Supplemental Table S1. Detailed informations of ADMA-containing peptides identified in chronic pancreatitis tissues.

Protein ID	Protein name	Annotations	Sequence window	Dimethyl (R) Probabilities	Dimethyl (R) Score diffs	Localization prob	PEP	Score	Number of Dimethyl (R)	Amino acid	Position in peptide	Charge	Mass error [ppm]	Intensity Ctrl 1	Intensity Ctrl 2	Intensity Ctrl 3	Intensity CP 1	Intensity CP 2	Intensity CP 3	Previous Reports
P05186-2	ALPL	Alkaline phosphatase, tissue-nonspecific isoz	LMHNIRDIDVIMGG	DIAYOLMHNIR(0.01)DIDVIN	DIAYOLMHNIR(-20.01)DID	0.990114	0.00396781	40.113	1	R	21	2	-0.02951	59428000	62387000	47221000	0	0	0	
O15013-7	ARHGEF10	Rho guanine nucleotide exchange factor 10	ALPVPRLQGIPKVTG	LQGIPKVTGR(1)	LQGIPKVTGR(75.85)	1	0.0363619	75.854		R	10	2	-0.57613	10695000	16326000	3479200	15466000	28951000	11093000	
Q8NFD5	ARID1B	AT-rich interactive domain-containing prote	MGRSOGSPMDPM	R(1)POLYGMGSNPHSOPO(	R(72.21)POLYGMGSNPHS(	1	2.53E-26	72.214	2	R	1	5	-0.28791	6377400	6421200	38138000	0	0	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q8NFD5	ARID1B	AT-rich interactive domain-containing prote	YGPPGPORYPIGIO(	R(1)POLYGMGSNPHSOPO(	R(54.7)POLYGMGSNPHSO	0.521221	2.53E-26	72.214	2	R	41	5	-0.21597	6377400	6421200	38138000	0	0	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q8NFD5	ARID1B	AT-rich interactive domain-containing prote	SSPYPGGSYGPPGP	R(1)POLYGMGSNPHSOPO(	R(72.21)POLYGMGSNPHS(	0.5	2.53E-26	72.214	2	R	33	5	-0.28791	6377400	6421200	14121000	0	0	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q8IVW6-4	ARID3B	AT-rich interactive domain-containing prote	RLSEEEQRLVQQAF(	LVQQAFQR(1)NFFSMAR(1)	LVQQAFQR(40.86)NFFSM/	1	0.00151945	50.787	2	R	8	4	-0.05951	10132000	9609200	61763000	27283000	19255000	16288000	
Q8IVW6-4	ARID3B	AT-rich interactive domain-containing prote	RLVOOAFORNFFSN	LVQOAFOR(1)NFFSMAR(1)	LVQOAFOR(40.86)NFFSM/	1	0.00151945	50.787	2	R	15	4	-0.05951	10132000	9609200	61763000	27283000	19255000	16288000	
Q8IZT6	ASPM	Abnormal spindle-like microcephaly-associat	SVIYIOAIFRGKKARR	R(1)HLKMMHIAATLIQR	R(48.94)HLKMMHIAATLIOF	0.999987	0.00878715	50.563	1	R	1	3	-4.0576	134950000	38463000	53996000	49751000	129420000	61455000	
Q9C0K0-2	BCL11B	B-cell lymphoma/leukemia 11B	EGRLPGTPPLFSPPP	DHPGFGEGRLPGTPPLFSPP	DHPGFGEGR(-36.52)LPGTI	0.990874	1.80E-11	48.867		R	22	5	0.83815	0	0	0	0	2391200	15845000	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
O00512	BCL9	B-cell CLL/lymphoma 9 protein	PSOTLOYFPRGEVP	IIPSEKPSOTLOYFPR(0.476)(	IIPSEKPSOTLOYFPR(-0.41)	0.523766	0.00125283	58.158	1	R	22	4	2.4907	2324900	13638000	9727300	0	6340000	0	Mol. Cell. Proteomics 13:372-387(2014)
Q86UU0-3	BCL9L	B-cell CLL/lymphoma 9-like protein	EAERFMTPRVREELL	EELLR(1)HQLLEKR	EELLR(57.65)HOLLEKR(-57.	0.999998	1.72E-05	96.015	1	R	5	4	0.82754	2268200	36278000	42950000	22945000	11803000	6907500	Front. Cell Dev. Biol. 8: 545934 (2020)
Q86UU0-3	BCL9L	B-cell CLL/lymphoma 9-like protein	PGGOGEAERFMTPI	VR(0.537)EELLR(0.463)HOLL	VR(0.64)EELLR(-0.64)HOLLI	0.53684	0.0266441	45.257	1	R	2	4	0.17825	0	0	0	0	0	4295000	Front. Cell Dev. Biol. 8: 545934 (2020)
P51587	BRCA2	Breast cancer type 2 susceptibility protein	HRVEOCVRNINLEEI	NINLEENR(1)QK	NINLEENR(76.9)QK	1	0.0354819	76.899		R	8	2	2.4496	31150000	17775000	27177000	16599000	10003000	14601000	
Q8TBZ0-2	CCDC110	Coiled-coil domain-containing protein 110	EENLDGNLNEDIKSI	R(1)ISELEALVK	R(77.06)ISELEALVK	1	0.0289583	77.058		R	1	2	0.10785	18367000	20454000	49962000	78196000	50972000	20317000	
Q8NCX0	CCDC150	Coiled-coil domain-containing protein 150	HSKDLKLLHLEVMN	LLHLEVMNLR(0.818)QQLR(	LLHLEVMNLR(6.53)QQLR(-	0.817942	0.0315883	42.809	1	R	10	3	-1.2921	0	54824000	0	0	0	0	Nat Commun 24;8:15571 (2017)
Q12834	CDC20	Cell division cycle protein 20 homolog	LYSOKATPGSSRKTC	TCR(0.999)YIPSLPDR(0.004)	TCR(28.44)YIPSLPDR(-26.2	0.998575	0.0176316	41.871	2	R	3	3	-0.3618	0	0	0	0	63633000	33566000	Mol. Cell. Proteomics 13:372-387(2014) ; Nat Commun 24;8:15571 (2017)
Q12834	CDC20	Cell division cycle protein 20 homolog	YIPSLPDRILDAPEIRI	TCR(0.999)YIPSLPDR(0.004)	TCR(28.44)YIPSLPDR(-26.2	0.997653	0.0176316	41.871	2	R	19	3	-0.3618	0	0	0	0	63633000	33566000	Mol. Cell. Proteomics 13:372-387(2014) ; Nat Commun 24;8:15571 (2017)
Q9UKI2	CDC42EP3	Cdc42 effector protein 3	YLKAANNKKGKKFK	LR(1)DILSPDMISPPLGDFR(1	LR(58.68)DILSPDMISPPLGD	1	0.00301984	58.676	2	R	2	2	-2.5838	185710000	359860000	195400000	37667000	0	0	
Q9UKI2	CDC42EP3	Cdc42 effector protein 3	DILSPDMISPPLGDFI	LR(1)DILSPDMISPPLGDFR(1	LR(58.68)DILSPDMISPPLGD	1	0.00301984	58.676	2	R	18	2	-2.5838	185710000	359860000	195400000	37667000	0	0	Mol. Cell. Proteomics 13:372-387(2014)
P0CG12	CHTF8	Chromosome transmission fidelity protein 8 l	MKEPRIFI	MKEPR(1)IFPR	MKEPR(62.62)IFPR(-62.62)	0.999999	0.023895	101.64	1	R	5	3	-1.4757	5251600	25575000	154610000	44009000	29275000	56192000	Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P0CG12	CHTF8	Chromosome transmission fidelity protein 8 l	ARAGGLLGTGSGLN	AGGLLGTGSGLNLR(1)MAGI	AGGLLGTGSGLNLR(38.23)I	0.99985	1.70E-13	86.856	1	R	14	3	1.5968	9403000	13311000	32780000	38382000	16471000	7872500	Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P0CG12	CHTF8	Chromosome transmission fidelity protein 8 l	PRTGALPGPGPLSNI	TGALPGPGPLSNPR(0.972)L(	TGALPGPGPLSNPR(15.48)L	0.972477	2.50E-13	91.128	1	R	14	3	-0.69648	0	10136000	31595000	20993000	21021000	9560700	Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P0CG12	CHTF8	Chromosome transmission fidelity protein 8 l	MKEPRIFPRE	MKEPR(0.282)IFPR(0.718)	MKEPR(-4.06)IFPR(4.06)	0.717955	0.014307	40.002	1	R	9	3	-0.9869	0	6140500	19910000	5406900	2903300	5325500	Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q8WTW3	COG1	Conserved oligomeric Golgi complex subunit	SQIRFGLLPLSMTSTI	FGLLPLSMTSTR(1)K	FGLLPLSMTSTR(50.91)K	1	0.00794025	50.909	1	R	12	2	-0.82008	124670000	0	86070000	18601000	0	0	
P23786	CPT2	Carnitine O-palmitoyltransferase 2, mitochor	ORSIVPTMHYODSL	SIVPTMHYODSLPR(1)LPIPK	SIVPTMHYODSLPR(58.98)L	1	0.00109174	66.335	1	R	14	4	-0.47841	45085000	2271900	41223000	50545000	85973000	115170000	Front. Cell Dev. Biol. 8: 545934 (2020)
O15320-9	CTAGE5;MIA2	cTAGE family member 5;Melanoma inhibitor	FPPPPPFAMRNVYP	NVYPPR(0.999)GFPPYLPPR	NVYPPR(30.18)GFPPYLPPR	0.999046	0.00410168	41.087	2	R	6	5	-0.15809	0	7379300	19522000	13508000	4041800	6113300	Nat Commun 24;8:15571 (2017)
O15320-9	CTAGE5;MIA2	cTAGE family member 5;Melanoma inhibitor	RNVYPPRGFPPYLPI	NVYPPR(0.999)GFPPYLPPR	NVYPPR(30.18)GFPPYLPPR	0.996172	0.00410168	41.087	2	R	15	5	-0.15809	0	7379300	19522000	13508000	4041800	6113300	Nat Commun 24;8:15571 (2017)
Q8N8A6	DDX51	ATP-dependent RNA helicase DDX51	MALFYVARY	ALFYVAR(1)YPGPDAAAAA(	ALFYVAR(78.03)YPGPDAA/	1	3.63E-15	86.946	1	R	7	3	-0.42411	16167000	0	0	0	18741000	0	
Q9Y485	DMXL1	DmX-like protein 1	ANHIFSCGADGTMI	NIGTGVMOIETGPANHIFSC	NIGTGVMOIETGPANHIFSC	1	0.00139115	44.807	1	R	29	2	1.6968	16269000	76169000	154740000	141990000	138140000	157420000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
Q8IVF4	DNAH10	Dynein heavy chain 10, axonemal	GDDLDKGVELLGVY	GVELLGVYER(1)ELAR(1)HEK	GVELLGVYER(45.86)ELAR(4	1	0.0127969	45.864	2	R	10	3	-3.3391	3147300	0	0	0	22199000	10464000	Nat Commun 24;8:15571 (2017)
Q8IVF4	DNAH10	Dynein heavy chain 10, axonemal	DKGVELLGVYERELA	GVELLGVYER(1)ELAR(1)HEK	GVELLGVYER(45.86)ELAR(4	1	0.0127969	45.864	2	R	14	3	-3.3391	3147300	0	0	0	22199000	10464000	Nat Commun 24;8:15571 (2017)
Q8IY82-2	DRC7	Dynein regulatory complex subunit 7	MOPEMDRVIEFYET	VIEFYETAR(0.902)VDGLMKI	VIEFYETAR(9.65)VDGLMKR	0.902226	0.0217033	47.201		R	9	3	-0.73613	0	0	0	0	53607000	44473000	
Q5VTE0	EF1A1P5;EEF1A	Putative elongation factor 1-alpha-like 3;Elor	GVNKMDSTEPPYSC	QLIVGVNKMDSTEPPYSQKF	QLIVGVNKMDSTEPPYSQK	1	0.00020265	64.507	1	R	20	4	0.49641	0	21399000	12541000	4985000	3417300	5203900	
Q9H4M9	EHD1	EH domain-containing protein 1	DDMLANDIARLMVI	LMVMVR(1)OEESLMPSOV\	LMVMVR(52.25)OEESLMPS	1	0.00401692	52.254	1	R	6	3	1.8243	26918000	18040000	227560000	96746000	13281000	22569000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
O60573	EIF4E2	Eukaryotic translation initiation factor 4E type	RLGPORLLFONLWK	LLFQNLWKPR(1)LNVP	LLFONLWKPR(62.92)LNVP	1	0.000370522	87.001	1	R	10	3	1.9401	9423700	103270000	12543000	0	0	1487900	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q04637-3	EIF4G1	Eukaryotic translation initiation factor 4 gamr	MNTPSOPR	NTPSQPR(1)QHFYPSR(1)	NTPSOPR(50.15)OHFYPSR	1	6.12E-22	97.551	1;2	R	7	4	0.14664	59158000	103680000	87124000	88466000	22509000	7785500	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q04637-3	EIF4G1	Eukaryotic translation initiation factor 4 gamr	MNTPSOPROHFYI	NTPSQPR(1)QHFYPSR(1)	NTPSOPR(50.15)OHFYPSR	1	0.00184011	60.628	2	R	14	4	0.14664	1921400	20139000	2455800	2439900	3718300	9794700	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P58107	EPPK1	Epiplakin	NKAARDSEHIDDETI	R(1)ALEAEQVEITVGR	R(44.62)ALEAEOVEITVGR(-	0.999965	0.0101332	44.616		R	1	4	-2.3821	0	0	0	1056900	2766200	13224000	
P0DP91	ERCC6	DNA excision repair protein ERCC-6	INKIIEOLSPOAATSR	IIEOLSPOAATSR(0.983)DINI	IIEOLSPOAATSR(17.61)DIN	0.982949	0.00807453	56.648	1	R	13	3	1.2698	20668000	4066100	37024000	25741000	34846000	30538000	
Q17RC7	EXOC3L4	Exocyst complex component 3-like protein 4	QRHLETLIRSYPDIRR	R(1)DHILAILALR	R(51.93)DHILAILALR(-51.93	0.999994	0.0120246	51.927	1	R	1	4	0.029741	7221200	19216000	29461000	37870000	15401000	65052000	
Q5T1M5	FKBP15	FK506-binding protein 15	ASFLMTEAROHNTE	QHNTEIR(1)MAVSK	QHNTEIR(89.55)MAVSK	1	0.0002422	89.548	1	R	7	3	-0.05018	63475000	74334000	45843000	67235000	104590000	162500000	Front. Cell Dev. Biol. 8: 545934 (2020)
Q9H479	FN3K	Fructosamine-3-kinase	MEQLLRA	MEQLLR(1)AELR	MEQLLR(83.56)AELR(-83.5	1	8.36E-09	114.93	1	R	6	2	0.43779	13687000	20964000	0	0	2499200	0	
P23945-3	FSHR	Follicle-stimulating hormone receptor	SLPSYGLENLKKLRAI	AR(1)STYNLKK	AR(81.3)STYNLKK	1	0.0337491	81.297		R	2	2	0.51357	0	0	22046000	0	0	0	
P35637-2	FUS	RNA-binding protein FUS	GGGGSGGYGOODI	GGR(1)GR(1)GGSGGGGGG	GGR(52.24)GR(52.24)GGSG	0.999994	0.00146758	52.784	2	R	3	4	-1.2657	0	4234400	10295000	0	5491900	0	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
P35637-2	FUS	RNA-binding protein FUS	GGSGGYGOODRGC	GGR(1)GR(1)GGSGGGGGG	GGR(52.24)GR(52.24)GGSG	0.999994	0.00146758	52.784	2	R	5	4	-1.2657	0	4234400	10295000	0	5491900	0	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
Q16538-2	GPR162	Probable G-protein coupled receptor 162	VKLLPGRHMLFPPLE	LLPGR(0.009)HMLFPPLER(	LLPGR(-20.27)HMLFPPLER	0.990699	0.0375517	40.113		R	14	3	1.0217	0	0	6470900	0	0	0	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
P24298	GPT	Alanine aminotransferase 1	LRAKVLTLDGMNPR	VLTLDGMNPR(0.406)VR(0.5	VLTLDGMNPR(-1.65)VR(1.(	0.593684	0.0246989	57.177	1	R	12	2	-1.6178	10998000	29014000	0	0	20790000	38184000	
Q05586-2	GRIN1	Glutamate receptor ionotropic, NMDA 1	KNVTALLMEAKELE/	VLOFDPGTKNVTALLMEAKE	VLOFDPGTKNVTALLMEAK	1	0.00679179	55.763	1	R	24	3	-0.49118	19827000	46309000	52342000	35989000	6070400	0	
Q99525	HIST1H4G	Histone H4-like protein type G	ENVIWYAVTNTEHA	VFLENVIWYAVTNTEHAKR(	VFLENVIWYAVTNTEHAKR(	1	0.000467235	79.771	1	R	19	4	-2.3436	6035700	0	0	24548000	69039000	181780000	
P09651-3	RNPA1;HNRNP/	Heterogeneous nuclear ribonucleoprotein A1	LSKOEMASASSSOR	ALSKOEMASASSSOR(0.006	ALSKOEMASASSSOR(-21.8	0.993544	7.45E-59	132.86	1	R	17	3	-0.22548	85602000	124560000	58242000	7814500	110500000	1868600	Mol. Cell. Proteomics 13:372-387(2014)
P09651-3	RNPA1;HNRNP/	Heterogeneous nuclear ribonucleoprotein A1	KALSKOEMASASSS	OEMASASSSOR(0.804)GR((	OEMASASSSOR(6.14)GR(-(	0.804455	8.85E-05	98.439	1	R	11	3	-1.154	24821000	54810000	75398000	0	8293900	0	Mol. Cell. Proteomics 13:372-387(2014)
P51991-2	HNRNPA3	Heterogeneous nuclear ribonucleoprotein A3	GGGYGSGGGSGGY	SSGSPYGGGYGSGGGSGGY	SSGSPYGGGYGSGGGSGGY	0.5	0.00772931	57.496	1	R	22	3	-0.51003	0	0	0	3940500	6881000	9217200	
P51991-2	HNRNPA3	Heterogeneous nuclear ribonucleoprotein A3	GGYGSGGGSGGYG	SSGSPYGGGYGSGGGSGGY	SSGSPYGGGYGSGGGSGGY	0.5	0.00772931	57.496	1	R	23	3	-0.51003	0	0	0	3940500	6881000	9217200	
Q99729-3	HNRNPAB	Heterogeneous nuclear ribonucleoprotein A/	EVYOOOOYGSGGF	EVYOOOOYGSGGR(0.454)(	EVYOOOOYGSGGR(-0.79)	0.545546	0.000186582	78.763	1	R	16	3	-0.26375	6638500	16116000	13217000	0	5641000	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q99729-3	HNRNPAB	Heterogeneous nuclear ribonucleoprotein A/	OPKEVYOOOOYGS	EVYOOOOYGSGGR(0.5)GN	EVYOOOOYGSGGR(0)GNF	0.5	0.000186582	78.763	1	R	13	3	0.061853	6638500	16116000	0	0	5641000	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q14103-3	HNRNPD	Heterogeneous nuclear ribonucleoprotein D(	GRGGDOOSGYGKV	R(1)GGHQNSYKPY	R(97.46)GGHQNSYKPY	1	3.05E-05	97.456		R	1	3	0.47607	111500000	30276000	175310000	14367000	129050000	14232000	Front. Cell Dev. Biol. 8: 545934 (2020)
O00839-2	HNRNPU	Heterogeneous nuclear ribonucleoprotein U	GGIGYPYPRAPVFP(	APVFPGR(1)GSYSNR(1)	APVFPGR(80.98)GSYSNR(8	1	1.35E-10	100.55	2	R	7	3	-0.25079	6706600	40568000	49356000	74171000	13372000	38561000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
O00839-2	HNRNPU	Heterogeneous nuclear ribonucleoprotein U	YPRAPVFPGRGSYSI	APVFPGR(1)GSYSNR(1)	APVFPGR(80.98)GSYSNR(8	1	1.35E-10	100.55	2	R	13	3	-0.25079	6706600	40568000	49356000	74171000	13372000	38561000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q1KMD3	HNRNPUL2	Heterogeneous nuclear ribonucleoprotein U-	DNRAYGOOYWGO	AYGOOYWGOPGNR(0.5)G(	AYGOOYWGOPGNR(0)GG	0.5	0.00804684	65.805	1	R	13	3	-1.3023	10061000	8270100	0	5048000	6131500	9926100	Mol. Cell. Proteomics 13:372-387(2014);Nat. Commun. 6:6428-6428(2015) ; Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q1KMD3	HNRNPUL2	Heterogeneous nuclear ribonucleoprotein U-	YGOOYWGOPGNR	AYGOOYWGOPGNR(0.5)G(	AYGOOYWGOPGNR(0)GG	0.5	0.00804684	65.805	1	R	17	3	-1.3023	10061000	8270100	0	5048000	6131500	9926100	Mol. Cell. Proteomics 13:372-387(2014);Nat. Commun. 6:6428-6428(2015) ; Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P98160	HSPG2	Basement membrane-specific heparan sulfat	AVSLEVAOPGPSNR	ATFSSVPLAASISAVSLEVAO	ATFSSVPLAASISAVSLEVAC	0.543206	0.0191808	48.867	1	R	29	3	0.29982	48106000	36990000	57168000	46516000	37989000	29653000	
O43837-2	IDH3B	Isocitrate dehydrogenase [NAD] subunit beta	FANVVHVKSLPGYN	LDLFANVVHVKSLPGYMTR(	LDLFANVVHVKSLPGYMTR	1	0.00915993	52.254	1	R	19	4	0.7091	0	0	0	0	33142000	0	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
A0A0C4DH67	.-8;IGKV1-9;IGKV1-27		LLIYAASTLOSGVPSI	LLIYAASTLQSGVPSR(1)	LLIYAASTLOSGVPSR(59.76)	1	0.00282234	59.757		R	16	2	-0.0241	0	41030000	0	0	11548000	0	Mol. Cell. Proteomics 13:372-387(2014)
Q15735	INPP5J	Phosphatidylinositol 4,5-bisphosphate 5-phc	OLPAKKNAALGPSE	NAALGPSEPR(0.871)LALAP	NAALGPSEPR(8.29)LALAPV	0.871002	0.0023467	66.965	1	R	10	3	0.33072	2070500	18306000	11317000	5197400	0	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q63ZY3-3	KANK2	KN motif and ankyrin repeat domain-contair	YPOYGALETRGGFN	GFYPOYGALETR(0.434)GGF	GFYPOYGALETR(-1.15)GGI	0.56578	0.0332579	53.403	1	R	18	3	-0.80009	0	7313500	0	1446600	6255700	1540300	
O43896	KIF1C	Kinesin-like protein KIF1C	KOEOLRLOGLOGS(	LOGLOGSGGR(0.878)GGGL	LOGLOGSGGR(8.56)GGGLI	0.877663	0.0237134	58.487	1	R	10	3	0.034562	1255400	6487700	2346800	5041500	3535200	2586600	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q8NEZ4-2	KMT2C	Histone-lysine N-methyltransferase 2C	YPGNIRSPVAPPLGF	SPVAPPLGPR(1)YAVFPK	SPVAPPLGPR(67.96)YAVFP	1	0.00330794	67.964	1	R	10	3	1.7361	15325000	23442000	21752000	15584000	9323400	8515000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
O14686	KMT2D	Histone-lysine N-methyltransferase 2D	DSRLLOEROLOLOC	QLQLQQQR(1)MQLAQK	OLOLOOOR(45.28)MOLA(	1	9.35E-34	162.93	1	R	8	3	-0.13673	12190000	72491000	65079000	33047000	10750000	7041000	Front. Cell Dev. Biol. 8: 545934 (2020)
P05783	KRT18	Keratin, type I cytoskeletal 18	GGSGSRISVSRSTSFI	STSFR(1)GGMGSGGLATGIA	STSFR(104.14)GGMGSGGL	1	3.10E-31	104.14	1	R	5	3	-1.082	30115000	0	0	0	0	0	Mol. Cell. Proteomics 13:372-387(2014) ;Front. Cell Dev. Biol. 8: 545934 (2020)
P35527	KRT9	Keratin, type I cytoskeletal 9	LGGRGGSGGSYGR(	GSR(1)GGSGGSYGGGGSGG	GSR(47.62)GGSGGSYGGG(	0.999983	0.0304395	47.728	1	R	3	3	1.0029	12973000	0	0	0	0	0	Nat Commun 24;8:15571 (2017);Nat Commun 24;8:15571 (2017)
P98164	LRP2	Low-density lipoprotein receptor-related prc	DWVGRHIYWSDVKI	R(1)IEVAKLDGR	R(88.95)IEVAKLDGR(-88.95	1	0.0134057	88.948	1	R	1	3	0.21759	34637000	55404000	0	170470000	81239000	109440000	Nat Commun 24;8:15571 (2017);Nat Commun 24;8:15571 (2017)
A6NIK2	LRRC10B	Leucine-rich repeat-containing protein 10B	PALLRMGRLHILDLD	LHILDLDR(1)NR(1)	LHILDLDR(57.6)NR(57.6)	1	0.0218196	68.735		R	8	3	-1.9098	48825000	207790000	67832000	48040000	24263000	56537000	Nat Commun 24;8:15571 (2017)
A6NIK2	LRRC10B	Leucine-rich repeat-containing protein 10B	LLRMGRLHILDLDRN	LHILDLDR(1)NR(1)	LHILDLDR(57.6)NR(57.6)	1	0.0218196	68.735		R	10	3	-1.9098	48825000	207790000	67832000	48040000	24263000	56537000	Nat Commun 24;8:15571 (2017)
Q49AS3	LRRC37A5P	Putative protein LRRC37A5P	EOOELRTVSMTAWI	TVSMTAWKPR(0.996)MNR(	TVSMTAWKPR(25.13)MNR	0.996418	0.0197109	54.471		R	10	3	1.7707	0	0	0	26631000	49319000	69547000	Mol. Cell. Proteomics 13:372-387(2014)
Q5JRA6-2	MIA3	Melanoma inhibitory activity protein 3	PLGSLGPREYFIPGTF	EYFIPGTR(1)LPPTHGPOEY	EYFIPGTR(56.65)LPPTHGF	0.999998	2.26E-08	76.186	1	R	8	4	-0.53073	0	8112400	28942000	8572600	7210300	0	Mol. Cell. Proteomics 13:372-387(2014) ; Nat Commun 24;8:15571 (2017)
Q5VWP3-2	MLIP	Muscular LMNA-interacting protein	PKSLAISSSLVSDVVF	SLAISSSLVSDVVR(1)	SLAISSSLVSDVVR(59.35)	1	0.000824729	67.993	1	R	14	2	1.6705	3736500	18446000	38194000	30460000	9440400	21486000	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017)
Q9Y3Q0	NAALAD2	N-acetylated-alpha-linked acidic dipeptidase	RAFIDPLGLPGKLFYI	LFYR(1)HIFAPSSHNK	LFYR(49.31)HIFAPSSHNK	1	0.029144	49.31	1	R	4	4	1.4641	49655000	0	3054700	0	0	0	
Q9NZG7	NINJ2	Ninjurin-2	MESAREI	ESAR(1)ENIDLOPGSSDPR	ESAR(53.99)ENIDLOPGSSD	0.999996	0.0233766	53.995		R	4	3	2.6843	0	0	0	31392000	29899000	31224000	
Q9Y466	NR2E1	Nuclear receptor subfamily 2 group E membe	MSKPAGSTSR	PAGSTSR(1)	PAGSTSR(40.92)	1	0.0336234	40.921		R	7	1	4.3213	248540000	160370000	190310000	0	19110000	6470200	Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017)
P30954	OR10J1	Olfactory receptor 10J1	MLLCFRFGNOSM	FGNQSMKR(1)	FGNQSMKR(50.12)	1	0.0261431	50.12		R	8	2	0.35597	7752100	5498000	14622000	22116000	0	0	Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017)
Q8NGG4	OR8H1;OR8H3	Olfactory receptor 8H1;Olfactory receptor 8H	LIYSLRNKEVKNALIR	NALIR(0.957)VMOR(0.46)R(	NALIR(11.01)VMOR(-1.12)I	0.957201	0.0139055	51.995		R	5	2	-4.0851	10792000	4898500	21433000	24823000	44372000	34476000	Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017)
Q8NGG4	OR8H1;OR8H3	Olfactory receptor 8H1;Olfactory receptor 8H	RNKEVKNALIRVMC	NALIR(0.957)VMOR(0.46)R(	NALIR(11.01)VMOR(-1.12)I	0.582625	0.0139055	51.995		R	10	2	-4.0851	10792000	4898500	21433000	24823000	44372000	34476000	Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017)
P11940	PABPC1	Polyadenylate-binding protein 1	STORVANTSTOTM(	VANTSTOTMGPR(0.998)PA	VANTSTOTMGPR(26.99)PA	0.998006	1.12E-06	81.665	1	R	12	3	0.83726	5077600	5955300	6253200	0	33273000	1670800	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P11940	PABPC1	Polyadenylate-binding protein 1	GPRPAAAAAAATPA	VANTSTOTMGPR(0.477)PA	VANTSTOTMGPR(-0.4)PA/	0.523187	0.00158387	63.857	1	R	25	3	1.2663	4661200	0	0	0	0	0	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
O94913	PCF11	Pre-mRNA cleavage complex 2 protein Pcf11	ALRFDGOPGOPSLL	FDGOPGOPSLLPR(0.999)FD	FDGOPGOPSLLPR(26.87)FI	0.998908	1.08E-09	77.681	2	R	13	5	0.17197	8221800	37152000	43427000	43480000	10766000	0	Mol. Cell. Proteomics 13:372-387(2014); Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
O94913	PCF11	Pre-mRNA cleavage complex 2 protein Pcf11	PRFDGLHGOPGPRF	FDGOPGOPSLLPR(0.912)FD	FDGOPGOPSLLPR(7.31)FD	0.563257	1.08E-09	77.681	2	R	27	5	-0.33312	8221800	37152000	43427000	43480000	10766000	0	Mol. Cell. Proteomics 13:372-387(2014); Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q9H307-2	PNN	Pinin	GRMCPATOKLIEES(	LIEESOR(1)KMNALFEGR(1)	LIEESOR(48.14)KMNALFEG	1	0.0103955	48.14	2	R	7	3	1.4411	3926000	129860000	22088000	12528000	7385200	2927900	Nat Commun 24;8:15571 (2017)
Q9H307-2	PNN	Pinin	LIEESORKMNALFEG	LIEESOR(1)KMNALFEGR(1)	LIEESOR(48.14)KMNALFEG	1	0.0103955	48.14	2	R	16	3	1.4411	3926000	129860000	22088000	12528000	7385200	2927900	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
O75334-5	;PPFIA1;PPFIA4	Liprin-alpha-2;Liprin-alpha-1;Liprin-alpha-4	LKSLFEHHKALDEKV	ALDEKVR(1)ER(1)	ALDEKVR(60.96)ER(60.96)	1	0.0408923	60.961		R	7	2	-1.1499	11653000	0	14384000	7773900	3469900	7515700	Nat Commun 24;8:15571 (2017)
O75334-5	;PPFIA1;PPFIA4	Liprin-alpha-2;Liprin-alpha-1;Liprin-alpha-4	SLFEHHKALDEKVRE	ALDEKVR(1)ER(1)	ALDEKVR(60.96)ER(60.96)	1	0.0408923	60.961		R	9	2	-1.1499	11653000	0	14384000	7773900	3469900	7515700	Nat Commun 24;8:15571 (2017)
Q13427-2	PPIG	Peptidyl-prolyl cis-trans isomerase G	ENOKTDAASKPFAE	PFAEVR(1)ILSCGELIPK	PFAEVR(56.78)ILSCGELIPK	1	0.0390696	56.783	1	R	6	2	0.49628	52139000	14715000	48131000	38143000	65054000	45802000	
Q6NYC8	PPP1R18	Phostensin	EKAERERLSQMPAW	LSQMPAWKR(1)GLLER(1)	LSQMPAWKR(46)GLLER(46	1	0.0162809	45.997	2	R	9	2	0.22234	1643400	0	0	0	4066100	1102200	PLoS ONE 8:E75669-E75669(2013); Nat Commun 24;8:15571 (2017)
Q6NYC8	PPP1R18	Phostensin	ERLSOMPAWKRGLI	LSQMPAWKR(1)GLLER(1)	LSQMPAWKR(46)GLLER(46	1	0.0162809	45.997	2	R	14	2	0.22234	1643400	0	0	0	4066100	1102200	PLoS ONE 8:E75669-E75669(2013); Nat Commun 24;8:15571 (2017)
Q9H7J1	PPP1R3E	Protein phosphatase 1 regulatory subunit 3E	GELPRVPRHVQIQL(	HVQIQLQR(1)DALR(1)	HVQIQLQR(45.43)DALR(45	1	0.0397734	45.433		R	8	3	-0.06152	1278100	9542700	14989000	3914400	487280	462950	
Q9H7J1	PPP1R3E	Protein phosphatase 1 regulatory subunit 3E	RVPRHVOIOLORDA	HVQIQLQR(1)DALR(1)	HVOIOLOR(45.43)DALR(45	1	0.0397734	45.433		R	12	3	-0.06152	1278100	9542700	14989000	3914400	487280	462950	
P01298-2	PPY	Pancreatic prohormone;Pancreatic hormone;	NATPEOMAOYAAD	R(1)YINMLTR(0.99)PR(0.01)	R(40.99)YINMLTR(20.09)PR	0.999921	0.025585	40.987		R	1	2	-1.0102	0	0	24721000	3121500	9488700	3838100	
P01298-2	PPY	Pancreatic prohormone;Pancreatic hormone;	AOYAADLRRYINML	R(1)YINMLTR(0.99)PR(0.01)	R(40.99)YINMLTR(20.09)PR	0.990291	0.025585	40.987		R	8	2	-1.0102	0	0	24721000	3121500	9488700	3838100	
Q8WXF1-2	PSPC1	Paraspeckle component 1	MMLRG	MMLR(1)GNLK	MMLR(103.02)GNLK	1	8.85E-15	148.21	1	R	4	2	-0.40595	5320500	8904900	6323000	8694300	3706500	2409200	
A1KZ92-2	PXDNL	Peroxidasin-like protein	RVKOGLTVDLEGKEI	VKQGLTVDLEGKEFR(1)	VKOGLTVDLEGKEFR(57.43	1	0.00526518	63.181	1	R	15	3	-0.97534	477750000	161830000	221480000	0	0	0	Nat Commun 24;8:15571 (2017)
Q5T8P6-5	RBM26	RNA-binding protein 26	DLYKKMOAGEEVTE	ELLDTELDLYKKMOAGEEVT	ELLDTELDLYKKMOAGEEVT	1	0.00304704	44.382		R	23	4	-1.5539	0	12627000	0	6609200	216310000	55045000	Nat Commun 24;8:15571 (2017)
Q5TC82-2	RC3H1	Roquin-1	YPVAPHPTOIRPSYL	YQQIESYYPVAPHPTQIR(0.4	YOQIESYYPVAPHPTOIR(-(	0.519044	0.0184181	46.027	1	R	23	4	0.90396	0	0	8166100	4007200	5274200	0	Nat Commun 24;8:15571 (2017)
Q9P2R6-2	RERE	Arginine-glutamic acid dipeptide repeats prc	PFASFHPGLNPLERE	ER(1)LALAGPOLR(0.862)PEI	ER(57.52)LALAGPOLR(7.96)	0.999998	0.00028591	57.52	2	R	2	4	0.005478	1391800	7357800	0	4648900	0	7573900	PubMed:25284789;Nat Commun 24;8:15571 (2017);**Front. Cell Dev. Biol. 8: 545934 (2020)**
Q9P2R6-2	RERE	Arginine-glutamic acid dipeptide repeats prc	ALAGPOLRPEMSYP	ER(1)LALAGPOLR(0.475)PEI	ER(40.96)LALAGPOLR(-0.4	0.525469	0.0164626	40.962	2	R	19	4	0.20393	0	0	0	2345800	0	0	PubMed:25284789;Nat Commun 24;8:15571 (2017);**Front. Cell Dev. Biol. 8: 545934 (2020)**
Q9P2R6-2	RERE	Arginine-glutamic acid dipeptide repeats prc	NPLERERLALAGPOI	ER(1)LALAGPOLR(0.96)PEM	ER(49.46)LALAGPOLR(13.8	0.960188	0.00028591	57.52	2	R	11	4	0.38198	1391800	7357800	0	2303000	0	7573900	PubMed:25284789;Nat Commun 24;8:15571 (2017);**Front. Cell Dev. Biol. 8: 545934 (2020)**
Q8TAI7	RHEBL1	GTPase RhebL1	IOEIARVENSYGOER	VIOEIAR(0.165)VENSYGOEF	VIOEIAR(-10.06)VENSYGO	0.91761	0.00182237	55.213		R	17	3	0.51861	55551000	17210000	64132000	64013000	84754000	20945000	PubMed:25284789;Nat Commun 24;8:15571 (2017)
Q8TAI7	RHEBL1	GTPase RhebL1	OLTOGIFTKVIOEIAF	VIOEIAR(0.954)VENSYGOEF	VIOEIAR(10.13)VENSYGOE	0.953732	0.00182237	55.213		R	7	3	-2.7062	55551000	17210000	64132000	59655000	84754000	20945000	
Q8TAI7	RHEBL1	GTPase RhebL1	VIOEIARVENSYGOE	VIOEIAR(0.165)VENSYGOEF	VIOEIAR(-10.06)VENSYGO	0.91761	0.0155707	46.408		R	16	3	0.51861	17220000	7861900	64132000	29866000	39544000	0	
Q01196-7	RUNX1	Runt-related transcription factor 1	AMRVSPHHPAPTPN	VSPHHPAPTPNPR(1)ASLNH	VSPHHPAPTPNPR(36.05)AS	0.999751	0.000197664	41.133	1	R	13	5	-1.1352	0	1774000	3047000	0	5159000	27201000	Front. Cell Dev. Biol. 8: 545934 (2020)
Q5PRF9	SAMD4B	Protein Smaug homolog 2	RMGLLSPSGIGGVSI	MGLLSPSGIGGVSPR(1)HAL	MGLLSPSGIGGVSPR(66.47)	1	1.83E-71	107.05	1	R	15	4	-0.80144	58260000	317410000	84252000	23533000	24376000	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q13435	SF3B2	Splicing factor 3B subunit 2	PODMGOIGVRTPL(	MGTPVPR(0.012)PPODMG(	MGTPVPR(-16.69)PPODM(	0.574982	6.49E-06	74.662	1	R	24	4	0.24061	101670000	0	0	23408000	0	8180400	Nat Commun 24;8:15571 (2017);Nat Commun 24;8:15571 (2017);Oncogene 22:5229-5237(2003);Front. Cell Dev. Biol. 8: 545934 (2020)
Q13435	SF3B2	Splicing factor 3B subunit 2	TPVPRPPODMGOI(	MGTPVPRPPODMGOIGVR(	MGTPVPR(-42.32)PPODM(	0.997576	9.05E-48	94.057	1	R	18	4	0.097479	0	193310000	144500000	0	58836000	0	Nat Commun 24;8:15571 (2017);Nat Commun 24;8:15571 (2017);Oncogene 22:5229-5237(2003);Front. Cell Dev. Biol. 8: 545934 (2020)
Q8ND83-3	SLAIN1	SLAIN motif-containing protein 1	LOHRVHSVGHFPVS	VHSVGHFPVSIR(1)QPLK	VHSVGHFPVSIR(52.27)OPL	1	4.61E-08	102.9	1	R	12	4	0.18942	4095100	38845000	33721000	16470000	4034800	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q9H2Y9-2	SLCO5A1	Solute carrier organic anion transporter famil	DEERPFALGMOFVL	PFALGMQFVLLR(1)	PFALGMQFVLLR(64.84)	1	0.0218428	64.836	1	R	12	2	3.6749	0	0	0	6269600	12425000	29684000	
Q08AF3-2	SLFN5	Schlafen family member 5	ECVVDAGKVTLGTC	VTLGTQQR(1)QEMDPR(1)	VTLGTOOR(44.62)OEMDPI	1	0.0277538	44.616		R	8	3	-0.22645	9545800	154100000	185280000	0	36268000	0	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
Q08AF3-2	SLFN5	Schlafen family member 5	GKVTLGTOOROEM	VTLGTQQR(1)QEMDPR(1)	VTLGTOOR(44.62)OEMDPI	1	0.0277538	44.616		R	14	3	-0.22645	9545800	154100000	185280000	0	36268000	0	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
Q9UQ35	SRRM2	Serine/arginine repetitive matrix protein 2	GANLTSPRVPLSAYE	MAPALSGANLTSPR(0.44)VF	MAPALSGANLTSPR(-1.05)\	0.560286	0.00106756	91.475	1	R	22	3	0.49626	5658000	143160000	100810000	48498000	11647000	0	Front. Cell Dev. Biol. 8: 545934 (2020)
O95210	STBD1	Starch-binding domain-containing protein 1	ERVAVMPAGSOOV	VAVMPAGSQQVSVR(1)	VAVMPAGSOOVSVR(45.1(	1	0.0301453	47.603	1	R	14	2	0.93559	44946000	40466000	11744000	0	0	0	
Q8NF91-4	SYNE1	Nesprin-1	TGKEDLEOKVASLEL	VASLELR(0.63)SOR(0.63)MS	VASLELR(0)SOR(0)MSR(1.5	0.63014	0.0126781	61.962		R	7	2	1.7213	110950000	146490000	125080000	144220000	82596000	73934000	Mol. Cell. Proteomics 13:372-387(2014);EMBO Rep. 3:268-273(2002) ; Nat Commun 24;8:15571 (2017)
Q8NF91-4	SYNE1	Nesprin-1	EDLEQKVASLELRSC	VASLELR(0.63)SOR(0.63)MS	VASLELR(0)SOR(0)MSR(1.5	0.63014	0.0126781	61.962		R	10	2	1.7213	110950000	146490000	125080000	144220000	82596000	73934000	Mol. Cell. Proteomics 13:372-387(2014);EMBO Rep. 3:268-273(2002) ; Nat Commun 24;8:15571 (2017)
Q8NF91-4	SYNE1	Nesprin-1	EOKVASLELRSORM	VASLELR(0.63)SOR(0.63)MS	VASLELR(0)SOR(0)MSR(1.5	0.73972	0.0126781	61.962		R	13	2	1.7213	110950000	146490000	125080000	144220000	82596000	73934000	Mol. Cell. Proteomics 13:372-387(2014);EMBO Rep. 3:268-273(2002) ; Nat Commun 24;8:15571 (2017)
O15061-2	SYNM	Synemin	OGKEOAMFDKKVC	VOLOR(1)MVDOR(1)SVISD	VOLOR(44.76)MVDOR(44.	1	0.0105944	44.765	2	R	5	2	-0.44575	37298000	65914000	165140000	130140000	98386000	24526000	Nat. Commun. 6:6428-6428(2015) ; Nat Commun 24;8:15571 (2017)
O15061-2	SYNM	Synemin	AMFDKKVOLORM\	VOLOR(1)MVDOR(1)SVISD	VOLOR(44.76)MVDOR(44.	1	0.0105944	44.765	2	R	10	2	-0.44575	37298000	65914000	165140000	130140000	98386000	24526000	Nat. Commun. 6:6428-6428(2015) ; Nat Commun 24;8:15571 (2017)
Q8N9I0	SYT2	Synaptotagmin-2	ELGGKTLVMAIYDFI	TLVMAIYDFDR(1)FSK	TLVMAIYDFDR(47.2)FSK	1	0.0298534	47.198	1	R	11	2	3.3078	0	0	6887700	23921000	55243000	38177000	
Q92804-2	TAF15	TATA-binding protein-associated factor 2N	GGYGGDRGGYGGC	SR(1)GGYGGDR(1)GGGSGY	SR(81.43)GGYGGDR(72.78)	1	0.00146017	81.428	2	R	2	3	-0.61849	39225000	80658000	140640000	7728000	127720000	14134000	Mol. Cell. Proteomics 13:372-387(2014);Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q92804-2	TAF15	TATA-binding protein-associated factor 2N	GGYGGDRSRGGYG	SR(1)GGYGGDR(1)GGGSGY	SR(81.43)GGYGGDR(72.78)	1	0.00146017	81.428	2	R	9	3	-0.61849	39225000	80658000	140640000	7728000	127720000	14134000	Mol. Cell. Proteomics 13:372-387(2014);Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q92804-2	TAF15	TATA-binding protein-associated factor 2N	GGGYGGDRGGGYG	SGGGYGGDR(0.037)GGGY(	SGGGYGGDR(-14.14)GGG\	0.9629	0.000774721	62.966	1	R	17	4	-0.12975	14560000	12123000	33986000	7315700	61038000	4196800	Mol. Cell. Proteomics 13:372-387(2014);Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q92804-2	TAF15	TATA-binding protein-associated factor 2N	GGYGGDRSGGGYG	SGGGYGGDR(0.5)GGGYG	SGGGYGGDR(0)GGGYGGD	0.5	0.00590177	50.425	1	R	9	3	-0.93304	4966900	6562300	10858000	0	16093000	0	Mol. Cell. Proteomics 13:372-387(2014);Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q92804-2	TAF15	TATA-binding protein-associated factor 2N	DKDGRGPMTGSSG(	GPMTGSSGGDR(1)GGFK	GPMTGSSGGDR(45.12)GGI	1	0.0171514	45.115	1	R	11	3	0.74418	0	14981000	14852000	0	0	0	Mol. Cell. Proteomics 13:372-387(2014);Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q68CZ2-2	TNS3	Tensin-3	PGLVOAOPRVPLTP	CPADNPGLVOAOPR(0.394)	CPADNPGLVOAOPR(-1.87	0.605853	3.13E-46	123.97	1	R	21	3	-0.61875	13764000	15034000	8250400	51979000	0	0	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q68CZ2-2	TNS3	Tensin-3	SRCPADNPGLVOA(	CPADNPGLVOAOPR(0.998)	CPADNPGLVOAOPR(26.23	0.997625	2.10E-72	132.59	1	R	14	3	-0.43568	0	26342000	7231400	0	33132000	118500000	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
O94842-3	TOX4	TOX high mobility group box family member	PPPLOAMOOPPPC	VR(1)INLQQPPPLQIK	VR(42.32)INLOOOPPPLOII	1	0.00806123	69.716	1	R	2	3	0.81326	36272000	82731000	65853000	31581000	7186300	2657700	Mol. Cell. Proteomics 13:372-387(2014);Front. Cell Dev. Biol. 8: 545934 (2020)
P53804-2	TTC3	E3 ubiquitin-protein ligase TTC3	RFDIAIIYYTRAIEYRP	AIEYR(1)PENYLLYGNR(1)	AIEYR(56.12)PENYLLYGNR(	1	0.0201482	56.122	2	R	5	3	-1.4921	9705300	0	36683000	0	0	0	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017)
P53804-2	TTC3	E3 ubiquitin-protein ligase TTC3	RAIEYRPENYLLYGN	AIEYR(1)PENYLLYGNR(1)	AIEYR(56.12)PENYLLYGNR(	1	0.0201482	56.122	2	R	15	3	-1.4921	9705300	0	36683000	0	0	0	Mol. Cell. Proteomics 13:372-387(2014) ;Nat Commun 24;8:15571 (2017)
Q5T4S7-3	UBR4	E3 ubiquitin-protein ligase UBR4	SEKLLRVCLNLPYFLF	VCLNLPYFLR(1)	VCLNLPYFLR(92.92)	1	0.00145963	92.925	1	R	10	2	3.2619	13096000	0	380710000	143090000	149970000	395410000	Anal. Chem. 75:3107-3114(2003); Nat Commun 24;8:15571 (2017)
O94874-2	UFL1	E3 UFM1-protein ligase 1	MRDEI	R(0.995)DELHVR(0.005)GGR	R(22.6)DELHVR(-22.6)GGR(	0.994526	0.0110084	53.17	1	R	1	2	-3.6512	9488400	23555000	31454000	73186000	111580000	115120000	Anal. Chem. 75:3107-3114(2003); Nat Commun 24;8:15571 (2017)
Q9C0J8	WDR33	pre-mRNA 3' end processing protein WDR33	IPFOOOKTPLLGDG	TPLLGDGPR(1)APFNOEGO:	TPLLGDGPR(176.54)APFNC	1	0	191.51	1	R	9	3	-0.03145	123810000	238990000	207710000	103460000	70057000	0	Front. Cell Dev. Biol. 8: 545934 (2020)
Q9C0J8	WDR33	pre-mRNA 3' end processing protein WDR33	SGTPSRGGRSGSNW	SGSNWGR(1)GSNMNSGPP	SGSNWGR(88.52)GSNMNS	1	1.01E-108	162.41	1	R	7	3	-0.44098	11910000	92699000	43147000	0	11824000	0	Front. Cell Dev. Biol. 8: 545934 (2020)
O43516-4	WIPF1	WAS/WASL-interacting protein family memb	ANTEKPTLNKTEOA(	TEQAGR(1)NALLSDISKGK	TEOAGR(73.91)NALLSDISK(	1	3.02E-07	99.011	1	R	6	3	-0.15778	0	3018300	33000000	20366000	17542000	7740500	
Q8TF74	WIPF2	WAS/WASL-interacting protein family memb	ANTEOPKLSRDEOR	GR(1)GALLQDICKGTK	GR(62.3)GALLQDICKGTK	1	0.00797198	87.298	1	R	2	3	0.78933	7077700	41875000	49157000	49199000	20276000	8122500	Front. Cell Dev. Biol. 8: 545934 (2020)
A6NGB9	WIPF3	WAS/WASL-interacting protein family memb	VSTDTSSLRRADPK(	GR(1)SALLADIQQGTR	GR(122.42)SALLADIOOGTR	1	8.30E-34	122.42	1	R	2	3	0.20339	2859200	0	29689000	31888000	15293000	18963000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P49750-3	YLPM1	YLP motif-containing protein 1	SSYLESPRGPRFDGP	SSYLESPR(0.44)GPR(0.922)F	SSYLESPR(-1.9)GPR(8.57)FI	0.638259	0.000285897	66.004		R	16	4	0.50121	0	0	0	74416000	0	0	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P49750-3	YLPM1	YLP motif-containing protein 1	GLLPDPPRSSYLESPI	SSYLESPR(1)GPR(1)FDGPR	SSYLESPR(50.32)GPR(45.42	0.999991	2.72E-06	72.891	2	R	8	3	-0.01768	31227000	95961000	73639000	68902000	45353000	65181000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
P49750-3	YLPM1	YLP motif-containing protein 1	PDPPRSSYLESPRGP	SSYLESPR(1)GPR(1)FDGPR	SSYLESPR(50.32)GPR(45.42	0.999971	2.72E-06	72.891	2	R	11	3	-0.01768	31227000	95961000	73639000	68902000	45353000	65181000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017);Front. Cell Dev. Biol. 8: 545934 (2020)
Q9UDV7-2	ZNF282	Zinc finger protein 282	FOFPPFPDRAPVFPI	APVFPDR(0.5)MMR(0.5)	APVFPDR(0)MMR(0)	0.5	0.0208299	44.692		R	7	2	3.9026	0	0	0	0	0	1839200	Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017)
Q9UDV7-2	ZNF282	Zinc finger protein 282	PPFPDRAPVFPDRM	APVFPDR(0.5)MMR(0.5)	APVFPDR(0)MMR(0)	0.5	0.0208299	44.692		R	10	2	3.9026	0	0	0	0	0	1839200	Exp. Cell Res. 315:1273-1286(2009) ;Nat Commun 24;8:15571 (2017)
A7E2V4-5	ZSWIM8	Zinc finger SWIM domain-containing protein	LLKKIPLGPSEMSTM	IPLGPSEMSTMR(1)	IPLGPSEMSTMR(41.28)	1	0.0196357	41.283	1	R	12	3	-0.09812	183560000	561550000	438510000	73822000	207840000	32349000	Mol. Cell. Proteomics 13:372-387(2014);Nat Commun 24;8:15571 (2017)
P22736-3			TCEGCKGFFKVPRSI	SPR(1)WGLLLEMER(1)	SPR(69.01)WGLLLEMER(69.	1	0.00535695	69.01	2	R	3	3	-1.161	75356000	314610000	670520000	197040000	216990000	208060000	
P22736-3			KVPRSPRWGLLLEM	SPR(1)WGLLLEMER(1)	SPR(69.01)WGLLLEMER(69.	1	0.00535695	69.01	2	R	12	3	-1.161	75356000	314610000	670520000	197040000	216990000	208060000	
P01619		Ig kappa chain V-III region B6	KPGOAPRLLIYGASS	LLIYGASSR(1)	LLIYGASSR(99.92)	1	0.0209382	100.82		R	9	2	-0.28893	6131600	4443600	33137000	61306000	66799000	304540000	
Q16587-5			GIPPOVSPLRPATRS	SR(1)GGTLAGHTQERPGH	SR(57)GGTLAGHTOER(-57)	0.999998	0.000522636	66.246	1	R	2	4	1.0975	0	26908000	96543000	34398000	13680000	33144000	Front. Cell Dev. Biol. 8: 545934 (2020)
Q9Y3Y2-4			PRGGLRGGRATRTLL	TLLR(0.992)GGMSLR(0.428)(	TLLR(18.48)GGMSLR(-1.34)	0.991883	0.0368414	60.59	2	R	4	2	-0.17223	0	0	0	0	0	75765000	Nat Commun 24;8:15571 (2017)
Q9Y3Y2-4			RATRTLLRGGMSLR(	TLLR(0.992)GGMSLR(0.428)(	TLLR(18.48)GGMSLR(-1.34)	0.58023	0.0368414	60.59	2	R	12	2	-0.17223	0	0	0	0	0	75765000	
Q5BJH7-4			MHPAGLAAAAAG	MHPAGLAAAAAGTPR(1)LP:	MHPAGLAAAAAGTPR(52.5	1	0.000593665	52.522	1	R	15	3	3.4324	0	0	0	0	1555100	0	Mol. Cell. Proteomics 13:372-387(2014);EMBO Rep. 3:268-273(2002) ; Nat Commun 24;8:15571 (2017)