	cuk6	Centrosomal protein of 120 kDa GN=CEP120 PE=1 SV=2
Q9UKX3	MYH13	15	6	91.3	0.001542	0.003073	1.45	cuk6	cuk5	Myosin-13 GN=MYH13 PE=2 SV=2
Q92598	HSPH1	14	6	91.4	0.017619	0.015603	1.27	cuk6	cuk5	Heat shock protein 105 kDa GN=HSPH1 PE=1 SV=1

P48735	IDH2	14	6	91.4	0.003639	0.005305	1.26	cuk5	cuk6	Isocitrate dehydrogenase [NADP]_ mitochondrial GN=IDH2 PE=1 SV=2
P34897	SHMT2	15	10	93.2	0.017089	0.015326	1.18	cuk6	cuk5	Serine hydroxymethyltransferase_ mitochondrial GN=SHMT2 PE=1 SV=3
P62424	RPL7A	15	8	95	0.001503	0.003031	1.78	cuk5	cuk6	60S ribosomal protein L7a GN=RPL7A PE=1 SV=2
Q15102	PAFAH1B3	10	8	96	0.040682	0.028156	1.13	cuk5	cuk6	Platelet-activating factor acetylhydrolase IB subunit gamma GN=PAFAH1B3 PE=1 SV=1
P38919	EIF4A3	13	6	97.1	0.004443	0.006088	1.68	cuk5	cuk6	Eukaryotic initiation factor 4A-III GN=EIF4A3 PE=1 SV=4
E7EVA0	MAP4	17	6	97.2	0.001099	0.00264	1.47	cuk6	cuk5	Microtubule-associated protein GN=MAP4 PE=1 SV=1
O00425	IGF2BP3	14	6	101	0.005476	0.006974	1.4	cuk5	cuk6	Insulin-like growth factor 2 mRNA-binding protein 3 GN=IGF2BP3 PE=1 SV=2
Q08211	DHX9	18	12	101	0.00053	0.001857	1.39	cuk5	cuk6	ATP-dependent RNA helicase A GN=DHX9 PE=1 SV=4
P06748	NPM1	9	4	102	0.007207	0.008317	1.51	cuk5	cuk6	Nucleophosmin GN=NPM1 PE=1 SV=2
Q06830	PRDX1	13	6	102	0.003163	0.004884	1.26	cuk6	cuk5	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
P49368	CCT3	14	8	102	0.018046	0.01584	1.27	cuk5	cuk6	T-complex protein 1 subunit gamma GN=CCT3 PE=1 SV=4
Q86U86	PBRM1	18	5	103	0.005098	0.006682	1.48	cuk6	cuk5	Protein polybromo-1 GN=PBRM1 PE=1 SV=1
P11940	PABPC1	16	5	104	0.010103	0.010358	1.72	cuk5	cuk6	Polyadenylate-binding protein 1 GN=PABPC1 PE=1 SV=2
Q14974	KPNB1	14	7	106	0.02063	0.01758	1.45	cuk5	cuk6	Importin subunit beta-1 GN=KPNB1 PE=1 SV=2
Q15084	PDIA6	13	8	106	3.54E-05	0.000603	1.35	cuk6	cuk5	Protein disulfide-isomerase A6 GN=PDIA6 PE=1 SV=1
O75128	COBL	19	8	106	0.037855	0.026985	1.18	cuk5	cuk6	Protein cordon-bleu GN=COBL PE=1 SV=2
Q3MJ40	CCDC144B	19	2	111	0.000668	0.002025	1.64	cuk6	cuk5	Coiled-coil domain-containing protein 144B GN=CCDC144B PE=2 SV=1
P02765	AHSG	13	9	112	0.00288	0.004646	1.43	cuk6	cuk5	Alpha-2-HS-glycoprotein GN=AHSG PE=1 SV=1
Q86YA3	ZGRF1	20	5	113	0.047906	0.032077	1.13	cuk5	cuk6	Protein ZGRF1 GN=ZGRF1 PE=1 SV=3
Q9UHF7	TRPS1	21	7	113	0.000408	0.001614	2.69	cuk6	cuk5	Zinc finger transcription factor Trps1 GN=TRPS1 PE=1 SV=2
Q9C0C2	TNKS1BP1	19	9	113	0.01398	0.013133	1.17	cuk5	cuk6	182 kDa tankyrase-1-binding protein GN=TNKS1BP1 PE=1 SV=4
P32119	PRDX2	10	5	114	0.002263	0.004009	1.2	cuk6	cuk5	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
Q6ZN16	MAP3K15	16	5	114	0.027781	0.021744	1.12	cuk6	cuk5	Mitogen-activated protein kinase kinase kinase 15 GN=MAP3K15 PE=1 SV=2
Q58FF3	HSP90B2P	16	6	114	0.042315	0.029123	1.24	cuk5	cuk6	Putative endoplasmin-like protein GN=HSP90B2P PE=5 SV=1
Q99832	CCT7	20	12	114	7.29E-05	0.000702	1.61	cuk6	cuk5	T-complex protein 1 subunit eta GN=CCT7 PE=1 SV=2
P27824	CANX	14	7	115	0.025462	0.020593	1.17	cuk6	cuk5	Calnexin GN=CANX PE=1 SV=2
Q5JSZ5	PRRC2B	18	6	116	0.005041	0.006661	1.22	cuk5	cuk6	Protein PRRC2B GN=PRRC2B PE=1 SV=2
Q9Y4I1	MYO5A	22	6	117	0.01922	0.016692	1.12	cuk5	cuk6	Unconventional myosin-Va GN=MYO5A PE=1 SV=2
A6QL64	ANKRD36	21	8	117	8.83E-06	0.000371	2.61	cuk6	cuk5	Ankyrin repeat domain-containing protein 36A GN=ANKRD36 PE=2 SV=3
Q9H4B7	TUBB1	10	2	119	0.000992	0.002547	1.66	cuk5	cuk6	Tubulin beta-1 chain GN=TUBB1 PE=1 SV=1
O60292	SIPA1L3	21	12	120	0.000129	0.000921	1.55	cuk6	cuk5	Signal-induced proliferation-associated 1-like protein 3 GN=SIPA1L3 PE=1 SV=3
P48741	HSPA7	14	3	121	0.00066	0.002025	2.49	cuk6	cuk5	Putative heat shock 70 kDa protein 7 GN=HSPA7 PE=5 SV=2
Q16658	FSCN1	16	9	121	0.00402	0.005708	1.1	cuk6	cuk5	Fascin GN=FSCN1 PE=1 SV=3
P04264	KRT1	17	6	122	7.71E-06	0.000371	1.67	cuk6	cuk5	Keratin_ type II cytoskeletal 1 GN=KRT1 PE=1 SV=6
Q7RTP6	MICAL3	23	6	123	0.00032	0.001426	1.55	cuk6	cuk5	[F-actin]-monooxygenase MICAL3 GN=MICAL3 PE=1 SV=2
P62805	H4C1	10	6	123	0.001052	0.002599	1.51	cuk6	cuk5	Histone H4 GN=HIST1H4A PE=1 SV=2
P17844	DDX5	18	7	123	0.009452	0.009875	1.2	cuk5	cuk6	Probable ATP-dependent RNA helicase DDX5 GN=DDX5 PE=1 SV=1
P55795	HNRNPH2	18	4	125	0.01235	0.01199	1.05	cuk6	cuk5	Heterogeneous nuclear ribonucleoprotein H2 GN=HNRNPH2 PE=1 SV=1
Q9UDT6	CLIP2	23	9	126	0.025636	0.020609	1.22	cuk5	cuk6	CAP-Gly domain-containing linker protein 2 GN=CLIP2 PE=1 SV=1
Q9NSB2	KRT84	20	8	132	0.006968	0.008121	1.54	cuk6	cuk5	Keratin_ type II cuticular Hb4 GN=KRT84 PE=2 SV=2
O75145	PPFIA3	22	11	133	0.000424	0.00165	2.51	cuk6	cuk5	Liprin-alpha-3 GN=PPFIA3 PE=1 SV=3
P08133	ANXA6	18	7	134	0.013787	0.012977	1.35	cuk6	cuk5	Annexin A6 GN=ANXA6 PE=1 SV=3
P36578	RPL4	18	8	134	0.00023	0.001222	1.65	cuk5	cuk6	60S ribosomal protein L4 GN=RPL4 PE=1 SV=5
P62701	RPS4X	16	6	137	0.003262	0.00492	1.25	cuk5	cuk6	40S ribosomal protein S4_ X isoform GN=RPS4X PE=1 SV=2
Q8IWJ2	GCC2	27	11	137	0.045661	0.031165	1.11	cuk6	cuk5	GRIP and coiled-coil domain-containing protein 2 GN=GCC2 PE=1 SV=4
A2RUR9	CCDC144A	22	2	141	0.000277	0.001321	1.85	cuk6	cuk5	Coiled-coil domain-containing protein 144A GN=CCDC144A PE=2 SV=1
Q8NB25	FAM184A	23	7	141	0.018016	0.01584	1.23	cuk5	cuk6	Protein FAM184A GN=FAM184A PE=2 SV=3
Q14240	EIF4A2	19	8	144	0.034262	0.025193	1.23	cuk6	cuk5	Eukaryotic initiation factor 4A-II GN=EIF4A2 PE=1 SV=2
K7ELL7	PRKCSH	18	10	145	0.000161	0.001035	1.39	cuk6	cuk5	Glucosidase 2 subunit beta GN=PRKCSH PE=1 SV=1
Q16695	H3-4	18	4	147	0.001342	0.002862	1.62	cuk6	cuk5	Histone H3.1t GN=HIST3H3 PE=1 SV=3
Q9NQT8	KIF13B	22	13	147	0.00026	0.001283	1.44	cuk6	cuk5	Kinesin-like protein KIF13B GN=KIF13B PE=1 SV=2
P48681	NES	24	9	150	0.000948	0.002506	1.25	cuk5	cuk6	Nestin GN=NES PE=1 SV=2
P60842	EIF4A1	19	6	152	0.01213	0.011846	1.23	cuk6	cuk5	Eukaryotic initiation factor 4A-I GN=EIF4A1 PE=1 SV=1
Q86UP2	KTN1	27	11	153	0.004448	0.006088	1.23	cuk5	cuk6	Kinectin GN=KTN1 PE=1 SV=1
P16401	H1-5	13	5	154	1.28E-05	0.000457	1.58	cuk5	cuk6	Histone H1.5 GN=HIST1H1B PE=1 SV=3
Q6FI13	H2AC18	17	6	154	0.004475	0.006089	1.43	cuk6	cuk5	Histone H2A type 2-A GN=HIST2H2AA3 PE=1 SV=3
P04843	RPN1	23	12	155	4.27E-05	0.000639	2.3	cuk6	cuk5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 GN=RPN1 PE=1 SV=1
E9PK25	CFL1	15	4	163	0.000542	0.00187	1.31	cuk6	cuk5	Cofilin-1 GN=CFL1 PE=1 SV=1
P50454	SERPINH1	20	7	164	0.00246	0.004279	1.16	cuk6	cuk5	Serpin H1 GN=SERPINH1 PE=1 SV=2
Q9HC77	CENPJ	26	9	166	0.008267	0.009151	1.19	cuk6	cuk5	Centromere protein J GN=CENPJ PE=1 SV=2
Q8TBY8	PMFBP1	26	12	166	0.008796	0.009388	1.36	cuk6	cuk5	Polyamine-modulated factor 1-binding protein 1 GN=PMFBP1 PE=2 SV=2
A6NHL2	TUBAL3	18	5	169	0.000281	0.001321	2.29	cuk5	cuk6	Tubulin alpha chain-like 3 GN=TUBAL3 PE=1 SV=2
Q15365	PCBP1	22	13	171	0.000121	0.000905	1.63	cuk6	cuk5	Poly(rC)-binding protein 1 GN=PCBP1 PE=1 SV=2
P16402	H1-3	14	3	173	0.00464	0.006281	1.58	cuk5	cuk6	Histone H1.3 GN=HIST1H1D PE=1 SV=2
Q15811	ITSN1	28	6	174	0.002741	0.004545	2.56	cuk6	cuk5	Intersectin-1 GN=ITSN1 PE=1 SV=3
P15880	RPS2	22	12	175	0.010276	0.010464	1.33	cuk5	cuk6	40S ribosomal protein S2 GN=RPS2 PE=1 SV=2
A0A0G2JIW1	HSPA1B	21	5	178	0.045294	0.030957	1.08	cuk6	cuk5	Heat shock 70 kDa protein 1B GN=HSPA1B PE=1 SV=1
Q9P219	CCDC88C	28	5	179	0.028535	0.022003	1.35	cuk6	cuk5	Protein Daple GN=CCDC88C PE=1 SV=3
Q8WX93	PALLD	28	15	183	0.023952	0.019596	1.25	cuk6	cuk5	Palladin GN=PALLD PE=1 SV=3
Q9NZI8	IGF2BP1	22	15	185	0.013057	0.012426	1.49	cuk5	cuk6	Insulin-like growth factor 2 mRNA-binding protein 1 GN=IGF2BP1 PE=1 SV=2
Q86UW6	N4BP2	27	11	189	0.008474	0.009223	1.27	cuk6	cuk5	NEDD4-binding protein 2 GN=N4BP2 PE=1 SV=2
P07237	P4HB	23	9	201	0.007835	0.008779	1.33	cuk6	cuk5	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
P54652	HSPA2	20	4	202	0.011323	0.011292	1.06	cuk5	cuk6	Heat shock-related 70 kDa protein 2 GN=HSPA2 PE=1 SV=1
Q16778	H2BC21	21	4	207	0.037952	0.026985	1.2	cuk6	cuk5	Histone H2B type 2-E GN=HIST2H2BE PE=1 SV=3
Q15366	PCBP2	21	6	207	0.000448	0.001688	1.56	cuk5	cuk6	Poly(rC)-binding protein 2 GN=PCBP2 PE=1 SV=1
P55196	AFDN	32	9	208	0.002224	0.003973	1.37	cuk6	cuk5	Afadin GN=AFDN PE=1 SV=3
P20700	LMNB1	26	11	214	0.014835	0.013845	1.33	cuk5	cuk6	Lamin-B1 GN=LMNB1 PE=1 SV=2
P22626	HNRNPA2B1	24	11	215	1.83E-05	0.000487	2.43	cuk6	cuk5	Heterogeneous nuclear ribonucleoproteins A2/B1 GN=HNRNPA2B1 PE=1 SV=2
Q14194	CRMP1	29	11	215	3.85E-05	0.000634	1.94	cuk6	cuk5	Dihydropyrimidinase-related protein 1 GN=CRMP1 PE=1 SV=1
Q14980	NUMA1	38	14	221	0.027853	0.021744	1.06	cuk5	cuk6	Nuclear mitotic apparatus protein 1 GN=NUMA1 PE=1 SV=2
P41219	PRPH	24	6	226	0.000101	0.000795	1.72	cuk6	cuk5	Peripherin GN=PRPH PE=1 SV=2
A0A087WWY3	FLNA	41	20	250	0.002898	0.004646	1.17	cuk6	cuk5	Filamin-A GN=FLNA PE=1 SV=1
Q14195	DPYSL3	28	14	269	8.41E-05	0.000745	1.88	cuk5	cuk6	Dihydropyrimidinase-related protein 3 GN=DPYSL3 PE=1 SV=1

P07197	NEFM	41	14	302	0.000485	0.001751	1.45	cuk6	cuk5	Neurofilament medium polypeptide GN=NEFM PE=1 SV=3
Q07065	CKAP4	36	16	309	0.002899	0.004646	1.25	cuk6	cuk5	Cytoskeleton-associated protein 4 GN=CKAP4 PE=1 SV=2
Q9BUF5	TUBB6	26	3	314	0.020938	0.017656	1.3	cuk6	cuk5	Tubulin beta-6 chain GN=TUBB6 PE=1 SV=1
Q16352	INA	33	16	315	0.005364	0.006923	1.19	cuk5	cuk6	Alpha-internexin GN=INA PE=1 SV=2
P04406	GAPDH	33	5	334	0.016616	0.015038	1.26	cuk5	cuk6	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
Q5TZA2	CROCC	59	18	354	0.002735	0.004545	1.36	cuk6	cuk5	Rootletin GN=CROCC PE=1 SV=1
P30101	PDIA3	36	19	364	0.003326	0.004996	1.46	cuk6	cuk5	Protein disulfide-isomerase A3 GN=PDIA3 PE=1 SV=4
Q6PEY2	TUBA3E	28	2	369	0.000224	0.001222	2.51	cuk6	cuk5	Tubulin alpha-3E chain GN=TUBA3E PE=1 SV=2
P08238	HSP90AB1	38	12	379	0.005829	0.007169	1.2	cuk6	cuk5	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
H0Y6I0	GOLGA4	58	26	382	0.000814	0.002274	1.43	cuk6	cuk5	Golgin subfamily A member 4 (Fragment) GN=GOLGA4 PE=1 SV=1
P14618	PKM	33	6	386	0.03179	0.023752	1.29	cuk5	cuk6	Pyruvate kinase PKM GN=PKM PE=1 SV=4
P22314	UBA1	54	18	408	0.027843	0.021744	1.16	cuk5	cuk6	Ubiquitin-like modifier-activating enzyme 1 GN=UBA1 PE=1 SV=3
P13639	EEF2	51	27	415	0.010023	0.010319	1.07	cuk6	cuk5	Elongation factor 2 GN=EEF2 PE=1 SV=4
A0A0B4J269	Not Found	43	3	572	0.004723	0.006342	1.41	cuk5	cuk6	Uncharacterized protein PE=1 SV=1
P04350	TUBB4A	47	6	599	0.017602	0.015603	1.32	cuk5	cuk6	Tubulin beta-4A chain GN=TUBB4A PE=1 SV=2
Q13509	TUBB3	54	10	613	0.000294	0.001359	1.54	cuk5	cuk6	Tubulin beta-3 chain GN=TUBB3 PE=1 SV=2
Q9BQE3	TUBA1C	46	6	617	0.00126	0.002829	2.33	cuk5	cuk6	Tubulin alpha-1C chain GN=TUBA1C PE=1 SV=1
P68032	ACTC1	54	11	688	0.005074	0.006682	1.39	cuk5	cuk6	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
Q13885	TUBB2A	50	2	735	0.0125	0.012064	1.29	cuk5	cuk6	Tubulin beta-2A chain GN=TUBB2A PE=1 SV=1
P60709	ACTB	66	15	1010	0.003374	0.005038	1.15	cuk5	cuk6	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1

Table S17: Identified allergy-related proteins following DMAT$_{A\beta1\text{-}6}$ and DMAT$_{A\beta17\text{-}23}$ compared to untreated cells. Herein, Cuk4=Aβ1-6; Cuk5=Aβ17-23; Cuk6= NoT.

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-Aβ$_{1\text{-}6}$ Antibody Treatment										
P29597	TYK2	8	2	42.1	0.000571	0.001291	2.23	cuk4	cuk6	Non-receptor tyrosine-protein kinase TYK2 GN=TYK2 PE=1 SV=3
P04083	ANXA1	9	3	54.8	0.000135	0.000622	2.02	cuk6	cuk4	Annexin A1 GN=ANXA1 PE=1 SV=2
P14625	HSP90B1	52	26	564	0.000312	0.000909	1.81	cuk6	cuk4	Endoplasmin GN=HSP90B1 PE=1 SV=1
Q15746	MYLK	10	6	64.8	5.01E-05	0.000431	1.77	cuk6	cuk4	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
P62937	PPIA	17	8	163	0.000441	0.001097	1.67	cuk6	cuk4	Peptidyl-prolyl cis-trans isomerase A GN=PPIA PE=1 SV=2
P16144	ITGB4	7	5	49	0.001351	0.002235	1.54	cuk4	cuk6	Integrin beta-4 GN=ITGB4 PE=1 SV=5
P00558	PGK1	20	9	150	0.004034	0.004466	1.47	cuk4	cuk6	Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3
O60343	TBC1D4	7	2	43	0.01107	0.008916	1.44	cuk6	cuk4	TBC1 domain family member 4 GN=TBC1D4 PE=1 SV=2
A0A1B0GV23	CTSD	9	6	48.6	0.008586	0.007434	1.42	cuk6	cuk4	Cathepsin D GN=CTSD PE=1 SV=1
P08670	VIM	52	22	676	0.000206	0.00075	1.38	cuk6	cuk4	Vimentin GN=VIM PE=1 SV=4
P12004	PCNA	6	4	44.8	0.019921	0.013809	1.35	cuk4	cuk6	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
P60709	ACTB	66	15	1010	0.001344	0.002235	1.3	cuk6	cuk4	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1
P68104	EEF1A1	32	4	335	0.002743	0.003524	1.23	cuk6	cuk4	Elongation factor 1-alpha 1 GN=EEF1A1 PE=1 SV=1
P02787	TF	62	25	655	0.002431	0.003274	1.2	cuk4	cuk6	Serotransferrin GN=TF PE=1 SV=3
Q06830	PRDX1	13	6	102	0.010672	0.008698	1.15	cuk6	cuk4	Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1
P10809	HSPD1	44	19	497	0.026764	0.017191	1.14	cuk4	cuk6	60 kDa heat shock protein_ mitochondrial GN=HSPD1 PE=1 SV=2
Anti-Aβ$_{17\text{-}23}$ Antibody Treatment										
P12004	PCNA	6	4	44.8	0.047014	0.031657	1.24	cuk5	cuk6	Proliferating cell nuclear antigen GN=PCNA PE=1 SV=1
Q15746	MYLK	10	6	64.8	0.002662	0.004452	1.17	cuk6	cuk5	Myosin light chain kinase_ smooth muscle GN=MYLK PE=1 SV=4
Q02413	DSG1	8	3	66.4	0.001401	0.002916	1.92	cuk6	cuk5	Desmoglein-1 GN=DSG1 PE=1 SV=2
Q03181	PPARD	7	2	67.2	0.003216	0.00492	1.43	cuk6	cuk5	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1
P60709	ACTB	66	15	1010	0.003374	0.005038	1.15	cuk5	cuk6	Actin_ cytoplasmic 1 GN=ACTB PE=1 SV=1

Table S18: Statistical overrepresentation test of the identified allergy related proteins following DMAT$_{A\beta1\text{-}6}$ and DMAT$_{A\beta17\text{-}23}$ by PANTHER. Herein, FDR indicates false discovery rate. Displaying only results for FDR $P < 0.05$.

Reactome pathways	Fold Enrichment	raw P value	FDR
Anti-Aβ$_{1\text{-}6}$ Antibody Treatment			
Interleukin-4 and Interleukin-13 signaling	43.64	2.07E-06	5.16E-03
Signaling by Interleukins	13.52	2.50E-05	2.08E-02
Anti-Aβ$_{17\text{-}23}$ Antibody Treatment			
No statistically significant results			

Table S19: Gene enriched term and their associated genes for the identified allergy related genes following ${}_{\text{Allg}}\text{DMAT}_{\text{A}\beta\text{1-6}}$ and ${}_{\text{Allg}}\text{DMAT}_{\text{A}\beta\text{17-23}}$.

Description	**Hits**	**LogP**	**Log(q-value)**
cellular response to chemical stress	ANXA1|MYLK|PRDX1|PCNA|PPIA	-6.744331056	-2.51991
Interleukin-4 and Interleukin-13 signaling	ANXA1|HSP90B1|TYK2|VIM	-6.565567193	-2.51991
response to steroid hormone	DSG1|PCNA|PPARD	-5.147369483	-1.5438
retina homeostasis	ACTB|PRDX1|TF	-5.010249598	-1.50866
cell activation	ACTB|ANXA1|HSPD1|PRDX1|PPIA	-4.833649323	-1.39005
Sudden infant death syndrome (SIDS) susceptibility pathways	HSPD1|TF|HSP90B1	-4.09410297	-0.8266
response to wounding	ACTB|ITGB4|PPARD|PPIA	-3.97583788	-0.7431
Signaling by Rho GTPases	ACTB|DSG1|MYLK	-3.909346136	-0.79979
Neutrophil degranulation	CTSD|DSG1|EEF1A1|PPIA	-3.79220745	-0.64964
positive regulation of hydrolase activity	CTSD|HSPD1|PCNA|TBC1D4	-3.699742806	-0.79979
regulation of vesicle-mediated transport	ANXA1|TF|TBC1D4	-2.59819305	-0.00566
Cellular responses to stress	EEF1A1|PRDX1|HSP90B1	-2.162574534	0

Table S20: Identified apoptosis-related proteins following $\text{DMAT}_{\text{A}\beta\text{1-6}}$, $\text{DMAT}_{\text{A}\beta\text{17-23}}$ compared to untreated cells. Herein, Cuk4=Aβ1-6; Cuk5=Aβ17-23; Cuk6= NoT.

Accession	Gene ID	Peptides	Unique peptides	Confidence score	Anova (p)	q Value	Max fold change	Highest Mean	Lowest Mean	Description
Anti-$\text{A}\beta_{1\text{-}6}$ Antibody Treatment										
Q8N163	CCAR2	8	4	41.6	0.006093	0.005976	2.09	cuk6	cuk4	Cell cycle and apoptosis regulator protein 2 GN=CCAR2 PE=1 SV=2
Q8IVF5	TIAM2	10	3	43.9	0.000421	0.001063	1.94	cuk4	cuk6	T-lymphoma invasion and metastasis-inducing protein 2 GN=TIAM2 PE=2 SV=4
P49773	HINT1	4	2	44.7	0.002123	0.003023	1.82	cuk6	cuk4	Histidine triad nucleotide-binding protein 1 GN=HINT1 PE=1 SV=2
P62979	RPS27A	6	3	46.9	0.022204	0.014975	2.3	cuk4	cuk6	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
P52756	RBM5	7	3	50.1	0.028247	0.017949	1.17	cuk6	cuk4	RNA-binding protein 5 GN=RBM5 PE=1 SV=2
J3KSB5	NF1	10	7	51.1	0.024678	0.016159	1.11	cuk4	cuk6	Neurofibromin (Fragment) GN=NF1 PE=1 SV=1
O43683	BUB1	9	4	51.3	0.045449	0.025635	1.27	cuk4	cuk6	Mitotic checkpoint serine/threonine-protein kinase BUB1 GN=BUB1 PE=1 SV=1
P01308	INS	5	3	51.6	0.000351	0.000964	1.82	cuk6	cuk4	Insulin GN=INS PE=1 SV=1
P04083	ANXA1	9	3	54.8	0.000135	0.000622	2.02	cuk6	cuk4	Annexin A1 GN=ANXA1 PE=1 SV=2
P17987	TCP1	10	4	67.5	0.001525	0.002411	1.44	cuk6	cuk4	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
Q03468	ERCC6	13	4	75.3	0.039195	0.022933	1.69	cuk4	cuk6	DNA excision repair protein ERCC-6 GN=ERCC6 PE=1 SV=1
P06748	NPM1	9	4	102	0.022784	0.015234	1.32	cuk6	cuk4	Nucleophosmin GN=NPM1 PE=1 SV=2
P07196	NEFL	15	3	113	0.006072	0.005968	1.95	cuk6	cuk4	Neurofilament light polypeptide GN=NEFL PE=1 SV=3
P32119	PRDX2	10	5	114	0.000697	0.001446	1.29	cuk6	cuk4	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
P08133	ANXA6	18	7	134	0.004933	0.005114	1.19	cuk6	cuk4	Annexin A6 GN=ANXA6 PE=1 SV=3
Q12931	TRAP1	18	8	143	0.00585	0.005786	1.3	cuk6	cuk4	Heat shock protein 75 kDa_ mitochondrial GN=TRAP1 PE=1 SV=3
P48681	NES	24	9	150	0.0002	0.000748	1.6	cuk4	cuk6	Nestin GN=NES PE=1 SV=2
P05787	KRT8	19	8	156	0.007764	0.00688	1.39	cuk4	cuk6	Keratin_ type II cytoskeletal 8 GN=KRT8 PE=1 SV=7
E9PK25	CFL1	15	4	163	0.024237	0.015964	1.1	cuk6	cuk4	Cofilin-1 GN=CFL1 PE=1 SV=1
Q15811	ITSN1	28	6	174	0.015478	0.011362	1.7	cuk6	cuk4	Intersectin-1 GN=ITSN1 PE=1 SV=3
Q05639	EEF1A2	17	2	202	0.029425	0.018498	1.14	cuk6	cuk4	Elongation factor 1-alpha 2 GN=EEF1A2 PE=1 SV=1
P61978	HNRNPK	30	4	248	0.004001	0.004466	1.43	cuk4	cuk6	Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1
Q9Y4L1	HYOU1	39	18	290	0.000318	0.000909	1.92	cuk4	cuk6	Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1
P04406	GAPDH	33	5	334	0.001352	0.002235	1.91	cuk4	cuk6	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P08238	HSP90AB1	38	12	379	0.015276	0.011267	1.24	cuk4	cuk6	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
P11021	HSPA5	43	25	466	0.008819	0.007601	1.47	cuk4	cuk6	Endoplasmic reticulum chaperone BiP GN=HSPA5 PE=1 SV=2
P10809	HSPD1	44	19	497	0.026764	0.017191	1.14	cuk4	cuk6	60 kDa heat shock protein_ mitochondrial GN=HSPD1 PE=1 SV=2
P14625	HSP90B1	52	26	564	0.000312	0.000909	1.81	cuk6	cuk4	Endoplasmin GN=HSP90B1 PE=1 SV=1
P68032	ACTC1	54	11	688	0.032896	0.020169	1.19	cuk6	cuk4	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1
Anti-$\text{A}\beta_{17\text{-}23}$ Antibody Treatment										
P49773	HINT1	4	2	44.7	0.000369	0.001531	2.22	cuk6	cuk5	Histidine triad nucleotide-binding protein 1 GN=HINT1 PE=1 SV=2
Q13247	SRSF6	5	4	45.3	0.008277	0.009151	1.47	cuk5	cuk6	Serine/arginine-rich splicing factor 6 GN=SRSF6 PE=1 SV=2
P62979	RPS27A	6	3	46.9	0.022825	0.018798	2.24	cuk5	cuk6	Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2
P52756	RBM5	7	3	50.1	0.025648	0.020609	1.26	cuk6	cuk5	RNA-binding protein 5 GN=RBM5 PE=1 SV=2
P01308	INS	5	3	51.6	0.000214	0.001222	1.37	cuk5	cuk6	Insulin GN=INS PE=1 SV=1
Q03181	PPARD	7	2	67.2	0.003216	0.00492	1.43	cuk6	cuk5	Peroxisome proliferator-activated receptor delta GN=PPARD PE=1 SV=1
P17987	TCP1	10	4	67.5	0.028958	0.02222	1.23	cuk6	cuk5	T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1
P61247	RPS3A	11	5	86.8	0.010061	0.010336	1.37	cuk5	cuk6	40S ribosomal protein S3a GN=RPS3A PE=1 SV=2
P06748	NPM1	9	4	102	0.007207	0.008317	1.51	cuk5	cuk6	Nucleophosmin GN=NPM1 PE=1 SV=2
P32119	PRDX2	10	5	114	0.002263	0.004009	1.2	cuk6	cuk5	Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5
P17844	DDX5	18	7	123	0.009452	0.009875	1.2	cuk5	cuk6	Probable ATP-dependent RNA helicase DDX5 GN=DDX5 PE=1 SV=1
P08133	ANXA6	18	7	134	0.013787	0.012977	1.35	cuk6	cuk5	Annexin A6 GN=ANXA6 PE=1 SV=3
P48681	NES	24	9	150	0.000948	0.002506	1.25	cuk5	cuk6	Nestin GN=NES PE=1 SV=2
E9PK25	CFL1	15	4	163	0.000542	0.00187	1.31	cuk6	cuk5	Cofilin-1 GN=CFL1 PE=1 SV=1
Q15811	ITSN1	28	6	174	0.002741	0.004545	2.56	cuk6	cuk5	Intersectin-1 GN=ITSN1 PE=1 SV=3
P07237	P4HB	23	9	201	0.007835	0.008779	1.33	cuk6	cuk5	Protein disulfide-isomerase GN=P4HB PE=1 SV=3
P04406	GAPDH	33	5	334	0.016616	0.015038	1.26	cuk5	cuk6	Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3
P08238	HSP90AB1	38	12	379	0.005829	0.007169	1.2	cuk6	cuk5	Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4
P68032	ACTC1	54	11	688	0.005074	0.006682	1.39	cuk5	cuk6	Actin_ alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1

Table S21: Statistical overrepresentation test of the identified apoptosis related proteins following DMAT$_{A\beta1-6}$ and DMAT$_{A\beta17-23}$ by PANTHER. Herein, FDR indicates false discovery rate. Displaying only results for FDR *P* < 0.05.

Reactome pathways	**Fold Enrichment**	**Raw P value**	**FDR**
Anti-Aβ_{1-6} Antibody Treatment			
No statistically significant results.			
Anti-Aβ_{17-23} Antibody Treatment			
Interleukin-12 signaling	70.67	1.19E-05	2.97E-02
Interleukin-12 family signaling	58.05	2.09E-05	2.61E-02

Table S22: Gene enriched term and their associated genes for the identified apoptosis related genes following $_{Apop}$DMAT$_{A\beta1-6}$ and $_{Apop}$DMAT$_{A\beta17-23}$.

Description	Hits	LogP	Log(q-value)
protein folding	HSPA5|HSP90AB1|HSPD1|P4HB|TCP1|HSP90B1|TRAP1	-8.56019	-4.48079
regulation of cellular response to stress	DDX5|ERCC6|HNRNPK|HSPA5|INS|NPM1|P4HB|TRAP1|HYOU1|CCAR2	-8.52645	-4.48079
Cellular responses to stress	HSPA5|HSP90AB1|P4HB|RPS3A|RPS27A|PRDX2|HSP90B1|HYOU1|CCAR2	-6.95421	-3.31828
apoptotic signaling pathway	ANXA6|DDX5|ERCC6|HINT1|NF1|PPARD	-6.29834	-2.79675
regulation of neuron apoptotic process	HSP90AB1|NEFL|NF1|HYOU1|NES	-5.82547	-2.17776
response to radiation	ANXA1|ERCC6|HSPA5|NF1|NPM1|CCAR2	-5.53327	-2.12697
biological process involved in symbiotic interaction	CFL1|GAPDH|HSP90AB1|HSPD1|TCP1	-5.49326	-2.12697
Interleukin-12 signaling	CFL1|P4HB|TCP1	-5.47365	-2.12697
regulation of mRNA splicing, via spliceosome	DDX5|HNRNPK|SRSF6|RBM5	-5.26269	-2.02994
positive regulation of protein localization to nucleus	HSP90AB1|INS|TCP1	-5.13179	-2.02792
negative regulation of catalytic activity	ANXA1|GAPDH|INS|NF1|NPM1|NES|CCAR2	-5.12847	-2.02792
supramolecular fiber organization	ACTC1|CFL1|HSP90AB1|NEFL|NF1|HSP90B1	-5.05744	-2.0001
positive regulation of apoptotic process	ANXA1|EEF1A2|HSPD1|NF1|RBM5|CCAR2	-5.02456	-2.0001
Axon guidance	CFL1|HSP90AB1|RPS3A|RPS27A|ITSN1	-4.72557	-1.80547
chaperone-mediated protein folding	HSPA5|TCP1|TRAP1	-4.36154	-1.61691
response to inorganic substance	ANXA1|ERCC6|HSPA5|NEFL|PRDX2	-3.93039	-1.41195
SARS-CoV Infections	DDX5|HSP90AB1|RPS27A	-3.89319	-1.40315
Cellular response to chemical stress	P4HB|RPS27A|PRDX2	-3.87704	-1.39368
7q11.23 copy number variation syndrome	CFL1|ERCC6|GAPDH	-3.84302	-1.38282
cell population proliferation	BUB1|HSPD1|PPARD|PRDX2|NES	-3.68703	-1.17577