Table S5 Analysis of N-termini that were unmodified upon secretome harvest and chemically dimethylated in the TAILS procedure (replicate 1).
This is a non-redundant, peptide-centric list, showing up to three proteins for each peptide identification.
The X! Tandem hyperscore and the mass deviation in ppm are shown.
The overall FDR is < 0.05 as calculated by PeptideProphet.
The prime sequence was experimentally identified, the corresponding non-prime sequence was bioinformatically derived.
The fold-change (Fc) value is based on ASAPratio.

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
CQDTQSQQLG	SQPSSNPTPSPLDASPR	PLCB3_HUMAN			1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3;	0.52	0.03	63.30	-1.58
M	VQAWYMDDAPGDPR	MTND_HUMAN			1,2-dihydroxy-3-keto-5-methylthiopentene	0.21	0.01	63.30	0.42
RYDDMAAAMK	AVTEQGHELSNEER	1433B_HUMAN			14-3-3 protein beta/alpha;	2.71	0.20	24.60	-2.52
RLGLALNFSV	FYYEILNSPDR	1433E_HUMAN			14-3-3 protein epsilon;	-1.49	0.08	43.50	-3.44
RYDDMAAAMK	NVTELNEPLSNEER	1433G_HUMAN			14-3-3 protein gamma;	2.09	0.21	72.60	-2.75
RYEDMAAFMK	GAVEKGEELSCEER	1433S_HUMAN			14-3-3 protein sigma;	0.41	0.06	81.30	4.36
YLKMKGDYFR	YLAEVACGDDR	1433T_HUMAN			14-3-3 protein theta;	0.44	0.02	36.00	4.08
RYDDMATCMK	AVTEQGAELSNEER	1433T_HUMAN			14-3-3 protein theta;	-0.16	0.02	76.60	-0.06
RYDDMAACMK	SVTEQGAELSNEER	1433Z_HUMAN			14-3-3 protein zeta/delta;	5.68	0.59	76.90	-1.52
YREKIETELR	DICNDVLSLLEK	1433Z_HUMAN			14-3-3 protein zeta/delta;	0.20	0.02	46.10	-2.96
LDTLSEESYK	DSTLIMQLLR	1433Z_HUMAN	1433B_HUMAN	1433E_HUMAN	14-3-3 protein zeta/delta;	0.14	0.02	51.20	-2.37
WEFGKRDSLG	AYASQDANEQGQDLGKR	TB182_HUMAN			182 kDa tankyrase-1-	2.26	0.22	28.70	-2.36
AAPDQPCVLF	ADAPEPGQALPVEEEAVTLAR	TB182_HUMAN			182 kDa tankyrase-1-binding protein;	1.28	0.04	43.50	-6.66
FQDSTEPRAS	RVPSSDEEVVEEPQSR	TB182_HUMAN			182 kDa tankyrase-1-binding protein;	1.06	0.09	39.40	0.21

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
QVKVIAATNR	VDILDPALLR	PRS6A_HUMAN			26S protease regulatory subunit 6A;	0.95	0.11	24.40	-3.36
RARIMQIHSR	KMNVSPDVNYEELAR	PRS6A_HUMAN			26S protease regulatory subunit 6A;	0.78	0.04	30.40	-3.43
IMQIHSRKMN	VSPDVNYEELAR	PRS6A_HUMAN			26S protease regulatory subunit 6A;	0.61	0.07	43.60	-1.61
ARIMQIHSRK	MNVSPDVNYEELAR	PRS6A_HUMAN			26S protease regulatory subunit 6A;	-2.25	0.21	36.30	-2.15
M	VLESTMVCVDNSEYMR	PSMD4_HUMAN			26S proteasome non-ATPase regulatory subunit	0.06	0.01	68.00	5.49
EAHKEAMSRK	LGQSESQGPPR	PSMD9_HUMAN			26S proteasome non-ATPase regulatory subunit	-0.04	0.00	32.00	-1.60
IYLARHVGLR	VGIPKETPALTINR	THIM_HUMAN			3-ketoacyl-CoA thiolase, mitochondrial;	4.57	0.54	33.10	0.44
SGWMPQAAPC	LSGAPQASAADVVVVHGR	THIK_HUMAN			3-ketoacyl-CoA thiolase, peroxisomal;	-1.49	0.13	50.90	0.73
GVQRGCGLRL	LSQTQGPPDYPR	RM49_HUMAN			39S ribosomal protein	0.68	0.05	39.80	-3.68
GEADRDTYRR	SAVPPGADKKAEAGAGSATEFQFR	RS10_HUMAN			40S ribosomal protein S10;	1.53	0.07	49.20	-1.32
EQFAWRHFYW	YLTNEGIQYLR	RS10_HUMAN			40S ribosomal protein	-1.16	0.08	31.40	-2.56
LARSGMKIGR	IEDVTPIPSDSTRR	RS14_HUMAN			40S ribosomal protein S14;	2.00	0.13	39.90	2.97
LARSGMKIGR	IEDVTPIPSDSTR	RS14_HUMAN			40S ribosomal protein	1.93	0.12	51.30	-0.55
GMKIGRIEDV	TPIPSDSTR	RS14_HUMAN			40S ribosomal protein S14;	1.62	0.05	29.40	-2.79
RSGMKIGRIE	DVTPIPSDSTR	RS14_HUMAN			40S ribosomal protein S14;	1.06	0.09	37.70	-1.23
LRALARSGMK	IGRIEDVTPIPSDSTR	RS14_HUMAN			40S ribosomal protein S14;	0.47	0.03	49.00	-3.25
CRVTGGMKVK	ADRDESSPYAAMLAAQDVAQR	RS14_HUMAN			40S ribosomal protein	0.23	0.01	57.10	-1.13
QKYVDEASKK	EIKDILIQYDR	RS16_HUMAN			40S ribosomal protein	0.51	0.03	32.10	1.76

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
RKADIDLTKR	AGELTEDEVER	RS18_HUMAN			40S ribosomal protein S18;	2.16	0.32	51.20	-3.45
LRKADIDLTK	RAGELTEDEVER	RS18_HUMAN			40S ribosomal protein S18;	0.47	0.03	39.60	0.76
MAFKDTGK	TPVEPEVAIHR	RS20_HUMAN			40S ribosomal protein S20;	-0.06	0.00	40.40	-2.74
KTYAICGAIR	RMGESDDSILR	RS21_HUMAN			40S ribosomal protein	3.04	0.38	39.10	-0.61
VTGRFNGQFK	TYAICGAIR	RS21_HUMAN			40S ribosomal protein S21;	0.06	0.00	44.00	-3.02
IIRNVKGPVR	EGDVLTLLESER	RS28_HUMAN			40S ribosomal protein	2.60	0.47	47.90	-1.08
GSQGQCTQVR	VEFMDDTSR	RS28_HUMAN			40S ribosomal protein	2.36	0.16	37.50	-3.01
RTGSQGQCTQ	VRVEFMDDTSR	RS28_HUMAN			40S ribosomal protein S28;	0.06	0.00	32.90	-3.47
KAELNEFLTR	ELAEDGYSGVEVR	RS3_HUMAN			40S ribosomal protein S3;	0.06	0.00	49.30	2.88
RKFVADGIFK	AELNEFLTR	RS3_HUMAN			40S ribosomal protein S3;	-0.23	0.01	43.80	-2.23
PDSIGKDIEK	ACQSIYPLHDVFVR	RS3A_HUMAN			40S ribosomal protein S3a;	0.99	0.03	34.40	-1.95
RIGRAGTVRR	QAVDVSPLR	RS5_HUMAN			40S ribosomal protein S5;	1.13	0.06	40.00	-2.66
TWEKLLLAAR	AIVAIENPADVSVISSR	RSSA_HUMAN			40S ribosomal protein SA;	4.00	0.43	54.70	-1.86
RNTGQRAVLK	FAAATGATPIAGR	RSSA_HUMAN			40S ribosomal protein SA;	-0.04	0.00	55.40	-0.81
GFHQEVFLGK	DLGGFDEDAEPR	CAB45_HUMAN			45 kDa calcium-binding	-0.79	0.05	68.50	0.59
EMRMQNNSSP	SISPNTSFTSDGSPSPLGGIKR	XRN2_HUMAN			5'-3' exoribonuclease 2;	1.41	0.11	37.20	4.42
QKEKRKRMKR	DQPAFTPSGILTPHALGSR	XRN2_HUMAN			5'-3' exoribonuclease 2;	-0.14	0.01	49.80	-1.30
SDSPKPPPQR	VTLTLPVLNAAR	6PGL_HUMAN			6-phosphogluconolactonase;	5.04	0.86	24.10	-3.47
GGSLVSMLAR	ELPAAVAPAGPASLAR	6PGL_HUMAN			6-	4.07	0.42	36.80	-1.25

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
RVTDALNATR	AAVEEGIVLGGGCALLR	CH60_HUMAN			60 kDa heat shock protein, mitochondrial;	2.23	0.25	89.30	0.18
LVIQQVFDNG	SIYNPEVLDITEETLHSR	RLA0_HUMAN			60S acidic ribosomal protein P0;	0.89	0.04	65.10	-0.89
VFDNGSIYNP	EVLDITEETLHSR	RLA0_HUMAN			60S acidic ribosomal protein P0;	-0.60	0.03	27.70	-2.03
RKNVNIYRDS	AIPVESDTDDEGAPR	NMD3_HUMAN			60S ribosomal export	0.94	0.09	69.40	-1.50
MSSKVSR	DTLYEAVR	RL10A_HUMAN			60S ribosomal protein L10a;	3.43	0.26	33.80	-2.71
KLVKKLAKKY	DAFLASESLIKQIPR	RL10A_HUMAN			60S ribosomal protein	-0.06	0.00	30.60	1.66
EELKLATQLT	GPVMPVR	RL13_HUMAN			60S ribosomal protein L13;	0.95	0.06	23.40	-6.25
AEELKLATQL	TGPVMPVR	RL13_HUMAN			60S ribosomal protein L13;	0.83	0.05	27.50	-4.37
KGDSSAEELK	LATQLTGPVMPVR	RL13_HUMAN			60S ribosomal protein L13;	-0.44	0.04	47.30	-3.24
ISVDPRRRNK	STESLQANVQR	RL13_HUMAN			60S ribosomal protein L13;	-0.44	0.03	59.20	-2.77
RYHTKVRAGR	GFSLEELR	RL13_HUMAN			60S ribosomal protein L13;	-0.76	0.03	27.00	-4.80
M	GAYKYIQELWR	RL15_HUMAN			60S ribosomal protein	-0.32	0.00	32.50	-2.87
KMKLPGRENK	TAVVVGTITDDVR	RL18_HUMAN			60S ribosomal protein	0.45	0.05	52.10	-1.16
GTHNMYREYR	DLTTAGAVTQCYR	RL18A_HUMAN			60S ribosomal protein	-0.89	0.08	63.20	-1.21
KLKADKARKK	LLADQAEAR	RL19_HUMAN			60S ribosomal protein	-0.04	0.00	32.40	-2.17
LQERIKVNGK	AGNLGGGVVTIER	RL22_HUMAN			60S ribosomal protein	1.57	0.14	63.10	-2.19
AVKFQRAITG	ASLADIMAKR	RL24_HUMAN			60S ribosomal protein	0.56	0.03	29.40	-3.58
RTRRAVKFQR	AITGASLADIMAKR	RL24_HUMAN			60S ribosomal protein L24;	0.40	0.03	26.50	-3.36
M	KFNPFVTSDR	RL26L_HUMAN	RL26_HUMAN		60S ribosomal protein	0.41	0.02	39.10	-1.57
EVQVVRGHYK	GQQIGKVVQVYR	RL26L_HUMAN	RL26_HUMAN		60S ribosomal protein	0.04	0.00	27.10	-4.43
MK	FNPFVTSDR	RL26L_HUMAN	RL26_HUMAN		60S ribosomal protein L26-like 1;	-0.12	0.01	32.30	-3.06
YNVRSMPIRK	DDEVQVVR	RL26_HUMAN	RL26L_HUMAN		60S ribosomal protein L26;	0.52	0.01	32.70	-5.06

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
QTRVNAAKNK	TGAAPIIDVVR	RL27A_HUMAN			60S ribosomal protein	-0.66	0.05	43.40	-2.89
KAKDQTKAQA	AAPASVPAQAPKR	RL29_HUMAN			60S ribosomal protein L29;	1.59	0.10	21.70	-1.82
AKAKAKDQTK	AQAAAPASVPAQAPKR	RL29_HUMAN			60S ribosomal protein L29;	0.56	0.05	41.30	-1.07
AKAKDQTKAQ	AAAPASVPAQAPKR	RL29_HUMAN			60S ribosomal protein L29;	0.14	0.01	31.30	-3.06
LGTACGKYYR	VCTLAIIDPGDSDIIR	RL30_HUMAN			60S ribosomal protein L30;	2.22	0.16	39.00	-0.06
ELGTACGKYY	RVCTLAIIDPGDSDIIR	RL30_HUMAN			60S ribosomal protein	0.67	0.03	33.00	-4.48
KKGGEKKKGR	SAINEVVTR	RL31_HUMAN			60S ribosomal protein L31;	1.13	0.09	33.60	-3.03
AKKGGEKKKG	RSAINEVVTR	RL31_HUMAN			60S ribosomal protein L31;	0.56	0.05	29.40	1.95
PRVRGGGTHR	SGQGAFGNMCR	RL4_HUMAN			60S ribosomal protein L4;	-0.49	0.02	39.30	-3.36
GDEYNVESID	GQPGAFTCYLDAGLAR	RL5_HUMAN			60S ribosomal protein L5;	-1.29	0.10	55.70	0.00
RVVKLRKMPR	YYPTEDVPR	RL6_HUMAN			60S ribosomal protein L6;	-1.25	0.06	31.00	-3.24
ALAKLVEAIR	TNYNDRYDEIR	RL7A_HUMAN			60S ribosomal protein	3.84	0.33	32.70	-3.69
SKKVISSANR	AVVGVVAGGGR	RL8_HUMAN			60S ribosomal protein L8;	3.41	0.58	37.90	-4.12
KPGDRGKLAR	ASGNYATVISHNPETK	RL8_HUMAN			60S ribosomal protein L8;	0.56	0.03	33.20	-4.87
FNDAQRQATK	DAGTIAGLNVMR	GRP78_HUMAN			78 kDa glucose-regulated protein;	2.58	0.21	47.60	0.40
EIIANDQGNR	ITPSYVAFTPEGER	GRP78_HUMAN			78 kDa glucose-regulated protein;	1.34	0.08	35.80	-0.81
KVLEDSDLKK	SDIDEIVLVGGSTR	GRP78_HUMAN			78 kDa glucose-regulated	0.85	0.03	39.40	-1.68
VEPWSQCSRS	CGGGVQER	ATS12_HUMAN			A disintegrin and metalloproteinase with	-4.68	1.20	20.10	-1.34

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
VTPFYNTLTK	GPEMEIHSGSGEER	ATS12_HUMAN			A disintegrin and metalloproteinase with	-6.27	0.00	26.20	-3.22
LPSRFIESAH	TELAKDDAAPAPPVADAKAQDR	AKAP1_HUMAN			A-kinase anchor protein 1,	2.19	0.18	38.20	-2.65
ALLTEEVLER	EVIAEEEPPTVTEPLPENR	AKA12_HUMAN			A-kinase anchor protein 12;	6.23	0.99	66.90	-1.33
PEDVLQPVQR	AEAERPEEQAEASGLK	AKA12_HUMAN			A-kinase anchor protein 12;	3.39	0.27	32.00	-0.17
IEVHQEEVVA	EVHVSTVEER	AKA12_HUMAN			A-kinase anchor protein 12;	2.27	0.14	29.70	-3.36
AVAEKVKEES	QLPGTGGPEDVLQPVQR	AKA12_HUMAN			A-kinase anchor protein	1.70	0.10	32.40	-2.53
SSKLVQNIIQ	TAVDQFVR	AKA12_HUMAN			A-kinase anchor protein	1.55	0.06	29.20	-4.46
VIAEEEPPTV	TEPLPENR	AKA12_HUMAN			A-kinase anchor protein	1.52	0.03	25.00	0.00
ETGSTFKKFF	TQGWAGWR	AKA12_HUMAN			A-kinase anchor protein 12;	1.31	0.07	29.10	-2.73
MAAAVADGTR	AATIIEER	AKA12_HUMAN			A-kinase anchor protein 12;	1.15	0.03	31.80	-3.11
VLQAVAEKVK	EESQLPGTGGPEDVLQPVQR	AKA12_HUMAN			A-kinase anchor protein 12;	0.76	0.04	56.10	-3.09
EEATPVQEVE	GGVPDIEEQERR	AKA12_HUMAN			A-kinase anchor protein 12;	0.74	0.06	31.10	-1.20
SPDTTEEATP	VQEVEGGVPDIEEQER	AKA12_HUMAN			A-kinase anchor protein	0.71	0.08	66.40	-2.22
SQEHDPGQGS	SSPEQAGSPTEGEGVSTWESFKR	AKA12_HUMAN			A-kinase anchor protein 12;	0.64	0.07	26.40	-0.12
ISASVTEPLE	QVEAEAALLTEEVLER	AKA12_HUMAN			A-kinase anchor protein 12;	0.59	0.07	90.10	-0.60
LTDSPDTTEE	ATPVQEVEGGVPDIEEQER	AKA12_HUMAN			A-kinase anchor protein	0.49	0.01	75.90	5.67
EPLEQVEAEA	ALLTEEVLER	AKA12_HUMAN			A-kinase anchor protein	0.38	0.03	36.90	0.66
EEATPVQEVE	GGVPDIEEQER	AKA12_HUMAN			A-kinase anchor protein	0.37	0.02	51.00	-1.03
AVSQLTDSPD	TTEEATPVQEVEGGVPDIEEQERR	AKA12_HUMAN			A-kinase anchor protein 12;	0.35	0.01	50.90	0.11
KDVPFFEGLE	GSIDTGITVSR	AKA12_HUMAN			A-kinase anchor protein	0.16	0.01	44.90	-2.64
EEVLEREVIA	EEEPPTVTEPLPENR	AKA12_HUMAN			A-kinase anchor protein 12;	0.11	0.01	72.70	2.37

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EATPVQEVEG	GVPDIEEQER	AKA12_HUMAN			A-kinase anchor protein 12;	-0.08	0.01	29.80	-3.32
EATPVQEVEG	GVPDIEEQERR	AKA12_HUMAN			A-kinase anchor protein	-0.10	0.01	32.70	-0.44
VLEREVIAEE	EPPTVTEPLPENR	AKA12_HUMAN			A-kinase anchor protein 12;	-0.25	0.02	46.00	0.13
SPDTTEEATP	VQEVEGGVPDIEEQERR	AKA12_HUMAN			A-kinase anchor protein 12;	-0.34	0.03	29.60	1.60
EAALLTEEVL	EREVIAEEEPPTVTEPLPENR	AKA12_HUMAN			A-kinase anchor protein	-0.49	0.04	56.20	1.62
SVTEPLEQVE	AEAALLTEEVLER	AKA12_HUMAN			A-kinase anchor protein 12;	-0.66	0.05	58.80	2.44
LTDSPDTTEE	ATPVQEVEGGVPDIEEQERR	AKA12_HUMAN			A-kinase anchor protein	-0.76	0.01	33.10	-0.13
EVLEREVIAE	EEPPTVTEPLPENR	AKA12_HUMAN			A-kinase anchor protein	-0.86	0.05	40.70	-1.34
TEEVLEREVI	AEEEPPTVTEPLPENR	AKA12_HUMAN			A-kinase anchor protein	-1.20	0.06	56.40	-1.09
DQFSRSVNVS	LTQEELDSGLDELSVR	AKAP2_HUMAN			A-kinase anchor protein 2;	3.24	0.25	40.80	-3.16
PGAVVLVGGL	SPPVHEATQPEPTER	AKAP2_HUMAN			A-kinase anchor protein	1.97	0.18	35.90	-3.05
LLQKQLQQQQ	QQPPSQLCTAPASSHER	AKAP2_HUMAN			A-kinase anchor protein 2;	1.91	0.12	35.40	-5.09
GLQQPQPRGI	RGSSAARPSGR	ABL2_HUMAN			Abelson tyrosine-protein	4.52	0.44	39.00	1.06
CLKSLDLFNC	EVTNLNDYR	AN32A_HUMAN	AN32B_HUMAN		Acidic leucine-rich nuclear phosphoprotein 32 family member A;	-0.32	0.02	30.20	-3.37
M	ILLEVNNR	ARPC2_HUMAN			Actin-related protein 2/3 complex subunit 2;	-0.27	0.01	44.10	-2.99
DENKFVDEED	GGDGQAGPDEGEVDSCLR	ARPC5_HUMAN			Actin-related protein 2/3 complex subunit 5;	-0.10	0.01	76.90	-3.13
TVASSSSLEK	SYELPDGQVITIGNER	ACTA_HUMAN	ACTBL_HUMAN	ACTBM_HUMAN	Actin, aortic smooth muscle;	2.62	0.10	98.30	-1.48
RKDLYANNVM	SGGTTMYPGIADR	ACTA_HUMAN	ACTB_HUMAN	ACTC_HUMAN	Actin, aortic smooth	1.31	0.13	35.40	-0.89
ASSSSLEKSY	ELPDGQVITIGNER	ACTA_HUMAN	ACTBL_HUMAN	ACTBM_HUMAN	Actin, aortic smooth	1.00	0.09	35.80	-2.93
DIRKDLYANN	VLSGGTTMYPGIADR	ACTA_HUMAN	ACTB_HUMAN	ACTC_HUMAN	Actin, aortic smooth	0.23	0.02	33.70	0.70

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
VASSSSLEKS	YELPDGQVITIGNER	ACTA_HUMAN	ACTBL_HUMAN	ACTBM_HUMAN	Actin, aortic smooth	-0.32	0.03	36.50	4.62
IRKDLYANNV	LSGGTTMYPGIADR	ACTA_HUMAN	ACTB_HUMAN	ACTC_HUMAN	Actin, aortic smooth muscle;	-0.37	0.02	43.60	0.27
AGFAGDDAPR	AVFPSIVGRPR	ACTB_HUMAN	ACTA_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	4.24	0.32	28.20	-0.81
VAPEEHPILL	TEAPLNPKANR	ACTB_HUMAN	ACTA_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	2.49	0.16	28.00	-2.58
WHHTFYNELR	VAPEEHPVLLTEAPLNPK	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	2.27	0.13	53.10	-2.24
DTAVLVIDNG	SGMCKAGFAGDDAPR	ACTB_HUMAN	ACTG_HUMAN	POTEE_HUMAN	Actin, cytoplasmic 1;	1.75	0.19	54.60	-0.38
EMATVASSSS	LEKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	1.63	0.07	58.60	1.17
WHHTFYNELR	VAPEEHPVLLTEAPLNPKANR	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	1.20	0.06	60.80	-2.49
ATVASSSSLE	KSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	0.95	0.03	63.20	-2.31
MDDDIAALV	VDNGSGMCKAGFAGDDAPR	ACTB_HUMAN			Actin, cytoplasmic 1;	0.92	0.07	33.70	-1.95
QGVMVGMGQK	DSYVGDEAQSKR	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.75	0.06	31.90	-1.26
IDNGSGMCKA	GFAGDDAPR	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.69	0.06	44.80	-2.34
FQQMWISKQE	YDESGPSIVHR	ACTB_HUMAN	ACTBM_HUMAN	ACTG_HUMAN	Actin, cytoplasmic 1;	0.65	0.07	43.20	4.27
DDTAVLVIDN	GSGMCKAGFAGDDAPR	ACTB_HUMAN	ACTG_HUMAN	POTEE_HUMAN	Actin, cytoplasmic 1;	0.48	0.03	40.40	-1.32
QEMATVASSS	SLEKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.35	0.02	50.10	3.54
QQMWISKQEY	DESGPSIVHR	ACTB_HUMAN	ACTBM_HUMAN	ACTG_HUMAN	Actin, cytoplasmic 1;	0.28	0.01	34.90	-0.71
TFQQMWISKQ	EYDESGPSIVHR	ACTB_HUMAN	ACTBM_HUMAN	ACTG_HUMAN	Actin, cytoplasmic 1;	0.23	0.01	47.60	-1.76
SLEKSYELPD	GQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTBL_HUMAN	Actin, cytoplasmic 1;	-0.02	0.00	56.50	-4.01
DYLMKILTER	GYSFTTTAER	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	-0.08	0.01	38.10	-3.08
LRLDLAGREL	TDYLMKILTER	ACTB_HUMAN	ACTA_HUMAN	ACTBL_HUMAN	Actin, cytoplasmic 1;	-0.25	0.01	25.30	-0.76
VPAMYVAIQA	VLSLYASGR	ACTB_HUMAN	ACTA_HUMAN	ACTBL_HUMAN	Actin, cytoplasmic 1;	-0.63	0.03	26.60	-6.03
VIDNGSGMCK	AGFAGDDAPR	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	-0.76	0.04	44.20	1.19

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
IMKCDVDIRK	DLYANTVLSGGTTMYPGIADR	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	-0.76	0.04	38.50	-1.87
GDGVTHTVPI	YEGYALPHAILR	ACTB_HUMAN	ACTBL_HUMAN	ACTG_HUMAN	Actin, cytoplasmic 1;	-0.79	0.04	34.00	-5.14
WDDMEKIWHH	TFYNELR	ACTB_HUMAN	ACTBL_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	-0.89	0.03	28.10	-3.07
ELRVAPEEHP	VLLTEAPLNPKANR	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	-1.12	0.10	29.70	-1.74
SGDGVTHTVP	IYEGYALPHAILR	ACTB_HUMAN	ACTBL_HUMAN	ACTG_HUMAN	Actin, cytoplasmic 1;	-1.20	0.06	42.70	-1.48
MATVASSSSL	EKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	-1.25	0.06	44.00	-2.99
DGVTHTVPIY	EGYALPHAILR	ACTB_HUMAN	ACTBL_HUMAN	ACTG_HUMAN	Actin, cytoplasmic 1;	-1.44	0.08	30.60	0.39
NVPAMYVAIQ	AVLSLYASGR	ACTB_HUMAN	ACTA_HUMAN	ACTBL_HUMAN	Actin, cytoplasmic 1;	-1.66	0.05	29.00	-7.19
ISLNPEQWSQ	LKEQISDIDDAVR	TCP4_HUMAN			Activated RNA polymerase II	1.62	0.11	38.80	-5.45
PASASQVAGI	TGVSDAYSQSLPGK	ASCC1_HUMAN			Activating signal	0.92	0.03	26.70	-3.09
PRWIVEERAD	ATNVNNWHWTER	AHSA1_HUMAN			Activator of 90 kDa heat shock protein ATPase	-0.76	0.05	28.40	-2.37
GRVTQLCRQY	SDMPPLTLEGIQDR	ACPM_HUMAN			Acyl carrier protein,	-0.44	0.02	67.60	4.36
GQIIRVPARM	AATLILEPAGR	ACOT1_HUMAN	ACOT2_HUMAN		Acyl-coenzyme A	1.21	0.05	37.80	-3.33
MER	QVLLSEPEEAAALYR	ACPH_HUMAN			Acylamino-acid-releasing enzyme;	4.85	0.78	55.10	2.27
AESFFQTKAL	DVSASDDEIAR	ACPH_HUMAN			Acylamino-acid-releasing enzyme;	1.55	0.12	44.20	-3.79
GCDGILGSGR	RPDGCGVCGGDDSTCR	ATL4_HUMAN			ADAMTS-like protein 4;	4.53	0.44	52.50	-0.61
MSDKLPYK	VADIGLAAWGR	SAHH_HUMAN			Adenosylhomocysteinase;	-0.04	0.00	43.00	-2.51
DIGLAAWGRK	ALDIAENEMPGLMR	SAHH_HUMAN			Adenosylhomocysteinase;	-0.12	0.01	43.60	-1.51
GAGKGTQAPR	LAENFCVCHLATGDMLR	KAD2_HUMAN			Adenylate kinase 2,	3.45	0.31	46.50	-4.42

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
M	APSVPAAEPEYPKGIR	KAD2_HUMAN			Adenylate kinase 2, mitochondrial;	0.38	0.02	27.00	-1.26
IKKRLETYYK	ATEPVIAFYEKR	KAD1_HUMAN			Adenylate kinase	0.23	0.01	22.80	-2.88
GSLAFLGADT	ARLDVASEFR	ADML_HUMAN			ADM;	-0.39	0.02	41.60	-4.52
RKFQATGSRP	AGEEDAGGPERPGDVVNVVFVDR	ADXL_HUMAN			Adrenodoxin-like protein, mitochondrial;	0.11	0.01	49.30	0.04
GFTCSCPAGR	GGAVCEKVLGAPVPAFEGR	AGRIN_HUMAN			Agrin;	6.44	0.68	45.40	0.36
KSELFGETAR	SIESTLDDLFR	AGRIN_HUMAN			Agrin;	5.51	0.89	51.50	-1.89
TCSFGSTCAR	SADGLTASCLCPATCR	AGRIN_HUMAN			Agrin;	4.84	0.57	36.50	4.92
RVGPTCADEK	SPCQPNPCHGAAPCR	AGRIN_HUMAN			Agrin;	4.77	0.30	38.40	-4.95
ASCLCPATCR	GAPEGTVCGSDGADYPGECQLLR	AGRIN_HUMAN			Agrin;	4.65	0.70	66.00	-0.94
RDLGPGKSVR	AIVDVHFDPTTAFR	AGRIN_HUMAN			Agrin;	4.46	0.23	34.40	-1.17
LLRPESCPAR	QAPVCGDDGVTYENDCVMGR	AGRIN_HUMAN			Agrin;	4.46	0.49	65.00	-1.89
CSAGQCVCPR	CEHPPPGPVCGSDGVTYGSACELR	AGRIN_HUMAN			Agrin;	4.09	0.37	55.90	-0.61
RGRPRCSCDR	VTCDGAYRPVCAQDGR	AGRIN_HUMAN			Agrin;	3.61	0.33	35.10	-2.53
GAPDFSKLAR	AAAVSSGFDGAIQLVSLGGR	AGRIN_HUMAN			Agrin;	3.59	0.35	85.70	5.41
AIQLVSLGGR	QLLTPEHVLR	AGRIN_HUMAN			Agrin;	3.13	0.12	26.70	-0.89
PKCGQCPDGR	ALGPAGCEADASAPATCAEMR	AGRIN_HUMAN			Agrin;	3.06	0.24	89.80	0.75
DLGKGAAVIR	SREPVTLGAWTR	AGRIN_HUMAN			Agrin;	2.99	0.16	45.10	-0.57
IRLLDVNNQR	LELGIGPGAATR	AGRIN_HUMAN			Agrin;	2.95	0.20	45.50	-2.20
VTYGSACELR	EAACLQQTQIEEAR	AGRIN_HUMAN			Agrin;	2.82	0.33	80.90	0.48
ASCLCPATCR	GAPEGTVCGSDGADYPGECQLLR	AGRIN_HUMAN			Agrin;	2.71	0.17	21.50	-1.77
QLLTPEHVLR	QVDVTSFAGHPCTR	AGRIN_HUMAN			Agrin;	2.00	0.14	32.10	-3.93
FYTPEMADPK	SELFGETAR	AGRIN_HUMAN			Agrin;	1.68	0.05	27.40	-3.08

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
NPCHGAAPCR	VLPEGGAQCECPLGR	AGRIN_HUMAN			Agrin;	1.40	0.13	62.00	-1.37
GVGECGDHPC	LPNPCHGGAPCQNLEAGR	AGRIN_HUMAN			Agrin;	0.20	0.01	25.20	-1.56
ELFGETARSI	ESTLDDLFR	AGRIN_HUMAN			Agrin;	0.06	0.00	33.10	-3.45
YNGNARGKDF	LALALLDGR	AGRIN_HUMAN			Agrin;	0.04	0.00	43.10	-1.55
ALAIVDGHLQ	LSYNLGSQPVVLR	AGRIN_HUMAN			Agrin;	0.04	0.00	35.50	-4.79
LYNGQKTDGK	GDFVSLALR	AGRIN_HUMAN			Agrin;	-0.32	0.01	36.90	-5.83
NVFKKFDGPC	DPCQGALPDPSR	AGRIN_HUMAN			Agrin;	-0.60	0.02	48.70	-1.93
SYNLGSQPVV	LRSTVPVNTNR	AGRIN_HUMAN			Agrin;	-0.73	0.07	30.50	-0.93
PHCEKGLVEK	SAGDVDTLAFDGR	AGRIN_HUMAN			Agrin;	-2.66	0.17	60.40	-1.47
AAAKAIQGLR	AVFDETYPDPVR	SYAC_HUMAN			Alanine--tRNA ligase, cytoplasmic;	2.36	0.31	33.30	-2.36
GSPDRPWAKP	EDPSLLEDPR	ALDR_HUMAN			Aldose reductase;	-2.08	0.09	26.80	0.08
ESESGSPEYR	QQSAVPLDEETHAGEDVAVFAR	PPB1_HUMAN			Alkaline phosphatase, placental type;	2.92	0.28	52.90	-2.54
LGLRLQLSLG	IIPVEEENPDFWNR	PPB1_HUMAN	PPBN_HUMAN		Alkaline phosphatase,	0.57	0.05	72.30	-2.35
YGNGPGYVLK	DGARPDVTESESGSPEYR	PPB1_HUMAN	PPBN_HUMAN		Alkaline phosphatase, placental type;	-0.04	0.00	33.50	1.26
QLSLGIIPVE	EENPDFWNR	PPB1_HUMAN	PPBN_HUMAN		Alkaline phosphatase, placental type;	-0.60	0.03	30.50	0.89
GYVLKDGARP	DVTESESGSPEYR	PPB1_HUMAN	PPBN_HUMAN		Alkaline phosphatase, placental type;	-0.63	0.06	47.90	-0.81
ESESGSPEYR	QQSAVPLDGETHAGEDVAVFAR	PPBN_HUMAN			Alkaline phosphatase, placental-like;	2.03	0.14	33.90	-1.80

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
AAGFCPAVLC	HPNSPLDEENLTQENQDR	AACT_HUMAN			Alpha-1-antichymotrypsin;	1.23	0.07	86.30	-1.89
LFFWTRPAPG	RPPSVSALDGDPASLTR	MGAT1_HUMAN			Alpha-1,3-mannosyl-	-0.82	0.06	33.60	-0.17
ILTLVVAACG	FVLWSSNGR	MGAT2_HUMAN			Alpha-1,6-mannosyl-	1.09	0.03	30.80	-2.01
DGKFSVVYAK	CDSSPDSAEDVR	FETUA_HUMAN			Alpha-2-HS-glycoprotein;	4.57	0.16	59.50	-0.44
GKFSVVYAKC	DSSPDSAEDVR	FETUA_HUMAN			Alpha-2-HS-glycoprotein;	-1.00	0.02	52.10	-2.23
WEQLLTTIAR	TINEVENQILTR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	4.28	0.39	72.20	-2.67
NFITAEELRR	ELPPDQAEYCIAR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	4.21	0.27	27.10	0.69
DPAWEKQQRK	TFTAWCNSHLR	ACTN1_HUMAN	ACTN2_HUMAN	ACTN3_HUMAN	Alpha-actinin-1;	2.74	0.27	27.80	0.28
KNFITAEELR	RELPPDQAEYCIAR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	1.79	0.05	43.00	-0.69
HTNYTMEHIR	VGWEQLLTTIAR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	1.47	0.12	49.00	4.10
NEHLMEDYEK	LASDLLEWIR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	1.25	0.11	36.10	-0.08
QLLTTIARTI	NEVENQILTR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	0.74	0.05	28.10	-2.00
MDHYD	SQQTNDYMQPEEDWDR	ACTN1_HUMAN			Alpha-actinin-1;	0.41	0.04	70.80	-0.77
YTMEHIRVGW	EQLLTTIAR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	0.32	0.02	34.50	-1.57
HLEQAEKGYE	EWLLNEIR	ACTN1_HUMAN	ACTN2_HUMAN	ACTN4_HUMAN	Alpha-actinin-1;	-0.04	0.00	25.80	-1.26
QHLEQAEKGY	EEWLLNEIR	ACTN1_HUMAN	ACTN2_HUMAN	ACTN4_HUMAN	Alpha-actinin-1;	-0.23	0.02	40.90	2.18
TLGPEEFKAC	LISLGYDIGNDPQGEAEFAR	ACTN1_HUMAN			Alpha-actinin-1;	-0.29	0.02	54.10	-2.18
EIGRISIEMH	GTLEDQLSHLR	ACTN1_HUMAN			Alpha-actinin-1;	-0.34	0.03	33.50	2.38
TNYTMEHIRV	GWEQLLTTIAR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	-0.52	0.05	48.20	-2.80
VGWEQLLTTI	ARTINEVENQILTR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	-0.73	0.05	35.10	-3.19

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
DGKEAMLKHR	DYETATLSDIKALIR	ACTN4_HUMAN			Alpha-actinin-4;	3.25	0.41	46.00	-3.17
NEVENQILTR	DAKGISQEQMQEFR	ACTN4_HUMAN			Alpha-actinin-4;	2.00	0.09	37.10	-4.64
KEAMLKHRDY	ETATLSDIKALIR	ACTN4_HUMAN			Alpha-actinin-4;	0.34	0.03	20.40	-0.33
LAAHQDRVEQ	IAAIAQELNELDYYDSHNVNTR	ACTN4_HUMAN			Alpha-actinin-4;	0.31	0.02	46.90	0.81
RVEQIAAIAQ	ELNELDYYDSHNVNTR	ACTN4_HUMAN			Alpha-actinin-4;	0.26	0.01	51.80	-0.84
NVNTRCQKIC	DQWDALGSLTHSR	ACTN4_HUMAN			Alpha-actinin-4;	-0.18	0.02	51.10	-0.39
EQIAAIAQEL	NELDYYDSHNVNTR	ACTN4_HUMAN			Alpha-actinin-4;	-0.47	0.05	29.50	-1.13
AAHQDRVEQI	AAIAQELNELDYYDSHNVNTR	ACTN4_HUMAN			Alpha-actinin-4;	-0.63	0.07	62.50	-4.85
NIQNFTTSWR	DGLAFNALIHR	ACTN4_HUMAN	SPTN4_HUMAN		Alpha-actinin-4;	-1.04	0.09	58.60	0.71
QDRVEQIAAI	AQELNELDYYDSHNVNTR	ACTN4_HUMAN			Alpha-actinin-4;	-1.08	0.09	60.10	-1.85
DLYTAKGLFR	AAVPSGASTGIYEALELR	ENOA_HUMAN	ENOB_HUMAN	ENOG_HUMAN	Alpha-enolase;	2.22	0.12	97.70	-1.25
FRAAVPSGAS	TGIYEALELR	ENOA_HUMAN	ENOB_HUMAN	ENOG_HUMAN	Alpha-enolase;	-0.08	0.00	29.10	0.75
WQKFTASAGI	QVVGDDLTVTNPKR	ENOA_HUMAN			Alpha-enolase;	-0.29	0.02	41.30	-4.16
VDLYTAKGLF	RAAVPSGASTGIYEALELR	ENOA_HUMAN	ENOB_HUMAN	ENOG_HUMAN	Alpha-enolase;	-0.34	0.02	58.70	-1.55
AKGLFRAAVP	SGASTGIYEALELR	ENOA_HUMAN	ENOB_HUMAN	ENOG_HUMAN	Alpha-enolase;	-0.52	0.03	60.00	-1.80
QDDWGAWQKF	TASAGIQVVGDDLTVTNPKR	ENOA_HUMAN			Alpha-enolase;	-0.66	0.05	41.50	0.38
HAGNKLAMQE	FMILPVGAANFR	ENOA_HUMAN			Alpha-enolase;	-0.79	0.03	43.70	-1.75
DDWGAWQKFT	ASAGIQVVGDDLTVTNPKR	ENOA_HUMAN			Alpha-enolase;	-0.82	0.04	37.40	-1.60
AGNKLAMQEF	MILPVGAANFR	ENOA_HUMAN			Alpha-enolase;	-0.82	0.06	37.90	-1.81
YTDKVVIGMD	VAASEFFR	ENOA_HUMAN			Alpha-enolase;	-1.29	0.06	23.60	-1.57
KAGYTDKVVI	GMDVAASEFFR	ENOA_HUMAN			Alpha-enolase;	-1.44	0.12	55.50	-2.45
AVPSGASTGI	YEALELR	ENOA_HUMAN	ENOB_HUMAN	ENOG_HUMAN	Alpha-enolase;	-1.44	0.08	26.70	-1.83
GYTDKVVIGM	DVAASEFFR	ENOA_HUMAN			Alpha-enolase;	-1.49	0.08	40.70	-2.71
LSTYCVDNNQ	GGPGEDGAQGEPAEPEDAEKSR	TXLNA_HUMAN			Alpha-taxilin;	0.20	0.01	56.10	-4.15

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TRSLAESELR	SAPYEFPEESPIEQLEER	AMPD2_HUMAN			AMP deaminase 2;	0.06	0.00	56.00	0.87
TTESVEEVVR	EVCSEQAETGPCR	A4_HUMAN			Amyloid beta A4 protein;	8.32	1.54	45.40	0.90
LAAWTARALE	VPTDGNAGLLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	3.75	0.21	53.00	2.04
LLAAWTARAL	EVPTDGNAGLLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	1.23	0.10	107.00	-1.85
LEVPTDGNAG	LLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	0.84	0.05	47.30	0.20
LLLAAWTARA	LEVPTDGNAGLLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	0.42	0.07	113.00	-1.41
LQPWHSFGAD	SVPANTENEVEPVDARPAADR	A4_HUMAN			Amyloid beta A4 protein;	0.29	0.02	33.60	0.00
SFGADSVPAN	TENEVEPVDARPAADR	A4_HUMAN			Amyloid beta A4 protein;	0.18	0.02	31.80	0.33
ADSVPANTEN	EVEPVDARPAADR	A4_HUMAN			Amyloid beta A4 protein;	0.06	0.00	27.60	-3.23
DDLQPWHSFG	ADSVPANTENEVEPVDARPAADR	A4_HUMAN			Amyloid beta A4 protein;	-0.10	0.01	41.00	-2.80
RALEVPTDGN	AGLLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	-0.20	0.01	46.50	-1.02
WHSFGADSVP	ANTENEVEPVDARPAADR	A4_HUMAN			Amyloid beta A4 protein;	-0.25	0.03	40.80	-2.16
SLDDLQPWHS	FGADSVPANTENEVEPVDARPAAD	A4_HUMAN			Amyloid beta A4 protein;	-0.25	0.03	48.20	-1.80
FGADSVPANT	ENEVEPVDARPAADR	A4_HUMAN			Amyloid beta A4 protein;	-0.58	0.05	30.30	-0.94
KAVIQHFQEK	VESLEQEAANER	A4_HUMAN			Amyloid beta A4 protein;	-1.08	0.11	50.90	-3.13
TTTTESVEEV	VREVCSEQAETGPCR	A4_HUMAN			Amyloid beta A4 protein;	-1.20	0.14	61.20	-2.87
FPFHSSEIQR	DELAPAGTGVSR	APLP1_HUMAN			Amyloid-like protein 1;	-0.02	0.00	37.20	-9.52
LLLRAQPAIG	SLAGGSPGAAEAPGSAQVAGLCG	APLP1_HUMAN			Amyloid-like protein 1;	-0.39	0.04	47.50	0.14
QNVREEPAVQ	FNSGTLALNR	TIE2_HUMAN			Angiopoietin-1 receptor;	0.42	0.01	24.80	-2.94
ALLSLAKGDR	SEDFGVNEDLADSDAR	ANXA1_HUMAN			Annexin A1;	3.03	0.31	72.60	-1.75
NEDLADSDAR	ALYEAGER	ANXA1_HUMAN			Annexin A1;	2.99	0.11	33.40	-0.75

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LEEVVLALLK	TPAQFDADELR	ANXA1_HUMAN			Annexin A1;	2.83	0.37	54.10	0.85
AALHKAIMVK	GVDEATIIDILTKR	ANXA1_HUMAN			Annexin A1;	1.83	0.24	26.20	-2.81
FRNALLSLAK	GDRSEDFGVNEDLADSDAR	ANXA1_HUMAN			Annexin A1;	1.66	0.19	89.50	-0.24
NRVYREELKR	DLAKDITSDTSGDFR	ANXA1_HUMAN			Annexin A1;	1.34	0.12	44.30	-2.71
RALYEAGERR	KGTDVNVFNTILTTR	ANXA1_HUMAN			Annexin A1;	1.22	0.27	40.90	-1.14
ELRAAMKGLG	TDEDTLIEILASR	ANXA1_HUMAN			Annexin A1;	0.51	0.05	67.30	-3.12
LAKGDRSEDF	GVNEDLADSDAR	ANXA1_HUMAN			Annexin A1;	0.38	0.02	55.70	-0.31
DADELRAAMK	GLGTDEDTLIEILASR	ANXA1_HUMAN			Annexin A1;	0.16	0.02	95.30	-0.69
AGERRKGTDV	NVFNTILTTR	ANXA1_HUMAN			Annexin A1;	-0.10	0.01	32.30	-2.07
REELKRDLAK	DITSDTSGDFR	ANXA1_HUMAN			Annexin A1;	-0.18	0.01	49.00	-1.21
KALTGHLEEV	VLALLKTPAQFDADELR	ANXA1_HUMAN			Annexin A1;	-0.27	0.01	32.40	2.20
YEAGERRKGT	DVNVFNTILTTR	ANXA1_HUMAN			Annexin A1;	-0.34	0.04	46.60	-1.75
HKAIMVKGVD	EATIIDILTKR	ANXA1_HUMAN			Annexin A1;	-0.44	0.03	26.40	-3.50
NALLSLAKGD	RSEDFGVNEDLADSDAR	ANXA1_HUMAN			Annexin A1;	-0.52	0.05	67.20	-0.72
LSLAKGDRSE	DFGVNEDLADSDAR	ANXA1_HUMAN			Annexin A1;	-0.58	0.06	71.70	-2.82
LLSLAKGDRS	EDFGVNEDLADSDAR	ANXA1_HUMAN			Annexin A1;	-0.69	0.07	85.40	-4.27
RAAMKGLGTD	EDTLIEILASR	ANXA1_HUMAN			Annexin A1;	-0.69	0.07	51.80	-0.46
AMKGLGTDED	TLIEILASR	ANXA1_HUMAN			Annexin A1;	-0.86	0.08	36.90	-4.57
AAMKGLGTDE	DTLIEILASR	ANXA1_HUMAN			Annexin A1;	-0.89	0.08	51.20	-1.72
LHKAIMVKGV	DEATIIDILTKR	ANXA1_HUMAN			Annexin A1;	-0.96	0.11	34.20	-4.46

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LRAAMKGLGT	DEDTLIEILASR	ANXA1_HUMAN			Annexin A1;	-1.00	0.16	63.80	-0.99
KAIMVKGVDE	ATIIDILTKR	ANXA1_HUMAN			Annexin A1;	-1.08	0.09	25.70	0.17
DELRAAMKGL	GTDEDTLIEILASR	ANXA1_HUMAN			Annexin A1;	-1.20	0.17	72.20	-2.30
SLAKGDRSED	FGVNEDLADSDAR	ANXA1_HUMAN			Annexin A1;	-1.29	0.16	50.90	-0.35
KASMKGLGTD	EDSLIEIICSR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	4.29	0.28	48.00	-3.21
DSLIEIICSR	TNQELQEINR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	3.60	0.29	51.30	-2.12
KLMVALAKGR	RAEDGSVIDYELIDQDAR	ANXA2_HUMAN			Annexin A2;	3.60	0.30	80.40	0.05
VTIVNILTNR	SNAQRQDIAFAYQR	ANXA2_HUMAN			Annexin A2;	3.24	0.19	37.60	-0.35
LNIETAIKTK	GVDEVTIVNILTNR	ANXA2_HUMAN			Annexin A2;	2.05	0.17	67.90	1.21
DASELKASMK	GLGTDEDSLIEIICSR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	0.24	0.03	81.80	-0.50
ILTNRSNAQR	QDIAFAYQR	ANXA2_HUMAN			Annexin A2;	-0.29	0.01	42.60	-1.32
KEMYKTDLEK	DIISDTSGDFR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-0.32	0.02	44.70	-3.83
KGRRAEDGSV	IDYELIDQDAR	ANXA2_HUMAN			Annexin A2;	-0.44	0.03	50.60	-0.58
INRVYKEMYK	TDLEKDIISDTSGDFR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-0.49	0.04	45.60	-0.48
NRVYKEMYKT	DLEKDIISDTSGDFR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-0.52	0.05	43.60	-2.64
RAEDGSVIDY	ELIDQDAR	ANXA2_HUMAN			Annexin A2;	-0.55	0.02	30.70	-2.71
AKGRRAEDGS	VIDYELIDQDAR	ANXA2_HUMAN			Annexin A2;	-0.58	0.04	47.10	-3.10
RRAEDGSVID	YELIDQDAR	ANXA2_HUMAN			Annexin A2;	-0.96	0.04	29.50	-2.94
SMKGLGTDED	SLIEIICSR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-1.20	0.06	34.50	-4.44

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
ASMKGLGTDE	DSLIEIICSR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-1.25	0.12	36.90	-7.98
TPPSAYGSVK	AYTNFDAER	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-1.39	0.04	23.80	-6.78
SELKASMKGL	GTDEDSLIEIICSR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-1.39	0.11	55.90	6.70
GRRAEDGSVI	DYELIDQDAR	ANXA2_HUMAN			Annexin A2;	-1.44	0.08	44.80	-3.54
LKASMKGLGT	DEDSLIEIICSR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-1.49	0.13	48.10	3.70
IETAIKTKGV	DEVTIVNILTNR	ANXA2_HUMAN			Annexin A2;	-2.25	0.32	35.60	1.19
HTLIRVMVSR	SEIDLFNIR	ANXA5_HUMAN			Annexin A5;	1.53	0.07	40.90	-3.08
DAETLRKAMK	GLGTDEESILTLLTSR	ANXA5_HUMAN			Annexin A5;	0.45	0.06	91.00	-1.49
MAQVLR	GTVTDFPGFDER	ANXA5_HUMAN			Annexin A5;	-3.25	0.00	41.10	-2.04
GKTTKMPCES	SPPESADTPTSTR	KI67_HUMAN			Antigen KI-67;	1.45	0.04	37.20	-3.20
EKAQALEDLA	GFKELFQTR	KI67_HUMAN			Antigen KI-67;	0.96	0.06	27.40	1.61
AGKTTKMPCE	SSPPESADTPTSTR	KI67_HUMAN			Antigen KI-67;	0.84	0.04	30.90	3.27
YMKHATKTAK	DALSSVQESQVAQQAR	APOC3_HUMAN			Apolipoprotein C-III;	-0.10	0.01	76.80	0.69
RKISVVSATK	GVPAGNSDTEGGQPGR	ACINU_HUMAN			Apoptotic chromatin	0.72	0.04	42.40	2.22
RRSSRVRQAR	AAKLSEGSQPAEEEEDQETPSR	ACINU_HUMAN			Apoptotic chromatin	0.60	0.04	54.20	-1.91
LTRRSISQQK	SGVSITIDDPVR	ACINU_HUMAN			Apoptotic chromatin	-0.14	0.01	43.10	-3.25
SFKRKISVVS	ATKGVPAGNSDTEGGQPGR	ACINU_HUMAN			Apoptotic chromatin	-0.20	0.02	63.10	0.00
LSDLHLLQSL	MAQSCSSALR	AQ12A_HUMAN	AQ12B_HUMAN		Aquaporin-12A;	3.32	0.50	28.00	6.14
VWPGDGLVPD	TAEPHVAPSPTLPSTEDVIR	GIT2_HUMAN			ARF GTPase-activating	-0.39	0.02	36.30	-1.49
VKVPGKRLPR	ATPATAPGTSPR	AGAP3_HUMAN			Arf-GAP with GTPase,	0.57	0.02	34.80	5.42
M	VLAELYVSDR	SYNC_HUMAN			Asparagine--tRNA ligase, cytoplasmic;	-2.79	0.19	25.60	-2.18

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
KEFNPTKPLL	SVNKSTSTPTSPGPR	ATX2L_HUMAN			Ataxin-2-like protein;	1.54	0.14	31.10	-2.61
APQPPPPQQH	QERPGAAAIGSAR	ATX2L_HUMAN			Ataxin-2-like protein;	0.59	0.04	31.10	-2.27
QRPLRGAKTL	SSPSNRPSGETSVPPPPAVGR	ATX2L_HUMAN			Ataxin-2-like protein;	0.08	0.00	36.70	-2.23
AAAAPARAPR	AAAAAATAPPSPGPAQPGPR	SAMD1_HUMAN			Atherin;	0.06	0.01	26.00	-2.62
AVGELLQEVS	GDSKDDAGIR	ABCF3_HUMAN			ATP-binding cassette sub-family F member 3;	3.86	0.23	32.00	-3.30
PPTAAHTANF	LLNASGSTSTPAPSR	ACLY_HUMAN			ATP-citrate synthase;	-0.55	0.06	56.50	-2.28
ILDDFIQNDR	AAECNIVVTQPR	DHX9_HUMAN			ATP-dependent RNA	2.48	0.17	38.90	-2.60
LGGIGQFLAK	AIEPPPLDAVIEAEHTLR	DHX9_HUMAN			ATP-dependent RNA	1.71	0.03	32.70	-1.50
LKAENNSEVG	ASGYGVPGPTWDR	DHX9_HUMAN			ATP-dependent RNA	0.98	0.06	30.80	6.44
AVIEAEHTLR	ELDALDANDELTPLGR	DHX9_HUMAN			ATP-dependent RNA helicase A;	0.94	0.08	64.20	-2.32
VRFLVLDEAD	GLLSQGYSDFINR	DDX1_HUMAN			ATP-dependent RNA	-1.16	0.05	44.20	-0.47
KMLEQLDMRR	DVQEIFR	DX39A_HUMAN	DX39B_HUMAN		ATP-dependent RNA helicase DDX39A;	4.50	0.88	30.80	-2.89
YVSIHSSGFR	DFLLKPELLR	DX39A_HUMAN	DX39B_HUMAN		ATP-dependent RNA	2.32	0.17	24.50	-0.23
IERVNIAFNY	DMPEDSDTYLHR	DX39A_HUMAN	DX39B_HUMAN		ATP-dependent RNA helicase DDX39A;	-0.16	0.02	22.60	-3.50
ENALGLDQQF	AGLDLNSSDNQSGGSTASKGR	DDX3X_HUMAN			ATP-dependent RNA helicase DDX3X;	1.98	0.23	43.80	-0.29
DREEALHQFR	SGKSPILVATAVAAR	DDX3X_HUMAN	DDX3Y_HUMAN		ATP-dependent RNA	1.41	0.12	31.40	-4.77
EEDSSNVDLP	YIPAENSPTR	DDX42_HUMAN			ATP-dependent RNA	0.09	0.01	25.10	-1.70
WGVRTMQARG	FGSDQSENVDR	ATIF1_HUMAN			ATPase inhibitor, mitochondrial;	1.42	0.11	35.40	-3.73
GVRTMQARGF	GSDQSENVDRGAGSIR	ATIF1_HUMAN			ATPase inhibitor,	-0.12	0.01	43.70	-3.74

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LLLLLPCEAEA	AAAAAAVSGSAAAEAKECDRPCV	ATRN_HUMAN			Attractin;	0.32	0.02	49.90	-3.14
PDMLVTKAVV	YRETDPSPEER	E41L1_HUMAN			Band 4.1-like protein 1;	0.23	0.01	28.10	-1.35
EVAENQQNQS	SDPEEEKGSQPPPAAESQSSLRR	E41L2_HUMAN			Band 4.1-like protein 2;	1.97	0.17	27.70	-2.16
ICCSEPPVVK	TEMVTISDASQR	E41L2_HUMAN			Band 4.1-like protein 2;	-1.39	0.11	48.10	-1.17
SPSTPAGWVR	EGDTVQLLCR	BCAM_HUMAN			Basal cell adhesion molecule;	4.18	0.81	26.80	3.53
RGQSGTYGCR	VEDYDAADDVQLSKTLELR	BCAM_HUMAN			Basal cell adhesion	1.42	0.13	38.20	-1.39
RHQTHGSLLR	LYQASPADSGEYVCR	PGBM_HUMAN			Basement membrane-specific heparan sulfate	6.73	2.16	56.70	-0.69
ELGSGLAVLR	SAEPLALGR	PGBM_HUMAN			Basement membrane-specific heparan sulfate proteoglycan core protein;	5.29	0.18	33.80	-2.44
KAQIHGGILR	LPAVEPTDQAQYLCR	PGBM_HUMAN			Basement membrane-	4.75	0.65	43.00	4.75
LRSPLPWQHR	LEGDTLIIPR	PGBM_HUMAN			Basement membrane-specific heparan sulfate	4.23	0.35	37.80	-3.20
GRAHSVEECR	CPIGYSGLSCESCDAHFTR	PGBM_HUMAN			Basement membrane-specific heparan sulfate	3.49	0.58	55.70	1.34
EGNPIQPGGK	CRPVNQEIVR	PGBM_HUMAN			Basement membrane-specific heparan sulfate	3.09	0.16	32.60	-2.84
PLVVEVHPAR	SIVPQGGSHSLR	PGBM_HUMAN			Basement membrane-specific heparan sulfate proteoglycan core protein;	2.58	0.13	26.70	-0.24
HRVTALREGR	RGSIQVDGEELVSGR	PGBM_HUMAN			Basement membrane-specific heparan sulfate proteoglycan core protein;	2.36	0.18	34.20	-4.96
CRCKNNVVGR	LCNECADGSFHLSTR	PGBM_HUMAN			Basement membrane-	2.30	0.17	33.50	-9.85
LAFPGHVFSR	SLPEVPETIELEVR	PGBM_HUMAN			Basement membrane-specific heparan sulfate	2.23	0.19	45.80	-2.25
AQPGPSNRPR	ALEVEECR	PGBM_HUMAN			Basement membrane-specific heparan sulfate	2.12	0.13	33.90	-3.00

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
GIVQSGGVVR	IAHVELADAGQYR	PGBM_HUMAN			Basement membrane-specific heparan sulfate	1.63	0.09	37.00	-4.41
GNPSVQGGQC	LPETNQAPLVVEVHPAR	PGBM_HUMAN			Basement membrane-	0.38	0.01	35.90	-0.32
VGEAGQGKDF	ISLGLQDGHLVFR	PGBM_HUMAN			Basement membrane-	-0.14	0.01	32.90	-2.95
GEAGQGKDFI	SLGLQDGHLVFR	PGBM_HUMAN			Basement membrane-	-0.37	0.02	38.60	-6.17
VHHVKEQYFK	SAAMTLNER	BCLF1_HUMAN			Bcl-2-associated transcription factor 1;	0.45	0.01	27.90	-3.41
EQRALQMEGL	QEDSILCLPAAYCER	BCOR_HUMAN			BCL-6 corepressor;	4.29	0.41	10.60	-2.00
LAGALLACLL	VLTADPPPPPLPAER	LFNG_HUMAN			Beta-1,3-N-acetylglucosaminyltransfe	1.97	0.08	36.50	0.69
ALLACLLVLT	ADPPPPPLPAER	LFNG_HUMAN			Beta-1,3-N-acetylglucosaminyltransfe	1.01	0.04	35.00	-2.57
YFSLLTRARR	DAGPPPGAAPR	LFNG_HUMAN			Beta-1,3-N-	0.59	0.01	52.70	-2.22
LLACLLVLTA	DPPPPPLPAER	LFNG_HUMAN			Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe;	0.21	0.00	46.60	4.28
ACLALAAALA	ALLLLPLPLPR	RFNG_HUMAN			Beta-1,3-N-	1.07	0.14	39.60	-2.97
LALAAALAAL	LLLPLPLPR	RFNG_HUMAN			Beta-1,3-N-acetylglucosaminyltransferase radical fringe;	0.35	0.01	31.00	-1.69
LPQLVGVSTP	LQGGSNSAAAIGQSSGELR	B4GT1_HUMAN			Beta-1,4-	-0.73	0.11	73.40	-1.80
DLSRLPQLVG	VSTPLQGGSNSAAAIGQSSGELR	B4GT1_HUMAN			Beta-1,4-galactosyltransferase 1;	-0.73	0.06	117.80	-0.95
AGRDLSRLPQ	LVGVSTPLQGGSNSAAAIGQSSGE	B4GT1_HUMAN			Beta-1,4-galactosyltransferase 1;	-0.82	0.09	85.20	0.84
RELGPLYTNI	TADIGTDPR	B4GT3_HUMAN			Beta-1,4-galactosyltransferase 3;	1.62	0.04	33.80	-6.36
LLVGSQLAVM	MYLSLGGFR	B4GT3_HUMAN			Beta-1,4-galactosyltransferase 3;	1.59	0.07	26.90	0.37
LVGSQLAVMM	YLSLGGFR	B4GT3_HUMAN			Beta-1,4-galactosyltransferase 3;	0.49	0.06	22.10	-1.81

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MMYLSLGGFR	SLSALFGR	B4GT3_HUMAN			Beta-1,4-galactosyltransferase 3;	-0.49	0.01	30.30	-2.94
SKDWSFYLLY	YTEFTPTEKDEYACR	B2MG_HUMAN			Beta-2-microglobulin;	1.03	0.13	56.00	-4.88
GVSLAVCKAG	AAEKGVPLYR	ENOB_HUMAN			Beta-enolase;	6.53	1.18	37.30	-1.55
LGVSLAVCKA	GAAEKGVPLYR	ENOB_HUMAN			Beta-enolase;	4.59	0.36	33.70	-0.08
GPLLWGCALG	LQGGMLYPQESPSR	BGLR_HUMAN			Beta-glucuronidase;	1.79	0.15	52.10	-0.31
AAAFAGRATA	LWPWPQNFQTSDQR	HEXA_HUMAN			Beta-hexosaminidase subunit alpha;	0.92	0.01	55.80	-3.11
LALCGAGTTA	AELSYSLR	MANBA_HUMAN			Beta-mannosidase;	0.55	0.02	27.00	-3.62
LKAQYKEKTG	KEYIPGQPPLSQSSDSSPTR	SYEP_HUMAN			Bifunctional glutamate/proline--tRNA	0.95	0.10	64.30	2.33
M	VQKESQATLEER	NCOAT_HUMAN			Bifunctional protein NCOAT;	1.43	0.13	26.40	-1.90
ALRDAGLAVR	DVSELTGFPEMLGGR	PUR9_HUMAN			Bifunctional purine biosynthesis protein	1.89	0.23	62.80	-3.18
ERRNENSEVD	TSAGSGSAPSVLHQR	BOD1L_HUMAN			Biorientation of	-0.60	0.02	25.70	-6.44
AEYLREKLQR	DLEAEHVEVEDTTLNR	BOLA2_HUMAN			BolA-like protein 2;	5.08	0.50	59.20	-2.89
LREKLQRDLE	AEHVEVEDTTLNR	BOLA2_HUMAN			BolA-like protein 2;	0.31	0.02	37.70	-1.56
GQGPITEDML	CAGYLEGER	BSSP4_HUMAN			Brain-specific serine	-4.24	0.80	20.20	2.20
KERLRQERMR	SREDEDALEQAR	BRD4_HUMAN			Bromodomain-containing protein 4;	-0.44	0.03	27.80	-3.71
IQIRRLKRLG	IEKTDPTTLTDEEINR	C1TC_HUMAN			C-1-tetrahydrofolate	0.84	0.05	46.50	-0.21
PVVVAVNAFK	TDTESELDLISR	C1TC_HUMAN			C-1-tetrahydrofolate	0.74	0.04	43.40	0.28
MIQYNNLNLK	TPVPSDIDISR	C1TC_HUMAN			C-1-tetrahydrofolate	0.34	0.02	29.40	-2.11
RRLKRLGIEK	TDPTTLTDEEINR	C1TC_HUMAN			C-1-tetrahydrofolate synthase, cytoplasmic;	0.20	0.02	47.00	-0.26
LASAVLLASL	LSLHLGTATR	CCL26_HUMAN			C-C motif chemokine 26;	3.06	0.33	9.10	-1.82
EHQVELELLR	DDNEQLITQYER	JIP4_HUMAN			C-Jun-amino-terminal	1.51	0.10	63.10	0.64
LVYLTQPGNG	NEGSVTGSCYCGKR	CXL16_HUMAN			C-X-C motif chemokine 16;	-0.02	0.00	42.10	-2.82

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LLLTPPGPLA	SAGPVSAVLTELR	CXCL6_HUMAN			C-X-C motif chemokine	0.20	0.00	52.40	-2.63
LTPPGPLASA	GPVSAVLTELR	CXCL6_HUMAN			C-X-C motif chemokine	-0.04	0.00	59.60	-1.88
LQQDVKLNGA	GLEVEDSDPEPEGEAEDR	CPMD8_HUMAN			C3 and PZP-like alpha-2-macroglobulin domain-	-6.27	0.00	20.50	-1.29
PILVVDSGPP	TLSSTGTLTIR	CAD22_HUMAN			Cadherin-22;	3.50	0.25	23.70	2.12
MESMAVATD	GGERPGVPAGSGLSASQR	CAMLG_HUMAN			Calcium signal-modulating cyclophilin	0.57	0.05	50.10	-0.23
SEEEIREAFR	VFDKDGNGYISAAELR	CALM_HUMAN			Calmodulin;	1.90	0.11	34.90	-1.32
AFRVFDKDGN	GYISAAELR	CALM_HUMAN			Calmodulin;	-0.16	0.01	41.10	-3.75
EVDADGNGTI	DFPEFLTMMAR	CALM_HUMAN			Calmodulin;	-2.44	0.27	37.90	-4.31
ISAISEAAAQ	YNPEPPPPR	CPNS1_HUMAN			Calpain small subunit 1;	1.33	0.06	30.70	-3.38
PPRTHYSNIE	ANESEEVRQFR	CPNS1_HUMAN			Calpain small subunit 1;	0.76	0.04	23.60	-3.15
AMRILGGVIS	AISEAAAQYNPEPPPPR	CPNS1_HUMAN			Calpain small subunit 1;	0.61	0.02	44.40	1.69
NPEPPPPRTH	YSNIEANESEEVR	CPNS1_HUMAN			Calpain small subunit 1;	0.49	0.05	62.80	-2.04
SSKTRGIEWK	RPTEICADPQFIIGGATR	CAN2_HUMAN			Calpain-2 catalytic	0.35	0.03	48.40	2.16
FDQTTISLQM	GTNKGASQAGMLAPGTR	CNN3_HUMAN			Calponin-3;	1.37	0.13	38.20	-4.12
TISLQMGTNK	GASQAGMLAPGTRR	CNN3_HUMAN			Calponin-3;	0.29	0.02	37.50	-3.62
LLGLLGLAVA	EPAVYFKEQFLDGDGWTSR	CALR_HUMAN			Calreticulin;	0.75	0.03	32.20	1.87
AVAEPAVYFK	EQFLDGDGWTSR	CALR_HUMAN			Calreticulin;	0.44	0.05	33.80	-9.96
KKVIDCLYTC	KEGLDLQVLEDSGR	CSTN1_HUMAN			Calsyntenin-1;	0.42	0.03	35.10	-1.79
HHFARAASEF	ESSEGVFLFPELR	CSTN1_HUMAN			Calsyntenin-1;	0.20	0.01	41.70	-2.78
FARAASEFES	SEGVFLFPELR	CSTN1_HUMAN			Calsyntenin-1;	-0.08	0.00	37.20	-7.38

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
RAASEFESSE	GVFLFPELR	CSTN1_HUMAN			Calsyntenin-1;	-0.79	0.03	36.50	7.68
ARAASEFESS	EGVFLFPELR	CSTN1_HUMAN			Calsyntenin-1;	-0.82	0.03	36.40	0.56
DEPEWVKTER	EQFVEFR	CALU_HUMAN			Calumenin;	2.86	0.11	23.70	-3.46
GNTDEPEWVK	TEREQFVEFR	CALU_HUMAN			Calumenin;	0.31	0.02	27.20	-3.27
NPVVKGRRRR	GAISAEVYTEEDAASYVR	KAP0_HUMAN			cAMP-dependent protein kinase type I-alpha	0.06	0.00	60.30	6.46
EKTISSEKAS	STPSSETQEEFVDDFR	CLIP1_HUMAN			CAP-Gly domain-containing linker protein	0.93	0.10	71.90	7.67
VNSLQQQPQA	ASPSVPEPHSLTPVAQADPLVR	CAPR1_HUMAN			Caprin-1;	0.67	0.03	35.20	-2.18
CLLLACPATA	TGPEVAQPEVDTTLGR	EST3_HUMAN			Carboxylesterase 3;	1.31	0.15	55.50	1.00
ATKNDIGPYE	CEIQNPVGASR	CEAM7_HUMAN			Carcinoembryonic antigen-related cell adhesion molecule 7;	0.11	0.01	24.20	-4.84
TELDDGIQAD	SGPINDTDANPR	CASP7_HUMAN			Caspase-7;	0.61	0.04	51.70	-3.64
PQCPTIKEIR	DQGSCGSCWAFGAVEAISDR	CATB_HUMAN			Cathepsin B;	2.00	0.16	48.90	2.95
PKPPQRVMFT	EDLKLPASFDAR	CATB_HUMAN			Cathepsin B;	0.44	0.03	38.60	-2.39
WTKWKAMHNR	LYGMNEEGWR	CATL1_HUMAN			Cathepsin L1;	4.48	0.40	20.00	-3.19
FQNRKPRKGK	VFQEPLFYEAPR	CATL1_HUMAN			Cathepsin L1;	1.97	0.11	48.00	1.84
ADLPKSWDWR	NVDGVNYASITR	CATZ_HUMAN			Cathepsin Z;	1.50	0.07	44.60	-1.57
NGLSEYLDLS	SPGPVEILTTVTESVTGISR	CD109_HUMAN			CD109 antigen;	1.52	0.04	44.10	3.62
LSEYLDLSSP	GPVEILTTVTESVTGISR	CD109_HUMAN			CD109 antigen;	-0.20	0.02	43.60	-2.48
LGYRKYQPNI	DVQESIHFLESEFSR	CD109_HUMAN			CD109 antigen;	-0.69	0.08	34.50	-4.09
SLNPSGEVTR	QIGDALPVSCTISASR	CD166_HUMAN			CD166 antigen;	4.21	0.39	36.20	-0.12
TVNSLNVSAI	SIPEHDEADEISDENR	CD166_HUMAN			CD166 antigen;	2.64	0.22	58.80	-5.25
SATVFRPGLG	WYTVNSAYGDTIIIPCR	CD166_HUMAN			CD166 antigen;	1.05	0.06	80.70	-0.53
RTVNSLNVSA	ISIPEHDEADEISDENR	CD166_HUMAN			CD166 antigen;	0.61	0.07	34.10	-0.70

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
FIAFRSSTKK	SVQYDDVPEYKDR	CD166_HUMAN			CD166 antigen;	0.48	0.04	31.30	0.24
TRYVQKGEYR	TNPEDIYPSNPTDDDVSSGSSSER	CD44_HUMAN			CD44 antigen;	3.15	0.18	28.40	-6.16
EASKSQEMVH	LVNKESSETPDQFMTADETR	CD44_HUMAN			CD44 antigen;	2.28	0.18	62.80	-1.95
EMVHLVNKES	SETPDQFMTADETR	CD44_HUMAN			CD44 antigen;	2.03	0.15	75.50	-1.93
ALSIGFETCR	YGFIEGHVVIPR	CD44_HUMAN			CD44 antigen;	1.76	0.04	38.50	-8.05
MVHLVNKESS	ETPDQFMTADETR	CD44_HUMAN			CD44 antigen;	0.98	0.02	68.60	-0.64
SQEMVHLVNK	ESSETPDQFMTADETR	CD44_HUMAN			CD44 antigen;	0.59	0.04	63.70	3.15
APPEEDCTSV	TDLPNAFDGPITITIVNR	CD44_HUMAN			CD44 antigen;	-0.34	0.04	52.90	3.26
GLCLVPLSLA	QIDLNITCR	CD44_HUMAN			CD44 antigen;	-0.76	0.01	32.60	-3.00
TSVTDLPNAF	DGPITITIVNR	CD44_HUMAN			CD44 antigen;	-1.60	0.15	49.00	-2.03
QKKKLCFKEN	AEQGEVDMESHR	CD99_HUMAN			CD99 antigen;	1.91	0.23	34.70	-2.96
M	VGGEAAAAVEELVSGVR	C2AIL_HUMAN			CDKN2AIP N-terminal-	0.37	0.03	37.10	-2.55
APENPVVEVR	EQAVEGGEVELSCLVPR	CADM4_HUMAN			Cell adhesion molecule 4;	4.59	0.34	63.80	-1.21
WCSVRQKGSY	LTHEASGLDEQGEAR	CADM4_HUMAN			Cell adhesion molecule 4;	2.75	0.29	47.80	-3.04
EADGDVPGPR	GEAEGQAEAKGDAPGPR	CGRE1_HUMAN			Cell growth regulator with	2.42	0.15	39.30	-1.53
EAKGDAPGPR	GEAGGQAEAEGDAPGPR	CGRE1_HUMAN			Cell growth regulator with EF hand domain protein	2.17	0.18	76.20	-1.82
LQSYLKGLGR	TEVQLEHLSR	CGRE1_HUMAN			Cell growth regulator with	0.38	0.01	22.70	-1.69
GRQSLLAKSP	LRQETQEAPGPR	CGRE1_HUMAN			Cell growth regulator with	-0.47	0.05	38.60	-2.54
TSDRGFQFVS	SSLPDICYR	CNBP_HUMAN			Cellular nucleic acid-binding protein;	1.18	0.09	43.60	-3.33

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LIPHINKQTS	STPSSLALTSASR	CE170_HUMAN			Centrosomal protein of 170 kDa;	1.35	0.07	35.90	1.07
GKKAEAAASA	LADADADLEER	CHM2A_HUMAN			Charged multivesicular	2.48	0.15	36.20	6.42
IVQVVCKKYR	GFTIPEAFR	CLIC1_HUMAN			Chloride intracellular channel protein 1;	-0.23	0.01	27.50	-4.20
AWEEVRGVFR	VAIQPVNDHAPVQTISR	CSPG4_HUMAN			Chondroitin sulfate proteoglycan 4;	2.42	0.40	34.00	4.91
RSSLSQQQLR	VVSDREEPEAAYR	CSPG4_HUMAN			Chondroitin sulfate	0.68	0.03	23.00	-0.19
DTNLDIRSGD	EVHYHVTAGPR	CSPG4_HUMAN			Chondroitin sulfate	-2.66	0.17	22.60	-1.69
LLLGSRPARG	AGPEPPVLPIR	CHRD_HUMAN			Chordin;	-0.32	0.02	31.10	-3.22
VAVVESMVTA	TEVAPPPPPVEVPIR	CHD4_HUMAN			Chromodomain-helicase-DNA-binding protein 4;	0.74	0.06	37.60	-1.78
VVESMVTATE	VAPPPPPVEVPIR	CHD4_HUMAN			Chromodomain-helicase-	0.51	0.03	51.70	-3.99
ASSPESPVLA	ASPEPWGPSPAASPESR	CHAP1_HUMAN			Chromosome alignment-	0.35	0.02	44.90	-2.73
NQNFYLSKQL	DEASGANDEIVQLR	CTRO_HUMAN			Citron Rho-interacting	0.61	0.06	68.10	-2.19
YNEHITKRVA	SSPAPPEGPSHPR	CTRO_HUMAN			Citron Rho-interacting kinase;	-0.69	0.08	54.40	-2.16
PDLALRMAVR	NNLAGAEELFAR	CLH1_HUMAN			Clathrin heavy chain 1;	2.02	0.12	44.00	-1.72
QESNGPTDSY	AAISQVDRLQSEPESIR	CLCA_HUMAN			Clathrin light chain A;	1.58	0.13	37.70	-4.10
DSYAAISQVD	RLQSEPESIR	CLCA_HUMAN			Clathrin light chain A;	-0.44	0.03	35.80	-2.25
PEFNNTDQID	LYDDVLTATSQPSDDR	CPSF7_HUMAN			Cleavage and polyadenylation	0.20	0.01	59.70	-1.04
NTDQIDLYDD	VLTATSQPSDDR	CPSF7_HUMAN			Cleavage and	-0.55	0.02	37.50	0.30
PSGVTEVVVK	LFDSDPITVTVPVEVSR	CLUS_HUMAN			Clusterin;	5.79	0.66	51.00	-0.95
RMKDQCDKCR	EILSVDCSTNNPSQAKLR	CLUS_HUMAN			Clusterin;	4.94	0.46	41.40	0.81
LDVMQDHFSR	ASSIIDELFQDR	CLUS_HUMAN			Clusterin;	3.34	0.46	56.00	-2.81
NPSQAKLRRE	LDESLQVAER	CLUS_HUMAN			Clusterin;	2.19	0.13	31.90	-1.00

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TNNPSQAKLR	RELDESLQVAER	CLUS_HUMAN			Clusterin;	1.24	0.03	37.00	-2.71
NNPSQAKLRR	ELDESLQVAER	CLUS_HUMAN			Clusterin;	0.13	0.01	51.10	-1.14
VTEVVVKLFD	SDPITVTVPVEVSR	CLUS_HUMAN			Clusterin;	-0.42	0.03	38.70	-2.22
WKMLNTSSLL	EQLNEQFNWVSR	CLUS_HUMAN			Clusterin;	-0.47	0.04	58.90	-1.64
VMQDHFSRAS	SIIDELFQDR	CLUS_HUMAN			Clusterin;	-0.76	0.05	48.10	0.00
DVMQDHFSRA	SSIIDELFQDR	CLUS_HUMAN			Clusterin;	-0.76	0.08	44.30	-3.68
GVTEVVVKLF	DSDPITVTVPVEVSR	CLUS_HUMAN			Clusterin;	-0.96	0.08	35.70	1.94
PSQAKLRREL	DESLQVAER	CLUS_HUMAN			Clusterin;	-1.00	0.04	36.80	0.19
QFNWVSRLAN	LTQGEDQYYLR	CLUS_HUMAN			Clusterin;	-1.00	0.10	46.30	-1.41
SGVTEVVVKL	FDSDPITVTVPVEVSR	CLUS_HUMAN			Clusterin;	-1.49	0.17	42.40	3.73
MSKRSKFALI	TWIGENVSGLQR	COTL1_HUMAN			Coactosin-like protein;	-2.79	0.19	33.60	-1.43
LLLLPGPAGS	EGAAPIAITCFTR	COCH_HUMAN			Cochlin;	5.90	0.43	62.90	-1.32
PKESHAFFTR	EFTGLEPIVSDVIR	COCH_HUMAN			Cochlin;	2.65	0.28	41.20	3.43
EPPVQTAVLT	ASAPAAQAGASQGLHALLEER	C2D1B_HUMAN			Coiled-coil and C2 domain-containing protein	-0.08	0.00	39.30	1.63
PPVQTAVLTA	SAPAAQAGASQGLHALLEER	C2D1B_HUMAN			Coiled-coil and C2 domain-containing protein 1B;	-0.58	0.02	34.60	1.74
LVFGLIWGLM	LLHYTFQQPR	CC126_HUMAN			Coiled-coil domain-containing protein 126;	-0.16	0.01	24.90	0.53
VSRTRRALVE	FESNPEETREPGSPPSVQR	CCD86_HUMAN			Coiled-coil domain-containing protein 86;	0.24	0.01	23.10	-3.21
PPASRAPQMR	AAPRPAPVAQPPAAAPPSAVGSSA	CHCH2_HUMAN	CHCH9_HUMAN		Coiled-coil-helix-coiled-coil-helix domain-	-0.63	0.05	57.70	-8.21
QMRAAPRPAP	VAQPPAAAPPSAVGSSAAAPR	CHCH2_HUMAN	CHCH9_HUMAN		Coiled-coil-helix-coiled-coil-helix domain-	-1.04	0.13	36.30	2.93
MRAAPRPAPV	AQPPAAAPPSAVGSSAAAPR	CHCH2_HUMAN	CHCH9_HUMAN		Coiled-coil-helix-coiled-	-1.25	0.12	28.40	-1.82

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
RGDPGPSGPP	GPPGDDGER	CO5A1_HUMAN			Collagen alpha-1(V) chain;	-4.24	0.00	23.60	-8.24
GRTDPAHDVR	VAVVQYSGTGQQRPER	CO6A1_HUMAN			Collagen alpha-1(VI) chain;	7.22	0.94	28.30	-1.66
QLLPPSPNNR	IALVITDGR	CO6A1_HUMAN			Collagen alpha-1(VI)	6.88	0.93	41.20	-3.24
FTGEALQYTR	DQLLPPSPNNR	CO6A1_HUMAN			Collagen alpha-1(VI)	3.55	0.10	26.00	-3.36
VNEAKHLGVK	VFSVAITPDHLEPR	CO6A1_HUMAN			Collagen alpha-1(VI)	3.34	0.28	40.20	-4.59
PHIRVLVTGK	TAEYDVAYGESHLFR	CO6A1_HUMAN			Collagen alpha-1(VI)	1.57	0.07	45.00	1.29
NGTKGYPGLK	GDEGEAGDPGDDNNDIAPR	CO6A1_HUMAN			Collagen alpha-1(VI) chain;	1.41	0.22	79.20	2.37
SAVDAMDFIN	DATDVNDALGYVTR	CO6A1_HUMAN			Collagen alpha-1(VI) chain;	0.45	0.04	76.80	-3.31
LASAVDAMDF	INDATDVNDALGYVTR	CO6A1_HUMAN			Collagen alpha-1(VI)	0.34	0.04	63.60	-0.45
FECQPARGPP	GLRGDPGFEGER	CO6A1_HUMAN			Collagen alpha-1(VI)	-0.02	0.00	33.30	-1.36
IKNNVEQVCC	SFECQPAR	CO6A1_HUMAN			Collagen alpha-1(VI)	-0.06	0.00	26.90	-0.68
VWNAGALHYS	DEVEIIQGLTR	CO6A1_HUMAN			Collagen alpha-1(VI)	-0.18	0.01	48.30	1.76
NEAKHLGVKV	FSVAITPDHLEPR	CO6A1_HUMAN			Collagen alpha-1(VI)	-0.20	0.01	24.30	-3.43
DAMDFINDAT	DVNDALGYVTR	CO6A1_HUMAN			Collagen alpha-1(VI) chain;	-0.23	0.02	59.30	-7.71
WNAGALHYSD	EVEIIQGLTR	CO6A1_HUMAN			Collagen alpha-1(VI)	-1.66	0.11	44.50	-4.44
ESGTRRGIPK	VIVVITDGR	COEA1_HUMAN			Collagen alpha-1(XIV) chain;	10.36	0.00	32.90	-4.10
LTESYCETWR	TEAPSATGQASSLLGGR	COIA1_HUMAN			Collagen alpha-1(XVIII) chain;	5.70	0.93	79.10	-1.10
QLEARTPLPR	GTDNEVAALQPPVVQLHDSNPYP	COIA1_HUMAN			Collagen alpha-1(XVIII)	4.26	0.52	44.50	0.15
GTFRAFLSSR	LQDLYSIVR	COIA1_HUMAN			Collagen alpha-1(XVIII)	4.01	0.33	30.50	-1.85
DWYIWQVIDQ	YSIPQVSIR	COMA1_HUMAN			Collagen alpha-1(XXII) chain;	4.11	0.28	26.70	0.92
PGFAGPPGPP	GPVGLPGEIGIR	CO9A2_HUMAN			Collagen alpha-2(IX)	-0.39	0.02	29.60	4.58
WKLLEVPEGR	TNFDNDIALVR	C1S_HUMAN			Complement C1s subcomponent;	1.93	0.08	47.90	-2.45
QVPDTESETR	ILLQGTPVAQMTEDAVDAER	CO3_HUMAN			Complement C3;	6.64	0.57	102.80	-1.83

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
ARASHLGLAR	SNLDEDIIAEENIVSR	CO3_HUMAN			Complement C3;	6.14	0.81	76.60	-3.79
SDEVQVGQQR	TFISPIKCR	CO3_HUMAN			Complement C3;	4.90	0.67	32.00	-1.10
RISLPESLKR	IPIEDGSGEVVLSR	CO3_HUMAN			Complement C3;	4.41	0.47	40.50	-1.00
RTLDPERLGR	EGVQKEDIPPADLSDQVPDTESET	CO3_HUMAN			Complement C3;	4.09	0.10	41.20	0.36
KPLSITVRTK	KQELSEAEQATR	CO3_HUMAN			Complement C3;	2.86	0.23	34.60	-3.38
THLPLALGSP	MYSIITPNILR	CO3_HUMAN			Complement C3;	2.76	0.39	36.60	-1.78
KKVEGTAFVI	FGIQDGEQR	CO3_HUMAN			Complement C3;	2.10	0.11	36.00	-2.50
LLTHLPLALG	SPMYSIITPNILR	CO3_HUMAN			Complement C3;	2.03	0.08	69.10	0.19
YIMAIEQTIK	SGSDEVQVGQQR	CO3_HUMAN			Complement C3;	1.83	0.17	55.00	-4.10
HHFISDGVRK	SLKVVPEGIR	CO3_HUMAN			Complement C3;	1.79	0.14	28.50	-2.86
ATRTMQALPY	STVGNSNNYLHLSVLR	CO3_HUMAN			Complement C3;	1.68	0.08	31.40	-2.55
QATRTMQALP	YSTVGNSNNYLHLSVLR	CO3_HUMAN			Complement C3;	1.65	0.12	29.60	-3.25
VGKSLYVSAT	VILHSGSDMVQAER	CO3_HUMAN			Complement C3;	1.37	0.06	44.20	-2.74
RTELRPGETL	NVNFLLR	CO3_HUMAN			Complement C3;	1.23	0.09	23.80	-0.88
VPDTESETRI	LLQGTPVAQMTEDAVDAER	CO3_HUMAN			Complement C3;	1.14	0.04	52.70	9.02
SLPESLKRIP	IEDGSGEVVLSR	CO3_HUMAN			Complement C3;	1.08	0.08	38.80	-5.12
QALPYSTVGN	SNNYLHLSVLR	CO3_HUMAN			Complement C3;	1.07	0.05	38.70	-3.57
EGVQKEDIPP	ADLSDQVPDTESETR	CO3_HUMAN			Complement C3;	0.90	0.07	57.40	-2.19
PLSITVRTKK	QELSEAEQATR	CO3_HUMAN			Complement C3;	0.90	0.05	36.00	-1.63
EVTVMQDFFI	DLRLPYSVVR	CO3_HUMAN			Complement C3;	0.62	0.04	32.30	-2.81
GVQKEDIPPA	DLSDQVPDTESETR	CO3_HUMAN			Complement C3;	0.56	0.04	30.80	2.47
LYGKKVEGTA	FVIFGIQDGEQR	CO3_HUMAN			Complement C3;	0.47	0.03	30.80	-4.71
SHLGLARSNL	DEDIIAEENIVSR	CO3_HUMAN			Complement C3;	0.32	0.02	51.60	-4.44

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LLALLQLKDF	DFVPPVVR	CO3_HUMAN			Complement C3;	0.32	0.03	22.70	4.05
QHARASHLGL	ARSNLDEDIIAEENIVSR	CO3_HUMAN			Complement C3;	0.16	0.01	42.80	2.03
VLLCLPAVWG	DCGLPPDVPNAQPALEGR	DAF_HUMAN			Complement decay-accelerating factor;	0.26	0.00	81.40	0.57
GTRKVGSQYR	LEDSVTYHCSR	CFAB_HUMAN			Complement factor B;	1.88	0.15	29.50	-1.36
RLMCAESNRR	DSCKGDSGGPLVCGGVLEGVVTS	CFAD_HUMAN			Complement factor D;	3.69	0.16	72.40	-0.96
DDQALGPELT	APAPEPPAEEPR	COG8_HUMAN			Conserved oligomeric	0.29	0.07	29.90	-0.08
VATGPYRAFR	VAAASGHCGAFSGSDSSR	F120A_HUMAN			Constitutive coactivator of PPAR-gamma-like protein	-0.44	0.05	47.00	-1.08
PTQTWSPVGA	GNPPDCDAPLASALPR	CNTP3_HUMAN			Contactin-associated	0.56	0.02	40.40	-3.81
NRGLDTGRRR	AAPEASGTPSSDAVSR	COR1A_HUMAN			Coronin-1A;	0.11	0.02	47.90	1.11
LEAEEWVSGR	DADPILISLR	COR1B_HUMAN			Coronin-1B;	5.71	0.69	48.10	-2.01
APGSSHLGAP	ASTTTAADATPSGSLAR	COR1B_HUMAN			Coronin-1B;	0.93	0.10	68.30	-0.68
RRNVLSDSRP	AMAPGSSHLGAPASTTTAADATPS	COR1B_HUMAN			Coronin-1B;	0.47	0.04	60.70	-0.67
AMAPGSSHLG	APASTTTAADATPSGSLAR	COR1B_HUMAN			Coronin-1B;	-0.04	0.00	68.10	-1.91
GDEESYEVFK	DLFDPIIEDR	KCRB_HUMAN			Creatine kinase B-type;	4.55	0.43	44.30	-3.09
VLKRLRLQKR	GTGGVDTAAVGGVFDVSNADR	KCRB_HUMAN			Creatine kinase B-type;	3.97	0.36	80.10	-2.86
EVLKRLRLQK	RGTGGVDTAAVGGVFDVSNADR	KCRB_HUMAN			Creatine kinase B-type;	3.36	0.36	76.80	2.79
ESYEVFKDLF	DPIIEDR	KCRB_HUMAN			Creatine kinase B-type;	0.52	0.01	29.60	-3.16
TSTIAPGVVM	ASSPALPTQPAEEAAR	CREB1_HUMAN			Cyclic AMP-responsive element-binding protein 1;	0.44	0.04	29.50	-1.41

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TTGQVVAMKK	IRLESEEEGVPSTAIR	CDK1_HUMAN			Cyclin-dependent kinase 1;	0.31	0.02	33.90	0.05
IQHQDMRILE	LTPEPDRPR	CDK13_HUMAN			Cyclin-dependent kinase	0.20	0.02	27.20	-1.25
VQEGHTAVVS	FLAAESDLHRR	CDN2D_HUMAN			Cyclin-dependent kinase 4 inhibitor D;	5.59	0.59	31.70	-4.99
MMC	GAPSATQPATAETQHIADQVR	CYTB_HUMAN			Cystatin-B;	0.44	0.04	33.40	-0.32
MMCG	APSATQPATAETQHIADQVR	CYTB_HUMAN			Cystatin-B;	0.31	0.03	28.10	-2.82
AGSSPGKPPR	LVGGPMDASVEEEGVR	CYTC_HUMAN			Cystatin-C;	6.98	1.26	61.70	-9.50
AGSSPGKPPR	LVGGPMDASVEEEGVRR	CYTC_HUMAN			Cystatin-C;	5.58	0.35	35.80	-7.37
AAGSSPGKPP	RLVGGPMDASVEEEGVR	CYTC_HUMAN			Cystatin-C;	2.11	0.11	54.00	-3.39
ARKQIVAGVN	YFLDVELGR	CYTC_HUMAN			Cystatin-C;	-0.86	0.05	26.50	-2.54
RKQIVAGVNY	FLDVELGR	CYTC_HUMAN			Cystatin-C;	-1.00	0.06	26.40	-6.61
CKPVFGVDCR	TVECPPVQQTACPPDSYETQVR	CRIM1_HUMAN			Cysteine-rich motor	4.90	0.43	67.40	-3.01
GFKRDHNGCR	TCQCINTEELCSER	CRIM1_HUMAN			Cysteine-rich motor neuron 1 protein;	1.90	0.21	59.10	-5.85
LLLARSGTRA	LVCLPCDESKCEEPR	CRIM1_HUMAN			Cysteine-rich motor neuron 1 protein;	0.37	0.01	40.90	-2.60
QGGVAICFTA	QCGEINCER	CRIM1_HUMAN			Cysteine-rich motor	-1.25	0.03	20.30	0.50
CRTVECPPVQ	QTACPPDSYETQVR	CRIM1_HUMAN			Cysteine-rich motor neuron 1 protein;	-1.34	0.07	57.30	-0.30
GSYIYEKPLA	EGPQVTGPIEVPAAR	CRIP2_HUMAN			Cysteine-rich protein 2;	2.61	0.15	59.50	4.88
AGSYIYEKPL	AEGPQVTGPIEVPAAR	CRIP2_HUMAN			Cysteine-rich protein 2;	2.40	0.16	59.70	0.68
TYVGSLRNGV	QSESLGTPR	CRLD2_HUMAN			Cysteine-rich secretory	4.75	0.44	28.90	-0.80
PQPQDLEFTK	LPNGLVIASLENYSPVSR	QCR2_HUMAN			Cytochrome b-c1 complex subunit 2, mitochondrial;	6.52	1.26	30.80	0.56

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EDEQKMLTES	GDPEEEEEEEEELVDPLTTVR	QCR6_HUMAN			Cytochrome b-c1 complex subunit 6, mitochondrial;	0.29	0.03	89.80	2.06
RIAREEIKKK	ILYEGTHLDPER	FA36A_HUMAN			Cytochrome c oxidase	0.38	0.03	37.70	-3.65
PAVAIQSVRC	YSHGSQETDEEFDAR	COX5A_HUMAN			Cytochrome c oxidase	0.48	0.06	57.30	-0.28
AVAIQSVRCY	SHGSQETDEEFDAR	COX5A_HUMAN			Cytochrome c oxidase	0.13	0.01	63.70	-2.01
PSGAAAMRSM	ASGGGVPTDEEQATGLER	COX5B_HUMAN			Cytochrome c oxidase	0.06	0.00	66.20	1.33
TEEEKQQILH	SEEFLSFFDHSTR	DC1I2_HUMAN			Cytoplasmic dynein 1 intermediate chain 2;	1.04	0.06	29.30	-1.72
VPPPMSPSSK	SVSTPSEAGSQDSGDGAVGSR	DC1I2_HUMAN			Cytoplasmic dynein 1	-0.66	0.05	39.30	-3.42
NAAEKLQVVG	RAGTGVDNVDLEAATR	SERA_HUMAN			D-3-phosphoglycerate	1.28	0.08	36.40	-1.02
EHKALVSHNG	SLINVGSLLQR	K1967_HUMAN			DBIRD complex subunit KIAA1967;	0.24	0.02	40.30	-4.21
WKLDVATDNF	FQNPELYIR	DCNL1_HUMAN			DCN1-like protein 1;	0.68	0.03	24.00	-2.40
VSQLFELEIE	ALPLDTPSSVETDISSSR	DAXX_HUMAN			Death domain-associated protein 6;	1.84	0.12	63.20	-2.21
VSSAGSLERD	STEVEISTGER	DOCK7_HUMAN			Dedicator of cytokinesis	-0.12	0.01	29.80	-1.29
GAGPRGSSLA	NPVPAAPLSAPGPCAAQPCR	DNER_HUMAN			Delta and Notch-like	0.66	0.05	42.20	-2.13
YPGLSISLRL	TGSSAQEEASGVALGEAPDHSYES	ECH1_HUMAN			Delta(3,5)-Delta(2,4)-	-1.39	0.18	81.90	-0.19
SAESSGQKSF	AANGIQAHPESSTGSDAR	TDIF2_HUMAN			Deoxynucleotidyltransferase terminal-interacting	1.18	0.09	32.90	-6.15
ESSGGWRDGR	ALINSPEGAVGR	DNS2A_HUMAN			Deoxyribonuclease-2-alpha;	2.67	0.27	43.40	-0.16
YERIVSRLRR	FGTVLTEHVAAAELGAR	RCL_HUMAN			Deoxyribonucleoside 5'-	3.27	0.15	35.00	-2.03
DRIAQLICER	IFYPEIEEVQALDDTER	DUT_HUMAN			Deoxyuridine 5'-	2.49	0.09	53.30	-6.96
ETPAISPSKR	ARPAEVGGMQLR	DUT_HUMAN			Deoxyuridine 5'-	0.40	0.03	55.80	-0.53
LLICFNVGSG	LHLQVLSTR	DSG2_HUMAN			Desmoglein-2;	1.58	0.09	30.90	-3.29
KHPHLVRQKR	AWITAPVALR	DSG2_HUMAN			Desmoglein-2;	0.86	0.05	37.30	-2.65
AIKKKFQGIK	HECQANGPEDLNR	DEST_HUMAN			Destrin;	1.34	0.06	31.30	-2.74
ALLALRLAAG	TDCPCPEPELCRPIR	DIAC_HUMAN			Di-N-acetylchitobiase;	-0.60	0.05	31.00	-2.53
VTIGFGVTLC	AVPIAQKSEPHSLSSEALMR	DBLOH_HUMAN			Diablo homolog, mitochondrial;	0.24	0.02	44.10	-1.17

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
GSHGLEIFQR	CYCGEGLSCR	DKK1_HUMAN			Dickkopf-related protein 1;	9.64	1.68	48.20	-2.40
KGQEGSVCLR	SSDCASGLCCAR	DKK1_HUMAN			Dickkopf-related protein 1;	5.89	0.30	59.80	-2.11
TLSSKMYHTK	GQEGSVCLR	DKK1_HUMAN			Dickkopf-related protein 1;	4.30	0.23	27.00	-2.51
EIEETITESF	GNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein	1.08	0.06	25.10	-2.74
NYQPYPCAED	EECGTDEYCASPTR	DKK1_HUMAN			Dickkopf-related protein 1;	1.07	0.12	68.30	2.58
GEVCTKQRKK	GSHGLEIFQR	DKK1_HUMAN	DKK2_HUMAN		Dickkopf-related protein	0.81	0.06	39.20	-1.19
TDEYCASPTR	GGDAGVQICLACR	DKK1_HUMAN			Dickkopf-related protein 1;	0.79	0.09	63.60	-0.36
TIDNYQPYPC	AEDEECGTDEYCASPTR	DKK1_HUMAN			Dickkopf-related protein 1;	0.68	0.09	90.80	-3.46
HTKGQEGSVC	LRSSDCASGLCCAR	DKK1_HUMAN			Dickkopf-related protein 1;	0.67	0.08	64.40	-1.03
DNYQPYPCAE	DEECGTDEYCASPTR	DKK1_HUMAN			Dickkopf-related protein 1;	0.61	0.08	77.30	-2.74
NHFRGEIEET	ITESFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein	0.53	0.06	33.70	-1.71
FRGEIEETIT	ESFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein	0.52	0.05	32.10	-4.71
PGILYPGGNK	YQTIDNYQPYPCAEDEECGTDEYC	DKK1_HUMAN			Dickkopf-related protein	0.47	0.04	57.60	-1.01
PYPCAEDEEC	GTDEYCASPTR	DKK1_HUMAN			Dickkopf-related protein 1;	0.40	0.04	47.50	-4.57
LYPGGNKYQT	IDNYQPYPCAEDEECGTDEYCASP	DKK1_HUMAN			Dickkopf-related protein	0.35	0.04	39.10	-0.60
CVSSDQNHFR	GEIEETITESFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein	0.32	0.03	65.20	-3.56
SDQNHFRGEI	EETITESFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein	-0.32	0.03	33.90	-4.15
DQNHFRGEIE	ETITESFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein	-0.34	0.03	24.20	-3.88
RFFRTTAVCK	DDLVTVKTPAFAESVTEGDVR	ODO2_HUMAN			Dihydrolipoyllysine-residue	0.67	0.03	69.30	1.13
MAP	VLSKDSADIESILALNPR	DPYD_HUMAN			Dihydropyrimidine dehydrogenase	1.97	0.13	43.60	-1.55

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
APLTAEIQQK	ILHLPTSWDWR	CATC_HUMAN			Dipeptidyl peptidase 1;	0.44	0.00	29.80	-1.51
MATTGTP	TADRGDAAATDDPAAR	DPP9_HUMAN			Dipeptidyl peptidase 9;	2.10	0.11	46.80	-0.37
LHQKHQRAKR	AVSHEDQFLR	ADA10_HUMAN			Disintegrin and	1.33	0.09	32.00	-3.90
LLLSWAAGMG	GQYGNPLNKYIR	ADA10_HUMAN			Disintegrin and	1.19	0.10	28.40	-2.30
GRFEGFIQTR	GGTFYVEPAER	ADA10_HUMAN			Disintegrin and	0.69	0.03	42.90	-2.06
LVWYQPDGTR	VVSEGHTLENCCYQGR	ADA15_HUMAN			Disintegrin and metalloproteinase domain-containing protein 15;	1.55	0.15	43.60	0.93
IEAGQYNSHL	YGTSVQSVR	DLG1_HUMAN	DLG2_HUMAN	DLG4_HUMAN	Disks large homolog 1;	1.85	0.08	27.70	7.12
KRRRVTSRER	VARPLPAEEPER	DNMT1_HUMAN			DNA (cytosine-5)-	1.07	0.06	28.80	-3.66
CVPALELTRK	MLTYDRRSEPQVGER	DPOLZ_HUMAN			DNA polymerase zeta catalytic subunit;	3.28	0.19	27.30	-0.70
DAYEAEGLAL	DDEDVEELTASQR	MCM2_HUMAN			DNA replication licensing factor MCM2;	0.11	0.01	48.10	-3.06
AGRGLGRMRR	GLLYDSDEEDEERPAR	MCM2_HUMAN			DNA replication licensing factor MCM2;	-0.16	0.02	47.40	-0.83
EEDQGIYQSK	VRELISDNQYR	MCM3_HUMAN			DNA replication licensing factor MCM3;	-0.29	0.03	41.90	-1.12
GRRRGPPRNY	AGEEEEEGSGSSEGFDPPATDR	DBPA_HUMAN			DNA-binding protein A;	0.38	0.02	35.40	-3.55
MPKLKPVELR	ELLNPVVEFVSHPSTTCR	PRKDC_HUMAN			DNA-dependent protein kinase catalytic subunit;	0.13	0.00	39.60	0.19
ARWPVAGQIR	ATQQQHDFTLTQTADGR	PRKDC_HUMAN			DNA-dependent protein kinase catalytic subunit;	-0.73	0.10	40.10	-0.41
YTIDSDWRFR	STVLTPMFVETQASQGTLQTR	PRKDC_HUMAN			DNA-dependent protein	-0.73	0.05	48.00	2.57
MEPD	GTYEPGFVGIR	RPB9_HUMAN			DNA-directed RNA polymerase II subunit	-0.08	0.01	31.20	-2.76
M	GKDYYQTLGLAR	DNJB1_HUMAN			DnaJ homolog subfamily	0.34	0.03	37.20	-5.64

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
M	VDYYEVLGVQR	DNJB6_HUMAN			DnaJ homolog subfamily B member 6;	-0.14	0.01	36.00	-2.18
QQERQRLGQR	QPPPSEPTQGPEIVPR	DNJC4_HUMAN			DnaJ homolog subfamily C member 4;	-2.34	0.12	31.10	-2.38
GTWAPAPGSA	SSEAPPLINEDVKR	RPN1_HUMAN			Dolichyl-diphosphooligosaccharide--protein	4.39	0.24	29.90	-3.51
AAPGEFRAIM	EMPSFYSHGLPR	DSRAD_HUMAN			Double-stranded RNA-	0.21	0.01	27.90	-1.10
NLAKNIGLTK	ARDINAVLIDMER	DSRAD_HUMAN			Double-stranded RNA-	0.00	0.00	38.40	0.64
RMAPTPIPTR	SPSDSSTASTPVAEQIER	DREB_HUMAN			Drebrin;	4.85	0.70	55.10	1.85
RRMAPTPIPT	RSPSDSSTASTPVAEQIER	DREB_HUMAN			Drebrin;	1.77	0.12	48.40	-0.68
ETRAAAPQAW	AGPMEEPPQAQAPPR	DREB_HUMAN			Drebrin;	1.46	0.07	41.50	-6.54
VLAENNQLLK	EADDVGPR	DYH5_HUMAN			Dynein heavy chain 5, axonemal;	-3.25	0.00	24.00	-9.96
LTMKAKSTVR	DIDPQNDLTFLR	DLRB1_HUMAN	DLRB2_HUMAN		Dynein light chain	2.90	0.22	37.10	0.27
FSEVELHNMK	LVPVVNNR	DAG1_HUMAN			Dystroglycan;	3.11	0.20	24.80	-1.81
VENGALLSWK	LGCSLNQNSVPDIHGVEAPAR	DAG1_HUMAN			Dystroglycan;	2.12	0.20	72.40	1.02
WKLGCSLNQN	SVPDIHGVEAPAR	DAG1_HUMAN			Dystroglycan;	-0.16	0.01	36.50	-3.61
HIPQTSSVFS	IEVYPEDHSELQSVR	DAG1_HUMAN			Dystroglycan;	-0.18	0.02	25.60	-1.14
GALLSWKLGC	SLNQNSVPDIHGVEAPAR	DAG1_HUMAN			Dystroglycan;	-0.27	0.02	51.60	-0.62
IPQTSSVFSI	EVYPEDHSELQSVR	DAG1_HUMAN			Dystroglycan;	-1.25	0.06	36.30	-4.00
DYLPAMRRRR	SSDPLGDTASNLGSAVDELMR	HUWE1_HUMAN			E3 ubiquitin-protein ligase HUWE1;	-0.08	0.01	43.40	-1.85
DADARVAITI	YCQASEEFLNGR	MGRN1_HUMAN			E3 ubiquitin-protein ligase MGRN1;	-2.79	0.19	22.90	-1.46

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
VEQFLQADLA	REPPADVWTPPAR	TRI25_HUMAN			E3 ubiquitin/ISG15 ligase	0.14	0.00	33.50	-0.98
QLQQEYTEMK	ALLDASETTSTR	TRI25_HUMAN			E3 ubiquitin/ISG15 ligase	-0.76	0.06	52.70	-3.46
HSNDQSPQIR	ASPSPQPSSQPLQIHR	EMAL4_HUMAN			Echinoderm microtubule-	0.31	0.03	31.10	-5.55
PKPEPEPPAR	APTASADAELSAQLSR	EFHD1_HUMAN			EF-hand domain-containing protein D1;	-2.08	0.26	38.50	-9.30
DCELSAKLLR	RADLNQGIGEPQSPSR	EFHD2_HUMAN			EF-hand domain-containing protein D2;	0.44	0.03	44.80	2.21
GGGAGTYRVG	SAQPSPPDDLDAGGLAQR	EH1L1_HUMAN			EH domain-binding	3.32	0.23	30.40	2.08
APPAGLGSAR	ETQAQACPQEGTEAHGAR	EH1L1_HUMAN			EH domain-binding	1.48	0.15	56.90	-0.56
TPGTETEVLG	TQKTEAGGSGVLQTR	EH1L1_HUMAN			EH domain-binding	0.96	0.11	34.70	-1.26
IEVGLLGVLG	IETGAAEGAILGTQEIASR	EH1L1_HUMAN			EH domain-binding	0.87	0.11	36.00	4.38
RPPETSPEMR	SSRQPAQDTAPTPAPR	EH1L1_HUMAN			EH domain-binding protein 1-like protein 1;	-0.08	0.01	28.40	-2.86
VKQLIVGVNK	MDSTEPPYSQKR	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	4.77	0.35	33.30	-0.27
RPTDKPLRLP	LQDVYKIGGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha	1.19	0.07	29.20	-1.97
DKPLRLPLQD	VYKIGGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha 1;	0.76	0.04	25.10	-4.51
TDKPLRLPLQ	DVYKIGGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha	0.73	0.04	32.50	-6.29
RLPLQDVYKI	GGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha	0.55	0.04	37.50	-3.40
LRLPLQDVYK	IGGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha 1;	-0.52	0.02	34.60	-3.30
VDMVPGKPMC	VESFSDYPPLGR	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	-0.58	0.01	27.00	-1.85
ISLWKFETSK	YYVTIIDAPGHR	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	-0.69	0.02	30.10	-4.10
SLWKFETSKY	YVTIIDAPGHR	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha	-0.93	0.07	27.30	-3.91
LWKFETSKYY	VTIIDAPGHR	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha	-3.25	0.31	22.10	-2.15
VKQLIVGVNK	MDSTEPAYSEKR	EF1A2_HUMAN			Elongation factor 1-alpha 2;	2.09	0.08	27.70	-2.72
TDSKDDDDID	LFGSDDEEESEEAKR	EF1B_HUMAN			Elongation factor 1-beta;	-0.42	0.04	33.10	-1.89
VLEKSSPGHR	ATAPQTQHVSPMR	EF1D_HUMAN			Elongation factor 1-delta;	2.71	0.22	30.30	-2.95

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
SGDHGELVVR	IASLEVENQSLR	EF1D_HUMAN			Elongation factor 1-delta;	1.76	0.24	58.80	-1.01
VILRDIARAR	ENIQKSLAGSSGPGASSGTSGDHG	EF1D_HUMAN			Elongation factor 1-delta;	0.75	0.07	48.50	-0.17
RENIQKSLAG	SSGPGASSGTSGDHGELVVR	EF1D_HUMAN			Elongation factor 1-delta;	0.67	0.07	45.70	-1.74
RARENIQKSL	AGSSGPGASSGTSGDHGELVVR	EF1D_HUMAN			Elongation factor 1-delta;	0.61	0.06	75.70	-1.44
ARARENIQKS	LAGSSGPGASSGTSGDHGELVVR	EF1D_HUMAN			Elongation factor 1-delta;	0.61	0.06	66.10	-1.22
YEQMNGPVAG	ASRQENGASVILR	EF1D_HUMAN			Elongation factor 1-delta;	0.20	0.01	28.00	-1.60
IARARENIQK	SLAGSSGPGASSGTSGDHGELVVR	EF1D_HUMAN			Elongation factor 1-delta;	-0.79	0.08	73.90	-2.03
ARENIQKSLA	GSSGPGASSGTSGDHGELVVR	EF1D_HUMAN			Elongation factor 1-delta;	-1.34	0.14	40.20	1.54
DYESYTWRKL	DPGSEETQTLVR	EF1G_HUMAN			Elongation factor 1-gamma;	-0.93	0.07	56.40	-1.02
VVAGFQWATK	EGALCEENMR	EF2_HUMAN			Elongation factor 2;	2.99	0.27	31.80	0.73
M	VNFTVDQIR	EF2_HUMAN			Elongation factor 2;	0.48	0.07	35.60	-3.73
RALLELQLEP	EELYQTFQR	EF2_HUMAN			Elongation factor 2;	-9.97	0.00	20.80	-0.56
LAEGGGAKFK	KYEEIDNAPEER	EFTU_HUMAN			Elongation factor Tu,	0.11	0.01	36.40	-3.58
SCSLSPTSLA	ETVHCDLQPVGPER	EGLN_HUMAN			Endoglin;	0.64	0.06	32.70	-4.62
MMKREYRGQR	SVKALADYIR	ERP44_HUMAN			Endoplasmic reticulum	0.72	0.03	24.70	-2.93
VLLTFGSVRA	DDEVDVDGTVEEDLGKSR	ENPL_HUMAN			Endoplasmin;	1.32	0.12	51.80	-2.83
GLVRLVHQER	TLAFPLTIR	EPCR_HUMAN			Endothelial protein C	1.23	0.08	28.20	-2.62
ILLLSGWAFC	SQDASDGLQR	EPCR_HUMAN			Endothelial protein C	0.21	0.00	43.70	-1.54
VYFCHLDIIW	VNTPEHVVPYGLGSPR	EDN1_HUMAN			Endothelin-1;	-1.08	0.05	33.80	-1.19
LAAGLVACLA	ALGIQYQTR	ECE1_HUMAN			Endothelin-converting	2.69	0.11	36.40	-2.87
TFGESRPELG	SEGLGSAAHGSQPDLR	EDC4_HUMAN			Enhancer of mRNA-decapping protein 4;	1.50	0.08	30.50	-2.35
PVRCPAWRPF	ASGANFEYIIAEKR	ECHM_HUMAN			Enoyl-CoA hydratase,	0.87	0.09	35.40	-4.00

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
QAHDNPQEKR	LAADDPEVR	EFNA1_HUMAN			Ephrin-A1;	3.50	0.19	30.00	-0.39
QPQRHFRVER	SQPVSQPLTYESGPDEVR	ES8L2_HUMAN			Epidermal growth factor receptor kinase substrate 8	0.61	0.05	40.60	-1.14
AQPQRHFRVE	RSQPVSQPLTYESGPDEVR	ES8L2_HUMAN			Epidermal growth factor	0.53	0.06	49.40	1.61
LRRLLQEREL	VEPLTPSGEAPNQALLR	EGFR_HUMAN			Epidermal growth factor	1.79	0.16	42.90	-0.44
VACIDRNGLQ	SCPIKEDSFLQR	EGFR_HUMAN			Epidermal growth factor	0.79	0.08	23.90	-3.84
ATNIKHFKNC	TSISGDLHILPVAFR	EGFR_HUMAN			Epidermal growth factor receptor;	-0.02	0.00	34.00	-0.12
QQCSGRCRGK	SPSDCCHNQCAAGCTGPR	EGFR_HUMAN			Epidermal growth factor	-0.52	0.06	24.30	-0.14
GRCRCPAGWR	GDTCQSDVDECSAR	EGFL7_HUMAN			Epidermal growth factor-like protein 7;	1.58	0.05	55.80	0.37
RPGRRVCAVR	AHGDPVSESFVQR	EGFL7_HUMAN			Epidermal growth factor-like protein 7;	1.12	0.12	44.20	-0.82
RYACCPGWKR	TSGLPGACGAAICQPPCR	EGFL7_HUMAN			Epidermal growth factor-like protein 7;	1.07	0.11	95.60	0.79
PRYACCPGWK	RTSGLPGACGAAICQPPCR	EGFL7_HUMAN			Epidermal growth factor-like protein 7;	1.05	0.08	66.90	-0.87
QPGRCRCPAG	WRGDTCQSDVDECSAR	EGFL7_HUMAN			Epidermal growth factor-like protein 7;	0.79	0.10	40.70	-1.12
DPVSESFVQR	VYQPFLTTCDGHR	EGFL7_HUMAN			Epidermal growth factor-like protein 7;	0.34	0.02	42.20	-3.20
PVSESFVQRV	YQPFLTTCDGHR	EGFL7_HUMAN			Epidermal growth factor-	-0.32	0.02	35.10	-1.57
VRGSLAEAVG	SPPPAATPTPTPPTR	EPN1_HUMAN			Epsin-1;	1.64	0.05	44.70	-0.07
AVWLLSSGHG	EEQPPETAAQR	ERO1A_HUMAN			ERO1-like protein alpha;	0.32	0.01	52.60	-3.18
EKNRETWYLS	WALDTNQEER	ERF3A_HUMAN	ERF3B_HUMAN		Eukaryotic peptide chain release factor GTP-	-0.14	0.01	26.30	-1.93
GVFNVQMEPK	VVTDTDETELAR	IF2A_HUMAN			Eukaryotic translation initiation factor 2 subunit	-0.16	0.02	47.60	-1.23
AKKAAKQEAR	SDKSPDLAPTPAPQSTPR	EIF2A_HUMAN			Eukaryotic translation initiation factor 2A;	1.20	0.10	42.10	6.71
M	APSTPLLTVR	EIF2A_HUMAN			Eukaryotic translation initiation factor 2A;	-0.27	0.02	16.80	-2.75
GEVHQAREDK	SLSEAPEDTSTR	EIF2D_HUMAN			Eukaryotic translation	-1.44	0.04	28.60	-0.15

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
PAAEELPGSH	AEPPVPAQGEAPGEQAR	EIF3B_HUMAN			Eukaryotic translation	0.91	0.08	63.30	-2.25
MQDAEN	VAVPEAAEER	EIF3B_HUMAN			Eukaryotic translation initiation factor 3 subunit	-0.18	0.01	33.40	-3.00
AKKKHDRKSK	RLDEEEEDNEGGEWER	EIF3C_HUMAN			Eukaryotic translation	-0.39	0.03	53.40	-4.68
LAKETFGVNN	AVYGIDAMNPSSR	EIF3J_HUMAN			Eukaryotic translation initiation factor 3 subunit	0.23	0.01	56.40	-3.05
FSKEVEERSR	ERPSQPEGLR	IF4G1_HUMAN			Eukaryotic translation	1.59	0.11	31.90	2.67
TGVAPTPVLM	NQPPQIAPKR	IF4G1_HUMAN			Eukaryotic translation	1.31	0.12	19.50	-0.98
SSASTSQSTR	AASIFGGAKPVDTAAR	IF4B_HUMAN			Eukaryotic translation	0.71	0.08	29.10	-2.50
GFGYAEFEDL	DSLLSALSLNEESLGNRR	IF4B_HUMAN			Eukaryotic translation	0.49	0.03	31.60	-0.85
VLGDGVQLPP	GDYSTTPGGTLFSTTPGGTR	4EBP1_HUMAN			Eukaryotic translation	-1.25	0.12	54.50	0.20
SRFRDGPPLR	GSNMDFREPTEEER	IF4H_HUMAN			Eukaryotic translation	1.28	0.07	27.00	-1.80
KPRTVATPLN	QVANPNSAIFGGARPR	IF4H_HUMAN			Eukaryotic translation initiation factor 4H;	0.86	0.07	28.60	-0.53
VEFDEVDSLK	EALTYDGALLGDR	IF4H_HUMAN			Eukaryotic translation	0.02	0.00	47.70	-0.35
RMDEISDHAK	VLTLSDDLER	IF5_HUMAN			Eukaryotic translation initiation factor 5;	0.04	0.00	26.80	-1.92
IKRNDFQLIG	IQDGYLSLLQDSGEVR	IF5A1_HUMAN			Eukaryotic translation initiation factor 5A-1;	1.43	0.08	76.50	0.82
NDFQLIGIQD	GYLSLLQDSGEVR	IF5A1_HUMAN			Eukaryotic translation initiation factor 5A-1;	1.07	0.07	59.50	-0.82
KRNDFQLIGI	QDGYLSLLQDSGEVR	IF5A1_HUMAN			Eukaryotic translation initiation factor 5A-1;	-0.29	0.03	65.40	2.16
MADDLD	FETGDAGASATFPMQCSALR	IF5A1_HUMAN	IF5AL_HUMAN		Eukaryotic translation	-0.55	0.03	98.30	-2.09
ADDLDFETGD	AGASATFPMQCSALR	IF5A1_HUMAN	IF5AL_HUMAN		Eukaryotic translation initiation factor 5A-1;	-0.63	0.02	66.00	-0.25
TTDQELQHIR	NSLPDTVQIR	IF6_HUMAN			Eukaryotic translation initiation factor 6;	1.62	0.12	37.10	-0.68
QLRQHSPQPG	VALLALEEER	EXTL1_HUMAN			Exostosin-like 1;	1.44	0.06	25.80	-1.37
EDNSEEYIRR	DLEGSDIDTR	XPO2_HUMAN			Exportin-2;	3.60	0.42	44.30	0.26
SYSHSSSSLS	EEPELSGGPPHITSSAPELR	ESYT1_HUMAN			Extended synaptotagmin-1;	0.62	0.04	38.60	-1.50

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
AVRGANTHLS	TFSFTKVDVGQQPLR	ESYT2_HUMAN			Extended synaptotagmin-2;	-4.68	0.00	35.70	-3.68
VLTYLAVASA	ASEGGFTATGQR	ECM1_HUMAN			Extracellular matrix	0.84	0.05	54.60	-1.48
MVFLVACALH	IALDLLPR	DMP4_HUMAN			Extracellular	-1.25	0.06	28.80	-4.34
ASYVRSRSIR	SVAIEVDGR	SULF2_HUMAN			Extracellular sulfatase Sulf-2;	0.38	0.02	44.90	-4.72
RSVAIEVDGR	VYHVGLGDAAQPR	SULF2_HUMAN			Extracellular sulfatase Sulf-2;	0.14	0.01	42.10	-3.04
ALQLEEERKR	AQEEAERLEADR	EZRI_HUMAN			Ezrin;	5.14	0.93	35.80	-0.83
ERELSEQIQR	ALQLEEER	EZRI_HUMAN			Ezrin;	3.46	0.08	34.10	-4.13
EAEKNERVQR	QLLTLSSELSQAR	EZRI_HUMAN			Ezrin;	2.61	0.25	46.90	0.34
ALLEEARRRK	EDEVEEWQHR	EZRI_HUMAN			Ezrin;	1.53	0.16	51.00	-2.24
YEHDDKLTPK	IGFPWSEIR	EZRI_HUMAN	MOES_HUMAN	RADI_HUMAN	Ezrin;	1.17	0.04	25.20	-1.85
EHDDKLTPKI	GFPWSEIR	EZRI_HUMAN	MOES_HUMAN	RADI_HUMAN	Ezrin;	1.00	0.03	25.30	-3.60
VSYHVQESLQ	DEGAEPTGYSAELSSEGIR	EZRI_HUMAN			Ezrin;	0.90	0.09	97.70	-0.85
YEPVSYHVQE	SLQDEGAEPTGYSAELSSEGIRDD	EZRI_HUMAN			Ezrin;	0.79	0.09	30.50	-1.14
YEPVSYHVQE	SLQDEGAEPTGYSAELSSEGIR	EZRI_HUMAN			Ezrin;	0.74	0.08	112.00	-2.83
LQDYEEKTKK	AERELSEQIQR	EZRI_HUMAN			Ezrin;	0.28	0.01	25.60	-3.37
VIKPIDKKAP	DFVFYAPR	EZRI_HUMAN	MOES_HUMAN	RADI_HUMAN	Ezrin;	0.06	0.00	30.60	-5.72
EFNEVFNDVR	LLLNNDNLLR	CAZA1_HUMAN	CAZA2_HUMAN		F-actin-capping protein subunit alpha-1;	2.34	0.13	47.70	-2.12
NNHTDMMEVD	GDVEIPPNKAVVLR	TBL1R_HUMAN			F-box-like/WD repeat-containing protein	0.11	0.00	31.40	-3.04
LPAESVTRVL	QPAVPVAALR	FBXL8_HUMAN			F-box/LRR-repeat protein	-1.44	0.12	26.90	-7.85

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
IAQITGPPDR	CQHAAEIITDLLR	FUBP1_HUMAN			Far upstream element-	2.64	0.06	30.70	-2.23
KPDDGTTPER	IAQITGPPDR	FUBP1_HUMAN			Far upstream element-binding protein 1;	2.05	0.06	30.80	-2.28
GFREVRNEYG	SRIGGNEGIDVPIPR	FUBP1_HUMAN			Far upstream element-binding protein 1;	0.20	0.01	42.00	2.92
PESKKLASQG	DSISSQLGPIHPPPR	FUBP2_HUMAN			Far upstream element-binding protein 2;	0.40	0.01	37.60	-0.43
ESKKLASQGD	SISSQLGPIHPPPR	FUBP2_HUMAN			Far upstream element-	0.34	0.02	40.80	-2.04
EDGDQPESKK	LASQGDSISSQLGPIHPPPR	FUBP2_HUMAN			Far upstream element-binding protein 2;	0.20	0.01	28.30	0.96
FVQHFSQIVR	VLTEDEMGHPEIGDAIAR	FPPS_HUMAN			Farnesyl pyrophosphate synthase;	1.36	0.10	34.40	-4.03
LEREERNQTQ	VLRQQQDEAYLASLR	FAF2_HUMAN			FAS-associated factor 2;	0.53	0.05	37.90	-1.98
PGLDGAQIPR	DPSQQELPR	FAS_HUMAN			Fatty acid synthase;	4.82	0.65	52.60	-4.28
AQQQTQLNLR	SLLVNPEGPTLMR	FAS_HUMAN			Fatty acid synthase;	1.57	0.39	37.10	-9.69
GLKMVVPGLD	GAQIPRDPSQQELPR	FAS_HUMAN			Fatty acid synthase;	-0.14	0.01	32.20	-1.68
MTTASTSQVR	QNYHQDSEAAINR	FRIH_HUMAN			Ferritin heavy chain;	1.38	0.12	38.30	1.33
LAQGRAETLA	GAMPNEAGGHPDAR	FHOD1_HUMAN			FH1/FH2 domain-containing protein 1;	-0.39	0.04	29.90	-1.49
HPRPDITWMK	DDQALTRPEAAEPR	FGRL1_HUMAN			Fibroblast growth factor	-0.66	0.06	38.00	-3.18
RKDFPESSLK	LVSSTLFGNTKPR	FGFP1_HUMAN			Fibroblast growth factor-binding protein 1;	-1.29	0.10	22.80	-2.75
RDQPFTILYR	DMDVVSGR	FBLN5_HUMAN			Fibulin-5;	1.86	0.15	31.30	-0.77
RLSPFMADIR	DAPQDFHPDR	FLNA_HUMAN			Filamin-A;	4.29	0.52	23.40	2.53

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
VRAGGPGLER	AEAGVPAEFSIWTR	FLNA_HUMAN			Filamin-A;	2.44	0.18	32.10	0.70
QTGGPHVKAR	VANPSGNLTETYVQDR	FLNA_HUMAN			Filamin-A;	1.51	0.13	87.10	-1.39
DVTYDGSPVP	SSPFQVPVTEGCDPSR	FLNA_HUMAN			Filamin-A;	1.47	0.10	49.90	-3.18
LHSVDVTYDG	SPVPSSPFQVPVTEGCDPSR	FLNA_HUMAN			Filamin-A;	0.69	0.07	60.50	-0.87
TQTVNYVPSR	EGPYSISVLYGDEEVPR	FLNA_HUMAN			Filamin-A;	0.28	0.01	73.00	0.72
LTQTGGPHVK	ARVANPSGNLTETYVQDR	FLNA_HUMAN			Filamin-A;	0.02	0.00	66.60	-2.42
FNEEHIPDSP	FVVPVASPSGDAR	FLNA_HUMAN			Filamin-A;	-0.18	0.01	41.50	-4.71
LVEPVDVVDN	ADGTQTVNYVPSR	FLNA_HUMAN			Filamin-A;	-0.25	0.01	49.90	-2.15
GLHSVDVTYD	GSPVPSSPFQVPVTEGCDPSR	FLNA_HUMAN			Filamin-A;	-0.76	0.04	67.80	2.51
PFKAKVTGQR	LVSPGSANETSSILVESVTR	FLNB_HUMAN			Filamin-B;	5.73	0.94	81.70	3.08
NEHLKCVNKR	IGNLQTDLSDGLR	FLNB_HUMAN			Filamin-B;	1.82	0.09	46.60	-5.59
GELVPHFPAR	VKVEPAVDTSR	FLNB_HUMAN			Filamin-B;	1.39	0.06	29.50	-2.94
FTVDCSQAGR	APLQVAVLGPTGVAEPVEVR	FLNC_HUMAN			Filamin-C;	5.23	1.00	63.50	-0.10
ETKREVRVEE	STQVGGDPFPAVFGDFLGR	FLNC_HUMAN			Filamin-C;	0.00	0.00	97.80	1.45
DVLQAADVDK	TVAGQDAVIVLLGTR	BLVRB_HUMAN			Flavin reductase (NADPH);	-0.16	0.01	56.20	-0.90
ACRMLGGRPR	CECAPDCSGLPAR	FSTL3_HUMAN			Follistatin-related protein 3;	5.99	0.82	51.10	-2.10
APDCSGLPAR	LQVCGSDGATYRDECELR	FSTL3_HUMAN			Follistatin-related protein	3.71	0.38	30.20	-1.57
CRMLGGRPRC	ECAPDCSGLPAR	FSTL3_HUMAN			Follistatin-related protein 3;	-1.00	0.08	41.40	-3.73
EGSEGSEGSF	RSHESPSDTEEDDR	FOXN3_HUMAN			Forkhead box protein N3;	-5.27	0.00	20.70	-0.41
GSLKTFRALL	TLAAGADGPPR	FJX1_HUMAN			Four-jointed box protein	-0.44	0.03	48.00	-5.22

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change (log$_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
SGRGSGGSDK	AGYSTDESSSSSLHATR	FXR2_HUMAN			Fragile X mental retardation syndrome-	-0.10	0.01	26.80	0.95
QSVYLMNLRK	SGTLGHPGSLDETTYER	FRDA_HUMAN			Frataxin, mitochondrial;	-1.44	0.16	34.70	-1.19
TCIFLPLLRG	HSLFTCEPITVPR	FZD6_HUMAN			Frizzled-6;	-4.24	0.80	43.90	-2.89
DESTGSIAKR	LQSIGTENTEENRR	ALDOA_HUMAN			Fructose-bisphosphate aldolase A;	5.05	0.69	32.30	-2.80
DESTGSIAKR	LQSIGTENTEENR	ALDOA_HUMAN			Fructose-bisphosphate	3.89	0.42	51.90	-0.99
DFAKWRCVLK	IGEHTPSALAIMENANVLAR	ALDOA_HUMAN			Fructose-bisphosphate aldolase A;	2.90	0.08	60.00	-0.94
ADESTGSIAK	RLQSIGTENTEENR	ALDOA_HUMAN			Fructose-bisphosphate aldolase A;	-0.29	0.03	40.60	-1.60
KGVVPLAGTD	GETTTQGLDGLSER	ALDOA_HUMAN	ALDOC_HUMAN		Fructose-bisphosphate	-0.39	0.04	75.80	-1.33
VVPLAGTDGE	TTTQGLDGLSER	ALDOA_HUMAN	ALDOC_HUMAN		Fructose-bisphosphate	-2.55	0.15	29.70	-3.43
VVGIKVDKGV	VPLAGTNGETTTQGLDGLSER	ALDOA_HUMAN			Fructose-bisphosphate aldolase A;	-5.27	0.00	64.50	-1.35
DESVGSMAKR	LSQIGVENTEENRR	ALDOC_HUMAN			Fructose-bisphosphate aldolase C;	1.47	0.07	31.30	-0.36
WRCVLKISER	TPSALAILENANVLAR	ALDOC_HUMAN			Fructose-bisphosphate aldolase C;	1.32	0.17	41.90	-3.51
IKVDKGVVPL	AGTDGETTTQGLDGLSER	ALDOC_HUMAN			Fructose-bisphosphate aldolase C;	-0.42	0.02	80.40	-1.36
GIKVDKGVVP	LAGTDGETTTQGLDGLSER	ALDOC_HUMAN			Fructose-bisphosphate	-1.55	0.09	48.10	-1.23
QTLKPSGFHE	DDPFFYDEHTLR	FXYD5_HUMAN			FXYD domain-containing ion transport regulator 5;	4.54	0.39	33.20	-2.78
LCALLAPGGA	YVLDDSDGLGR	GALC_HUMAN			Galactocerebrosidase;	0.08	0.00	40.10	-1.29
HLKEAGALDR	LLDLPAAASSEDIER	GALA_HUMAN			Galanin peptides;	1.78	0.14	67.60	-2.97
LHLKEAGALD	RLLDLPAAASSEDIER	GALA_HUMAN			Galanin peptides;	1.55	0.17	62.60	0.11
KEAGALDRLL	DLPAAASSEDIER	GALA_HUMAN			Galanin peptides;	1.02	0.05	58.40	-2.08

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AKSFVLNLGK	DSNNLCLHFNPR	LEG1_HUMAN			Galectin-1;	3.46	0.32	32.20	-1.19
TQGVNDGDMR	LADGGATNQGR	LG3BP_HUMAN			Galectin-3-binding protein;	8.81	1.36	41.50	-1.29
AGVVCTNETR	STHTLDLSR	LG3BP_HUMAN			Galectin-3-binding protein;	3.49	0.14	38.60	-1.04
PSALDTNSSK	STSSFPCPAGHFNGFR	LG3BP_HUMAN			Galectin-3-binding protein;	3.30	0.19	48.40	-1.56
YLPTIQSCWN	YGFSCSSDELPVLGLTKSGGSDR	LG3BP_HUMAN			Galectin-3-binding	2.88	0.19	35.60	2.37
AVPSELALLK	AVDTWSWGER	LG3BP_HUMAN			Galectin-3-binding	2.49	0.07	27.90	-6.47
STHTLDLSRE	LSEALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding protein;	2.00	0.14	55.10	-2.14
RSTHTLDLSR	ELSEALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding protein;	1.46	0.06	67.90	-6.54
PRIYTSPTWS	AFVTDSSWSAR	LG3BP_HUMAN			Galectin-3-binding protein;	0.67	0.02	26.90	-4.20
LVYQSRRGPL	VKYSSDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding protein;	0.62	0.06	40.20	-1.00
WGERASHEEV	EGLVEKIR	LG3BP_HUMAN			Galectin-3-binding	0.56	0.05	30.00	-2.07
YQSRRGPLVK	YSSDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding protein;	0.56	0.03	55.70	-0.80
QSCWNYGFSC	SSDELPVLGLTKSGGSDR	LG3BP_HUMAN			Galectin-3-binding	0.44	0.01	31.20	0.69
TWSWGERASH	EEVEGLVEKIR	LG3BP_HUMAN			Galectin-3-binding	0.41	0.04	35.20	-1.17
KSQLVYQSRR	GPLVKYSSDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding protein;	0.40	0.01	45.10	-1.16
SRRGPLVKYS	SDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding protein;	0.38	0.02	45.20	-2.53
VYQSRRGPLV	KYSSDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding	0.31	0.01	44.20	-1.96
QKKTLQALEF	HTVPFQLLAR	LG3BP_HUMAN			Galectin-3-binding	0.29	0.02	39.80	-0.83
QAEAWPSVPT	DLLQLLLPR	LG3BP_HUMAN			Galectin-3-binding protein;	0.18	0.02	44.40	-3.05
KPRIYTSPTW	SAFVTDSSWSAR	LG3BP_HUMAN			Galectin-3-binding protein;	0.13	0.01	42.50	1.78
TQAEAWPSVP	TDLLQLLLPR	LG3BP_HUMAN			Galectin-3-binding	0.02	0.00	44.00	-3.06

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
YKPRIYTSPT	WSAFVTDSSWSAR	LG3BP_HUMAN			Galectin-3-binding protein;	-0.04	0.00	42.80	-1.11
TYKPRIYTSP	TWSAFVTDSSWSAR	LG3BP_HUMAN			Galectin-3-binding protein;	-0.08	0.01	59.60	-1.90
EALFQKKTLQ	ALEFHTVPFQLLAR	LG3BP_HUMAN			Galectin-3-binding protein;	-0.12	0.00	26.00	-2.32
RGPLVKYSSD	YFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding protein;	-0.12	0.01	27.40	0.25
AEAWPSVPTD	LLQLLLPR	LG3BP_HUMAN			Galectin-3-binding protein;	-0.14	0.01	23.50	-3.20
LFQKKTLQAL	EFHTVPFQLLAR	LG3BP_HUMAN			Galectin-3-binding	-0.18	0.00	38.10	-3.21
ALTQAEAWPS	VPTDLLQLLLPR	LG3BP_HUMAN			Galectin-3-binding	-0.34	0.04	36.70	-2.41
GPLVKYSSDY	FQAPSDYR	LG3BP_HUMAN			Galectin-3-binding	-0.37	0.02	23.60	-5.30
HTLDLSRELS	EALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding	-0.49	0.04	43.70	-2.09
ALFQKKTLQA	LEFHTVPFQLLAR	LG3BP_HUMAN			Galectin-3-binding protein;	-0.52	0.01	35.50	-2.68
THTLDLSREL	SEALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding	-0.66	0.03	55.20	-2.03
QWGTVCDNLW	DLTDASVVCR	LG3BP_HUMAN			Galectin-3-binding	-0.76	0.06	59.30	-1.88
TRSTHTLDLS	RELSEALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding protein;	-0.76	0.03	42.40	-2.80
TLDLSRELSE	ALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding protein;	-0.96	0.02	34.00	1.62
GAYPATGPYG	APAGPLIVPYNLPLPGGVVPR	LEG3_HUMAN			Galectin-3;	1.11	0.16	76.10	-0.33
ANRIALDFQR	GNDVAFHFNPR	LEG3_HUMAN			Galectin-3;	0.73	0.04	32.90	-0.92
QNGSSMKPRA	DVAFHFNPR	LEG3_HUMAN	LEG4_HUMAN	LEG8_HUMAN	Galectin-3;	-0.20	0.02	25.90	-1.59
HLKKPSQLSS	FSWDNCDEGKDPAVIR	SAP3_HUMAN			Ganglioside GM2 activator;	0.29	0.02	36.60	-1.88

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AHLKKPSQLS	SFSWDNCDEGKDPAVIR	SAP3_HUMAN			Ganglioside GM2 activator;	-0.10	0.01	30.70	-7.25
GEDWVFVSSK	DADLTDTAQTR	FCL_HUMAN			GDP-L-fucose synthase;	1.83	0.12	51.10	-4.05
KKGGVASGFK	HVVPNEVVVQR	GELS_HUMAN			Gelsolin;	0.73	0.08	37.90	-2.52
AASAILTAQL	DEELGGTPVQSR	GELS_HUMAN			Gelsolin;	0.47	0.04	41.00	-2.35
KNWRDPDQTD	GLGLSYLSSHIANVER	GELS_HUMAN			Gelsolin;	-0.02	0.00	31.60	0.17
DQTDGLGLSY	LSSHIANVER	GELS_HUMAN			Gelsolin;	-0.10	0.00	28.40	-1.98
ETLIKKRKAR	SLLPLSTSLDHR	GEMI5_HUMAN			Gem-associated protein 5;	0.73	0.01	40.50	-1.53
LSVEPSQQLD	TASTEETDPETSQPEPNRPSELDLR	GEMI5_HUMAN			Gem-associated protein 5;	-0.73	0.06	52.80	-2.89
ISRGVQVLPR	DTASLSTTPSESPR	GEPH_HUMAN			Gephyrin;	2.27	0.21	40.10	-1.35
AELTKVFEIR	NTEDLTEEWLR	GMFB_HUMAN			Glia maturation factor beta;	7.12	1.51	45.60	-4.25
LQSLTCDLES	LRGTNESLER	GFAP_HUMAN			Glial fibrillary acidic	-0.08	0.01	35.30	-9.47
IHQGTKMIPC	DFLIPVQTQHPIR	G6PI_HUMAN			Glucose-6-phosphate isomerase;	-0.42	0.02	37.00	-4.56
NFFRMVISNP	AATQSDIDFLIEEIER	DCE1_HUMAN			Glutamate decarboxylase 1;	-6.27	0.00	37.10	0.05
PIRTFQDLSK	QVEMSYGTVR	GRID1_HUMAN			Glutamate receptor delta-	-6.27	0.00	25.10	-4.57
M	GLLSQGSPLSWEETKR	GSH1_HUMAN			Glutamate--cysteine ligase catalytic subunit;	0.68	0.04	36.40	-0.32
MSGESAR	SLGKGSAPPGPVPEGSIR	GSTO1_HUMAN			Glutathione S-transferase omega-1;	2.89	0.16	24.50	-1.87
MPP	YTVVYFPVR	GSTP1_HUMAN			Glutathione S-transferase P;	0.79	0.06	35.80	-2.30
LGRTLGLYGK	DQQEAALVDMVNDGVEDLR	GSTP1_HUMAN			Glutathione S-transferase P;	0.00	0.00	72.30	-3.76

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MAFRVPTANV	SVVDLTCR	G3PT_HUMAN	G3P_HUMAN		Glyceraldehyde-3-phosphate dehydrogenase, testis-specific;	-0.16	0.01	30.60	-3.68
NGKLTGMAFR	VPTANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	4.36	0.52	60.30	1.67
YDNEFGYSNR	VVDLMAHMASK	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	2.82	0.21	32.20	-1.94
NDHFVKLISW	YDNEFGYSNR	G3P_HUMAN			Glyceraldehyde-3-	0.26	0.02	39.70	-3.39
PELNGKLTGM	AFRVPTANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	0.00	0.00	52.50	-4.33
LNGKLTGMAF	RVPTANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	-0.06	0.01	55.10	-0.58
GMAFRVPTAN	VSVVDLTCR	G3P_HUMAN	G3PT_HUMAN		Glyceraldehyde-3-phosphate dehydrogenase;	-0.39	0.01	28.70	-3.23
LTGMAFRVPT	ANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	-0.49	0.06	52.70	-2.77
KLTGMAFRVP	TANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-	-0.96	0.08	63.50	-3.30
SEKRKQISVR	GLAGLGDVAEVR	PYGB_HUMAN			Glycogen phosphorylase,	1.22	0.10	55.50	-3.86
RATRAFVAAR	SFVQGLGVASDVVR	GPC1_HUMAN			Glypican-1;	3.01	0.25	59.80	-3.14
IYGAKGFSLS	DVPQAEISGEHLR	GPC1_HUMAN			Glypican-1;	1.11	0.07	26.70	-3.58
MALSTASDDR	CWNGMAR	GPC1_HUMAN			Glypican-1;	1.06	0.04	29.60	-6.06
KPLPAGRISR	SISESAFSAR	GPC4_HUMAN			Glypican-4;	-3.08	0.00	34.20	-4.04
RDLSENNDQR	QQLQALSEPQPR	GOLM1_HUMAN			Golgi membrane protein 1;	4.12	0.44	40.80	2.67
DVFNVEDQKR	DTINLLDQR	GOLM1_HUMAN			Golgi membrane protein	3.70	0.22	38.20	-1.25
ENPEMEGPER	DQLVIPDGQEEEQEAAGEGR	GOLM1_HUMAN			Golgi membrane protein	2.81	0.26	66.20	-1.41
RDRLPQEPGR	EQVVEDRPVGGR	GOLM1_HUMAN			Golgi membrane protein 1;	1.72	0.05	26.70	-1.39

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
PEMEGPERDQ	LVIPDGQEEEQEAAGEGR	GOLM1_HUMAN			Golgi membrane protein 1;	-0.14	0.01	85.00	-0.61
QIKDFKEKIQ	QDADSVITVGR	GCP60_HUMAN			Golgi resident protein	4.44	0.25	25.10	0.42
AGYTCNVKAR	SCEKEVVSAQPATFLAR	GRN_HUMAN			Granulins;	2.05	0.16	51.20	0.51
DNQTCCRDNR	QGWACCPYR	GRN_HUMAN			Granulins;	1.88	0.11	33.30	-0.90
KKLPAQRTNR	AVALSSSVMCPDAR	GRN_HUMAN			Granulins;	1.06	0.08	67.80	-1.07
RTNRAVALSS	SVMCPDAR	GRN_HUMAN			Granulins;	0.99	0.03	34.70	-4.02
NQTCCRDNRQ	GWACCPYR	GRN_HUMAN			Granulins;	0.66	0.03	34.10	0.27
LTKLPAHTVG	DVKCDMEVSCPDGYTCCR	GRN_HUMAN			Granulins;	0.47	0.05	63.90	-0.22
PAQRTNRAVA	LSSSVMCPDAR	GRN_HUMAN			Granulins;	0.23	0.01	33.40	-3.42
QRTNRAVALS	SSVMCPDAR	GRN_HUMAN			Granulins;	0.09	0.01	33.90	0.86
LVAAGRRAAG	ASVATELR	GROA_HUMAN			Growth-regulated alpha	1.91	0.06	26.70	-2.16
ALELRPRGEA	AEGPAAAAAAAAAAAAAGVGGE	GDF11_HUMAN			Growth/differentiation factor 11;	0.20	0.01	53.60	-3.23
VLENTKRSRR	NLGLDCDEHSSESR	GDF11_HUMAN			Growth/differentiation factor 11;	-0.02	0.00	31.00	-1.81
GGHLHLRISR	AALPEGLPEASR	GDF15_HUMAN			Growth/differentiation factor 15;	2.04	0.18	42.90	-5.38
VLSWLPHGGA	LSLAEASR	GDF15_HUMAN			Growth/differentiation factor 15;	0.57	0.02	25.50	0.11
GALSLAEASR	ASFPGPSELHSEDSR	GDF15_HUMAN			Growth/differentiation factor 15;	-0.39	0.02	39.00	-3.71
ALSLAEASRA	SFPGPSELHSEDSR	GDF15_HUMAN			Growth/differentiation	-1.04	0.04	27.70	-1.20
ETTSEAWSVE	VLPSDSEAPDLKQEER	GAPD1_HUMAN			GTPase-activating protein and VPS9 domain-	1.35	0.12	30.40	-2.89
TACYFATIHT	DSSLLLADITDKFGQR	GUAD_HUMAN			Guanine deaminase;	-0.89	0.12	45.00	0.38

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
NKTVMAHGCY	LSAEELNVFHER	GUAD_HUMAN			Guanine deaminase;	-0.89	0.05	53.40	-0.41
TNKTVMAHGC	YLSAEELNVFHER	GUAD_HUMAN			Guanine deaminase;	-0.93	0.05	55.80	-2.43
LQAEVTALKT	LVITSTPASPNR	R3GEF_HUMAN			Guanine nucleotide exchange factor for Rab-	-0.69	0.06	30.90	-3.56
TREGNVRVSR	ELAGHTGYLSCCR	GBB1_HUMAN			Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit	0.13	0.01	43.40	-3.99
TREGNVRVSR	ELPGHTGYLSCCR	GBB2_HUMAN	GBB4_HUMAN		Guanine nucleotide-	0.11	0.01	38.60	-1.77
MTKIKADPD	GPEAQAEACSGER	NHP2_HUMAN			H/ACA ribonucleoprotein	-0.08	0.00	72.10	-1.29
M	FLQYYLNEQGDR	NOP10_HUMAN			H/ACA ribonucleoprotein complex subunit 3;	0.21	0.01	67.90	2.64
EGEEEQAINR	QTALYTLK	HEAT1_HUMAN			HEAT repeat-containing protein 1;	3.64	0.26	23.20	4.32
VPAYFNDSQR	QATKDAGVIAGLNVLR	HS71L_HUMAN	HSP71_HUMAN		Heat shock 70 kDa	4.84	0.37	31.90	-0.06
QASIEIDSLY	EGIDFYTSITR	HS71L_HUMAN	HSP71_HUMAN	HSP7C_HUMAN	Heat shock 70 kDa protein 1-like;	-0.29	0.02	30.60	-1.42
TVTNAVVTVP	AYFNDSQR	HS71L_HUMAN	GRP75_HUMAN	HSP71_HUMAN	Heat shock 70 kDa protein 1-like;	-1.55	0.05	33.20	-3.19
TFTTYSDNQP	GVLIQVYEGER	HS71L_HUMAN	HSP71_HUMAN	HSP7C_HUMAN	Heat shock 70 kDa protein 1-like;	-2.25	0.11	30.50	-4.01
GVDFYKSITR	ARFEELCSDLFR	HSP71_HUMAN	HSP76_HUMAN	HSP77_HUMAN	Heat shock 70 kDa	3.30	0.14	33.50	-1.14
FNDSQRQATK	DAGVIAGLNVLR	HSP71_HUMAN	HS71L_HUMAN		Heat shock 70 kDa	1.45	0.13	55.00	-3.42
SIDAGVFEVK	ATAGDTHLGGEDFDNR	HSP71_HUMAN	HS71L_HUMAN	HSP76_HUMAN	Heat shock 70 kDa protein 1A/1B;	1.24	0.08	54.00	-2.05
KALRDAKLDK	AQIHDLVLVGGSTR	HSP71_HUMAN			Heat shock 70 kDa	0.42	0.03	36.90	-2.41
FNDSQRQATK	DAGAIAGLNVLR	HSP76_HUMAN			Heat shock 70 kDa protein 6;	7.20	1.34	47.30	-0.25
EIIANDQGNR	TTPSYVAFTDTER	HSP76_HUMAN	HS71L_HUMAN	HSP71_HUMAN	Heat shock 70 kDa protein 6;	6.43	0.42	53.70	-1.85
VPAYFNDSQR	QATKDAGAIAGLNVLR	HSP76_HUMAN			Heat shock 70 kDa	2.96	0.43	36.60	-0.42
SCVGVFQQGR	VEILANDQGNR	HSP76_HUMAN	HSP77_HUMAN		Heat shock 70 kDa protein 6;	2.37	0.16	47.80	-2.31

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
GAIAGLNVLR	IINEPTAAAIAYGLDR	HSP76_HUMAN	HSP71_HUMAN		Heat shock 70 kDa protein 6;	2.36	0.20	76.50	-1.22
SCVGVFQHGK	VEIIANDQGNR	HSP7C_HUMAN	GRP78_HUMAN	HS71L_HUMAN	Heat shock cognate 71 kDa protein;	4.47	0.32	39.90	-2.15
KEIAEAYLGK	TVTNAVVTVPAYFNDSQR	HSP7C_HUMAN			Heat shock cognate 71	2.94	0.13	37.90	-3.18
VPAYFNDSQR	QATKDAGTIAGLNVLR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	2.55	0.21	53.30	-2.73
GIDFYTSITR	ARFEELNADLFR	HSP7C_HUMAN	HSP72_HUMAN		Heat shock cognate 71	1.91	0.09	48.10	-2.25
NDSQRQATKD	AGTIAGLNVLR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	1.80	0.17	42.30	-3.39
FEELNADLFR	GTLDPVEKALR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	1.07	0.06	34.00	-2.76
TIEDGIFEVK	STAGDTHLGGEDFDNR	HSP7C_HUMAN	HSP72_HUMAN		Heat shock cognate 71 kDa protein;	0.73	0.05	55.40	-1.97
KALRDAKLDK	SQIHDIVLVGGSTR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	0.71	0.07	48.60	-4.03
IGDAAKNQVA	MNPTNTVFDAKR	HSP7C_HUMAN			Heat shock cognate 71	0.60	0.02	24.40	-2.82
DFYTSITRAR	FEELNADLFR	HSP7C_HUMAN	HSP72_HUMAN		Heat shock cognate 71 kDa protein;	0.47	0.02	39.80	-0.08
IDFYTSITRA	RFEELNADLFR	HSP7C_HUMAN	HSP72_HUMAN		Heat shock cognate 71 kDa protein;	0.18	0.01	39.30	-1.25
FNDSQRQATK	DAGTIAGLNVLR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	-0.08	0.01	63.60	-0.97
RDAKLDKSQI	HDIVLVGGSTR	HSP7C_HUMAN	HS71L_HUMAN		Heat shock cognate 71	-0.49	0.03	36.20	1.44
FYTSITRARF	EELNADLFR	HSP7C_HUMAN	HSP72_HUMAN		Heat shock cognate 71 kDa protein;	-0.52	0.05	37.10	-3.07
YTSITRARFE	ELNADLFR	HSP7C_HUMAN	HSP72_HUMAN		Heat shock cognate 71 kDa protein;	-0.79	0.05	34.20	-1.09

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
IEIDSLYEGI	DFYTSITR	HSP7C_HUMAN	HS71L_HUMAN	HSP71_HUMAN	Heat shock cognate 71 kDa protein;	-0.82	0.03	24.80	-0.48
IEDGIFEVKS	TAGDTHLGGEDFDNR	HSP7C_HUMAN	HS71L_HUMAN	HSP71_HUMAN	Heat shock cognate 71	-1.08	0.09	38.40	-1.40
EDGIFEVKST	AGDTHLGGEDFDNR	HSP7C_HUMAN	HS71L_HUMAN	HSP71_HUMAN	Heat shock cognate 71 kDa protein;	-1.25	0.15	51.30	-4.48
DSQRQATKDA	GTIAGLNVLR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	-1.66	0.11	40.40	-3.81
KEQITKFFLK	DISTTLNADEAVAR	HS105_HUMAN	HS74L_HUMAN		Heat shock protein 105	-0.47	0.05	59.70	3.64
SQSCYIAVAR	AGGIETIANEFSDR	HS105_HUMAN			Heat shock protein 105	-0.93	0.05	47.40	-4.71
IMQDKLEKER	NDAKNAVEEYVYEFR	HS105_HUMAN			Heat shock protein 105	-0.96	0.04	41.00	2.41
VAAPAYSRAL	SRQLSSGVSEIR	HSPB1_HUMAN			Heat shock protein beta-1;	1.10	0.07	48.90	-4.08
AAPAYSRALS	RQLSSGVSEIR	HSPB1_HUMAN			Heat shock protein beta-1;	0.47	0.04	43.20	-1.74
TLTVEAPMPK	LATQSNEITIPVTFESR	HSPB1_HUMAN			Heat shock protein beta-1;	0.08	0.01	51.10	5.63
LIPEYLNFIR	GVVDSEDLPLNISR	HS90A_HUMAN	H90B3_HUMAN	HS90B_HUMAN	Heat shock protein HSP 90-alpha;	6.98	0.48	75.20	-0.32
FSVEGQLEFR	ALLFVPR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	4.27	0.34	25.20	0.83
FYSNKEIFLR	ELISNSSDALDKIR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	3.50	0.22	25.60	-2.41
HIYYITGETK	DQVANSAFVER	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	1.79	0.10	48.10	-0.24
ADDTSAAVTE	EMPPLEGDDDTSR	HS90A_HUMAN	HS904_HUMAN		Heat shock protein HSP 90-alpha;	1.62	0.03	40.80	-0.13
RRIKEIVKKH	SQFIGYPITLFVEKER	HS90A_HUMAN			Heat shock protein HSP	0.72	0.03	25.80	-1.55
IGRGTKVILH	LKEDQTEYLEER	HS90A_HUMAN	H90B3_HUMAN	H90B4_HUMAN	Heat shock protein HSP	0.49	0.06	47.70	-1.91
RGTKVILHLK	EDQTEYLEERR	HS90A_HUMAN	H90B3_HUMAN	HS90B_HUMAN	Heat shock protein HSP 90-alpha;	0.40	0.04	38.10	-0.20
EYLNFIRGVV	DSEDLPLNISR	HS90A_HUMAN	H90B3_HUMAN	HS90B_HUMAN	Heat shock protein HSP 90-alpha;	0.31	0.02	37.20	0.77
WESSAGGSFT	VRTDTGEPMGR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	0.29	0.01	30.60	-0.16

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
KHNDDEQYAW	ESSAGGSFTVR	HS90A_HUMAN	HS902_HUMAN	HS90B_HUMAN	Heat shock protein HSP 90-alpha;	0.11	0.01	33.60	-5.47
VRRVFIMDNC	EELIPEYLNFIR	HS90A_HUMAN	HS904_HUMAN		Heat shock protein HSP 90-alpha;	0.09	0.01	39.20	-2.61
RMKENQKHIY	YITGETKDQVANSAFVER	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	0.04	0.00	40.80	-3.77
KLYVRRVFIM	DNCEELIPEYLNFIR	HS90A_HUMAN	HS904_HUMAN		Heat shock protein HSP	-0.02	0.00	32.20	1.58
MGYMAAKKHL	EINPDHSIIETLR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.04	0.00	31.50	-1.65
GYMAAKKHLE	INPDHSIIETLR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.10	0.01	34.30	-2.22
GRGTKVILHL	KEDQTEYLEER	HS90A_HUMAN	H90B3_HUMAN	H90B4_HUMAN	Heat shock protein HSP	-0.12	0.01	37.30	0.13
PEYLNFIRGV	VDSEDLPLNISR	HS90A_HUMAN	H90B3_HUMAN	HS90B_HUMAN	Heat shock protein HSP	-0.25	0.02	35.20	-3.03
TRMKENQKHI	YYITGETKDQVANSAFVER	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.27	0.03	37.40	-1.06
RGTKVILHLK	EDQTEYLEER	HS90A_HUMAN	H90B3_HUMAN	H90B4_HUMAN	Heat shock protein HSP 90-alpha;	-0.29	0.03	47.20	-1.72
WEDHLAVKHF	SVEGQLEFR	HS90A_HUMAN	H90B3_HUMAN	HS902_HUMAN	Heat shock protein HSP 90-alpha;	-0.42	0.03	37.30	-3.27
TMGYMAAKKH	LEINPDHSIIETLR	HS90A_HUMAN			Heat shock protein HSP	-0.52	0.05	33.20	-2.85
ELIPEYLNFI	RGVVDSEDLPLNISR	HS90A_HUMAN	HS90B_HUMAN		Heat shock protein HSP 90-alpha;	-0.55	0.05	39.20	-2.70
IMDSCDELIP	EYLNFIR	HS90A_HUMAN	HS904_HUMAN	HS90B_HUMAN	Heat shock protein HSP 90-alpha;	-0.58	0.03	26.20	-2.73
ALLFVPRRAP	FDLFENR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.60	0.05	26.00	-2.36
LNFIRGVVDS	EDLPLNISR	HS90A_HUMAN	H90B3_HUMAN	HS90B_HUMAN	Heat shock protein HSP	-0.66	0.05	33.60	-4.58
SVKDLVILLY	ETALLSSGFSLEDPQTHANR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.69	0.06	51.70	-1.67
LVILLYETAL	LSSGFSLEDPQTHANR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.73	0.06	40.40	-0.61
GTKVILHLKE	DQTEYLEER	HS90A_HUMAN	H90B3_HUMAN	H90B4_HUMAN	Heat shock protein HSP	-0.82	0.07	35.90	-3.94

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
ENQKHIYYIT	GETKDQVANSAFVER	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.89	0.08	37.70	-0.29
ILLYETALLS	SGFSLEDPQTHANR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-1.00	0.06	23.50	-3.89
AAKKHLEINP	DHSIIETLR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-1.16	0.08	24.20	-2.77
KDLVILLYET	ALLSSGFSLEDPQTHANR	HS90A_HUMAN			Heat shock protein HSP	-1.49	0.08	33.50	-3.69
FYSNKEIFLR	ELISNASDALDKIR	HS90B_HUMAN	ENPL_HUMAN	H90B2_HUMAN	Heat shock protein HSP	4.28	0.31	36.60	-5.43
KVEKVTISNR	LVSSPCCIVTSTYGWTANMER	HS90B_HUMAN			Heat shock protein HSP 90-beta;	3.84	0.19	53.40	-1.14
DEVAAEEPNA	AVPDEIPPLEGDEDASR	HS90B_HUMAN	H90B3_HUMAN		Heat shock protein HSP	1.37	0.08	60.40	5.00
GYMMAKKHLE	INPDHPIVETLR	HS90B_HUMAN			Heat shock protein HSP 90-beta;	0.88	0.06	31.70	-7.25
TMGYMMAKKH	LEINPDHPIVETLR	HS90B_HUMAN			Heat shock protein HSP 90-beta;	0.28	0.01	28.90	-0.42
NRRRLSELLR	YHTSQSGDEMTSLSEYVSR	HS90B_HUMAN			Heat shock protein HSP 90-beta;	0.08	0.01	60.10	-2.26
VRRVFIMDSC	DELIPEYLNFIR	HS90B_HUMAN			Heat shock protein HSP 90-beta;	-0.39	0.06	42.50	-3.27
AVKDLVVLLF	ETALLSSGFSLEDPQTHSNR	HS90B_HUMAN			Heat shock protein HSP 90-beta;	-1.44	0.27	35.70	0.27
DGIFEVKSTA	GDTHLGGEDFDNR	HSP72_HUMAN	HS71L_HUMAN	HSP71_HUMAN	Heat shock-related 70 kDa protein 2;	0.26	0.02	40.10	-1.16
ASWAKSAGAK	SSGGREDLESSGLQR	HN1_HUMAN			Hematological and	1.90	0.15	28.80	-1.43
WAKSAGAKSS	GGREDLESSGLQR	HN1_HUMAN			Hematological and neurological expressed 1	1.04	0.04	41.50	-0.28
LRQRASNKVQ	DSAPVETPR	HMOX1_HUMAN			Heme oxygenase 1;	-0.63	0.02	27.30	-0.50
KTNVKAAWGK	VGAHAGEYGAEALER	HBA_HUMAN			Hemoglobin subunit alpha;	-0.69	0.06	58.60	-3.20

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AVTALWGKVN	VDEVGGEALGR	HBB_HUMAN			Hemoglobin subunit beta;	0.00	0.00	36.00	-1.06
SQLSELHCDK	LHVDPENFR	HBB_HUMAN	HBD_HUMAN		Hemoglobin subunit beta;	-0.08	0.01	28.50	-1.29
VTALWGKVNV	DEVGGEALGR	HBB_HUMAN			Hemoglobin subunit beta;	-0.16	0.01	44.60	-6.69
AMAFSAEQDL	QLCVGGCPPSQR	RGMC_HUMAN			Hemojuvelin;	4.62	0.71	39.30	-3.17
ASSLYSSPVN	SSAPLAEDIDPELAR	HGS_HUMAN			Hepatocyte growth factor-regulated tyrosine kinase substrate;	0.93	0.04	53.50	1.05
SSAPPASSLY	SSPVNSSAPLAEDIDPELAR	HGS_HUMAN			Hepatocyte growth factor-regulated tyrosine kinase	0.74	0.04	91.20	-2.58
SDSDSKADSD	GAKPEPVAMAR	HDGR2_HUMAN			Hepatoma-derived growth factor-related protein 2;	-0.20	0.01	33.90	-1.59
IQGHRVEVKK	AVPKEDIYSGGGGGGSR	ROA0_HUMAN			Heterogeneous nuclear	1.13	0.10	43.80	-1.02
ESPKEPEQLR	KLFIGGLSFETTDESLR	RA1L2_HUMAN	ROA1_HUMAN		Heterogeneous nuclear ribonucleoprotein A1-like 2;	-0.08	0.00	41.30	2.98
GGGQYFAKPR	NQGGYGGSSSSSSYGSGR	ROA1_HUMAN			Heterogeneous nuclear	2.18	0.20	74.90	-1.33
LRKLFIGGLS	FETTDESLR	ROA1_HUMAN	RA1L2_HUMAN		Heterogeneous nuclear ribonucleoprotein A1;	0.94	0.05	26.90	0.79
MSK	SESPKEPEQLR	ROA1_HUMAN			Heterogeneous nuclear ribonucleoprotein A1;	0.51	0.01	37.10	-1.99
VKKIFVGGIK	EDTEEYNLR	ROA3_HUMAN			Heterogeneous nuclear ribonucleoprotein A3;	0.60	0.05	26.70	-4.90
KKDLTEYLSR	FGEVVDCTIKTDPVTGR	HNRDL_HUMAN			Heterogeneous nuclear ribonucleoprotein D-like;	1.86	0.09	34.90	-3.53
GGLSWDTSKK	DLTEYLSR	HNRDL_HUMAN			Heterogeneous nuclear ribonucleoprotein D-like;	0.32	0.03	30.10	-0.20
ESEGAKIDAS	KNEEDEGHSNSSPR	HNRPD_HUMAN			Heterogeneous nuclear	3.57	0.13	29.50	-3.41
AMKTKEPVKK	IFVGGLSPDTPEEKIR	HNRPD_HUMAN			Heterogeneous nuclear ribonucleoprotein D0;	0.88	0.08	34.50	-1.20
HRTEMDWVLK	HSGPNSADSANDGFVR	HNRPF_HUMAN			Heterogeneous nuclear ribonucleoprotein F;	0.00	0.00	65.20	0.00

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
NFFSPLNPVR	VHIEIGPDGR	HNRH1_HUMAN	HNRH2_HUMAN	HNRPF_HUMAN	Heterogeneous nuclear	0.88	0.06	36.20	0.62
GGEGFVVKVR	GLPWSCSADEVQR	HNRH1_HUMAN			Heterogeneous nuclear ribonucleoprotein H;	0.71	0.04	52.10	-3.19
NSVEMDWVLK	HTGPNSPDTANDGFVR	HNRH1_HUMAN	HNRH2_HUMAN		Heterogeneous nuclear ribonucleoprotein H;	0.11	0.01	73.30	-1.69
TEGGEGFVVK	VRGLPWSCSADEVQR	HNRH1_HUMAN			Heterogeneous nuclear ribonucleoprotein H;	-0.08	0.01	49.30	-0.95
GFDDYGGYNN	YGYGNDGFDDR	HNRH3_HUMAN			Heterogeneous nuclear ribonucleoprotein H3;	0.73	0.04	23.60	0.00
FDDYGGYNNY	GYGNDGFDDR	HNRH3_HUMAN			Heterogeneous nuclear	-0.06	0.00	33.20	-3.67
GGRPMPPSRR	DYDDMSPR	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	5.33	0.44	28.10	-4.96
EEEQAFKRSR	NTDEMVELR	HNRPK_HUMAN			Heterogeneous nuclear	4.63	0.79	36.40	-3.08
PSEWQMAYEP	QGGSGYDYSYAGGR	HNRPK_HUMAN			Heterogeneous nuclear	2.08	0.13	45.90	-1.50
DTWSPSEWQM	AYEPQGGSGYDYSYAGGR	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	0.82	0.08	93.80	0.05
EWQMAYEPQG	GSGYDYSYAGGR	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	0.81	0.05	47.60	-2.73
TWSPSEWQMA	YEPQGGSGYDYSYAGGR	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	0.81	0.08	60.50	-3.49
DMEEEQAFKR	SRNTDEMVELR	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	0.51	0.03	36.70	-3.54
KGGKNIKALR	TDYNASVSVPDSSGPER	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	0.42	0.04	71.00	-3.65
VECLNYQHYK	GSDFDCELR	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	0.38	0.01	33.20	-3.62
GGKNIKALRT	DYNASVSVPDSSGPER	HNRPK_HUMAN			Heterogeneous nuclear	-0.06	0.01	47.00	-1.11
VIGKGGKNIK	ALRTDYNASVSVPDSSGPER	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	-0.23	0.02	39.60	-2.74
DRVVECIKII	LDLISESPIKGR	HNRPK_HUMAN			Heterogeneous nuclear	-0.23	0.01	31.90	-2.43
RGGRGGSRAR	NLPLPPPPPR	HNRPK_HUMAN			Heterogeneous nuclear	-1.00	0.02	39.10	-3.41

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EYESQAKRLK	TEEGEIDYSAEEGENRR	HNRLL_HUMAN			Heterogeneous nuclear	0.18	0.02	44.30	-3.33
EKNIKRGGNR	FEPYANPTKR	HNRPM_HUMAN			Heterogeneous nuclear ribonucleoprotein M;	0.62	0.02	25.10	-0.23
MERGNFGGSF	AGSFGGAGGHAPGVAR	HNRPM_HUMAN			Heterogeneous nuclear	0.13	0.01	43.00	-1.14
ALKRGEIIAK	QGGGGGGGSVPGIER	HNRPM_HUMAN			Heterogeneous nuclear	-0.20	0.01	47.70	-6.39
MRPFEGFQRK	AIVICPTDEDLKDR	HNRL1_HUMAN			Heterogeneous nuclear	0.49	0.03	34.90	-4.35
ELMERLQAAL	DDEEAGGRPAMEPGNGSLDLGGD	HNRPU_HUMAN			Heterogeneous nuclear	1.31	0.14	68.50	-1.05
LKAELMERLQ	AALDDEEAGGRPAMEPGNGSLDL	HNRPU_HUMAN			Heterogeneous nuclear ribonucleoprotein U;	1.09	0.12	82.50	-3.77
GKSSGPTSLF	AVTVAPPGAR	HNRPU_HUMAN			Heterogeneous nuclear ribonucleoprotein U;	0.80	0.02	28.10	-2.05
KFIEIAARKK	RNFILDQTNVSAAAQR	HNRPU_HUMAN			Heterogeneous nuclear ribonucleoprotein U;	-0.39	0.04	49.60	2.45
RGAAKEAAGK	SSGPTSLFAVTVAPPGAR	HNRPU_HUMAN			Heterogeneous nuclear ribonucleoprotein U;	-0.52	0.02	43.70	-4.93
HHLRDYFEEY	GKIDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	1.71	0.09	32.00	-1.82
EHHLRDYFEE	YGKIDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear	1.02	0.08	48.00	-1.43
HLRDYFEEYG	KIDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	0.91	0.09	27.50	-1.44
DYFEEYGKID	TIEIITDR	ROA2_HUMAN			Heterogeneous nuclear	0.81	0.07	26.80	-2.02
RDYFEEYGKI	DTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	0.76	0.05	37.40	-2.99
LRDYFEEYGK	IDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	0.41	0.04	39.00	-2.55
QEVQSSRSGR	GGNFGFGDSR	ROA2_HUMAN			Heterogeneous nuclear	0.40	0.01	44.00	-0.86
FRKLFIGGLS	FETTEESLR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	0.34	0.02	26.60	-2.54
VDKIVLQKYH	TINGHNAEVR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	-0.02	0.00	23.00	0.87
MEK	TLETVPLER	ROA2_HUMAN			Heterogeneous nuclear	-0.32	0.03	27.20	-1.10

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
SPSPLLSSSF	DLDYDFQR	HNRPC_HUMAN			Heterogeneous nuclear ribonucleoproteins C1/C2;	0.96	0.06	37.10	-4.34
YYDRMYSYPA	RVPPPPPIAR	HNRPC_HUMAN			Heterogeneous nuclear	0.74	0.05	28.70	-1.86
FQRDYYDRMY	SYPARVPPPPPIAR	HNRPC_HUMAN			Heterogeneous nuclear	0.37	0.03	38.50	-1.03
EHPSPSPLLS	SSFDLDYDFQR	HNRPC_HUMAN			Heterogeneous nuclear ribonucleoproteins C1/C2;	0.20	0.01	44.00	-5.56
EQKAAKLKEK	YEKDIAAYR	HMGB1_HUMAN	HMGB2_HUMAN		High mobility group protein B1;	0.32	0.01	27.60	-3.46
ACLASGSVLR	LVDAVLGAEIR	HDAC6_HUMAN			Histone deacetylase 6;	4.57	0.73	30.40	-5.15
VGMSLVALKK	ALAAAGYDVEKNNSR	H11_HUMAN	H12_HUMAN	H13_HUMAN	Histone H1.1;	0.49	0.03	35.60	-4.37
KTKAVSRSQR	AGLQFPVGR	H2A1A_HUMAN	H2A1B_HUMAN	H2A1C_HUMAN	Histone H2A type 1-A;	2.01	0.07	40.40	-1.23
YMAAVLEYLT	AEILELAGNAAR	H2A1B_HUMAN	H2A1C_HUMAN	H2A1D_HUMAN	Histone H2A type 1-B/E;	0.20	0.02	52.00	1.35
VYMAAVLEYL	TAEILELAGNAAR	H2A1B_HUMAN	H2A1C_HUMAN	H2A1D_HUMAN	Histone H2A type 1-B/E;	-1.16	0.05	46.50	-2.42
GISSKAMGIM	NSFVNDIFER	H2B1B_HUMAN	H2B1C_HUMAN	H2B1D_HUMAN	Histone H2B type 1-B;	0.67	0.03	32.50	-0.24
ISSKAMGIMN	SFVNDIFER	H2B1B_HUMAN	H2B1C_HUMAN	H2B1D_HUMAN	Histone H2B type 1-B;	-0.55	0.02	36.20	-1.47
ALREIRRYQK	STELLIR	H31T_HUMAN	H31_HUMAN	H32_HUMAN	Histone H3.1t;	3.61	0.22	27.60	-3.25
RLARRGGVKR	ISGLIYEETR	H4_HUMAN			Histone H4;	2.11	0.18	48.00	-5.29
CDLPKISQLD	GVDDGTESDTSVTATTR	MLL1_HUMAN			Histone-lysine N-methyltransferase MLL;	0.53	0.07	85.50	-1.49
QNKALSSAVQ	ASPTSPGGSPSSPSSGQR	MLL1_HUMAN			Histone-lysine N-methyltransferase MLL;	0.28	0.03	48.30	1.43
IATYQANYGF	SNDGASSSTANVEDVHAR	HTSF1_HUMAN			HIV Tat-specific factor 1;	0.45	0.05	53.00	-2.75
EREERLRGWE	AFLNAPEANR	HTSF1_HUMAN			HIV Tat-specific factor 1;	0.24	0.01	29.60	-3.16
SEAGSHTVQR	MYGCDVGSDWR	1A02_HUMAN	1A69_HUMAN		HLA class I	3.30	0.24	36.80	-1.24

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AVGYVDDTQF	VRFDSDAASQR	1A02_HUMAN	1A03_HUMAN	1A11_HUMAN	HLA class I	-0.47	0.02	44.80	-1.01
ISVGYVDDTQ	FVRFDNDAASPR	HLAE_HUMAN			HLA class I	0.62	0.03	30.10	-2.04
SRPGRGEPRF	IAVGYVDDTQFVR	1B15_HUMAN	1A01_HUMAN	1A02_HUMAN	HLA class I histocompatibility	-3.66	0.46	52.30	-0.07
PAEITLTWQR	DGEDQTQDTELVETRPAGDR	1B07_HUMAN	1B08_HUMAN	1B13_HUMAN	HLA class I histocompatibility	3.75	0.35	34.80	-0.44
ISVGYVDDTQ	FVRFDSDAASPR	1B07_HUMAN	1B08_HUMAN	1B14_HUMAN	HLA class I histocompatibility	0.65	0.03	35.90	-1.22
SVGYVDDTQF	VRFDSDAASPR	1B07_HUMAN	1B08_HUMAN	1B14_HUMAN	HLA class I	0.16	0.01	40.00	-1.75
AGEPRFISVG	YVDDTQFVR	1B07_HUMAN	1A01_HUMAN	1A02_HUMAN	HLA class I	0.09	0.01	29.30	-4.84
AVGYVDDTQF	VQFDSDAASPR	1C05_HUMAN	1C08_HUMAN		HLA class I histocompatibility antigen, Cw-5 alpha chain;	2.84	0.24	30.10	6.14
SEAGSHTIQR	MYGCDLGPDGR	1C06_HUMAN	1B13_HUMAN	1B35_HUMAN	HLA class I	3.87	0.25	41.10	5.91
EAAREAEQRR	AYLEGTCVEWLR	1C06_HUMAN	1A02_HUMAN	1A29_HUMAN	HLA class I	3.03	0.16	56.20	0.85
DYIALNEDLR	SWTAADTAAQITQR	1C06_HUMAN	1B07_HUMAN	1B08_HUMAN	HLA class I histocompatibility	2.90	0.18	55.40	1.42
GYVDDTQFVR	FDSDAASPR	1C06_HUMAN	1B07_HUMAN	1B08_HUMAN	HLA class I	2.58	0.65	33.60	-4.42
GAGEPRFISV	GYVDDTQFVR	1C06_HUMAN	1A01_HUMAN	1A02_HUMAN	HLA class I	0.20	0.01	41.20	-1.87
FDLDPETPAN	GYRSLVHTAR	LIPS_HUMAN			Hormone-sensitive lipase;	1.53	0.07	25.00	0.92
LTRAVTTVTQ	STPVPGPSVPPPEELQVSPGPR	HCFC1_HUMAN			Host cell factor 1;	0.65	0.05	54.40	2.44
AFKVKPFVVR	DAVVYPILVEFTR	HYOU1_HUMAN			Hypoxia up-regulated	1.53	0.31	34.50	-1.29
LLMLGMGCWA	REVLVPEGPLYR	IGSF8_HUMAN			Immunoglobulin superfamily member 8;	-1.49	0.08	39.40	-3.76
WTLSNLCRNK	NPAPPIDAVEQILPTLVR	IMA2_HUMAN			Importin subunit alpha-2;	-0.16	0.02	37.70	-1.97
KRRNVSSFPD	DATSPLQENR	IMA2_HUMAN			Importin subunit alpha-2;	-1.55	0.05	49.60	-4.55
EAAMFDSLLM	DSYVSSTTGESVITR	IMA7_HUMAN			Importin subunit alpha-7;	0.31	0.04	60.00	2.14
LEAAQKFLER	AAVENLPTFLVELSR	IMB1_HUMAN			Importin subunit beta-1;	3.35	0.45	51.90	-1.66

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LLPLLGGTQT	AIVFIKQPSSQDALQGR	PTK7_HUMAN			Inactive tyrosine-protein kinase 7;	0.49	0.04	55.10	-0.57
LCCRRDHYVD	FQELGWR	INHBE_HUMAN			Inhibin beta E chain;	2.27	0.16	24.20	-3.53
LFSDVCRVES	GENCSSPAPR	ITPR1_HUMAN			Inositol 1,4,5-trisphosphate receptor type 1;	-3.92	0.00	30.10	3.15
LTSAEVIVPR	DQTPDENEEVIVR	IF2B2_HUMAN			Insulin-like growth factor	0.78	0.05	63.90	0.44
FLAFASCCIA	AYRPSETLCGGELVDTLQFVCGDR	IGF2_HUMAN			Insulin-like growth factor II;	0.40	0.02	79.60	1.08
WQCAPCSAEK	LALCPPVSASCSEVTR	IBP1_HUMAN			Insulin-like growth factor-binding protein 1;	5.82	0.55	63.40	0.17
VSASCSEVTR	SAGCGCCPMCALPLGAACGVATAI	IBP1_HUMAN			Insulin-like growth factor-	2.67	0.19	61.90	-0.64
LTVQVGVTAG	APWQCAPCSAEKLALCPPVSASCS	IBP1_HUMAN			Insulin-like growth factor-	0.32	0.01	55.30	-0.72
FRCPPCTPER	LAACGPPPVAPPAAVAAVAGGAR	IBP2_HUMAN			Insulin-like growth factor-binding protein 2;	7.57	0.44	86.60	-1.21
KLIQGAPTIR	GDPECHLFYNEQQEAR	IBP2_HUMAN			Insulin-like growth factor-binding protein 2;	7.06	0.69	67.80	-3.91
PKKLRPPPAR	TPCQQELDQVLER	IBP2_HUMAN			Insulin-like growth factor-	6.64	0.50	52.10	-1.46
GCGCCSVCAR	LEGEACGVYTPR	IBP2_HUMAN			Insulin-like growth factor-	3.50	0.22	45.80	-2.03
CWCVNPNTGK	LIQGAPTIR	IBP2_HUMAN			Insulin-like growth factor-binding protein 2;	3.15	0.19	33.50	-4.01
QCKMSLNGQR	GECWCVNPNTGKLIQGAPTIR	IBP2_HUMAN			Insulin-like growth factor-binding protein 2;	2.72	0.20	42.20	-2.22
ARMPCAELVR	EPGCGCCSVCAR	IBP2_HUMAN			Insulin-like growth factor-	1.70	0.13	35.80	-3.61
YTERCGSGLR	CQPSPDEARPLQALLDGR	IBP3_HUMAN			Insulin-like growth factor-binding protein 3;	4.39	0.13	28.10	0.97
RGPPVARAGA	SSAGLGPVVR	IBP3_HUMAN			Insulin-like growth factor-	2.60	0.11	38.00	-1.54

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LLRGPPVARA	GASSAGLGPVVR	IBP3_HUMAN			Insulin-like growth factor-binding protein 3;	2.42	0.20	55.30	-4.61
VVRCEPCDAR	ALAQCAPPPAVCAELVR	IBP3_HUMAN			Insulin-like growth factor-binding protein 3;	2.23	0.12	65.10	0.43
GHAKDSQRYK	VDYESQSTDTQNFSSESKR	IBP3_HUMAN			Insulin-like growth factor-binding protein 3;	1.74	0.22	21.70	-1.59
GNASESEEDR	SAGSVESPSVSSTHR	IBP3_HUMAN			Insulin-like growth factor-	1.47	0.06	40.70	-0.92
LERLAASQSR	THEDLYIIPIPNCDR	IBP4_HUMAN			Insulin-like growth factor-	5.05	0.20	35.60	-2.44
VKLPGGLEPK	GELDCHQLADSFR	IBP4_HUMAN			Insulin-like growth factor-binding protein 4;	4.62	0.35	45.20	-0.12
PPCSEEKLAR	CRPPVGCEELVR	IBP4_HUMAN			Insulin-like growth factor-	2.99	0.17	40.10	-3.33
LAAGPGPSLG	DEAIHCPPCSEEKLAR	IBP4_HUMAN			Insulin-like growth factor-	-0.76	0.04	35.60	-2.27
QDTEMGPCRR	HLDSVLQQLQTEVYR	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	5.89	0.39	81.00	0.75
QCRSSQGQRR	GPCWCVDR	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	2.42	0.18	37.70	-2.13
QGVQAGCPGG	CVEEEDGGSPAEGCAEAEGCLRR	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	2.32	0.16	36.00	-3.04
LQQLQTEVYR	GAQTLYVPNCDHR	IBP6_HUMAN			Insulin-like growth factor-	2.14	0.11	63.20	-0.64
LAASPGGALA	RCPGCGQGVQAGCPGGCVEEEDG	IBP6_HUMAN			Insulin-like growth factor-	1.81	0.16	95.00	2.24
GTSTTPSQPN	SAGVQDTEMGPCRR	IBP6_HUMAN			Insulin-like growth factor-	1.02	0.07	26.60	-3.01
LQTEVYRGAQ	TLYVPNCDHR	IBP6_HUMAN			Insulin-like growth factor-	0.92	0.04	24.70	-2.15
EMGPCRRHLD	SVLQQLQTEVYR	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	0.61	0.04	64.00	1.88
DTEMGPCRRH	LDSVLQQLQTEVYR	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	0.06	0.00	72.00	3.82
GPCRRHLDSV	LQQLQTEVYR	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	-0.27	0.02	29.90	-1.38
RETIKGIQKR	EASNCFAIR	ITM2B_HUMAN			Integral membrane protein 2B;	0.08	0.00	43.10	-1.00

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TIKGIQKREA	SNCFAIR	ITM2B_HUMAN			Integral membrane protein 2B;	0.06	0.00	32.90	-0.11
ETIKGIQKRE	ASNCFAIR	ITM2B_HUMAN			Integral membrane protein 2B;	-0.20	0.01	29.40	-3.62
PNSDPPFSFK	NVISLTEDVDEFR	ITB4_HUMAN			Integrin beta-4;	3.13	0.14	40.20	-1.59
DRSFTSQMLS	SQPPPHGDLGAPQNPNAKAAGSR	ITB4_HUMAN			Integrin beta-4;	0.13	0.01	50.40	-2.39
VEQRAFHDLK	VAPGYYTLTADQDAR	ITB4_HUMAN			Integrin beta-4;	-0.44	0.04	32.70	-1.97
GKTCECDDRR	CEDLDGVVCGGHGTCSCGR	ITGBL_HUMAN			Integrin beta-like protein 1;	7.02	1.19	75.30	-2.21
ERDCRAVYDR	YSDDFCSGHGQCNCGR	ITGBL_HUMAN			Integrin beta-like protein 1;	6.50	1.11	29.80	0.36
TKKKSNQMCK	NSQDIICSNAGTCHCGR	ITGBL_HUMAN			Integrin beta-like protein	3.44	0.50	46.60	0.56
DCKAGWYGKK	CEHPQSCTLSAEESIR	ITGBL_HUMAN			Integrin beta-like protein 1;	3.21	0.33	43.30	-2.64
YKEILLLTGL	DNITDEELDR	AIM2_HUMAN			Interferon-inducible	5.48	0.39	32.30	-2.80
AIGHLDRQQR	EDITQSAQHALR	ILF3_HUMAN			Interleukin enhancer-binding factor 3;	1.86	0.14	34.80	-1.00
HVAVKVLQDM	GLPTGAEGR	ILF3_HUMAN			Interleukin enhancer-	0.53	0.03	32.10	-2.35
KLHVAVKVLQ	DMGLPTGAEGR	ILF3_HUMAN			Interleukin enhancer-	0.29	0.02	27.00	-2.56
YFYGILQSDA	SERCDDWGLDTMR	IL1AP_HUMAN			Interleukin-1 receptor accessory protein;	0.64	0.06	34.10	-0.54
DPPRATEPVA	TSNPAGDPVGSTR	INF2_HUMAN			Inverted formin-2;	1.20	0.05	30.40	-2.10
RPSPLVKAHK	SVQANLDQSQR	INF2_HUMAN			Inverted formin-2;	0.74	0.04	53.80	-2.03
GDAQALKPLK	FSSNQPPAAGSSR	INF2_HUMAN			Inverted formin-2;	-0.20	0.01	28.80	1.50
ASLGPQARRE	ASSSSPEAGEGQIR	ISCA2_HUMAN			Iron-sulfur cluster assembly 2 homolog,	0.20	0.02	47.90	-4.06
AAVALPGSGA	EGDGGWRPGGPGAVAEEER	JMJD8_HUMAN			JmjC domain-containing	0.08	0.01	40.30	-0.41
AILLCSLALG	SVTVHSSEPEVR	JAM1_HUMAN			Junctional adhesion molecule A;	-0.27	0.02	29.80	-4.33
LLSLALETAG	EEAQGDKIIDGAPCAR	KLK7_HUMAN			Kallikrein-7;	2.28	0.18	39.10	-1.96
AAHCKMNEYT	VHLGSDTLGDR	KLK7_HUMAN			Kallikrein-7;	-9.97	0.00	29.50	-0.91

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
QLRLALLVAA	GAPEVLVSAPR	KDEL2_HUMAN			KDEL motif-containing protein 2;	-0.27	0.02	53.50	-3.56
VRRGLAGATT	LGDMIYVSGGFDGSR	KLH12_HUMAN			Kelch-like protein 12;	-4.24	0.80	25.20	2.67
GYGSSFGGVD	GLLAGGEKATMQNLNDR	K1C17_HUMAN			Keratin, type I cytoskeletal 17;	0.83	0.09	48.20	0.05
ILGATIENSR	IVLQIDNAR	K1C18_HUMAN	K1C19_HUMAN		Keratin, type I cytoskeletal 18;	6.20	0.66	40.40	-4.11
SVENDIHGLR	KVIDDTNITR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	5.87	1.17	32.70	-0.73
SLEIDLDSMR	NLKASLENSLR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	5.25	0.50	32.10	-1.46
AETTLTELRR	TVQSLEIDLDSMR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	5.18	0.22	53.60	-3.39
AAETTLTELR	RTVQSLEIDLDSMR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	2.85	0.11	31.90	-0.18
HYFKIIEDLR	AQIFANTVDNAR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	1.88	0.14	44.50	-1.11
VKYETELAMR	QSVENDIHGLR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	1.30	0.13	38.40	-1.31
GWFGEGILTG	NEKETMQSLNDR	K1C18_HUMAN	KRT35_HUMAN		Keratin, type I cytoskeletal 18;	0.76	0.06	22.90	-3.06
IDLDSMRNLK	ASLENSLR	K1C18_HUMAN			Keratin, type I	0.75	0.02	29.20	-4.35
STTVVTTQSA	EVGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.60	0.05	51.80	-2.60
GIAGGLAGMG	GIQNEKETMQSLNDR	K1C18_HUMAN			Keratin, type I	0.57	0.04	42.50	6.66
TVVTTQSAEV	GAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.52	0.02	44.60	-0.76
DLAKIMADIR	AQYDELAR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.29	0.01	33.90	-2.01

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
YFKIIEDLRA	QIFANTVDNAR	K1C18_HUMAN			Keratin, type I	0.14	0.01	40.10	-1.17
RGGMGSGGLA	TGIAGGLAGMGGIQNEKETMQSL	K1C18_HUMAN			Keratin, type I	0.14	0.01	70.50	-1.58
TVEVDAPKSQ	DLAKIMADIR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.02	0.00	23.10	-2.08
TGIAGGLAGM	GGIQNEKETMQSLNDR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.02	0.00	41.80	1.22
TNYRSLGSVQ	APSYGARPVSSAASVYAGAGGSG	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.12	0.01	45.80	-1.25
ELRRTVQSLE	IDLDSMR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.12	0.01	20.20	-2.83
LEDGEDFNLG	DALDSSNSMQTIQKTTTR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.18	0.02	32.20	-1.07
QIEESTTVVT	TQSAEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I	-0.18	0.01	85.20	-1.77
LTELRRTVQS	LEIDLDSMR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.23	0.02	26.50	1.78
IEESTTVVTT	QSAEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.23	0.02	80.60	-0.70
VQAPSYGARP	VSSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.23	0.02	72.30	-2.63
LGSVQAPSYG	ARPVSSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I	-0.29	0.02	83.80	-2.77
GLTVEVDAPK	SQDLAKIMADIR	K1C18_HUMAN			Keratin, type I	-0.29	0.02	35.80	-0.49
TFSTNYRSLG	SVQAPSYGARPVSSAASVYAGAG	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.34	0.04	63.60	-1.29
SLGSVQAPSY	GARPVSSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I	-0.39	0.04	84.50	1.53
ESTTVVTTQS	AEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.47	0.04	81.60	-0.53
APSYGARPVS	SAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.49	0.04	76.10	-1.20
ESTTVVTTQS	AEVGAAETTLTELRR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.52	0.05	23.60	-0.61

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EESTTVVTTQ	SAEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.52	0.05	76.50	-1.71
EESTTVVTTQ	SAEVGAAETTLTELRR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.55	0.02	28.60	-4.48
TRSTFSTNYR	SLGSVQAPSYGAR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.58	0.03	52.20	-2.86
NEKETMQSLN	DRLASYLDR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.79	0.08	35.50	-1.40
GSVQAPSYGA	RPVSSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.82	0.07	53.90	-1.92
YWSQQIEEST	TVVTTQSAEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.86	0.08	94.60	4.84
ELDKYWSQQI	EESTTVVTTQSAEVGAAETTLTELI	K1C18_HUMAN			Keratin, type I	-0.89	0.10	45.90	-0.43
SHYFKIIEDL	RAQIFANTVDNAR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.93	0.11	58.70	0.46
VVTTQSAEVG	AAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.96	0.08	41.00	-3.00
TRSTFSTNYR	SLGSVQAPSYGARPVSSAASVYAG	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.96	0.08	61.70	-0.59
GYGGVLTASD	GLLAGNEKLTMQNLNDR	K1C19_HUMAN			Keratin, type I cytoskeletal 19;	0.00	0.00	31.10	-1.85
GLDIEIATYR	RLLEGEESR	KRT84_HUMAN			Keratin, type II cuticular	4.50	0.17	15.90	1.07
VNQSLLTPLN	LQIDPSIQR	K2C5_HUMAN			Keratin, type II cytoskeletal 5;	0.21	0.02	29.70	-1.00
GASRPRVAVR	SAYGGPVGAGIR	K2C7_HUMAN			Keratin, type II cytoskeletal 7;	-3.25	0.31	51.00	-9.74
SVILSMDNNR	NLDLDSIIDEVR	K2C71_HUMAN			Keratin, type II cytoskeletal 71;	-2.34	0.12	29.50	0.63
EIESVKKQCA	NLETAIADAEQR	K2C73_HUMAN	K2C71_HUMAN		Keratin, type II	2.80	0.19	44.70	-2.65
ELAIKDANAK	LSELEAALQR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	4.14	0.22	47.70	-2.68
GLTDEINFLR	QLYEEEIR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	2.74	0.17	31.80	-0.27

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change (log$_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
YMNKVELESR	LEGLTDEINFLR	K2C8_HUMAN			Keratin, type II	2.66	0.19	59.90	-0.76
AEIEGLKGQR	ASLEAAIADAEQR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	2.25	0.19	59.70	-1.67
LDMDSIIAEV	KAQYEDIANR	K2C8_HUMAN	K2C75_HUMAN		Keratin, type II cytoskeletal 8;	1.49	0.12	24.40	-1.96
SVVLSMDNSR	SLDMDSIIAEVK	K2C8_HUMAN			Keratin, type II	0.73	0.05	56.60	-1.87
VTVNQSLLSP	LVLEVDPNIQAVR	K2C8_HUMAN			Keratin, type II	0.64	0.05	55.30	-1.27
NQSLLSPLVL	EVDPNIQAVR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	0.53	0.06	37.20	-0.60
EMNRNISRLQ	AEIEGLKGQR	K2C8_HUMAN			Keratin, type II	0.40	0.02	38.90	-1.45
LAIKDANAKL	SELEAALQR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	0.38	0.02	37.30	-3.14
SLLQQQKTAR	SNMDNMFESYINNLRR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	0.35	0.01	42.60	-1.28
EQIKTLNNKF	ASFIDKVR	K2C8_HUMAN	K22E_HUMAN	K22O_HUMAN	Keratin, type II	0.20	0.02	33.10	-2.69
SLLSPLVLEV	DPNIQAVR	K2C8_HUMAN			Keratin, type II	0.04	0.00	27.00	-1.69
KEQIKTLNNK	FASFIDKVR	K2C8_HUMAN	K22E_HUMAN	K22O_HUMAN	Keratin, type II cytoskeletal 8;	0.02	0.00	19.40	-0.26
ITAVTVNQSL	LSPLVLEVDPNIQAVR	K2C8_HUMAN			Keratin, type II	0.00	0.00	76.30	-2.33
QSLLSPLVLE	VDPNIQAVR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.02	0.00	31.00	-3.75
TSPGLSYSLG	SSFGSGAGSSSFSRTSSSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.04	0.00	21.90	-1.65
AEQRGELAIK	DANAKLSELEAALQR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.08	0.00	51.80	-1.29
PGLSYSLGSS	FGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.14	0.01	32.70	-2.45
VNQSLLSPLV	LEVDPNIQAVR	K2C8_HUMAN			Keratin, type II	-0.14	0.01	37.10	-2.10
TAVTVNQSLL	SPLVLEVDPNIQAVR	K2C8_HUMAN			Keratin, type II	-0.14	0.01	75.90	-0.06
TVNQSLLSPL	VLEVDPNIQAVR	K2C8_HUMAN			Keratin, type II	-0.16	0.01	40.20	-1.52

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
SPGLSYSLGS	SFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.23	0.02	39.80	-6.07
YGGLTSPGLS	YSLGSSFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.29	0.03	98.70	-0.79
GLSYSLGSSF	GSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.34	0.01	28.00	4.28
EGLKGQRASL	EAAIADAEQR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.44	0.02	47.50	-1.18
GGLTSPGLSY	SLGSSFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.49	0.05	85.90	-1.18
TSPGLSYSLG	SSFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.52	0.02	80.80	-2.07
IEGLKGQRAS	LEAAIADAEQR	K2C8_HUMAN			Keratin, type II	-0.55	0.05	39.90	-1.72
GLSSAYGGLT	SPGLSYSLGSSFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.55	0.06	97.10	0.05
DMDSIIAEVK	AQYEDIANR	K2C8_HUMAN	K2C75_HUMAN		Keratin, type II cytoskeletal 8;	-0.58	0.04	40.90	-1.71
TTSGYAGGLS	SAYGGLTSPGLSYSLGSSFGSGAGS	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.69	0.06	95.10	3.77
MDSIIAEVKA	QYEDIANR	K2C8_HUMAN	K2C75_HUMAN		Keratin, type II cytoskeletal 8;	-0.79	0.04	23.40	-4.60
KHGDDLRRTK	TEISEMNR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.82	0.02	30.50	-3.25
MNKVELESRL	EGLTDEINFLR	K2C8_HUMAN			Keratin, type II	-1.00	0.10	51.00	-0.90
LEGLTDEINF	LRQLYEEEIR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-1.04	0.09	33.50	-0.72
AYMNKVELES	RLEGLTDEINFLR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-1.34	0.07	30.10	0.25
VELESRLEGL	TDEINFLR	K2C8_HUMAN	K2C6A_HUMAN	K2C6B_HUMAN	Keratin, type II cytoskeletal 8;	-1.34	0.07	32.50	-1.45
NKVELESRLE	GLTDEINFLR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-1.39	0.11	39.40	-3.79
QDLLNVKMAL	DIEIATYR	K2C8_HUMAN	GFAP_HUMAN	K2C4_HUMAN	Keratin, type II cytoskeletal 8;	-1.49	0.17	31.00	-2.08

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AARMSRSSGR	SGSMDPSGAHPSVR	KHDR1_HUMAN			KH domain-containing, RNA-binding, signal	-0.10	0.01	32.30	-2.53
MSRSSGRSGS	MDPSGAHPSVR	KHDR1_HUMAN			KH domain-containing,	-0.25	0.01	30.40	4.73
HHPPTVTLSI	EPQTVQEGER	KIRR1_HUMAN			Kin of IRRE-like protein 1;	-9.97	0.00	28.60	-3.06
ESHKTIKQMQ	SSFTSSEQELER	KTN1_HUMAN			Kinectin;	0.49	0.04	63.10	-0.63
GVPKRVYELH	GSSPAVSSEECTPSR	KIF14_HUMAN			Kinesin-like protein	0.98	0.11	55.90	4.05
HSCRGGVDTA	AAPAGGAPPAHAPGPGR	LAGE3_HUMAN			L antigen family member	0.08	0.00	35.90	1.01
WKISGLPVTR	VIGSGCNLDSAR	LDHA_HUMAN	LDH6A_HUMAN	LDHB_HUMAN	L-lactate dehydrogenase A	5.05	0.49	44.10	-0.86
GQNGISDLVK	VTLTSEEEAR	LDHA_HUMAN			L-lactate dehydrogenase A chain;	2.11	0.11	44.50	-2.66
IEDKLKGEMM	DLQHGSLFLR	LDHA_HUMAN			L-lactate dehydrogenase A chain;	-2.16	0.19	29.00	-1.80
VIEDKLKGEM	MDLQHGSLFLR	LDHA_HUMAN			L-lactate dehydrogenase A	-2.79	0.19	36.30	-2.59
VAWKISGFPK	NRVIGSGCNLDSAR	LDH6A_HUMAN	LDHA_HUMAN		L-lactate dehydrogenase	0.60	0.05	38.70	-2.51
NCPEFVPRQH	YQKETESAPGSPR	LARP1_HUMAN			La-related protein 1;	1.45	0.17	41.30	-5.13
PTDALANKLF	GAPEPSTIAR	LARP1_HUMAN			La-related protein 1;	0.72	0.03	31.80	-1.94
QKNRVKPQFR	SSGGSEHSTEGSVSLGDGQLNR	LARP4_HUMAN			La-related protein 4;	0.14	0.02	66.60	-1.32
IGPSKERTLS	ADASVNTLPVVVSR	LAR4B_HUMAN			La-related protein 4B;	0.35	0.04	33.50	-3.09
TLLKVDLENR	CQSLTEDLEFR	LMNB1_HUMAN			Lamin-B1;	3.26	0.22	51.30	-4.63
TPVPPRMGSR	AGGPTTPLSPTR	LMNB1_HUMAN			Lamin-B1;	1.60	0.08	48.30	-0.68
VRGRELTGLK	ALYETELADAR	LMNB1_HUMAN			Lamin-B1;	1.01	0.09	39.90	-0.31
VRGRELTGLK	ALYETELADARR	LMNB1_HUMAN			Lamin-B1;	0.71	0.05	29.20	1.73
LKVDLENRCQ	SLTEDLEFR	LMNB1_HUMAN			Lamin-B1;	0.35	0.02	26.40	3.15
LLKVDLENRC	QSLTEDLEFR	LMNB1_HUMAN			Lamin-B1;	0.09	0.01	31.00	-5.74
HAKLENARLS	SEMNTSTVNSAR	LMNB1_HUMAN			Lamin-B1;	-0.08	0.01	39.20	-3.32
TLMRVDLENR	CQSLQEELDFR	LMNB2_HUMAN			Lamin-B2;	2.92	0.13	51.40	-1.38

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MATPLPGR	AGGPATPLSPTR	LMNB2_HUMAN			Lamin-B2;	2.69	0.20	55.60	-2.08
ELAAALSDKR	GLESDVAELR	LMNB2_HUMAN			Lamin-B2;	1.42	0.08	41.10	-1.61
NSKGPPDFSS	DEEREPTPVLGSGAAAAGR	LAP2A_HUMAN	LAP2B_HUMAN		Lamina-associated polypeptide 2, isoform	-0.06	0.01	56.80	-3.35
KLREQGTESR	SSTPLPTISSSAENTR	LAP2B_HUMAN	LAP2A_HUMAN		Lamina-associated polypeptide 2, isoforms	1.76	0.10	46.00	-1.97
ILKEMFPYEA	STPTGISASCR	LAP2B_HUMAN			Lamina-associated polypeptide 2, isoforms	1.10	0.09	34.00	-5.89
VNRVTGNFKH	ASPILPITEFSDIPR	LAP2B_HUMAN			Lamina-associated polypeptide 2, isoforms	0.97	0.07	60.40	0.77
SCRRPIKGAA	GRPLELSDFR	LAP2B_HUMAN			Lamina-associated	0.86	0.05	35.20	-1.56
NRVTGNFKHA	SPILPITEFSDIPR	LAP2B_HUMAN			Lamina-associated	0.84	0.05	36.30	9.01
VVNRVTGNFK	HASPILPITEFSDIPR	LAP2B_HUMAN			Lamina-associated polypeptide 2, isoforms	0.42	0.01	46.30	-0.33
HPLDSPHVCR	RCNCESDFTDGTCEDLTGR	LAMA5_HUMAN			Laminin subunit alpha-5;	6.16	1.19	76.50	-4.99
ERLLWEMRAR	DLGAPQAAAEAELAAAQR	LAMA5_HUMAN			Laminin subunit alpha-5;	5.78	0.65	108.00	-3.59
PYFNLAEGAR	IAASATCGEEAPAR	LAMA5_HUMAN			Laminin subunit alpha-5;	5.47	0.59	67.70	-2.51
NCQACTCDPR	GALDQLCGAGGLCR	LAMA5_HUMAN			Laminin subunit alpha-5;	5.00	0.47	68.00	-4.94
SCEPRTGVCR	CRPNTQGPTCSEPAR	LAMA5_HUMAN			Laminin subunit alpha-5;	4.94	0.45	46.20	-0.80
ELCLCPASYR	GDSCQECAPGFYR	LAMA5_HUMAN			Laminin subunit alpha-5;	4.68	0.71	59.30	-2.48
AAEAQDTATR	VQSQLQAMQENVER	LAMA5_HUMAN			Laminin subunit alpha-5;	4.63	0.46	63.30	-3.38
HYLPDLHHLR	LELEEAATPEGHAVR	LAMA5_HUMAN			Laminin subunit alpha-5;	4.30	0.20	50.40	4.78
GPQTLERITR	DDAAICTTEYSR	LAMA5_HUMAN			Laminin subunit alpha-5;	4.17	0.33	54.80	-2.10
ASNAIDGTER	WWQSPPLSR	LAMA5_HUMAN			Laminin subunit alpha-5;	3.68	0.19	31.00	-2.87
DVNQDRLTQR	AIEASNAYSR	LAMA5_HUMAN			Laminin subunit alpha-5;	3.65	0.20	25.10	-5.13
AYPTPGHVHR	GQLQLVEGNFR	LAMA5_HUMAN			Laminin subunit alpha-5;	3.46	0.21	43.90	-1.40
GGRCDPHTGR	CNCPPGLSGER	LAMA5_HUMAN			Laminin subunit alpha-5;	3.25	0.15	42.00	-5.10
TLQATLHAAR	DTLASVFR	LAMA5_HUMAN			Laminin subunit alpha-5;	2.62	0.22	34.30	-2.77

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
DAANPKGCTR	CFCFGATER	LAMA5_HUMAN			Laminin subunit alpha-5;	2.46	0.14	33.80	-4.93
VVLLLDDLER	AGALLPAIHEQLR	LAMA5_HUMAN			Laminin subunit alpha-5;	2.23	0.16	38.40	-0.85
LDQAKEELER	LAASLDGAR	LAMA5_HUMAN			Laminin subunit alpha-5;	2.22	0.06	29.80	-1.77
LPEGCDEAGR	CLCQPEFAGPHCDR	LAMA5_HUMAN			Laminin subunit alpha-5;	2.12	0.13	31.10	-2.31
DPDTGQCRCR	VGFEGATCDR	LAMA5_HUMAN			Laminin subunit alpha-5;	1.69	0.13	26.80	2.46
GTEATLGHAK	TLLAAIR	LAMA5_HUMAN			Laminin subunit alpha-5;	0.80	0.05	33.90	-3.18
GGPVGHSIHC	EVCDHCVVLLLDDLER	LAMA5_HUMAN			Laminin subunit alpha-5;	0.65	0.03	41.50	-0.15
SIHCEVCDHC	VVLLLDDLER	LAMA5_HUMAN			Laminin subunit alpha-5;	0.57	0.05	43.50	-1.39
KCRPNVTGRR	CDTCSPGFHGYPR	LAMA5_HUMAN			Laminin subunit alpha-5;	0.44	0.03	37.00	-3.79
DYFGCRSCRC	DIGGALGQSCEPR	LAMA5_HUMAN			Laminin subunit alpha-5;	0.38	0.02	51.10	-0.14
HCEVCDHCVV	LLLDDLER	LAMA5_HUMAN			Laminin subunit alpha-5;	0.26	0.02	26.00	-2.86
TREQVLPAGQ	IVNCDCSAAGTQGNACR	LAMA5_HUMAN			Laminin subunit alpha-5;	0.11	0.02	68.10	-1.54
ETSKKIAHAK	AVAAEAQDTATR	LAMA5_HUMAN			Laminin subunit alpha-5;	0.00	0.00	64.30	-0.32
DKSYDFISHC	AAQGYHISPSSSSLFCR	LAMA5_HUMAN			Laminin subunit alpha-5;	-0.06	0.00	46.90	-5.01
RHETAQQLEV	LEQQSTSLGQDAR	LAMA5_HUMAN			Laminin subunit alpha-5;	-0.08	0.01	46.20	-2.66
AQQLGQLALN	LSSIILDVNQDR	LAMA5_HUMAN			Laminin subunit alpha-5;	-0.16	0.01	27.50	1.49
RPGRIPTSSR	CGNTIPDDDNQVVSLSPGSR	LAMB1_HUMAN			Laminin subunit beta-1;	5.41	0.79	83.50	3.15
KVDDIICDSR	YSDIEPSTEGEVIFR	LAMB1_HUMAN			Laminin subunit beta-1;	2.93	0.23	54.90	-4.57
RVESLSQVEV	ILQHSAADIAR	LAMB1_HUMAN			Laminin subunit beta-1;	0.04	0.00	28.60	-3.25
TNLRIKFVKL	HTLGDNLLDSR	LAMB1_HUMAN			Laminin subunit beta-1;	0.02	0.00	24.70	-7.92
PGRIPTSSRC	GNTIPDDDNQVVSLSPGSR	LAMB1_HUMAN			Laminin subunit beta-1;	-0.02	0.00	41.40	-3.64
TSSRCGNTIP	DDDNQVVSLSPGSR	LAMB1_HUMAN			Laminin subunit beta-1;	-0.20	0.02	37.20	0.07

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
PGYYFATLDH	YLYEAEEANLGPGVSIVER	LAMB1_HUMAN			Laminin subunit beta-1;	-1.08	0.07	34.50	1.82
LAGAIAERVR	SLADVDAILAR	LAMB2_HUMAN			Laminin subunit beta-2;	3.84	0.35	58.40	-5.80
AIRGAVADTR	DTEQTLYQVQER	LAMB2_HUMAN			Laminin subunit beta-2;	3.66	0.48	51.30	-2.60
VCGAPGDAPC	ATSPCGGAGCRDEDGQPR	LAMB2_HUMAN			Laminin subunit beta-2;	2.34	0.12	21.90	-0.21
ARHTQAELQR	ALAEGGSILSR	LAMB2_HUMAN			Laminin subunit beta-2;	2.15	0.13	41.40	-5.26
SLRRTLQGLQ	LDLPLEEETLSLPR	LAMB3_HUMAN			Laminin subunit beta-3;	-2.16	0.10	33.80	-0.48
GSTNGQCDIR	TGQCECQPGITGQHCER	LAMC1_HUMAN			Laminin subunit gamma-1;	7.28	1.14	63.10	-1.51
NCPTGTTGKR	CELCDDGYFGDPLGR	LAMC1_HUMAN			Laminin subunit gamma-1;	7.02	1.37	62.50	-0.28
SFRVDRRDTR	LSAEDLVLEGAGLR	LAMC1_HUMAN			Laminin subunit gamma-1;	4.48	0.61	72.00	-2.79
GRNGPVRLCR	LCQCSDNIDPNAVGNCNR	LAMC1_HUMAN			Laminin subunit gamma-1;	4.45	0.60	49.50	-2.57
NLQSGQGCER	CDCHALGSTNGQCDIR	LAMC1_HUMAN			Laminin subunit gamma-1;	3.52	0.39	71.00	2.48
IDECNIETGR	CVCKDNVEGFNCER	LAMC1_HUMAN			Laminin subunit gamma-1;	3.39	0.36	35.20	-1.79
ECLPCDCNGR	SQECYFDPELYR	LAMC1_HUMAN			Laminin subunit gamma-1;	2.85	0.17	54.60	-3.55
SRLQNIRNTI	EETGNLAEQAR	LAMC1_HUMAN			Laminin subunit gamma-1;	2.85	0.15	30.20	-1.52
EASLEWSSER	QDIAVISDSYFPR	LAMC1_HUMAN			Laminin subunit gamma-	2.04	0.08	48.60	-3.70

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
ISRLQNIRNT	IEETGNLAEQAR	LAMC1_HUMAN			Laminin subunit gamma-1;	1.25	0.11	30.70	-2.56
RVAKTANDTS	TEAYNLLLR	LAMC1_HUMAN			Laminin subunit gamma-1;	1.19	0.05	26.20	-4.61
LLLRTLAGEN	QTAFEIEELNR	LAMC1_HUMAN			Laminin subunit gamma-1;	1.11	0.09	52.00	3.32
AAAAAGCAQA	AMDECTDEGGRPQR	LAMC1_HUMAN			Laminin subunit gamma-1;	0.79	0.06	36.40	-0.54
SSQISRLQNI	RNTIEETGNLAEQAR	LAMC1_HUMAN			Laminin subunit gamma-1;	0.51	0.04	52.70	0.52
CNIETGRCVC	KDNVEGFNCER	LAMC1_HUMAN			Laminin subunit gamma-1;	0.34	0.01	35.30	0.21
VAKTANDTST	EAYNLLLR	LAMC1_HUMAN			Laminin subunit gamma-1;	0.26	0.02	26.30	-2.84
DIVRVAKTAN	DTSTEAYNLLLR	LAMC1_HUMAN			Laminin subunit gamma-1;	-0.06	0.01	59.70	-1.26
VRVAKTANDT	STEAYNLLLR	LAMC1_HUMAN			Laminin subunit gamma-1;	-1.55	0.05	39.70	-0.33
ASDKTQQAER	ALGSAAADAQR	LAMC2_HUMAN			Laminin subunit gamma-	3.87	0.21	40.70	-1.60
AEQALQDILR	DAQISEGASR	LAMC2_HUMAN			Laminin subunit gamma-2;	2.96	0.20	42.20	-1.88
RRVQPPAQTR	RSTPLGQQQPAPR	LTBP2_HUMAN			Latent-transforming growth factor beta-binding protein 2;	0.13	0.02	39.90	-1.36
RVQPPAQTRR	STPLGQQQPAPR	LTBP2_HUMAN			Latent-transforming	0.02	0.00	48.60	-1.60
SDECRCVSGR	CVPRPGGAVCECPGGFQLDASR	LTBP3_HUMAN			Latent-transforming growth factor beta-	2.77	0.21	49.00	0.45
SNGYYYHTQR	LECIDNDECADEEPACEGGR	LTBP4_HUMAN			Latent-transforming growth factor beta-	6.72	1.46	51.30	0.72
RQGPVGSGRR	ECYFDTAAPDACDNILAR	LTBP4_HUMAN			Latent-transforming growth factor beta-	4.07	0.64	67.20	-3.47

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
FHCACPAGFR	SRGPGAPCQDVDECAR	LTBP4_HUMAN			Latent-transforming growth factor beta-	3.63	0.37	48.20	-2.38
AVARAEAAAR	AEAAAPYTVLAQSAPR	LTBP4_HUMAN			Latent-transforming	2.06	0.11	39.00	3.40
APSGDLSLRR	DVDECQLFR	LTBP4_HUMAN			Latent-transforming growth factor beta-	1.68	0.09	43.90	-0.17
LLLLPPPGSC	AAEGSPGTPDESTPPPR	MESD_HUMAN			LDLR chaperone MESD;	0.52	0.02	60.60	0.47
VLPLASPGAA	LTGEQLLGSLLR	LFTY1_HUMAN			Left-right determination factor 1;	1.33	0.19	39.10	-1.58
ASLVTAKLVN	TTITPEPEPKPQPNSR	LUZP1_HUMAN			Leucine zipper protein 1;	1.51	0.14	35.30	-1.95
KGSRNMPGLS	AATLASLGGTSSR	LRRF1_HUMAN			Leucine-rich repeat flightless-interacting	0.28	0.02	63.20	-2.29
VSQEAAQVLE	SAGEGPLDVR	LRRF2_HUMAN			Leucine-rich repeat flightless-interacting	0.83	0.03	33.60	-1.06
LLPALTVLDI	HDNQLTSLPSAIR	LRC40_HUMAN			Leucine-rich repeat-containing protein 40;	-4.68	0.00	32.30	-3.90
LIVQWPNQDS	LQAVVDGLEAFSAHR	PRAML_HUMAN			Leucine-rich repeat-	1.58	0.11	30.70	-0.79
ELVALMSAIR	DGETPDPEDPSR	LKHA4_HUMAN			Leukotriene A-4 hydrolase;	2.16	0.07	36.30	-0.74
HIPTSAPVYQ	QPQQQPVAQSYGGYKEPAAPVSIQ	LASP1_HUMAN			LIM and SH3 domain protein 1;	1.34	0.15	31.90	-0.50
AAPSSGQIYG	SGPQGYNTQPVPVSGQCPPPSTR	LPP_HUMAN			Lipoma-preferred partner;	0.53	0.03	36.40	-2.41
ITPAAFSTLT	TASVEESESTSSAR	LRBA_HUMAN			Lipopolysaccharide-responsive and beige-like	0.26	0.01	48.30	-1.22
LFVCLGNICR	SPIAEAVFR	PPAC_HUMAN			Low molecular weight phosphotyrosine protein	3.24	0.16	41.50	-6.19
WWKCDGQKDC	SDGSDELALCPQR	LRP2_HUMAN			Low-density lipoprotein receptor-related protein 2;	3.35	0.31	23.10	-7.65
CLHQRRVALA	ELQEADGQCPVDR	PPA6_HUMAN			Lysophosphatidic acid phosphatase type 6;	0.00	0.00	51.00	4.19

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
SLATAALLGH	ILLHDFLLVPR	LYAG_HUMAN			Lysosomal alpha-glucosidase;	2.01	0.05	43.20	0.95
ATAALLGHIL	LHDFLLVPR	LYAG_HUMAN			Lysosomal alpha-glucosidase;	1.14	0.05	30.80	-1.14
AQAHPGRPRA	VPTQCDVPPNSR	LYAG_HUMAN			Lysosomal alpha-	-0.20	0.01	23.50	0.64
APQPIPRRSW	SPALTIENEHIR	MA2B1_HUMAN			Lysosomal alpha-mannosidase;	-0.34	0.03	33.40	-1.20
LVSWASRGEA	APDQDEIQR	PPGB_HUMAN			Lysosomal protective protein;	0.96	0.02	22.50	-1.27
SWASRGEAAP	DQDEIQRLPGLAKQPSFR	PPGB_HUMAN			Lysosomal protective protein;	0.81	0.04	33.30	-0.69
GNEKSIIDCK	FNAESQGCNHEEDAGVR	LOXL2_HUMAN			Lysyl oxidase homolog 2;	4.06	0.54	36.80	-1.85
SPDGPSRFRK	AYKPEQPLVR	LOXL2_HUMAN			Lysyl oxidase homolog 2;	-1.00	0.06	22.40	-1.65
SEVRCRGYER	TLSDCPALEGSQNGCQHENDAAV	LOXL4_HUMAN			Lysyl oxidase homolog 4;	4.30	0.68	43.60	6.32
SAREALFGAR	LGQGLGPIHLSEVR	LOXL4_HUMAN			Lysyl oxidase homolog 4;	1.33	0.04	38.80	-3.25
RPPKTKPQRK	GSWAEEPR	LOXL4_HUMAN			Lysyl oxidase homolog 4;	0.55	0.09	26.50	-5.38
KHKAEEVEDE	TVELDVSDEEMAR	MPH6_HUMAN			M-phase phosphoprotein 6;	0.29	0.02	31.60	-6.04
EGRRSTRDRR	SPAEPEGGPASEGAARPLPR	CSF1_HUMAN			Macrophage colony-stimulating factor 1;	0.84	0.04	27.00	-1.77
GGAQNRSYSK	LLCGLLAER	MIF_HUMAN			Macrophage migration inhibitory factor;	6.37	1.02	40.40	-0.37
IGKIGGAQNR	SYSKLLCGLLAER	MIF_HUMAN			Macrophage migration	3.17	0.07	46.10	-0.51
MP	MFIVNTNVPR	MIF_HUMAN			Macrophage migration inhibitory factor;	0.09	0.00	37.10	-1.80
YMLGSAMSRP	IIHFGSDYEDR	PRIO_HUMAN			Major prion protein;	-0.52	0.03	36.10	-2.16
EQLPDCLKGC	DVVVIPAGVPR	MDHM_HUMAN			Malate dehydrogenase, mitochondrial;	-1.49	0.13	27.40	0.87

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
CGLCSLGAVG	APRPCQAPQQWEGR	EPDR1_HUMAN			Mammalian ependymin-related protein 1;	1.60	0.14	22.90	-0.82
SCSNFAVQHR	YLFEEDNLLR	MATN2_HUMAN			Matrilin-2;	-1.55	0.09	36.30	-1.04
SASTSSHNLQ	SIFNIGSR	MATR3_HUMAN			Matrin-3;	-0.04	0.00	30.30	-1.72
PNKDTSENAD	GQSDENKDDYTIPDEYR	MATR3_HUMAN			Matrin-3;	-0.18	0.01	51.00	-2.46
LGCLGLGVAA	EDAEVHAENWLR	MMP15_HUMAN			Matrix metalloproteinase-15;	0.76	0.08	30.20	-5.27
LLGCLGLGVA	AEDAEVHAENWLR	MMP15_HUMAN			Matrix metalloproteinase-15;	0.23	0.01	36.10	0.13
HRRDQIIEKD	AALCVLIDEMNER	MED7_HUMAN			Mediator of RNA polymerase II transcription subunit 7;	-0.69	0.01	26.60	-2.88
PPPLPRLKRR	DFTPAELR	PGRC1_HUMAN			Membrane-associated progesterone receptor	0.86	0.03	30.60	-2.76
IFLLYKIVRG	DQPAASGDSDDDEPPPLPR	PGRC1_HUMAN			Membrane-associated progesterone receptor component 1;	0.80	0.02	86.30	-2.04
ALSVLPGSRA	LRPGDCEVCISYLGR	MANF_HUMAN			Mesencephalic astrocyte-derived neurotrophic factor;	0.52	0.03	72.10	-0.77
EPGLQTTAVV	SMGSGDHQFNLAEILSQNYSVR	MIER2_HUMAN			Mesoderm induction early response protein 2;	-5.27	0.00	48.30	7.63
AESAEVLLPR	LVSCPGPLDQDQQEAAR	MSLN_HUMAN			Mesothelin;	10.36	0.00	95.20	0.52
PPNISSLSPR	QLLGFPCAEVSGLSTER	MSLN_HUMAN			Mesothelin;	6.01	0.87	77.50	1.64
PQACTRFFSR	ITKANVDLLPR	MSLN_HUMAN			Mesothelin;	5.89	0.44	30.00	-3.39
LPRGAPERQR	LLPAALACWGVR	MSLN_HUMAN			Mesothelin;	4.81	0.30	56.10	-2.66
LPVLGQPIIR	SIPQGIVAAWR	MSLN_HUMAN			Mesothelin;	3.97	0.44	22.70	-3.83
GSLLSEADVR	ALGGLACDLPGR	MSLN_HUMAN			Mesothelin;	3.81	0.33	48.60	4.48
PQDLDTCDPR	QLDVLYPKAR	MSLN_HUMAN			Mesothelin;	2.86	0.26	30.40	-4.28

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
WSVSTMDALR	GLLPVLGQPIIR	MSLN_HUMAN			Mesothelin;	2.78	0.17	39.50	-4.60
PAALACWGVR	GSLLSEADVR	MSLN_HUMAN			Mesothelin;	1.67	0.11	40.60	0.09
CTRFFSRITK	ANVDLLPR	MSLN_HUMAN			Mesothelin;	1.46	0.04	34.60	-3.24
GGLACDLPGR	FVAESAEVLLPR	MSLN_HUMAN			Mesothelin;	1.41	0.07	56.40	-3.82
SAEVLLPRLV	SCPGPLDQDQQEAAR	MSLN_HUMAN			Mesothelin;	1.06	0.10	52.80	-0.35
NFSTAIPDFH	AVLAGPGGPGNGLR	GRM1_HUMAN			Metabotropic glutamate	0.51	0.02	25.10	-1.74
QSRHLACLPR	EPGLCTWQSLR	TIMP1_HUMAN			Metalloproteinase	5.65	0.25	33.50	-1.38
YQRYEIKMTK	MYKGFQALGDAADIR	TIMP1_HUMAN			Metalloproteinase	1.57	0.07	46.40	-2.04
YEIKMTKMYK	GFQALGDAADIR	TIMP1_HUMAN			Metalloproteinase	1.18	0.12	63.90	-2.05
LLWLIAPSRA	CTCVPPHPQTAFCNSDLVIR	TIMP1_HUMAN			Metalloproteinase	1.10	0.05	62.00	-0.96
QALGDAADIR	FVYTPAMESVCGYFHR	TIMP1_HUMAN			Metalloproteinase inhibitor 1;	1.03	0.04	53.30	1.45
QAKFFACIKR	SDGSCAWYR	TIMP2_HUMAN			Metalloproteinase inhibitor 2;	6.51	0.38	39.90	-1.42
LATLLRPADA	CSCSPVHPQQAFCNADVVIR	TIMP2_HUMAN			Metalloproteinase inhibitor 2;	1.07	0.06	70.50	-2.23
LLRPADACSC	SPVHPQQAFCNADVVIR	TIMP2_HUMAN			Metalloproteinase	0.79	0.06	78.00	-2.08
ATLLRPADAC	SCSPVHPQQAFCNADVVIR	TIMP2_HUMAN			Metalloproteinase	0.60	0.05	60.20	-2.57
LEGMLSQSVS	SQYNMAGVR	ICLN_HUMAN			Methylosome subunit pICln;	1.31	0.08	30.00	-1.51
ATEPEPSGSI	ANPAASTSPSLSHR	MAP1B_HUMAN			Microtubule-associated protein 1B;	2.20	0.23	26.70	0.21
VSPCEFEHRK	AVPMAPAPASPGSSNDSSAR	MAP1S_HUMAN			Microtubule-associated protein 1S;	0.29	0.02	39.70	1.05
SSMKKTTTLS	GTAPAAGVVPSR	MAP4_HUMAN			Microtubule-associated	0.38	0.01	42.10	-1.61
SMKKTTTLSG	TAPAAGVVPSR	MAP4_HUMAN			Microtubule-associated protein 4;	-0.04	0.00	52.50	-5.03
VRQGTLKKAR	YNAQCQETIR	MK_HUMAN			Midkine;	0.51	0.05	43.50	-0.46

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
TKVRQGTLKK	ARYNAQCQETIR	MK_HUMAN			Midkine;	0.06	0.01	46.70	0.84
EESLKTDHPE	IGEGKPTPALSEEASSSSIR	IMMT_HUMAN			Mitochondrial inner	0.55	0.04	50.60	-2.11
SLYFGENRLR	STQAATQVVLNVPETR	MPPB_HUMAN			Mitochondrial-processing peptidase subunit beta;	-0.02	0.00	63.00	4.92
VLMDGSVKLV	TPEGSPVR	M4K1_HUMAN			Mitogen-activated protein kinase kinase kinase	3.09	0.40	26.30	-2.07
M	VGGGGVGGGLLENANPLIYQR	MIP18_HUMAN			Mitotic spindle-associated MMXD complex subunit	0.24	0.01	49.00	-0.92
VFKQPISCVK	EEIQETQTPTHSR	MK67I_HUMAN			MKI67 FHA domain-interacting nucleolar	0.40	0.02	28.10	-6.53
ELKTAMSTPH	VAEPAENEQDEQDENGAEASADL	MOES_HUMAN			Moesin;	5.69	0.79	61.00	0.73
LEKTRAELKT	AMSTPHVAEPAENEQDEQDENGA	MOES_HUMAN			Moesin;	4.62	0.83	42.00	-0.12
KTRAELKTAM	STPHVAEPAENEQDEQDENGAEAS	MOES_HUMAN			Moesin;	3.67	0.34	75.20	0.59
SEAEKLAKER	QEAEEAKEALLQASR	MOES_HUMAN			Moesin;	1.57	0.11	30.10	-3.87
EAVEWQQKAQ	MVQEDLEKTR	MOES_HUMAN			Moesin;	1.55	0.11	23.20	-2.14
LLLPLVHVSA	TTPEPCELDDEDFR	CD14_HUMAN			Monocyte differentiation	1.26	0.07	58.80	-1.14
KIPEELKPWL	VDDWDLITR	MO4L1_HUMAN			Mortality factor 4-like protein 1;	1.16	0.08	32.20	-0.86
IPEELKPWLV	DDWDLITR	MO4L1_HUMAN			Mortality factor 4-like	0.49	0.03	31.10	-2.71
IPEELKPWLV	EDWDLVTR	MO4L2_HUMAN			Mortality factor 4-like protein 2;	0.98	0.05	32.80	-2.26
CESPRSVECR	AEDAPGVPLR	MUC5A_HUMAN			Mucin-5AC;	2.58	0.30	37.00	-1.14
CSPDVGLTCR	NREQASGLCYNYQIR	MUC5A_HUMAN			Mucin-5AC;	2.09	0.17	35.80	-1.26
DDEAPDAETT	AAATTATTAAPTTATTAASTTAR	MUCL1_HUMAN			Mucin-like protein 1;	-3.25	0.31	31.30	0.05
ELLDSPGKVL	LQSKDQITAGNAAR	PUR6_HUMAN			Multifunctional protein	2.76	0.26	35.20	-3.27

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
RLMQGDQILM	VNGEDVR	MPDZ_HUMAN			Multiple PDZ domain protein;	3.39	0.06	21.00	-1.59
PMLQTVAKNK	DQGTYEDYVEGLR	MYL6_HUMAN			Myosin light polypeptide	0.04	0.00	59.60	-3.17
FTEDQTAEFK	EAFQLFDR	MYL6_HUMAN			Myosin light polypeptide	-1.86	0.14	24.70	-1.98
MERELEKSQR	SQISSVNSDVEALRR	MPRIP_HUMAN			Myosin phosphatase Rho-	-0.42	0.03	28.80	-1.41
PSAEKVPTTK	STLWQEEMR	MPRIP_HUMAN			Myosin phosphatase Rho-interacting protein;	-0.44	0.02	39.90	-1.49
VRAMEAEAAG	LREQLEEEAAAR	MYH14_HUMAN			Myosin-14;	1.55	0.14	36.70	-0.83
KGNLRVKQLK	RQLEEAEEEASR	MYH14_HUMAN			Myosin-14;	0.68	0.04	33.50	2.44
LEEKRRLEAR	IAQLEEELEEEQGNTELINDR	MYH9_HUMAN			Myosin-9;	2.89	0.28	55.90	-0.16
QKNMALKKIR	ELESQISELQEDLESER	MYH9_HUMAN			Myosin-9;	2.77	0.27	67.50	-3.10
YDKLEKTKTR	LQQELDDLLVDLDHQR	MYH9_HUMAN			Myosin-9;	2.31	0.13	65.00	-2.07
FSALESQLQD	TQELLQEENR	MYH9_HUMAN			Myosin-9;	2.22	0.14	29.90	-2.41
ANASRRKLQR	ELEDATETADAMNR	MYH9_HUMAN			Myosin-9;	1.53	0.18	49.50	-0.82
EKLQLQEQLQ	AETELCAEAEELR	MYH9_HUMAN			Myosin-9;	0.88	0.10	76.50	-3.29
KTKTRLQQEL	DDLLVDLDHQR	MYH9_HUMAN			Myosin-9;	0.73	0.06	45.90	-0.80
KKKMQQNIQE	LEEQLEEEESAR	MYH9_HUMAN			Myosin-9;	0.69	0.05	50.70	-1.34
QVRRTEKKLK	DVLLQVDDERR	MYH9_HUMAN			Myosin-9;	0.67	0.06	29.00	-0.29
EKTKTRLQQE	LDDLLVDLDHQR	MYH9_HUMAN			Myosin-9;	0.53	0.04	45.40	-2.50
KLEKTKTRLQ	QELDDLLVDLDHQR	MYH9_HUMAN			Myosin-9;	0.48	0.03	57.50	1.32
DFSALESQLQ	DTQELLQEENR	MYH9_HUMAN			Myosin-9;	0.31	0.02	47.00	-4.56
KASTRLKQLK	RQLEEAEEEAQR	MYH9_HUMAN			Myosin-9;	0.29	0.03	50.40	-5.65

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
DKLEKTKTRL	QQELDDLLVDLDHQR	MYH9_HUMAN			Myosin-9;	0.20	0.01	35.10	2.14
EVSSLKNKLR	RGDLPFVVPR	MYH9_HUMAN			Myosin-9;	-0.34	0.03	29.00	-2.10
LEKTKTRLQQ	ELDDLLVDLDHQR	MYH9_HUMAN			Myosin-9;	-0.49	0.03	41.70	-2.85
LFGFLWEASG	GLDSGASRDDDLLLPYPR	NAGPA_HUMAN			N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase;	0.76	0.05	54.50	-2.56
LRGASNLTWR	SDVLVEYQGEGR	GNS_HUMAN			N-acetylglucosamine-6-sulfatase;	0.06	0.00	40.70	-4.20
SVDQVKAQLR	TALASGGVLDASGDYR	B3GN1_HUMAN			N-acetyllactosaminide	4.85	0.39	68.00	-4.55
REPGEFALLR	SCQEVFDKLAR	B3GN1_HUMAN			N-acetyllactosaminide beta-1,3-N-	1.53	0.19	37.20	-2.13
KHKKEVGKLK	SMDLSEYIIR	NAT10_HUMAN			N-acetyltransferase 10;	-0.16	0.01	44.50	-2.93
DSPIPGAGAY	ADDTAGAAAATGNGDILMR	ASPG_HUMAN			N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	3.99	0.25	33.00	-3.46
DKSKPGQFIR	SVDPDSPAEASGLR	NHRF1_HUMAN			Na(+)/H(+) exchange regulatory cofactor NHE-	2.93	0.23	45.10	-1.82
NGEIQKENSR	EALAEAALESPRPALVR	NHRF1_HUMAN			Na(+)/H(+) exchange regulatory cofactor NHE-	2.81	0.12	28.70	-5.05
GVQVREELLR	AQEAPGQAEPPAAAEVQGAGNEN	NHRF1_HUMAN			Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	1.30	0.06	47.90	9.59
IQKENSREAL	AEAALESPRPALVR	NHRF1_HUMAN			Na(+)/H(+) exchange regulatory cofactor NHE-	0.71	0.04	30.20	-3.64
LRAQEAPGQA	EPPAAAEVQGAGNENEPR	NHRF1_HUMAN			Na(+)/H(+) exchange	0.66	0.05	112.20	-0.97
QKENSREALA	EAALESPRPALVR	NHRF1_HUMAN			Na(+)/H(+) exchange	0.31	0.02	22.90	-2.70
QEAPGQAEPP	AAAEVQGAGNENEPR	NHRF1_HUMAN			Na(+)/H(+) exchange regulatory cofactor NHE-	-0.37	0.02	85.40	-0.06
RNLHKTVMQN	GAGGALFVHR	NDUV2_HUMAN			NADH dehydrogenase	-0.66	0.03	46.30	1.38
ELLAEKMAVD	GGCGDTGDWEGR	UBA3_HUMAN			NEDD8-activating	-0.58	0.03	63.80	-1.54
IKNVNTALNT	TQIPSSIEDIFNDDR	ULA1_HUMAN			NEDD8-activating	1.06	0.10	59.50	-2.07

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
FEQNVQRSMR	GGYIGSTYFER	UBC12_HUMAN			NEDD8-conjugating enzyme Ubc12;	-1.55	0.09	33.30	-3.97
QESSRRPQRK	SLYESFVSSSDR	NELFE_HUMAN			Negative elongation factor	-0.58	0.03	47.20	-3.83
LGRRAPGAAA	ARSGSAPQSPGASIR	NEO1_HUMAN			Neogenin;	-1.93	0.15	36.50	-0.68
LGKGEYQESL	RSLEEEGQELPQSADVQR	NEST_HUMAN			Nestin;	1.53	0.21	56.60	-1.24
PSPTYTPILE	DAPGPQPQAEGSQEASWGVQGR	NEST_HUMAN			Nestin;	1.52	0.14	62.30	0.44
GEFLESDSVS	VSVPWDDSLR	NEST_HUMAN			Nestin;	0.95	0.07	43.40	5.24
FLQARTPTLA	STPIPPTPQAPSPAVDAEIR	NEST_HUMAN			Nestin;	0.31	0.01	43.00	-5.21
PGLSMFAGQA	AQPDPCSDENGHPR	NET1_HUMAN			Netrin-1;	0.23	0.01	25.00	-7.43
STELDVVESR	AQLLVVGSPGPVPR	L1CAM_HUMAN			Neural cell adhesion	6.49	0.76	42.80	-3.88
PSITWRGDGR	DLQELGDSDKYFIEDGR	L1CAM_HUMAN			Neural cell adhesion molecule L1;	3.25	0.35	36.70	-1.31
DYSDQGNYSC	VASTELDVVESR	L1CAM_HUMAN			Neural cell adhesion molecule L1;	1.43	0.12	44.20	3.00
DVKGPQVALK	GSRVDIETPNLEGTLTGPR	AHNK_HUMAN			Neuroblast differentiation-associated protein	0.74	0.04	48.00	-3.72
WTREVFSSCS	SEVVLSGDDEEYQR	AHNK_HUMAN			Neuroblast differentiation-associated protein	0.13	0.01	80.40	0.79
YTTKIKPRLK	SEDGVEGDLGETQSR	AHNK_HUMAN			Neuroblast differentiation-associated protein	-0.25	0.03	59.60	-2.92
GGSEGGRRRR	ELDPMDVR	NOTC1_HUMAN			Neurogenic locus notch homolog protein 1;	1.97	0.13	24.00	-1.49
QPCRAGGTCS	SDGMGFHCTCPPGVQGR	NOTC3_HUMAN			Neurogenic locus notch	-1.34	0.14	21.10	-1.21
FALLAAGVAP	LSWDLPEPR	NMB_HUMAN			Neuromedin-B;	0.09	0.01	28.00	-4.10
ALLAAGVAPL	SWDLPEPR	NMB_HUMAN			Neuromedin-B;	0.00	0.00	25.80	-4.08

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
GARQRGLGGR	GLQEAAEER	VGF_HUMAN			Neurosecretory protein	2.38	0.11	41.00	-3.97
GSAPEVRGAR	NSEPQDEGELFQGVDPR	VGF_HUMAN			Neurosecretory protein VGF;	1.83	0.11	79.80	-3.65
GVAAPFPKAR	RPESALLGGSEAGER	VGF_HUMAN			Neurosecretory protein	1.49	0.10	53.70	-2.76
PEASDPSEEL	EALASLLQELR	VGF_HUMAN			Neurosecretory protein	-1.04	0.11	48.50	-1.02
EAEAEERRLQ	EQEELENYIEHVLLR	VGF_HUMAN			Neurosecretory protein VGF;	-1.34	0.10	54.80	-0.67
ESPGPERVWR	ASWGEFQAR	VGF_HUMAN			Neurosecretory protein	-2.00	0.16	31.10	-3.41
SSPRPPRPSS	NPGLSLDAR	NTR2_HUMAN			Neurotensin receptor type 2;	2.87	0.17	27.10	-3.91
IDELEPRRPR	YRVPDVLVADPPIAR	GANAB_HUMAN			Neutral alpha-glucosidase	0.08	0.00	39.10	-1.69
LTSRLQGVGA	LGQAASDNSGPEDAKR	NOMO1_HUMAN	NOMO2_HUMAN	NOMO3_HUMAN	Nodal modulator 1;	0.23	0.02	41.30	-1.25
REQEIRMGQM	AMGGAMGINNR	NONO_HUMAN			Non-POU domain-	0.59	0.04	33.80	-3.30
AFSQFGPIER	AVVIVDDR	NONO_HUMAN	SFPQ_HUMAN		Non-POU domain-containing octamer-	-0.04	0.00	33.70	-1.19
ELALKATLVE	SSTSGFTPGGGGSSVSMIASR	NASP_HUMAN			Nuclear autoantigenic sperm protein;	0.16	0.02	93.90	-4.65
LKATLVESST	SGFTPGGGGSSVSMIASR	NASP_HUMAN			Nuclear autoantigenic	0.08	0.01	98.00	-1.54
QATEMLYMRL	DTMNTTCVDR	NCBP1_HUMAN			Nuclear cap-binding protein subunit 1;	-6.27	0.00	22.60	-6.49
IQKLQRQRLR	SRPQGLTEAEQR	NFKB2_HUMAN			Nuclear factor NF-kappa-B p100 subunit;	0.08	0.01	34.10	-3.35
NLNKTIQNSS	VSPTSSSSSSSTGETQTQSSSR	NUFP2_HUMAN			Nuclear fragile X mental retardation-interacting protein 2;	1.12	0.09	38.10	1.17
IPARSQAPLE	SSLDSLGDVFLDSGR	NUMA1_HUMAN			Nuclear mitotic apparatus	0.44	0.03	72.30	-3.37
ASSTSLVALS	AEATPATTGVPDAR	NU214_HUMAN			Nuclear pore complex protein Nup214;	0.73	0.07	47.60	-0.72

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
VSDSHFQRVS	AAVLPLVHPLPEGLR	NCOR1_HUMAN			Nuclear receptor corepressor 1;	0.11	0.01	41.90	0.87
GPSYSNNLAK	AGLNGASCHLEYSPER	RORG_HUMAN			Nuclear receptor ROR-gamma;	-3.66	0.46	31.20	0.11
VRNRKVVDYS	QFQESDDADEDYGR	NUCKS_HUMAN			Nuclear ubiquitous casein and cyclin-dependent	1.27	0.13	68.50	0.29
RGPPRQRQPR	EDGNEEDKENQGDETQGQQPPQR	YBOX1_HUMAN			Nuclease-sensitive	1.55	0.19	63.90	-1.53
RNYQQNYQNS	ESGEKNEGSESAPEGQAQQR	YBOX1_HUMAN			Nuclease-sensitive element-binding protein 1;	1.47	0.17	51.20	0.28
GPPRNYQQNY	QNSESGEKNEGSESAPEGQAQQR	YBOX1_HUMAN			Nuclease-sensitive	1.29	0.20	47.30	1.28
PRNYQQNYQN	SESGEKNEGSESAPEGQAQQR	YBOX1_HUMAN			Nuclease-sensitive	1.04	0.11	69.10	0.31
RRPYGRRPQY	SNPPVQGEVMEGADNQGAGEQG	YBOX1_HUMAN			Nuclease-sensitive	0.95	0.10	66.50	-1.44
EAELNAKAQR	LSQETEALGR	NUCB1_HUMAN			Nucleobindin-1;	3.16	0.22	40.70	3.36
SQGRLEAQKR	ELQQAVLHMEQR	NUCB1_HUMAN			Nucleobindin-1;	1.07	0.07	47.80	-2.12
SRSITRKRKR	EDSAPPSSVAR	NOG1_HUMAN			Nucleolar GTP-binding	-0.20	0.01	29.50	-1.66
SKISEKRKKK	LRLLEQQELR	NOL10_HUMAN			Nucleolar protein 10;	0.49	0.05	36.00	-2.92
IEEKGAVEAL	AAALAHISGATSVDQR	DDX21_HUMAN			Nucleolar RNA helicase 2;	1.35	0.07	31.10	-0.25
LAIKCHWTQR	AAVIGDVIR	DDX21_HUMAN			Nucleolar RNA helicase 2;	1.31	0.10	30.80	-4.35
EEKGAVEALA	AALAHISGATSVDQR	DDX21_HUMAN			Nucleolar RNA helicase 2;	0.90	0.08	44.60	-3.73
KTGISDVFAK	NDLAVVDVR	NUCL_HUMAN			Nucleolin;	2.26	0.07	36.40	-3.21
KTLFVKGLSE	DTTEETLKESFDGSVR	NUCL_HUMAN			Nucleolin;	1.63	0.16	32.20	-2.03
SQPSKTLFVK	GLSEDTTEETLKESFDGSVR	NUCL_HUMAN			Nucleolin;	1.28	0.10	27.40	-1.06
PELKTGISDV	FAKNDLAVVDVR	NUCL_HUMAN			Nucleolin;	0.91	0.03	32.80	-3.18
LPYKVTQDEL	KEVFEDAAEIR	NUCL_HUMAN			Nucleolin;	0.75	0.04	33.00	-2.56

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
NLPYKVTQDE	LKEVFEDAAEIR	NUCL_HUMAN			Nucleolin;	0.69	0.04	43.60	-3.49
PYKVTQDELK	EVFEDAAEIR	NUCL_HUMAN			Nucleolin;	0.57	0.03	51.80	-1.82
AKNLPYKVTQ	DELKEVFEDAAEIR	NUCL_HUMAN			Nucleolin;	0.52	0.03	52.60	-2.32
NFNKSAPELK	TGISDVFAKNDLAVVDVR	NUCL_HUMAN			Nucleolin;	0.42	0.03	35.20	-2.11
YKVTQDELKE	VFEDAAEIR	NUCL_HUMAN			Nucleolin;	-0.08	0.00	29.50	-1.94
FNKSAPELKT	GISDVFAKNDLAVVDVR	NUCL_HUMAN			Nucleolin;	-0.23	0.01	52.90	-1.32
KSAPELKTGI	SDVFAKNDLAVVDVR	NUCL_HUMAN			Nucleolin;	-0.23	0.01	30.20	-3.14
SAPELKTGIS	DVFAKNDLAVVDVR	NUCL_HUMAN			Nucleolin;	-0.25	0.02	42.90	1.54
LKADKDYHFK	VDNDENEHQLSLR	NPM_HUMAN			Nucleophosmin;	2.85	0.22	31.50	-3.30
DKDYHFKVDN	DENEHQLSLR	NPM_HUMAN			Nucleophosmin;	-0.29	0.02	23.70	3.53
ATLKMSVQPT	VSLGGFEITPPVVLR	NPM_HUMAN			Nucleophosmin;	-0.96	0.13	63.90	-1.48
LKMSVQPTVS	LGGFEITPPVVLR	NPM_HUMAN			Nucleophosmin;	-1.00	0.04	34.60	-8.10
VQPTVSLGGF	EITPPVVLR	NPM_HUMAN			Nucleophosmin;	-1.16	0.03	25.60	-2.74
TLKMSVQPTV	SLGGFEITPPVVLR	NPM_HUMAN			Nucleophosmin;	-1.39	0.07	48.70	-0.92
QPTVSLGGFE	ITPPVVLR	NPM_HUMAN			Nucleophosmin;	-1.60	0.10	25.00	-3.55
AEQRGQNLLL	TNLQTIQGILER	TPR_HUMAN			Nucleoprotein TPR;	0.93	0.07	39.50	-0.28
DGYEADDAEG	GDGTDPGTETEESMGGGEGNHR	TPR_HUMAN			Nucleoprotein TPR;	0.20	0.02	34.70	1.22
YEADDAEGGD	GTDPGTETEESMGGGEGNHR	TPR_HUMAN			Nucleoprotein TPR;	-0.79	0.07	57.90	-2.78
EGLNVVKTGR	VMLGETNPADSKPGTIR	NDKA_HUMAN	NDK8_HUMAN	NDKB_HUMAN	Nucleoside diphosphate kinase A;	3.15	0.23	35.40	-4.50
MANLER	TFIAIKPDGVQR	NDKA_HUMAN	NDKB_HUMAN		Nucleoside diphosphate kinase A;	1.58	0.10	21.70	-1.35
NVVKTGRVML	GETNPADSKPGTIR	NDKA_HUMAN	NDK8_HUMAN	NDKB_HUMAN	Nucleoside diphosphate	-0.60	0.04	35.10	-3.60

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
PQILAALQER	LDGLVETPTGYIESLPR	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	4.36	0.37	37.00	-1.11
QNPQILAALQ	ERLDGLVETPTGYIESLPR	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	1.66	0.12	53.40	-1.75
LKARQLTVQM	MQNPQILAALQER	NP1L1_HUMAN			Nucleosome assembly	1.34	0.11	64.10	-1.23
QVRCAHIEAK	FYEEVHDLER	NP1L1_HUMAN	NP1L4_HUMAN		Nucleosome assembly protein 1-like 1;	0.69	0.03	31.20	1.54
YEEVHDLERK	YAVLYQPLFDKR	NP1L1_HUMAN			Nucleosome assembly	0.20	0.01	27.10	-2.97
ILAALQERLD	GLVETPTGYIESLPR	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	-0.04	0.00	79.70	-0.78
DLDDDAEAIL	AADFEIGHFLR	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	-1.34	0.07	27.90	-1.75
LLLSGRPTRA	DSKVFGDLDQVR	OLM2A_HUMAN			Olfactomedin-like protein 2A;	1.07	0.08	42.30	-1.38
FLSFLSFSET	CYTLGIIPR	O10Z1_HUMAN			Olfactory receptor 10Z1;	-2.92	0.22	25.00	-7.18
GRVDEGPQPR	SVEPQDAGPLER	OGFR_HUMAN			Opioid growth factor	-0.29	0.01	40.10	-2.49
RNIEPHLKKA	MQTVYLR	ORC5_HUMAN			Origin recognition complex subunit 5;	4.45	0.24	25.10	-4.90
FGFYRSGQAK	ETIPLQETSLYTQDR	PPT1_HUMAN			Palmitoyl-protein thioesterase 1;	5.17	0.46	39.80	-1.92
QHQGVFGLPR	CPGESSHICDFIR	PPT1_HUMAN			Palmitoyl-protein thioesterase 1;	4.22	0.36	31.40	-2.24
VDSEWFGFYR	SGQAKETIPLQETSLYTQDR	PPT1_HUMAN			Palmitoyl-protein	1.20	0.09	57.00	-1.54
KALRERWLLE	GTPSSASEGDEDLR	PALM_HUMAN			Paralemmin-1;	1.83	0.17	59.40	-2.07
IEVTPSVLRA	NMPLHVR	PARD3_HUMAN			Partitioning defective 3 homolog;	1.42	0.13	33.40	-0.56
QQPQSSSPVY	GSSAKTSSVSNPQDSVGSPCSR	PAXI_HUMAN			Paxillin;	1.09	0.07	48.60	-3.68
SVAPANSALG	QTQPSDQDTLVQR	PDLI5_HUMAN			PDZ and LIM domain	2.17	0.13	23.80	-0.91

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TGRISNSATY	SGSVAPANSALGQTQPSDQDTLVQ	PDLI5_HUMAN			PDZ and LIM domain	0.41	0.04	41.70	4.45
AVLEELRQTR	ADLHAVQGWAAR	PTX3_HUMAN			Pentraxin-related protein	5.85	0.82	36.70	0.00
CAPGAPAEAR	LTSALDELLQATR	PTX3_HUMAN			Pentraxin-related protein PTX3;	5.57	0.41	68.90	0.75
EAQRPEEAGR	ALAAVLEELR	PTX3_HUMAN			Pentraxin-related protein	4.70	0.22	52.30	-2.78
LQRLREELGR	LAESLARPCAPGAPAEAR	PTX3_HUMAN			Pentraxin-related protein PTX3;	2.93	0.14	50.20	2.20
PGAPAEARLT	SALDELLQATR	PTX3_HUMAN			Pentraxin-related protein PTX3;	2.72	0.20	32.10	-2.41
AARSWLPAGC	ETAILFPMR	PTX3_HUMAN			Pentraxin-related protein PTX3;	1.13	0.06	25.20	-2.08
APGAPAEARL	TSALDELLQATR	PTX3_HUMAN			Pentraxin-related protein PTX3;	0.04	0.00	43.70	-1.78
SSGRVLGRFR	GKGSGGLNLGNFFASR	AMD_HUMAN			Peptidyl-glycine alpha-amidating	0.82	0.03	36.80	-0.73
KTEWLDGKHV	AFGKVKER	PAL4A_HUMAN	PAL4G_HUMAN		Peptidyl-prolyl cis-trans isomerase A-like 4A/B/C;	7.97	0.99	16.90	0.20
SCFHRIIPGF	MCQGGDFTR	PAL4A_HUMAN	PPIA_HUMAN		Peptidyl-prolyl cis-trans isomerase A-like 4A/B/C;	-0.89	0.03	30.00	-6.42
GKHVVFGKVK	EGMNIVEAMER	PPIA_HUMAN			Peptidyl-prolyl cis-trans isomerase A;	5.29	0.37	29.10	-4.59
FGYKGSCFHR	IIPGFMCQGGDFTR	PPIA_HUMAN	PAL4A_HUMAN		Peptidyl-prolyl cis-trans isomerase A;	1.53	0.07	31.50	-0.43
M	VNPTVFFDIAVDGEPLGR	PPIA_HUMAN			Peptidyl-prolyl cis-trans isomerase A;	0.24	0.03	90.80	0.25
FMLGKQEVIR	GWEEGVAQMSVGQR	FKB1A_HUMAN			Peptidyl-prolyl cis-trans	2.02	0.19	67.20	1.98
M	GVQVETISPGDGR	FKB1A_HUMAN			Peptidyl-prolyl cis-trans isomerase FKBP1A;	0.26	0.02	60.70	0.30
VTGQAAPVAG	LGSDAELQIER	FKBP9_HUMAN			Peptidyl-prolyl cis-trans isomerase FKBP9;	0.89	0.04	39.10	-1.19

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
TGKVSASFTS	TAMVPETTHEAAAIDEDVLR	PPIL2_HUMAN			Peptidyl-prolyl cis-trans isomerase-like 2;	-0.16	0.01	56.40	-1.04
RVLQEKKQKM	DKLLGELHTLR	PCM1_HUMAN			Pericentriolar material 1 protein;	4.01	0.65	22.50	-2.00
MSADGAEAD	GSTQVTVEEPVQQPSVVDR	PLIN3_HUMAN			Perilipin-3;	0.81	0.12	68.00	-5.02
NIPLVSDPKR	TIAQDYGVLKADEGISFR	PRDX1_HUMAN			Peroxiredoxin-1;	2.74	0.16	34.30	-1.03
TIAQDYGVLK	ADEGISFR	PRDX1_HUMAN			Peroxiredoxin-1;	1.20	0.02	29.90	-4.01
FIIDGKGVLR	QITVNDLPVGR	PRDX1_HUMAN	PRDX2_HUMAN		Peroxiredoxin-1;	0.78	0.05	37.40	1.93
YLEDSGHTLR	GLFIIDDKGILR	PRDX1_HUMAN	PRDX4_HUMAN		Peroxiredoxin-1;	0.62	0.03	29.40	-1.47
KRTIAQDYGV	LKADEGISFR	PRDX1_HUMAN			Peroxiredoxin-1;	-0.86	0.05	28.10	0.91
GLFIIDGKGV	LRQITVNDLPVGR	PRDX1_HUMAN	PRDX2_HUMAN		Peroxiredoxin-1;	-2.08	0.18	43.90	-3.89
IIDGKGVLRQ	ITVNDLPVGR	PRDX2_HUMAN	PRDX1_HUMAN		Peroxiredoxin-2;	-1.00	0.06	26.60	-0.54
TPRKEGGLGP	LNIPLLADVTR	PRDX2_HUMAN			Peroxiredoxin-2;	-2.16	0.19	41.30	-2.14
LLLFLLPAGA	VQGWETEERPR	PRDX4_HUMAN			Peroxiredoxin-4;	-0.18	0.02	21.80	-2.19
SWGILFSHPR	DFTPVCTTELGR	PRDX6_HUMAN			Peroxiredoxin-6;	2.34	0.22	37.40	4.77
MP	GGLLLGDVAPNFEANTTVGR	PRDX6_HUMAN			Peroxiredoxin-6;	0.90	0.12	62.80	-2.91
TSLTHTSRPP	AALTPVPLSQGDLSHPPR	PHF23_HUMAN			PHD finger protein 23;	0.21	0.01	31.80	-1.85
GEDKGGYVIK	ASEGPAFFPGR	SYFB_HUMAN			Phenylalanine--tRNA ligase beta subunit;	0.40	0.03	37.10	-6.83
LRKKGILPPK	ESLKELEEEAEEEQR	PDCL3_HUMAN			Phosducin-like protein 3;	0.71	0.05	46.30	-2.20
LVYEQDRPLK	CDEPILSNR	PEBP1_HUMAN			Phosphatidylethanolamine-binding protein 1;	1.81	0.07	33.70	-1.94
VWLVYEQDRP	LKCDEPILSNR	PEBP1_HUMAN			Phosphatidylethanolamine-binding protein 1;	0.91	0.07	36.40	-0.42
WDGLDSGKLY	TLVLTDPDAPSR	PEBP1_HUMAN			Phosphatidylethanolamine-	-0.63	0.06	35.20	5.30

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
SWDGLDSGKL	YTLVLTDPDAPSR	PEBP1_HUMAN			Phosphatidylethanolamine-binding protein 1;	-2.08	0.09	49.20	-0.74
IPENRIRSTR	SVENLPECGITHEQR	PI4KB_HUMAN			Phosphatidylinositol 4-kinase beta;	-0.34	0.03	36.60	-4.27
KDCVGPEVEK	ACANPAAGSVILLENLR	PGK1_HUMAN			Phosphoglycerate kinase 1;	3.00	0.15	67.90	2.17
IEAFRASLSK	LGDVYVNDAFGTAHR	PGK1_HUMAN	PGK2_HUMAN		Phosphoglycerate kinase 1;	2.11	0.18	66.60	-1.50
EAFRASLSKL	GDVYVNDAFGTAHR	PGK1_HUMAN	PGK2_HUMAN		Phosphoglycerate kinase	-0.89	0.07	33.90	-4.69
CVGPEVEKAC	ANPAAGSVILLENLR	PGK1_HUMAN			Phosphoglycerate kinase 1;	-1.08	0.05	72.80	0.19
RASLSKLGDV	YVNDAFGTAHR	PGK1_HUMAN	PGK2_HUMAN		Phosphoglycerate kinase 1;	-1.20	0.06	28.30	3.89
PEVEKACANP	AAGSVILLENLR	PGK1_HUMAN			Phosphoglycerate kinase	-1.66	0.16	39.10	-3.10
IVPQIKAGKR	VLIAAHGNSLR	PGAM1_HUMAN	PGAM2_HUMAN		Phosphoglycerate mutase	1.40	0.06	39.10	-2.88
TERNWSLPNR	AVEPQLQEEER	PLTP_HUMAN			Phospholipid transfer protein;	3.41	0.21	47.40	-4.13
LELVKQEGLR	FLEQELETITIPDLR	PLTP_HUMAN			Phospholipid transfer protein;	2.03	0.21	29.90	-2.00
PVLYHAGTVL	LNSLLDTVPVR	PLTP_HUMAN			Phospholipid transfer	0.09	0.01	31.40	-1.82
GISVLEMSHR	SSDFAKIINNTENLVR	SERC_HUMAN			Phosphoserine	2.20	0.11	30.90	-2.71
VGSAGVTVVI	VRDDLLGFALR	SERC_HUMAN			Phosphoserine	0.52	0.02	44.80	-0.38
KVIFLQGGGC	GQFSAVPLNLIGLKAGR	SERC_HUMAN			Phosphoserine	0.37	0.02	32.00	-1.72
VRGHWFLSPR	TEYTVAVQTASK	PHIPL_HUMAN			Phytanoyl-CoA hydroxylase-interacting protein-like;	3.91	0.23	29.80	-3.91
ALLLWSSLGA	DDGVAEVLAR	CQ101_HUMAN			PKHD domain-containing	-0.08	0.01	46.80	-2.13
LPPPPCPAHS	ATRFDPTWESLDAR	FUCO2_HUMAN			Plasma alpha-L-fucosidase;	1.06	0.07	35.20	-5.12
YNQKSIHSFM	THPEFAIEEELPR	AT2B4_HUMAN			Plasma membrane calcium-transporting ATPase 4;	1.66	0.05	32.00	0.75
PYNQKSIHSF	MTHPEFAIEEELPR	AT2B4_HUMAN			Plasma membrane calcium-transporting	0.84	0.02	52.00	-2.55

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MPG	HLQEGFGCVVTNR	PAIRB_HUMAN			Plasminogen activator inhibitor 1 RNA-binding	0.81	0.07	36.90	-1.81
GGGVGGPGAK	SAAQAAAQTNSNAAGKQLR	PAIRB_HUMAN			Plasminogen activator	-0.55	0.06	40.40	-3.47
IWPPCVEVKR	CTGCCNTSSVKCQPSR	PDGFA_HUMAN			Platelet-derived growth	1.56	0.13	22.50	-1.79
KRPLPIRRKR	SIEEAVPAVCKTR	PDGFA_HUMAN			Platelet-derived growth factor subunit A;	1.53	0.08	45.60	-2.22
GCGYLAHVLA	EEAEIPR	PDGFA_HUMAN			Platelet-derived growth	1.21	0.06	30.20	-1.60
GCGYLAHVLA	EEAEIPREVIER	PDGFA_HUMAN			Platelet-derived growth	1.03	0.12	31.10	1.67
EAEAAREKQR	ALQALEELR	PLEC_HUMAN			Plectin;	3.91	0.54	41.10	-4.48
QLAEGTAQQR	LAAEQELIR	PLEC_HUMAN			Plectin;	2.53	0.13	40.80	-0.28
IEEFRAKIER	ARSDEGQLSPATR	PLEC_HUMAN			Plectin;	2.48	0.09	41.60	-3.03
RMVEGYQGLR	CDNFTSSWR	PLEC_HUMAN			Plectin;	2.09	0.15	27.10	-1.91
KQRLEAEAGR	FRELAEEAAR	PLEC_HUMAN			Plectin;	1.80	0.10	28.30	0.00
QLGRQLRYYR	ESADPLGAWLQDAR	PLEC_HUMAN			Plectin;	1.67	0.10	61.00	2.44
ATKASLKKLR	AQAEAQQPTFDALRDELR	PLEC_HUMAN			Plectin;	1.65	0.14	40.50	-2.06
MPLADSQAVR	EQLRQEQALLEEIER	PLEC_HUMAN			Plectin;	1.51	0.07	35.10	-2.35
AAVDAQQQKR	SIQEELQQLR	PLEC_HUMAN			Plectin;	1.42	0.09	48.10	-1.18
VRLQLEATER	QRGGAEGELQALR	PLEC_HUMAN			Plectin;	1.39	0.07	41.60	3.04
LKAEATEAAR	QRSQVEEELFSVR	PLEC_HUMAN			Plectin;	1.20	0.05	29.60	-1.47
QLQRGERSVR	DVAEVDTVR	PLEC_HUMAN			Plectin;	0.95	0.12	37.70	-1.35
LQQRCRPDQL	TGLSLLPLSEKAAR	PLEC_HUMAN			Plectin;	0.74	0.05	32.30	-5.70
RRKVSAQRLQ	EAGILSAEELQR	PLEC_HUMAN			Plectin;	0.72	0.05	59.20	-0.52

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
IIDRRSGRQY	DIDDAIAKNLIDR	PLEC_HUMAN			Plectin;	0.67	0.06	33.00	-4.67
MEELVRSQVM	DEATALQLR	PLEC_HUMAN			Plectin;	0.47	0.03	40.20	-1.24
SAPRADAKAY	SDPSTGEPATYGELQQR	PLEC_HUMAN			Plectin;	0.45	0.04	45.80	-6.92
LLQETQALQQ	SFLSEKDSLLQR	PLEC_HUMAN			Plectin;	0.45	0.03	25.30	1.14
YTQLLRRCRR	DDGTGQLLLPLSDAR	PLEC_HUMAN			Plectin;	0.40	0.03	43.60	-1.31
LPSDMAVALL	EAQAGTGHIIDPATSAR	PLEC_HUMAN			Plectin;	0.18	0.01	35.70	1.44
VVPATTQRTL	ARPGPEPAPATDER	PLEC_HUMAN			Plectin;	0.13	0.02	42.10	-1.87
QLQRGERSVR	DVAEVDTVRR	PLEC_HUMAN			Plectin;	-0.10	0.01	28.70	-1.43
PSDMAVALLE	AQAGTGHIIDPATSAR	PLEC_HUMAN			Plectin;	-0.23	0.01	32.20	-2.68
EAAVDAQQQK	RSIQEELQQLR	PLEC_HUMAN			Plectin;	-0.49	0.04	33.70	-1.74
RLTVDEAVRK	GLVGPELHDR	PLEC_HUMAN			Plectin;	-0.55	0.02	40.90	-1.33
LLPLSEKAAR	ARQEELYSELQAR	PLEC_HUMAN			Plectin;	-0.58	0.06	52.20	2.03
KGRLCFEGLR	SLVPAAELLESR	PLEC_HUMAN			Plectin;	-0.58	0.03	47.10	-2.42
MLSGNAGGFR	SRSSSVGSSSSYPISPAVSR	PLEC_HUMAN			Plectin;	-0.76	0.04	48.80	-3.88
VAYQRGYLNK	DTHDQLSEPSEVR	PLEC_HUMAN			Plectin;	-0.82	0.06	38.10	-1.87
ALSAPRADAK	AYSDPSTGEPATYGELQQR	PLEC_HUMAN			Plectin;	-0.86	0.08	82.40	2.57
EAGVSDMKLG	DQGPPEEAEDR	PODXL_HUMAN			Podocalyxin;	0.20	0.01	30.70	-0.08
TVTNAVGMGR	AEQVIFVR	PVRL2_HUMAN			Poliovirus receptor-related protein 2;	1.11	0.07	35.50	-2.22
ILSPWGAEVK	AEPVEVVAPR	PARP1_HUMAN			Poly [ADP-ribose]	1.00	0.10	44.10	-2.10

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TSSESIPQTA	TQPAISPPPKPTVSR	PAPOA_HUMAN			Poly(A) polymerase alpha;	1.95	0.13	31.20	0.49
NNLIGCIIGR	QGANINEIR	PCBP1_HUMAN			Poly(rC)-binding protein 1;	1.91	0.14	27.40	-4.22
LSQSPQGRVM	TIPYQPMPASSPVICAGGQDR	PCBP1_HUMAN			Poly(rC)-binding protein 1;	1.85	0.20	58.60	1.80
KGGSKIKEIR	ESTGAQVQVAGDMLPNSTER	PCBP1_HUMAN	PCBP2_HUMAN	PCBP3_HUMAN	Poly(rC)-binding protein 1;	1.66	0.09	83.80	0.89
LDAYSIQGQH	TISPLDLAKLNQVAR	PCBP1_HUMAN			Poly(rC)-binding protein 1;	1.50	0.12	29.50	-1.46
EVKGYWASLD	ASTQTTHELTIPNNLIGCIIGR	PCBP1_HUMAN			Poly(rC)-binding protein	0.99	0.06	63.70	1.60
PASTHELTIP	NDLIGCIIGR	PCBP2_HUMAN	PCBP3_HUMAN		Poly(rC)-binding protein 2;	1.28	0.07	36.90	2.67
PEVKGYWGLD	ASAQTTSHELTIPNDLIGCIIGR	PCBP2_HUMAN			Poly(rC)-binding protein 2;	0.89	0.05	50.30	-0.04
QQQQLTNLQM	AAVTMGFGDPLSPLQSMAAQR	PUF60_HUMAN			Poly(U)-binding-splicing factor PUF60;	0.61	0.06	33.50	-2.25
TNLQMAAVTM	GFGDPLSPLQSMAAQR	PUF60_HUMAN			Poly(U)-binding-splicing	0.57	0.03	66.90	-3.64
QVVNLYVKNL	DDGIDDERLR	PABP1_HUMAN	PABP3_HUMAN		Polyadenylate-binding protein 1;	1.36	0.10	25.70	-0.97
ITRYQVVNLY	VKNLDDGIDDER	PABP1_HUMAN	PABP3_HUMAN		Polyadenylate-binding protein 1;	0.89	0.05	42.50	-2.14
VKVMTDESGK	SKGFGFVSFER	PABP1_HUMAN	PABP3_HUMAN		Polyadenylate-binding	0.65	0.03	23.60	-1.29
STQTVGPRPA	AAAAAAATPAVR	PABP1_HUMAN	PABP3_HUMAN		Polyadenylate-binding	0.45	0.02	43.90	-0.37
LKATEMVEVG	ADDDEGGAERGEAGDLR	PTRF_HUMAN			Polymerase I and	0.90	0.10	27.40	-4.25
EVLKATEMVE	VGADDDEGGAERGEAGDLR	PTRF_HUMAN			Polymerase I and transcript release factor;	0.87	0.10	27.40	-3.12
KATEMVEVGA	DDDEGGAERGEAGDLR	PTRF_HUMAN			Polymerase I and	0.81	0.08	26.70	-2.77
EDAAALELSS	DEAVEVEEVIEESR	PTRF_HUMAN			Polymerase I and transcript release factor;	0.78	0.05	76.90	-0.84

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
IREGQVEVLK	ATEMVEVGADDDEGGAERGEAGI	PTRF_HUMAN			Polymerase I and transcript release factor;	0.51	0.06	53.50	-1.20
GQVEVLKATE	MVEVGADDDEGGAER	PTRF_HUMAN			Polymerase I and	0.38	0.04	55.40	-0.32
IREGQVEVLK	ATEMVEVGADDDEGGAER	PTRF_HUMAN			Polymerase I and	0.31	0.03	93.50	0.11
SLERQAGQIK	KLEVNEAELLR	PTRF_HUMAN			Polymerase I and transcript release factor;	0.18	0.02	28.30	-2.31
LKTSRDKLRK	SFTPDHVVYAR	PTRF_HUMAN			Polymerase I and transcript release factor;	-0.06	0.00	34.10	-2.56
DAERVDQAYR	ENGFNIYVSDK	GLT10_HUMAN			Polypeptide N-	1.89	0.21	31.00	-2.90
FAFLWVLGIA	YYMYSGGGSALAGGAGGGAGR	GALT2_HUMAN			Polypeptide N-acetylgalactosaminyltrans	0.56	0.05	104.40	-1.57
AFLWVLGIAY	YMYSGGGSALAGGAGGGAGR	GALT2_HUMAN			Polypeptide N-	0.52	0.05	113.90	-1.54
FLWVLGIAYY	MYSGGGSALAGGAGGGAGR	GALT2_HUMAN			Polypeptide N-	0.41	0.04	99.40	-0.19
LWVLGIAYYM	YSGGGSALAGGAGGGAGR	GALT2_HUMAN			Polypeptide N-	0.18	0.02	88.60	-1.72
LTVAYIFVEL	LVSTFHASAGAGR	GALT4_HUMAN			Polypeptide N-	0.42	0.03	21.10	-2.07
ALAASAAAVD	AGMAMAGQSPVLR	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	0.11	0.01	64.00	-1.75
AFGLSVPNVH	GALAPLAIPSAAAAAAAAGR	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	-0.16	0.01	84.80	0.64
MD	GIVPDIAVGTKR	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	-0.32	0.02	49.50	-2.39
MAE	APPRRLGLGPPPGDAPR	KCNQ4_HUMAN			Potassium voltage-gated channel subfamily KQT	0.35	0.02	36.20	-4.15
HVPNSVRLWK	AAVELEEPEDAR	PRP6_HUMAN			Pre-mRNA-processing factor 6;	0.48	0.03	43.50	0.66
SAPSTSRTTA	SEPVEQSEATSKDCSR	FL2D_HUMAN			Pre-mRNA-splicing	1.33	0.18	24.10	-1.34
AANPVDFLSK	ASEIMVDDEELAQHPATTEDIR	RRMJ3_HUMAN			pre-rRNA processing protein FTSJ3;	0.04	0.00	79.10	-0.72
VIASSKKAKR	DLIDNSFNR	RRMJ3_HUMAN			pre-rRNA processing	-0.89	0.03	29.60	-3.46
TQEMLEEAKK	NLQEEIDALESR	PFD4_HUMAN			Prefoldin subunit 4;	2.34	0.14	59.20	-1.25
DLERQSEQQR	ETLAQLQQEFQR	PFD6_HUMAN			Prefoldin subunit 6;	4.34	0.36	49.80	-0.79

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
QLAAKEAKLR	DLEDSLAR	LMNA_HUMAN			Prelamin-A/C;	6.50	0.42	37.40	-2.43
RLAVYIDRVR	SLETENAGLR	LMNA_HUMAN			Prelamin-A/C;	5.42	0.69	43.50	3.58
ETENAGLRLR	ITESEEVVSR	LMNA_HUMAN			Prelamin-A/C;	5.03	0.46	37.00	-8.41
ALSTALSEKR	TLEGELHDLR	LMNA_HUMAN			Prelamin-A/C;	4.55	0.27	31.10	-2.80
ALDMEINAYR	KLLEGEEER	LMNA_HUMAN	LMNB1_HUMAN	LMNB2_HUMAN	Prelamin-A/C;	3.65	0.41	36.00	-6.04
LDNARQSAER	NSNLVGAAHEELQQSR	LMNA_HUMAN			Prelamin-A/C;	3.62	0.30	51.10	-0.73
NGKQREFESR	LADALQELR	LMNA_HUMAN			Prelamin-A/C;	3.32	0.10	36.50	-2.74
FSQHARTSGR	VAVEEVDEEGKFVR	LMNA_HUMAN			Prelamin-A/C;	2.59	0.14	30.70	-3.25
TVTRSYRSVG	GSGGGSFGDNLVTR	LMNA_HUMAN			Prelamin-A/C;	2.46	0.09	58.90	-1.32
NTWGCGNSLR	TALINSTGEEVAMR	LMNA_HUMAN			Prelamin-A/C;	2.44	0.26	55.40	-1.25
LSPTRITRLQ	EKEDLQELNDR	LMNA_HUMAN			Prelamin-A/C;	1.15	0.07	35.90	4.22
HSPPTDLVWK	AQNTWGCGNSLR	LMNA_HUMAN			Prelamin-A/C;	0.71	0.06	43.60	0.86
TPSQRRATRS	GAQASSTPLSPTR	LMNA_HUMAN			Prelamin-A/C;	0.61	0.04	39.90	-5.51
SASGSGAQVG	GPISSGSSASSVTVTR	LMNA_HUMAN			Prelamin-A/C;	0.59	0.06	73.70	-1.51
ADKASASGSG	AQVGGPISSGSSASSVTVTR	LMNA_HUMAN			Prelamin-A/C;	0.52	0.07	79.90	0.27
SVTVTRSYRS	VGGSGGGSFGDNLVTR	LMNA_HUMAN			Prelamin-A/C;	0.42	0.04	57.70	-3.56
VTVTRSYRSV	GGSGGGSFGDNLVTR	LMNA_HUMAN			Prelamin-A/C;	0.38	0.02	71.00	-2.83
SSVTVTRSYR	SVGGSGGGSFGDNLVTR	LMNA_HUMAN			Prelamin-A/C;	0.28	0.02	99.10	0.50
DAENRLQTMK	EELDFQKNIYSEELR	LMNA_HUMAN			Prelamin-A/C;	0.18	0.01	33.50	1.16

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
HHHGSHCSSS	GDPAEYNLR	LMNA_HUMAN			Prelamin-A/C;	0.16	0.01	40.60	-5.05
ARQSAERNSN	LVGAAHEELQQSR	LMNA_HUMAN			Prelamin-A/C;	0.16	0.01	33.30	-5.56
LHHHHGSHCS	SSGDPAEYNLR	LMNA_HUMAN			Prelamin-A/C;	0.08	0.01	47.20	-5.17
SLETENAGLR	LRITESEEVVSR	LMNA_HUMAN			Prelamin-A/C;	0.06	0.00	36.30	-1.99
QRRATRSGAQ	ASSTPLSPTR	LMNA_HUMAN			Prelamin-A/C;	-0.02	0.00	35.20	7.61
ASSVTVTRSY	RSVGGSGGGSFGDNLVTR	LMNA_HUMAN			Prelamin-A/C;	-0.02	0.00	44.20	-1.08
ETPSQRRATR	SGAQASSTPLSPTR	LMNA_HUMAN			Prelamin-A/C;	-0.02	0.00	67.80	-1.36
PSQRRATRSG	AQASSTPLSPTR	LMNA_HUMAN			Prelamin-A/C;	-0.06	0.00	52.10	-2.97
SAERNSNLVG	AAHEELQQSR	LMNA_HUMAN			Prelamin-A/C;	-0.25	0.01	27.20	2.24
CGTCGQPADK	ASASGSGAQVGGPISSGSSASSVTV	LMNA_HUMAN			Prelamin-A/C;	-0.47	0.06	118.80	0.38
QKQLAAKEAK	LRDLEDSLAR	LMNA_HUMAN			Prelamin-A/C;	-0.47	0.04	33.80	-0.33
MGNWQIKRQN	GDDPLLTYR	LMNA_HUMAN			Prelamin-A/C;	-0.66	0.06	31.10	-3.99
KDLEALLNSK	EAALSTALSEKR	LMNA_HUMAN			Prelamin-A/C;	-0.76	0.04	23.70	-0.30
NDRLAVYIDR	VRSLETENAGLR	LMNA_HUMAN			Prelamin-A/C;	-0.96	0.08	41.90	3.91
LETENAGLRL	RITESEEVVSR	LMNA_HUMAN			Prelamin-A/C;	-1.00	0.10	34.80	0.52
PPTDLVWKAQ	NTWGCGNSLR	LMNA_HUMAN			Prelamin-A/C;	-1.12	0.07	23.50	-0.08
PPRTVSGRYK	STTSVSEEDVSSR	PAWR_HUMAN			PRKC apoptosis WT1 regulator protein;	-1.16	0.10	63.50	-0.99

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LASLLGAALA	GPVLGLKECTR	SAP_HUMAN			Proactivator polypeptide;	2.39	0.05	64.60	-2.46
PRSKPQPKDN	GDVCQDCIQMVTDIQTAVR	SAP_HUMAN			Proactivator polypeptide;	0.67	0.04	98.90	-0.63
GASSTTSTGR	SSQSSSQQFSGIGR	DDX17_HUMAN			Probable ATP-dependent RNA helicase DDX17;	0.20	0.02	63.00	-2.08
GGGGGRSRYR	TTSSANNPNLMYQDECDRR	DDX17_HUMAN			Probable ATP-dependent	-0.34	0.03	29.30	3.29
LREHGEKKKR	SREDAGDNDDTEGAIGVR	DDX47_HUMAN			Probable ATP-dependent RNA helicase DDX47;	0.00	0.00	61.50	-0.16
DELPKFEKNF	YQEHPDLAR	DDX5_HUMAN			Probable ATP-dependent RNA helicase DDX5;	1.20	0.09	28.00	1.04
DVEDVKFVIN	YDYPNSSEDYIHR	DDX5_HUMAN			Probable ATP-dependent RNA helicase DDX5;	-0.02	0.00	36.90	-3.89
EEIMSEKENK	TIVFVETKR	DDX5_HUMAN			Probable ATP-dependent	-0.63	0.04	22.90	0.43
DKQTQNDLVT	GANLMDIIR	DDX59_HUMAN			Probable ATP-dependent	3.65	0.29	33.90	-2.13
M	KDSLVLLGR	CIAO1_HUMAN			Probable cytosolic iron-sulfur protein assembly	0.69	0.04	36.20	-0.25
KVNKGIYLKE	EKGVTLLYYGR	GP133_HUMAN			Probable G-protein coupled receptor 133;	1.91	0.09	25.50	-6.36
APDDYERINR	QLIEAKMALQDR	AT11C_HUMAN			Probable phospholipid-	5.56	1.11	39.70	-2.38
YAVRDTIALC	TAESIDTLR	AT11C_HUMAN			Probable phospholipid-transporting ATPase IG;	3.27	0.32	33.50	-0.77
YCLHGQCIYL	VDMSQNYCR	EREG_HUMAN			Proepiregulin;	1.52	0.13	23.60	-4.99
LGGQKCSVIR	DSLLQDGEFSMDLR	PROF1_HUMAN			Profilin-1;	6.80	0.45	81.00	-0.30
EVGVLVGKDR	SSFYVNGLTLGGQKCSVIR	PROF1_HUMAN			Profilin-1;	3.32	0.28	35.10	-1.17
GVHGGLINKK	CYEMASHLR	PROF1_HUMAN			Profilin-1;	2.50	0.15	38.60	-2.01
PSVWAAVPGK	TFVNITPAEVGVLVGKDR	PROF1_HUMAN			Profilin-1;	2.36	0.05	31.30	-0.66

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
GDCTMDIRTK	SQGGEPTYNVAVGR	PROF2_HUMAN			Profilin-2;	-0.25	0.01	55.00	-3.62
SAPSIPTPAY	QSSPAGGHAPTPPTPAPR	PDC6I_HUMAN			Programmed cell death 6-	0.69	0.03	30.50	1.82
APSIPTPAYQ	SSPAGGHAPTPPTPAPR	PDC6I_HUMAN			Programmed cell death 6-	0.61	0.02	36.30	-1.90
EAKHREAEMR	NSILAQVLDQSAR	PDCD5_HUMAN			Programmed cell death protein 5;	4.42	0.68	64.20	-2.70
LGGGRDRKVR	DLQEADLDLLR	HBEGF_HUMAN			Proheparin-binding EGF-	0.44	0.04	43.70	-0.08
MKVLRAWL	LCLLMLGLALR	PRRP_HUMAN			Prolactin-releasing peptide;	0.06	0.01	26.30	-1.46
SGPFEPDLYK	SEMEVQDAELKALLQSSASR	PA2G4_HUMAN			Proliferation-associated protein 2G4;	0.40	0.02	47.30	-1.42
FIANVAHTFV	VDVAQGTQVTGR	PA2G4_HUMAN			Proliferation-associated protein 2G4;	-0.47	0.03	43.60	-0.24
VQQAVARRPR	DLPAIQPR	PROSC_HUMAN			Proline synthase co-transcribed bacterial homolog protein;	0.41	0.01	34.50	-1.48
SLAAVLLAVY	YGLIWVPTR	PRR24_HUMAN			Proline-rich protein 24;	0.06	0.00	29.50	-0.97
YFSYSHLVCR	TAIEEVQAER	P3H1_HUMAN			Prolyl 3-hydroxylase 1;	0.13	0.01	30.30	-2.47
CEGGHVLHHG	VCQENCPER	PCSK5_HUMAN			Proprotein convertase subtilisin/kexin type 5;	5.23	0.26	29.60	-1.23
THLAGVVSGR	DAGVAKGASMR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	7.08	1.35	21.00	-2.32
PTRMATAVAR	CAPDEELLSCSSFSR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	5.02	0.36	77.00	-0.78
QSDHREIEGR	VMVTDFENVPEEDGTR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	4.80	0.27	63.90	0.64
EAQGGKLVCR	AHNAFGGEGVYAIAR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	4.70	0.54	89.70	-0.83
RQRLIHFSAK	DVINEAWFPEDQR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	0.24	0.01	44.00	-7.16

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AAHVAGIAAM	MLSAEPELTLAELR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-0.66	0.03	36.70	0.56
VAGIAAMMLS	AEPELTLAELR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-0.93	0.04	32.10	-2.04
AHVAGIAAMM	LSAEPELTLAELR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-0.96	0.04	48.50	-1.22
SQLVQPVGPL	VVLLPLAGGYSR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-1.04	0.06	34.10	-1.25
VITVGATNAQ	DQPVTLGTLGTNFGR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-1.08	0.09	63.80	-1.24
LIHFSAKDVI	NEAWFPEDQR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-1.08	0.09	32.70	-1.66
RCCLLPQANC	SVHTAPPAEASMGTR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-1.20	0.08	27.70	-2.97
CLYSPASAPE	VITVGATNAQDQPVTLGTLGTNFG	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-1.20	0.11	46.10	-0.97
LEFIRKSQLV	QPVGPLVVLLPLAGGYSR	PCSK9_HUMAN			Proprotein convertase	-1.39	0.15	56.10	-2.24
GLEFIRKSQL	VQPVGPLVVLLPLAGGYSR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-1.39	0.15	68.40	-3.76
LNCQGKGTVS	GTLIGLEFIR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	-1.44	0.12	36.90	-4.59
KSQLVQPVGP	LVVLLPLAGGYSR	PCSK9_HUMAN			Proprotein convertase	-1.86	0.07	36.40	-0.72
QLLRVWGAPR	NSDPALGLDDDPDAPAAQLAR	PCSK1_HUMAN			ProSAAS;	5.80	0.70	99.10	3.63
PELLRYLLGR	ILAGSADSEGVAAPR	PCSK1_HUMAN			ProSAAS;	4.19	0.40	71.10	-0.69
AAGAVQELAR	ALAHLLEAER	PCSK1_HUMAN			ProSAAS;	2.63	0.16	30.90	2.17
PRRFRRSVPR	GEAAGAVQELAR	PCSK1_HUMAN			ProSAAS;	2.32	0.13	60.00	-1.92

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AAPRRLRRAA	DHDVGSELPPEGVLGALLR	PCSK1_HUMAN			ProSAAS;	1.31	0.08	59.40	-2.05
VKEPRGLSAA	SPPLAETGAPR	PCSK1_HUMAN			ProSAAS;	1.28	0.08	35.50	-2.76
PVKEPRGLSA	ASPPLAETGAPR	PCSK1_HUMAN			ProSAAS;	1.11	0.03	31.10	1.00
GVAAPRRLRR	AADHDVGSELPPEGVLGALLR	PCSK1_HUMAN			ProSAAS;	1.09	0.01	73.70	-2.61
RRLRRAADHD	VGSELPPEGVLGALLR	PCSK1_HUMAN			ProSAAS;	1.02	0.11	40.30	-1.40
ETGAPRRFRR	SVPRGEAAGAVQELAR	PCSK1_HUMAN			ProSAAS;	0.90	0.03	65.10	-1.34
LLRVWGAPRN	SDPALGLDDDPDAPAAQLAR	PCSK1_HUMAN			ProSAAS;	0.87	0.08	90.20	2.21
RNSDPALGLD	DDPDAPAAQLAR	PCSK1_HUMAN			ProSAAS;	-0.14	0.01	31.90	0.00
VDFNNWKDWE	DDSDEDMSNFDR	TEBP_HUMAN			Prostaglandin E synthase 3;	0.40	0.04	52.10	4.14
GVLGDLQAAP	EAQVSVQPNFQQDKFLGR	PTGDS_HUMAN			Prostaglandin-H2 D-isomerase;	4.31	0.45	30.20	0.74
LLGVLGDLQA	APEAQVSVQPNFQQDKFLGR	PTGDS_HUMAN			Prostaglandin-H2 D-isomerase;	3.47	0.17	38.00	-1.90
PGSSSSSSSR	SQSAAVTPSSTTSSTR	ADRM1_HUMAN			Proteasomal ubiquitin receptor ADRM1;	0.88	0.03	55.70	-0.63
RARVECQSHR	LTVEDPVTVEYITR	PSA7L_HUMAN	PSA7_HUMAN		Proteasome subunit alpha type-7-like;	3.73	0.39	39.40	-4.21
KICALDDNVC	MAFAGLTADAR	PSA7_HUMAN			Proteasome subunit alpha type-7;	-1.66	0.05	29.60	-1.29
GYVDMLGVAY	EAPSLATGYGAYLAQPLLR	PSB4_HUMAN			Proteasome subunit beta	-0.37	0.04	43.90	-0.69
EEPGIEMLHG	TTTLAFKFR	PSB5_HUMAN			Proteasome subunit beta	0.29	0.02	16.90	0.09
YKLPKVRKTG	TTIAGVVYKDGIVLGADTR	PSB7_HUMAN			Proteasome subunit beta	0.67	0.04	63.90	-1.14
GQATAADQEK	NPEGDGLLEYSTFNFWR	AF1Q_HUMAN			Protein AF1q;	-6.27	0.00	40.70	-3.80
QRRRKFLNLR	FRTGSGQGPSSTGQPGR	AHNK2_HUMAN			Protein AHNAK2;	2.21	0.22	51.70	-5.04

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
PRAQPTPGMS	REGEGEGLQSLEIGIAR	AHNK2_HUMAN			Protein AHNAK2;	1.93	0.10	40.60	0.00
QSVVEVPYAR	SEAHLTELLEEICDR	CNPY2_HUMAN			Protein canopy homolog 2;	0.16	0.00	33.10	-0.76
LPSKCEVCKL	LSTELQAELSR	CNPY4_HUMAN			Protein canopy homolog 4;	1.21	0.05	40.10	-3.14
FLVALIIWCY	LREESEADQWLR	CSMT1_HUMAN			Protein CCSMST1;	0.84	0.05	49.10	-1.79
CFLVALIIWC	YLREESEADQWLR	CSMT1_HUMAN			Protein CCSMST1;	0.24	0.01	35.90	-0.70
EDSEVLMMIK	TQSSLVPALTDFVR	CUTA_HUMAN			Protein CutA;	2.72	0.07	46.80	-1.54
IAVGKGSSLK	RLPVFGMEPR	CYR61_HUMAN			Protein CYR61;	-1.49	0.04	51.20	-0.89
MEDQDGLLGK	ELGFDASEVELTR	CYR61_HUMAN			Protein CYR61;	-1.55	0.14	48.40	-2.67
LLHLTRLALS	TCPAACHCPLEAPKCAPGVGLVR	CYR61_HUMAN			Protein CYR61;	-1.79	0.06	38.40	-2.35
ASKVSAQILK	SNLASMEQQIVHLER	DIAP2_HUMAN			Protein diaphanous homolog 2;	0.13	0.01	35.40	1.23
FAPWCGHCKR	LAPEYEAAATR	PDIA3_HUMAN			Protein disulfide-	4.93	0.57	44.20	-1.56
SGYPTLKIFR	DGEEAGAYDGPR	PDIA3_HUMAN			Protein disulfide-isomerase A3;	2.22	0.09	44.90	-0.16
SRKTFSHELS	DFGLESTAGEIPVVAIR	PDIA3_HUMAN			Protein disulfide-	0.90	0.09	40.10	1.05
LLAAARLAAA	SDVLELTDDNFESR	PDIA3_HUMAN			Protein disulfide-isomerase A3;	0.06	0.01	85.40	-1.56
NRPEDYQGGR	TGEAIVDAALSALR	PDIA6_HUMAN			Protein disulfide-	3.54	0.48	63.40	-0.64
ARKMKFALLK	GSFSEQGINEFLR	PDIA6_HUMAN			Protein disulfide-isomerase A6;	0.74	0.03	71.60	-2.83
SCTFFLAVNG	LYSSSDDVIELTPSNFNR	PDIA6_HUMAN			Protein disulfide-isomerase A6;	0.11	0.01	76.60	-0.05
CLAVAALVRA	DAPEEEDHVLVLR	PDIA1_HUMAN			Protein disulfide-	0.45	0.00	40.00	-1.68
KLKAEGSEIR	LAKVDATEESDLAQQYGVR	PDIA1_HUMAN			Protein disulfide-isomerase;	-1.34	0.10	41.70	-0.98
YTYSENRVEK	DGLILTSR	PARK7_HUMAN			Protein DJ-1;	4.23	0.51	30.00	-4.32
M	AVTGWLESLR	DPCD_HUMAN			Protein DPCD;	-0.39	0.01	43.20	1.11

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EQMLEGQTQV	AENPHSEYGLTDNVER	DPY30_HUMAN			Protein dpy-30 homolog;	0.59	0.06	45.20	-3.22
LLSLGRFVRG	DGVGGDPAVALPHR	LMAN1_HUMAN			Protein ERGIC-53;	-0.37	0.01	70.50	-1.79
YVISQVFEIK	MDASLGNLFAR	FAM3C_HUMAN			Protein FAM3C;	0.28	0.02	48.10	-1.88
VISQVFEIKM	DASLGNLFAR	FAM3C_HUMAN			Protein FAM3C;	0.13	0.01	50.80	-4.37
LLFHPPRAHL	LTIKETIR	FA83B_HUMAN			Protein FAM83B;	7.55	1.37	25.90	-6.60
RDAEKKDQMK	ADLTALFLPR	FLII_HUMAN			Protein flightless-1	-0.47	0.03	44.50	0.09
SLESQPPPLQ	TQACPESSCLR	HEXI1_HUMAN			Protein HEXIM1;	0.73	0.04	26.00	-6.43
WQSRAFPQLG	GRPGPEGEGSLESQPPPLQTQACP	HEXI1_HUMAN			Protein HEXIM1;	0.09	0.01	49.30	-2.82
GATPVQDERD	SGSDGEDDVNEQHSGSDTGSVER	IWS1_HUMAN			Protein IWS1 homolog;	1.08	0.13	49.80	0.00
PSASMTRLMR	SRTASGSSVTSLDGTR	NDRG1_HUMAN			Protein NDRG1;	-0.82	0.09	39.90	-2.23
LLLPASLTGG	VGSLNLEELSEMR	OS9_HUMAN			Protein OS-9;	0.04	0.00	58.40	-2.05
QKSLLSSTST	TTKITTGSSSAGTQSSTSNR	MYPT1_HUMAN			Protein phosphatase 1 regulatory subunit 12A;	2.01	0.30	47.30	4.38
SLSTMSSSLY	ASSQLNRPNSLVGITSAYSR	MYPT1_HUMAN			Protein phosphatase 1 regulatory subunit 12A;	-0.14	0.01	53.90	-1.99
GGPGPRVYFQ	SPPGAAGEGPGGADDEGPVRR	PP14B_HUMAN			Protein phosphatase 1	1.89	0.12	37.20	1.06
SGGPGPRVYF	QSPPGAAGEGPGGADDEGPVRR	PP14B_HUMAN			Protein phosphatase 1 regulatory subunit 14B;	1.35	0.07	44.50	-1.47
EAALLHEEAT	MTIEELLTR	PPM1G_HUMAN			Protein phosphatase 1G;	0.44	0.02	26.30	-0.09
VSKKASPEAA	STPRDPIDVDLPEEAER	PML_HUMAN			Protein PML;	0.00	0.00	45.90	-0.76
KNLDSGHCVP	EPSSSGQR	PRC2A_HUMAN			Protein PRRC2A;	-3.08	0.26	27.80	-5.89

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
NKYVQQEKQN	TASLSK	PRUNE_HUMAN			Protein prune homolog;	3.42	0.29	10.20	-7.20
RELPSFLGKR	TDEAAFQKLMSNLDSNR	S10A4_HUMAN			Protein S100-A4;	1.89	0.07	34.10	-2.70
QALHLRSWLL	SRQGPAETGGQGQPQGPGLR	SCO2_HUMAN			Protein SCO2 homolog,	0.64	0.04	53.40	-2.29
PPSRVSVIQF	LEAPIGDEDAEEAAAEKR	SCRIB_HUMAN			Protein scribble homolog;	0.97	0.11	34.50	-2.33
DEEALHYLTR	VEVTEFEDIKSGYR	SET_HUMAN			Protein SET;	1.13	0.16	38.80	-2.54
TTFVNHPQVS	ALLGEEDEEALHYLTR	SET_HUMAN			Protein SET;	-1.04	0.06	56.40	-1.32
HPQVSALLGE	EDEEALHYLTR	SET_HUMAN			Protein SET;	-1.08	0.07	30.00	-0.14
FVNHPQVSAL	LGEEDEEALHYLTR	SET_HUMAN			Protein SET;	-1.39	0.11	45.10	-0.29
KDMERLTSLR	AGIEGPLLASDVGR	SON_HUMAN			Protein SON;	-0.02	0.00	42.70	-5.32
DRKKLYSLLG	IDLTAPSNNSSPR	SBNO1_HUMAN			Protein strawberry notch homolog 1;	1.89	0.12	26.50	-3.50
NQDEINKNVM	SAFGLTDDQVSGPPSAPAEDR	TFG_HUMAN			Protein TFG;	1.18	0.21	104.20	-1.07
INKNVMSAFG	LTDDQVSGPPSAPAEDR	TFG_HUMAN			Protein TFG;	0.98	0.09	90.00	0.73
KNVMSAFGLT	DDQVSGPPSAPAEDR	TFG_HUMAN			Protein TFG;	0.74	0.06	55.10	-3.31
EINKNVMSAF	GLTDDQVSGPPSAPAEDR	TFG_HUMAN			Protein TFG;	0.41	0.04	86.10	0.60
QDEINKNVMS	AFGLTDDQVSGPPSAPAEDR	TFG_HUMAN			Protein TFG;	0.20	0.02	50.50	-2.48
SAFGLTDDQV	SGPPSAPAEDR	TFG_HUMAN			Protein TFG;	0.16	0.01	34.60	0.45
EHTGAIDVLS	ADLESADLLGDHR	TMED8_HUMAN			Protein TMED8;	-0.04	0.00	37.10	-2.15
PIPDEHLILK	TTFEDLIQR	SC31A_HUMAN			Protein transport protein Sec31A;	0.38	0.01	33.90	-2.59
NIPPIQRVPR	DIPAMLPAAR	YIPF3_HUMAN			Protein YIPF3;	-0.93	0.02	34.90	-2.57
PLQLCALVHC	APPAAGQQQPPREPPAAPGAWR	LYOX_HUMAN			Protein-lysine 6-oxidase;	2.51	0.10	44.80	-1.80

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MSPWQVMLFR	KSPQELLCGASLISDR	THRB_HUMAN			Prothrombin;	0.32	0.01	50.90	-1.25
SPWQVMLFRK	SPQELLCGASLISDR	THRB_HUMAN			Prothrombin;	0.08	0.00	76.30	-7.26
FPQSIDVLES	VPINTPLAR	FAT2_HUMAN			Protocadherin Fat 2;	5.27	0.50	14.60	-3.27
VEDEDEAGLQ	KSLKFNLMSDAPGDSPR	PCDH1_HUMAN			Protocadherin-1;	6.43	1.15	34.40	-9.95
ILLNAAWLKR	DAESIHQYLLQR	PSA_HUMAN			Puromycin-sensitive aminopeptidase;	2.33	0.20	39.50	-0.20
EMAMAASSSS	VEKSYELPDGQVITIGNER	ACTBM_HUMAN			Putative beta-actin-like	1.96	0.11	49.40	-2.58
DSEQEMAMAA	SSSSVEKSYELPDGQVITIGNER	ACTBM_HUMAN			Putative beta-actin-like protein 3;	1.33	0.09	47.00	3.68
M	AGGEAGVTLGQPHLSR	IF2GL_HUMAN	IF2G_HUMAN		Putative eukaryotic	0.41	0.03	44.60	-1.51
SIYYITGESK	EQVANSAFVER	H90B3_HUMAN	HS90B_HUMAN		Putative heat shock protein HSP 90-beta-3;	0.92	0.06	38.60	-3.99
PADSKPGTIR	GDFCIQVGR	NDK8_HUMAN	NDKA_HUMAN	NDKB_HUMAN	Putative nucleoside diphosphate kinase;	2.53	0.15	45.00	-3.24
MNSGPVVAMV	WEGLNVVKTGR	NDK8_HUMAN	NDKA_HUMAN	NDKB_HUMAN	Putative nucleoside diphosphate kinase;	-1.25	0.09	19.00	-2.26
LTVAWILGTF	YYLWQDNR	GLTL1_HUMAN			Putative polypeptide N-acetylgalactosaminyltrans	-0.79	0.05	33.30	-1.94
FEKAAFQKQN	DTPKGPQPPTVSPIR	NOP2_HUMAN			Putative ribosomal RNA methyltransferase NOP2;	0.82	0.03	29.20	-3.03
RSRGFGFITF	TNPEHASVAMR	RBM3_HUMAN			Putative RNA-binding	0.09	0.00	33.20	-3.46
AGSDLRRRRR	DLGPHAEGQLAPR	S38AA_HUMAN			Putative sodium-coupled neutral amino acid transporter 10;	1.24	0.10	48.00	-1.87
EGLMKVEAAR	LSAQDPVVAVAEDGR	S38AA_HUMAN			Putative sodium-coupled neutral amino acid	0.73	0.03	55.00	2.69
EPFPTMQKTP	TQPPELR	YQ024_HUMAN			Putative uncharacterized protein FLJ43826;	7.29	0.83	21.10	-0.69
SARNSRMFGH	LSPVRIPHLR	YA034_HUMAN	YI024_HUMAN		Putative UPF0607 protein ENSP00000383783;	-0.29	0.01	25.50	-4.02
HEGQHPAQLR	SDVCTPGGTTIYGLHALEQGGLR	P5CR3_HUMAN			Pyrroline-5-carboxylate	-0.06	0.00	35.80	0.53

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AHQVARYRPR	APIIAVTR	KPYM_HUMAN			Pyruvate kinase isozymes	10.36	0.00	37.20	-2.42
ADTFLEHMCR	LDIDSPPITAR	KPYM_HUMAN			Pyruvate kinase isozymes	5.45	0.30	56.30	-1.14
DIDSPPITAR	NTGIICTIGPASR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	2.95	0.22	60.90	-4.25
PVLCKDPVQE	AWAEDVDLR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	2.27	0.18	36.90	-2.61
FIQTQQLHAA	MADTFLEHMCR	KPYM_HUMAN			Pyruvate kinase isozymes	0.75	0.06	29.30	-3.89
TAFIQTQQLH	AAMADTFLEHMCR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	0.59	0.04	44.60	-1.58
QTQQLHAAMA	DTFLEHMCR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	0.02	0.00	25.60	-1.45
DLKFGVEQDV	DMVFASFIR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	-0.79	0.03	24.60	-0.71
IENHEGVRRF	DEILEASDGIMVAR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	-0.82	0.04	68.50	-2.19
DTFLEHMCRL	DIDSPPITAR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	-1.12	0.05	22.80	-2.95
GAVEASFKCC	SGAIIVLTKSGR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	-1.49	0.13	29.50	3.22
VYKKFDLGQD	VIDFTGHALALYR	GDIA_HUMAN	GDIB_HUMAN		Rab GDP dissociation	-0.25	0.02	26.70	0.99
DVYKKFDLGQ	DVIDFTGHALALYR	GDIA_HUMAN	GDIB_HUMAN		Rab GDP dissociation inhibitor alpha;	-3.08	0.26	33.60	-0.12
FTGHALALYR	TDDYLDQPCYETINR	GDIB_HUMAN			Rab GDP dissociation inhibitor beta;	4.49	0.52	71.50	0.93
VSISDLLVPK	DLGTESQIFISR	GDIB_HUMAN			Rab GDP dissociation inhibitor beta;	3.38	0.23	48.40	2.94
EEEIKIPVVC	ALTQEESSAQLSNEEEHLDSTR	RABE1_HUMAN			Rab GTPase-binding effector protein 1;	0.47	0.04	59.90	0.04
IAAQMLSFVM	DDPDFESEGSDTQR	PARF_HUMAN			Rab-like protein 6;	0.47	0.03	48.30	-0.80
QDQTTVRTVA	SATTAIEIR	REPS1_HUMAN			RalBP1-associated Eps	-0.52	0.02	26.50	-0.90
LALKVFVAGR	NRLENDGATALAEAFR	RAGP1_HUMAN			Ran GTPase-activating	2.21	0.14	33.10	-2.70
SDRAWVWNTH	ADFADECPKPELLAIR	RANG_HUMAN			Ran-specific GTPase-	1.24	0.08	32.70	-3.34

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
KMRAKLFRFA	SENDLPEWKER	RANG_HUMAN			Ran-specific GTPase-activating protein;	0.49	0.03	27.60	2.24
LFKMRAKLFR	FASENDLPEWKER	RANG_HUMAN			Ran-specific GTPase-activating protein;	0.40	0.03	33.70	-2.50
EETAPEDAQK	SSSPAPADIAQTVQEDLR	G3BP1_HUMAN			Ras GTPase-activating protein-binding protein 1;	1.20	0.10	78.80	-2.76
NIPPQRGPRP	IREAGEQGDIEPR	G3BP1_HUMAN			Ras GTPase-activating protein-binding protein 1;	1.03	0.10	44.60	-1.73
TAPEDAQKSS	SPAPADIAQTVQEDLR	G3BP1_HUMAN			Ras GTPase-activating protein-binding protein 1;	0.96	0.08	75.70	1.44
PPQRGPRPIR	EAGEQGDIEPR	G3BP1_HUMAN			Ras GTPase-activating protein-binding protein 1;	-0.27	0.03	47.50	-1.22
FVQGIFVEKY	DPTIEDSYR	RAP1A_HUMAN	RAP1B_HUMAN	RASH_HUMAN	Ras-related protein Rap-1A;	-0.32	0.01	28.70	-5.40
SGISIGSSDG	SELSEETSWPAFER	RGPS2_HUMAN			Ras-specific guanine	-1.72	0.23	19.30	0.23
TKEDEMPVGR	NVLELSNVVR	PTPRF_HUMAN			Receptor-type tyrosine-protein phosphatase F;	4.13	0.35	34.20	-1.02
KWTEYRVWVR	AHTDVGPGPESSPVLVR	PTPRF_HUMAN			Receptor-type tyrosine-protein phosphatase F;	1.74	0.06	30.40	-6.81
PVTYYGIQYR	AAGTEGPFQEVDGVATTR	PTPRF_HUMAN			Receptor-type tyrosine-protein phosphatase F;	-0.44	0.01	48.10	-4.90
LTEELIKALQ	DLENAASGDATVR	RPR1B_HUMAN			Regulation of nuclear pre-	3.37	0.18	31.10	0.67
DPGRHVMLLR	AVPGGAGDASVLPSLPR	RMD3_HUMAN			Regulator of microtubule	-0.04	0.00	31.00	-3.00
LYCLLRREPR	QALAGTFR	RL3R2_HUMAN			Relaxin-3 receptor 2;	3.23	0.15	26.90	-3.59
LLALVAGVLG	NEFSILKSPGSVVFR	RENR_HUMAN			Renin receptor;	0.71	0.04	31.20	-2.11
LERKPAAGLS	AAPVPTAPAAGAPLMDFGNDFVP	RTN4_HUMAN			Reticulon-4;	0.51	0.06	49.40	-1.87
LLLLAPVAAP	AGSGDPDDPGQPQDAGVPR	TIG1_HUMAN			Retinoic acid receptor responder protein 1;	0.24	0.02	30.30	-4.98
DYMVGSYGPR	AEEYEFLTPVEEAPKGMLAR	GDIR1_HUMAN			Rho GDP-dissociation inhibitor 1;	2.46	0.13	43.80	-4.28

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
FQEPTEPKTK	AAAPGVEDEPLLR	RIR2_HUMAN			Ribonucleoside-diphosphate reductase subunit M2;	0.02	0.00	49.20	-1.38
ASLSSAAATG	TSTSTPAAPTAR	RL1D1_HUMAN			Ribosomal L1 domain-containing protein 1;	1.30	0.06	32.50	2.59
EDSASASLSS	AAATGTSTSTPAAPTAR	RL1D1_HUMAN			Ribosomal L1 domain-containing protein 1;	1.16	0.07	72.50	-1.02
LSSAAATGTS	TSTPAAPTAR	RL1D1_HUMAN			Ribosomal L1 domain-containing protein 1;	0.95	0.03	28.70	-1.80
MEDSASASLS	SAAATGTSTSTPAAPTAR	RL1D1_HUMAN			Ribosomal L1 domain-	0.93	0.07	67.30	3.76
MTAEFKKTDK	SILVSPTGPSR	RRP1B_HUMAN			Ribosomal RNA	0.57	0.04	28.20	-3.74
EETMEEQKTK	VGDGDLSAEEIPENEVSLR	RRP1B_HUMAN			Ribosomal RNA processing protein 1 homolog B;	-0.25	0.03	71.30	3.25
KLELEEDSEM	DLPAFADSDDDLER	BMS1_HUMAN			Ribosome biogenesis protein BMS1 homolog;	0.23	0.01	67.60	0.50
EALLEAGQAR	DAQDVQASQAEADQQQTR	RRBP1_HUMAN			Ribosome-binding protein 1;	5.55	1.33	104.60	0.00
QLKTQLEWTE	AILEDEQTQR	RRBP1_HUMAN			Ribosome-binding protein 1;	1.39	0.09	37.40	-1.29
PYKTLVSTVG	SMVFNEGEAQR	RRBP1_HUMAN			Ribosome-binding protein 1;	-0.39	0.02	43.00	-8.91
EAGQARDAQD	VQASQAEADQQQTR	RRBP1_HUMAN			Ribosome-binding protein 1;	-1.00	0.10	52.10	5.46
LQEQQRLLAQ	LDPSLVAFLR	RPAP1_HUMAN			RNA polymerase II-associated protein 1;	0.64	0.06	32.20	0.86
SRRDVYLSPR	DDGYSTKDSYSSR	RBMX_HUMAN	RMXL1_HUMAN		RNA-binding motif protein, X chromosome;	0.96	0.07	23.90	-0.45
SDHPSGGSYR	DSYESYGNSR	RBMX_HUMAN	RMXL1_HUMAN		RNA-binding motif protein, X chromosome;	-0.52	0.02	35.90	-0.41

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EPREGQKLPK	SRTAYSGGAEDLER	RBMX2_HUMAN			RNA-binding motif	-0.42	0.04	64.40	-1.42
VLASQALSQG	SEPSSENANDTIILR	RBM10_HUMAN			RNA-binding protein 10;	0.08	0.00	59.40	-0.42
YRTQSSASLA	ASYAAQQHPQAAASYR	RBM14_HUMAN			RNA-binding protein 14;	0.81	0.06	35.70	0.63
IKGAIEVLIR	EYSSELNAPSQESDSHPR	RBM25_HUMAN			RNA-binding protein 25;	1.47	0.13	28.80	-1.94
KLPVDSVFNK	FEDEDSDDVPR	RBM25_HUMAN			RNA-binding protein 25;	1.07	0.11	51.50	1.10
RKKLPVDSVF	NKFEDEDSDDVPR	RBM25_HUMAN			RNA-binding protein 25;	0.62	0.05	34.30	-4.87
EGMSKRKRKR	SVQEGENPDDGVR	RBM34_HUMAN			RNA-binding protein 34;	0.84	0.07	63.50	-1.95
M	VKLFIGNLPR	RBM4B_HUMAN	RBM4_HUMAN		RNA-binding protein 4B;	0.79	0.01	39.10	-1.71
FGSEEGSRAR	MREDYDSVEQDGDEPGPQR	RBM8A_HUMAN			RNA-binding protein 8A;	1.82	0.18	59.10	-0.27
RAGDWQCPNP	GCGNQNFAWR	EWS_HUMAN			RNA-binding protein EWS;	3.37	0.29	28.80	-3.71
SQAPSQYSQQ	SSSYGQQSSFR	EWS_HUMAN			RNA-binding protein EWS;	2.39	0.11	36.20	-2.60
EGRGMPPPLR	GGPGGPGGPGGPMGR	EWS_HUMAN			RNA-binding protein EWS;	0.20	0.01	67.80	3.46
SFRQDHPSSM	GVYGQESGGFSGPGENR	EWS_HUMAN			RNA-binding protein	0.16	0.01	85.70	-3.23
QAPSQYSQQS	SSYGQQSSFR	EWS_HUMAN			RNA-binding protein EWS;	0.11	0.01	36.90	-1.36
DHPSSMGVYG	QESGGFSGPGENR	EWS_HUMAN			RNA-binding protein EWS;	0.09	0.00	58.90	-1.77
GSYSQAPSQY	SQQSSSYGQQSSFR	EWS_HUMAN			RNA-binding protein EWS;	0.04	0.00	71.30	-2.55
QDHPSSMGVY	GQESGGFSGPGENR	EWS_HUMAN			RNA-binding protein EWS;	-0.20	0.01	53.60	-1.91
ECNQCKAPKP	DGPGGGPGGSHMGGNYGDDR	FUS_HUMAN			RNA-binding protein FUS;	1.06	0.07	34.10	-5.29
QCKAPKPDGP	GGGPGGSHMGGNYGDDR	FUS_HUMAN			RNA-binding protein FUS;	0.08	0.01	61.90	-3.76

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EVLQTLQDLI	AYFQPPEEEMR	RYR3_HUMAN			Ryanodine receptor 3;	4.65	0.43	26.30	-6.87
ASGTTTTAVK	IGIIGGTGLDDPEILEGR	MTAP_HUMAN			S-methyl-5'-thioadenosine phosphorylase;	2.01	0.16	67.20	0.49
EEIRKTFNIK	NDFTEEEEAQVR	SKP1_HUMAN			S-phase kinase-associated	2.52	0.27	35.90	-0.87
FGQDEDVTSK	AFTGREFDELNPSAQR	AT2A2_HUMAN			Sarcoplasmic/endoplasmic reticulum calcium	0.47	0.02	34.10	-3.26
SSAASELAEA	SSEELAEAPTEAPSPEAR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	2.85	0.27	59.10	-0.68
ESTAHAQSSK	ADSLLAVVKR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	1.15	0.12	29.80	0.44
SAASELAEAS	SEELAEAPTEAPSPEAR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	0.60	0.04	67.20	-0.99
VEQSSAASEL	AEASSEELAEAPTEAPSPEAR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor	0.53	0.06	85.20	0.23
LAEASSEELA	EAPTEAPSPEAR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	0.47	0.03	53.30	-0.23
ASELAEASSE	ELAEAPTEAPSPEAR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	0.34	0.03	67.10	-1.12
EQSSAASELA	EASSEELAEAPTEAPSPEAR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	0.32	0.04	76.50	1.42
QSSAASELAE	ASSEELAEAPTEAPSPEAR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	0.14	0.02	67.50	0.86
ELYKAHEWAR	AIIESDQEQGR	SCRN1_HUMAN			Secernin-1;	0.94	0.11	40.10	0.24
GRSRSNQLPK	AAWIPHVENR	SCG2_HUMAN			Secretogranin-2;	-1.86	0.14	32.10	-2.60
NEQINDEMKR	SGQLGIQEEDLR	SCG2_HUMAN			Secretogranin-2;	-3.08	0.52	49.20	0.07
VIQHRPSRQY	ATLDVYNPFETR	SCAM3_HUMAN			Secretory carrier-	0.42	0.03	52.90	-1.99
LLLGAPRGCA	EGVAAALTPER	PLA2R_HUMAN			Secretory phospholipase A2 receptor;	-0.42	0.02	48.40	-2.87
VKGSSQPQAR	VYLTFDELR	SEM3C_HUMAN			Semaphorin-3C;	1.52	0.06	37.30	-3.63

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TVFNGPFAHK	EGPNHQLISYQGR	SEM3C_HUMAN			Semaphorin-3C;	-0.37	0.03	35.00	-4.56
WASLLTGAWP	SFPTQDHLPATPR	SEM3F_HUMAN			Semaphorin-3F;	0.38	0.01	33.30	-4.54
GGLLLHGGSS	GPSPGPSVPR	SEM3G_HUMAN			Semaphorin-3G;	0.82	0.04	32.90	-3.25
AARLWGLGIG	AEVWWNLVPR	SEM4C_HUMAN			Semaphorin-4C;	0.71	0.01	48.30	4.16
LLLLLGGAHG	LFPEEPPPLSVAPR	SEM6B_HUMAN			Semaphorin-6B;	2.03	0.06	37.70	-2.21
DGVRGSPPVP	SGPPMEEDGLR	SENP3_HUMAN			Sentrin-specific protease 3;	0.65	0.06	19.00	-5.56
INPETPGYVG	FANLPNQVHR	SEPT2_HUMAN			Septin-2;	0.69	0.07	35.70	-2.28
PAPVSQLQSR	LEPKPQPPVAEATPR	SEPT9_HUMAN			Septin-9;	1.30	0.04	39.90	-3.38
GPRGFYGTFD	VHLDLEDR	SPTC1_HUMAN			Serine	-3.08	0.26	21.70	0.00
YETLYANGSR	TETQVGIYILSSSGDGAQHR	PRS23_HUMAN			Serine protease 23;	2.69	0.15	58.70	-0.98
GSSGKSRRKR	QIYGYDSR	PRS23_HUMAN			Serine protease 23;	-0.32	0.01	30.20	-1.74
ANDVSDVIKR	ESTLNMVVR	HTRA1_HUMAN			Serine protease HTRA1;	3.34	0.22	31.40	-5.29
HRPPVIVLQR	GACGQGQEDPNSLR	HTRA1_HUMAN			Serine protease HTRA1;	3.11	0.22	50.50	-1.58
ASAQLSRAGR	SAPLAAGCPDRCEPAR	HTRA1_HUMAN			Serine protease HTRA1;	-0.04	0.00	25.00	2.04
ASAQLSRAGR	SAPLAAGCPDR	HTRA1_HUMAN			Serine protease HTRA1;	-0.04	0.00	49.40	-3.50
M	VLDLDLFR	SYSC_HUMAN			Serine--tRNA ligase,	0.59	0.02	32.20	-3.41
ATRPSPSPER	SSTGPEPPAPTPLLAER	SRRM2_HUMAN			Serine/arginine repetitive	5.93	0.81	63.60	6.80
PTAANYPSSS	RTPQAPASANLVGPR	SRRM2_HUMAN			Serine/arginine repetitive	0.64	0.03	37.40	-1.53

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
TSRTTPRRSR	SVSPCSNVESR	SRRM2_HUMAN			Serine/arginine repetitive matrix protein 2;	0.21	0.02	40.30	-4.38
RHGGSPQPLA	TTPLSQEPVNPPSEASPTR	SRRM2_HUMAN			Serine/arginine repetitive	-0.12	0.00	59.90	0.10
EQSRFQSDSS	SYPTVDSNSLLGQSR	SRRM2_HUMAN			Serine/arginine repetitive	-0.58	0.03	27.50	0.60
GDVCYADVYR	DGTGVVEFVR	SRSF1_HUMAN			Serine/arginine-rich	3.01	0.22	35.00	-2.71
FAFVRFHDKR	DAEDAMDAMDGAVLDGR	SRSF2_HUMAN			Serine/arginine-rich splicing factor 2;	3.77	0.36	73.00	-4.60
AFRVLSSLLS	SCSDSVALYSFCR	STK36_HUMAN			Serine/threonine-protein	-2.66	0.34	30.20	1.76
LLNAPTKRPR	SSTVTEAPIAVVTSR	NEK9_HUMAN			Serine/threonine-protein kinase Nek9;	1.83	0.17	45.10	-0.26
EPAKTAQALS	SGSGSQETKIPISLVLR	OXSR1_HUMAN			Serine/threonine-protein kinase OSR1;	0.74	0.04	34.00	0.44
IPQDRPTSEE	LLKHIFVLR	TAOK1_HUMAN			Serine/threonine-protein kinase TAO1;	7.35	1.34	15.90	-7.02
LVGGPEYVHC	LLPPLESLATVEETVVR	2AAA_HUMAN			Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha	-0.42	0.04	54.20	-1.21
NKCVPNSNER	YYGYTGAFR	TRFE_HUMAN	TRFL_HUMAN		Serotransferrin;	2.43	0.09	18.80	-4.08
QNALLVRYTK	KVPQVSTPTLVEVSR	ALBU_HUMAN			Serum albumin;	6.91	1.17	33.20	4.30
KTPVSDRVTK	CCTESLVNR	ALBU_HUMAN			Serum albumin;	1.96	0.13	36.50	2.74
LVTDLTKVHT	ECCHGDLLECADDR	ALBU_HUMAN			Serum albumin;	0.24	0.02	49.60	-1.57
NALLVRYTKK	VPQVSTPTLVEVSR	ALBU_HUMAN			Serum albumin;	-0.47	0.03	26.50	-2.65
EGHSEASLAS	ALVEGEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-response protein;	1.73	0.14	39.40	-2.62
FAEGHSEASL	ASALVEGEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-	1.58	0.11	26.50	-2.49
AEGHSEASLA	SALVEGEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-	1.45	0.07	52.40	-1.54
EASLASALVE	GEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-	1.44	0.07	37.20	-0.72
VALEQAQKVR	YEGSYALTSEEAER	SDPR_HUMAN			Serum deprivation-response protein;	1.34	0.14	63.80	-2.02
TNYSFHCNVC	HHSGNTYFLR	ASH2L_HUMAN			Set1/Ash2 histone methyltransferase	6.28	0.65	12.40	-4.28

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MSGLR	VYSTSVTGSR	SH3L3_HUMAN			SH3 domain-binding glutamic acid-rich-like	2.75	0.12	28.10	-0.83
AGGGGPAPLS	SAAPSPLSSSLGTAGHR	SH3K1_HUMAN			SH3 domain-containing kinase-binding protein 1;	0.14	0.01	41.70	-3.87
PNAQTPSHLG	ATLPVGQPVGGDPEVR	SHC1_HUMAN			SHC-transforming protein	1.07	0.10	72.20	0.68
MMNADMDAVD	AENQVELEEKTR	SCOC_HUMAN			Short coiled-coil protein;	0.92	0.07	35.20	-2.99
VVVMVGSFCV	CYVPYAAFAMYMVNNR	OPSB_HUMAN			Short-wave-sensitive opsin 1;	-4.68	0.00	24.10	-0.65
RHITLDKTWK	GSDHSASLEPGELAELVR	SIAS_HUMAN			Sialic acid synthase;	-0.47	0.02	50.30	-2.79
M	VLLESEQFLTELTR	SRP14_HUMAN			Signal recognition particle 14 kDa protein;	0.35	0.05	76.40	-1.52
LQVLRQFVRH	ESETTTSLVLER	SSBP_HUMAN			Single-stranded DNA-binding protein,	-0.29	0.04	44.70	-1.29
EMPQDLRSPA	RTPPSEEDSAEAER	SGTA_HUMAN			Small glutamine-rich tetratricopeptide repeat-containing protein alpha;	0.74	0.03	44.60	-1.62
SGHLGEVLIR	CNNVLYIR	RUXF_HUMAN			Small nuclear	3.09	0.13	36.40	-0.46
MQLANTEEYI	DGALSGHLGEVLIR	RUXF_HUMAN			Small nuclear ribonucleoprotein F;	-1.00	0.06	35.90	-5.09
HLKAVKMTLK	NREPVQLETLSIR	SMD1_HUMAN			Small nuclear ribonucleoprotein Sm D1;	0.18	0.01	38.60	-4.21
PLSVLTQSVK	NNTQVLINCR	SMD2_HUMAN			Small nuclear	2.90	0.18	33.10	-4.84
NITVTYRDGR	VAQLEQVVYIR	SMD3_HUMAN			Small nuclear ribonucleoprotein Sm D3;	3.21	0.25	40.80	-1.20
LAAARVELPG	TAVPSVPEDAAPASR	S12A2_HUMAN			Solute carrier family 12 member 2;	2.34	0.22	39.30	-4.28
GPANHTEAST	NDSGAWLR	S22AK_HUMAN			Solute carrier family 22	4.10	0.15	21.70	-2.01
LVVHGPGDLR	LENYPIPEPGPNEVLLR	DHSO_HUMAN			Sorbitol dehydrogenase;	3.54	0.28	55.90	5.31
LPPSTLSQDR	LDAPPPPAAPLPR	SORT_HUMAN			Sortilin;	1.13	0.11	45.50	-0.74
PPSTLSQDRL	DAPPPPAAPLPR	SORT_HUMAN			Sortilin;	0.13	0.01	43.50	-1.70

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
AFPRGGRWRR	SAPGEDEECGRVR	SORT_HUMAN			Sortilin;	-0.47	0.06	33.80	-2.07
VKKIHENEKR	LEAGDHPVELLAR	SPRC_HUMAN			SPARC;	8.97	0.68	44.70	-3.59
LSHTELAPLR	APLIPMEHCTTR	SPRC_HUMAN			SPARC;	3.18	0.21	30.60	-1.58
KLHLDYIGPC	KYIPPCLDSELTEFPLR	SPRC_HUMAN			SPARC;	2.12	0.03	33.60	-4.19
PCKYIPPCLD	SELTEFPLR	SPRC_HUMAN			SPARC;	-0.16	0.01	36.40	5.50
IHENEKRLEA	GDHPVELLAR	SPRC_HUMAN			SPARC;	-0.82	0.04	23.80	-1.31
CKYIPPCLDS	ELTEFPLR	SPRC_HUMAN			SPARC;	-1.00	0.04	30.90	0.10
GPCKYIPPCL	DSELTEFPLR	SPRC_HUMAN			SPARC;	-1.34	0.07	30.60	-4.75
KKIHENEKRL	EAGDHPVELLAR	SPRC_HUMAN			SPARC;	-4.24	0.00	33.90	-3.57
ALLKKHEALM	SDLSAYGSSIQALR	SPTA2_HUMAN			Spectrin alpha chain, non-erythrocytic 1;	0.45	0.04	56.40	0.07
PSPTSDRKAK	TALPAQSAATLPAR	SPTB2_HUMAN			Spectrin beta chain, non-	0.14	0.01	63.30	-0.21
LELSLQLSQL	DLEDTQIPTSR	SPAT5_HUMAN			Spermatogenesis-associated protein 5;	1.24	0.14	29.60	-2.38
GEAPANGLRR	AAAPEAYVQK	SGPP2_HUMAN			Sphingosine-1-phosphate phosphatase 2;	4.07	0.26	25.80	-0.72
LPSHTKIKYR	QTTQDAPEEVR	CWC15_HUMAN			Spliceosome-associated protein CWC15 homolog;	-0.34	0.01	33.70	1.15
QKTVIPGMPT	VIPPGLTR	SF01_HUMAN			Splicing factor 1;	1.20	0.05	22.00	-1.59
PIRTPARKLT	ATPTPLGGMTGFHMQTEDR	SF3B1_HUMAN			Splicing factor 3B subunit 1;	0.49	0.04	28.40	0.48
ATPTPGHIMS	MTPEQLQAWR	SF3B1_HUMAN			Splicing factor 3B subunit	-0.18	0.00	41.30	-3.63

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EIAKMGTPVP	RPPQDMGQIGVR	SF3B2_HUMAN			Splicing factor 3B subunit 2;	0.72	0.03	31.30	3.38
IGLQNGVLLR	TVLDPVTGDLSDTR	SF3B3_HUMAN			Splicing factor 3B subunit 3;	5.23	0.68	51.30	7.77
M	FLYNLTLQR	SF3B3_HUMAN			Splicing factor 3B subunit 3;	0.16	0.01	30.40	-2.26
TALLPTMTPD	GLAVTPTPVPVVGSQMTR	U2AF2_HUMAN			Splicing factor U2AF 65 kDa subunit;	-0.76	0.08	66.50	1.25
GFGFIKLESR	ALAEIAKAELDDTPMR	SFPQ_HUMAN			Splicing factor, proline-	2.80	0.19	34.10	-0.72
GGRGGLHDFR	SPPPGMGLNQNR	SFPQ_HUMAN			Splicing factor, proline- and glutamine-rich;	0.91	0.04	29.10	-2.15
FEYEYSQRWK	SLDEMEKQQR	SFPQ_HUMAN			Splicing factor, proline-	0.88	0.03	55.40	-2.50
MMGSDMRTER	FGQGGAGPVGGQGPR	SFPQ_HUMAN			Splicing factor, proline-	0.29	0.02	60.10	-1.23
LEEQARAKTQ	TPPVSPAPQPTEER	SRC8_HUMAN			Src substrate cortactin;	1.17	0.08	46.80	0.00
ELSYRGPVSG	TEPEPVYSMEAADYR	SRC8_HUMAN			Src substrate cortactin;	1.13	0.04	41.70	1.51
AASFKAELSY	RGPVSGTEPEPVYSMEAADYR	SRC8_HUMAN			Src substrate cortactin;	0.67	0.04	65.50	-0.13
QSSSTVGQSF	SEQHISQLQESIR	SRPK1_HUMAN			SRSF protein kinase 1;	0.75	0.05	43.40	-1.57
LEPVACGSVL	SEGSPLTEQEESSPSHDR	SRPK2_HUMAN			SRSF protein kinase 2;	0.66	0.05	27.20	-0.05
NDSVSPRKSR	VAAQNSAEVVR	STC1_HUMAN			Stanniocalcin-1;	3.78	0.29	56.30	-1.54
KLNVCSIAKR	NPEAITEVVQLPNHFSNR	STC1_HUMAN			Stanniocalcin-1;	3.54	0.26	42.50	-3.63
DIQVKELEKR	ASGQAFELILSPR	STMN1_HUMAN			Stathmin;	2.04	0.12	55.70	-0.63
ELEKRASGQA	FELILSPR	STMN1_HUMAN			Stathmin;	0.18	0.01	32.50	-2.28
FNDSQRQATK	DAGQISGLNVLR	GRP75_HUMAN			Stress-70 protein, mitochondrial;	-0.29	0.03	36.20	-2.03

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EFSHLRPEQR	LALLHEGTGPR	SMC3_HUMAN			Structural maintenance of chromosomes protein 3;	0.89	0.05	26.10	-4.17
SSAAAHRYSR	EANAPGPVPGER	SUMF1_HUMAN			Sulfatase-modifying factor 1;	-0.47	0.02	36.40	-1.71
SQHKGVAVRR	VLNTEANVVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	5.16	0.49	33.80	-3.06
AEETNSAVCR	DFNIPGFPTVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	4.56	0.25	28.80	-1.86
LSQHKGVAVR	RVLNTEANVVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	4.28	0.68	28.50	-0.31
AVPGANAAPR	SALYSPSDPLTLLQADTVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	3.35	0.43	103.60	-0.72
DFPAAGSAAR	RDVQNVAAAPELAMGALELESR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	3.15	0.19	57.10	0.76
SRVPVLMESR	SFYTAYLQR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	2.78	0.10	40.60	-5.18
GPLEVRRVGR	SSKQLVDIPEGQLEAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.64	0.12	39.80	-1.75
FPAAGSAARR	DVQNVAAAPELAMGALELESR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.60	0.21	59.80	-1.26
RPPKLHPGLR	AAPGQEPPEHMAELQR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.58	0.09	29.50	0.73
PLGQWHLSKR	DTGAALLAESR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.45	0.12	64.30	-2.12
VRRVGRSSKQ	LVDIPEGQLEAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.09	0.08	39.40	-1.02
EATLNFLKAH	FSPSNIILDFPAAGSAAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.02	0.13	40.80	0.21
RRVGRSSKQL	VDIPEGQLEAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.00	0.09	52.10	-1.66
LAVPGANAAP	RSALYSPSDPLTLLQADTVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	0.75	0.04	64.70	0.45
RVGRSSKQLV	DIPEGQLEAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	0.48	0.03	35.90	-3.53
WPPACPPLEP	AKLEEIDGFFAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	0.47	0.02	29.20	-2.93
VRKFGVTDFP	SCYLLFR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	0.11	0.01	29.70	-8.30

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
AHFSPSNIIL	DFPAAGSAAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	0.02	0.00	37.70	-6.56
EGSRPPACPR	LDPIQPSDVLSLLDNR	QSOX2_HUMAN			Sulfhydryl oxidase 2;	2.69	0.30	45.10	1.53
M	VEKEEAGGGISEEEAAQYDR	SAE1_HUMAN			SUMO-activating enzyme subunit 1;	0.98	0.11	65.60	0.85
GFHVHEFGDN	TAGCTSAGPHFNPLSR	SODC_HUMAN			Superoxide dismutase [Cu-	0.44	0.03	30.40	-4.04
GLHGFHVHEF	GDNTAGCTSAGPHFNPLSR	SODC_HUMAN			Superoxide dismutase [Cu-Zn];	-0.96	0.04	40.80	-1.70
RKKSLEGMKK	ARVGGSDEEASGIPSR	SSF1_HUMAN			Suppressor of SWI4 1 homolog;	0.29	0.03	43.50	-2.84
CTNGVLLDSR	CDYSCSSGYHLEGDR	SRPX2_HUMAN			Sushi repeat-containing protein SRPX2;	3.15	0.27	41.40	-4.41
NKVSEHVGSR	TQDECILHFLR	SMRC1_HUMAN	SMRC2_HUMAN		SWI/SNF complex subunit SMARCC1;	2.55	0.11	36.40	-2.39
TAVVAVEPDR	RNQSPVDQGATGASQGLLDR	SDC1_HUMAN			Syndecan-1;	-0.29	0.03	74.50	0.43
FVGGVAESIR	ETEVIDPQDLLEGR	SDC4_HUMAN			Syndecan-4;	4.01	0.20	48.80	3.77
SEDVSNKVSM	SSTVQGSNIFER	SDC4_HUMAN			Syndecan-4;	2.01	0.07	43.40	-3.82
LLLFFVGGVA	ESIRETEVIDPQDLLEGR	SDC4_HUMAN			Syndecan-4;	0.49	0.01	73.20	-1.36
LFFVGGVAES	IRETEVIDPQDLLEGR	SDC4_HUMAN			Syndecan-4;	0.47	0.02	72.60	-1.31
ERNLVSWESQ	TQPQVQVQDEEITEDDLR	STX7_HUMAN			Syntaxin-7;	0.23	0.03	80.40	6.61
DSTDLVAKLR	AFHNEAQVNPER	TCPA_HUMAN			T-complex protein 1 subunit alpha;	0.40	0.02	33.40	-0.83
AAKVLVDMSR	VQDDEVGDGTTSVTVLAAELLR	TCPB_HUMAN			T-complex protein 1 subunit beta;	2.78	0.46	113.60	-0.09
LGEACTIVLR	GATQQILDEAER	TCPB_HUMAN			T-complex protein 1 subunit beta;	1.62	0.09	42.90	-5.27
MSVNAVMKVI	DPATATSVDLR	TCPD_HUMAN			T-complex protein 1 subunit delta;	-0.34	0.02	33.50	-2.12
ALEIIPRQLC	DNAGFDATNILNKLR	TCPH_HUMAN			T-complex protein 1	-0.69	0.06	33.60	-2.71

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
VAQALEVIPR	TLIQNCGASTIR	TCPG_HUMAN			T-complex protein 1 subunit gamma;	3.10	0.29	52.40	3.89
PLAVKLQTYK	TAVETAVLLLR	TCPG_HUMAN			T-complex protein 1 subunit gamma;	0.11	0.01	36.10	0.66
DGAISTIVLR	GSTDNLMDDIER	TCPQ_HUMAN			T-complex protein 1 subunit theta;	3.21	0.21	43.90	0.22
LVCCSAKNLR	DIDEVSSLLR	TCPQ_HUMAN			T-complex protein 1	3.14	0.27	45.30	1.70
MIEIMEMKHK	SETDTSLIR	TCPZ_HUMAN			T-complex protein 1	-1.16	0.03	43.40	-2.74
VANSTANLVK	TIKALDGAFTEENR	TLN1_HUMAN			Talin-1;	1.73	0.10	37.90	-1.85
AAAQAAYLVG	VSDPNSQAGQQGLVEPTQFAR	TLN1_HUMAN			Talin-1;	1.68	0.16	30.10	-2.35
TIMCVTESIF	SSMGDAGEMVR	TLN1_HUMAN	TLN2_HUMAN		Talin-1;	1.55	0.11	29.10	-2.82
KFFYSDQNVD	SRDPVQLNLLYVQAR	TLN1_HUMAN	TLN2_HUMAN		Talin-1;	-1.12	0.05	50.40	-2.05
LQRSQSLPHS	ATVTLGGTSDPSTLSSSALSER	TB22A_HUMAN			TBC1 domain family member 22A;	-0.04	0.00	89.90	5.52
LDILKNKAKR	SLTSSLENIFSR	TBCD4_HUMAN			TBC1 domain family	-0.27	0.02	58.60	-1.58
MEASSDGGFR	SQENSPSPPR	TSH3_HUMAN			Teashirt homolog 3;	3.10	0.10	20.80	-3.81
YRLGPASAAD	TGSEAKPGALAEGAAEPEPQR	TE2IP_HUMAN			Telomeric repeat-binding factor 2-interacting	-0.34	0.04	53.50	0.51
PAACAGDMAD	AASPCSVVNDLR	THOP1_HUMAN			Thimet oligopeptidase;	-0.04	0.00	40.80	-4.16
M	VGVKPVGSDPDFQPELSGAGSR	TXNL1_HUMAN			Thioredoxin-like protein 1;	0.51	0.05	54.90	-0.93
GEDLEVNIAK	VDVTEQPGLSGR	TMX1_HUMAN			Thioredoxin-related	0.31	0.02	36.60	0.62
RTIYTTRISL	TTFNIQDGPDFQDR	THIOM_HUMAN			Thioredoxin,	-0.23	0.02	63.10	-1.78
AAVHYDRSGR	SLGTADVHFER	THOC4_HUMAN			THO complex subunit 4;	0.06	0.00	28.00	-1.66
AVRTSVPLHR	SRDETPALAGTDASR	THSD4_HUMAN			Thrombospondin type-1 domain-containing protein	-0.66	0.03	30.40	-2.46

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
SMVLELRGLR	TIVTTLQDSIR	TSP1_HUMAN			Thrombospondin-1;	3.71	0.36	42.60	-1.41
STTGTGEHLR	NALWHTGNTPGQVR	TSP1_HUMAN	TSP2_HUMAN		Thrombospondin-1;	3.04	0.23	25.80	1.52
IDGDGILNER	DNCQYVYNVDQR	TSP1_HUMAN			Thrombospondin-1;	1.96	0.18	50.40	-0.44
NFQGVLQNVR	FVFGTTPEDILR	TSP1_HUMAN			Thrombospondin-1;	1.92	0.10	60.40	-1.62
SSMVLELRGL	RTIVTTLQDSIR	TSP1_HUMAN			Thrombospondin-1;	-0.73	0.05	31.80	-2.57
FLMHVCGTNR	IPESGGDNSVFDIFELTGAAR	TSP1_HUMAN			Thrombospondin-1;	-1.49	0.13	47.50	1.70
DLQAICGISC	DELSSMVLELR	TSP1_HUMAN			Thrombospondin-1;	-2.00	0.16	45.20	4.82
VLFLMHVCGT	NRIPESGGDNSVFDIFELTGAAR	TSP1_HUMAN			Thrombospondin-1;	-2.00	0.16	80.00	-1.36
GVLFLMHVCG	TNRIPESGGDNSVFDIFELTGAAR	TSP1_HUMAN			Thrombospondin-1;	-2.00	0.24	74.30	-3.46
TDNNGEGDAC	AADIDGDGILNER	TSP1_HUMAN			Thrombospondin-1;	-2.08	0.26	44.10	-3.01
QGVLQNVRFV	FGTTPEDILR	TSP1_HUMAN			Thrombospondin-1;	-2.92	0.00	23.70	-2.79
LLLLCFFTSA	SQDLQVIDLLTVGESR	TSP3_HUMAN			Thrombospondin-3;	2.33	0.33	78.20	-0.89
LLCFFTSASQ	DLQVIDLLTVGESR	TSP3_HUMAN			Thrombospondin-3;	1.37	0.19	67.60	-0.06
PGYKAEGKYK	DDPVDLR	TR150_HUMAN			Thyroid hormone receptor-associated protein 3;	0.59	0.03	27.20	-1.74
HSNKKEQEFR	SIFQHIQSAQSQR	TR150_HUMAN			Thyroid hormone receptor-	-0.27	0.03	34.20	7.41
SPRERSPALK	SPLQSVVVR	TR150_HUMAN			Thyroid hormone receptor-associated protein 3;	-0.39	0.01	28.80	-3.95
PLDSPGRRKR	DTNAPESFKDTAESR	TRIPB_HUMAN			Thyroid receptor-	0.92	0.08	26.90	-2.67
SRDLEQPTYR	YESSSYTDQFSR	ZO1_HUMAN			Tight junction protein ZO-	0.09	0.01	43.40	-1.13
EKMDHKARLQ	RMQELQEAQNAR	ZO2_HUMAN			Tight junction protein ZO-	0.62	0.07	40.00	3.11

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
EEPLVSSITR	SSEPVQHEESIR	ZO2_HUMAN			Tight junction protein ZO-2;	0.16	0.02	35.70	-2.10
DGEGGAYTDN	ELDEPAEEPLVSSITR	ZO2_HUMAN			Tight junction protein ZO-2;	-0.32	0.02	71.10	0.27
EDTDGEGGAY	TDNELDEPAEEPLVSSITR	ZO2_HUMAN			Tight junction protein ZO-	-0.52	0.03	80.00	1.35
EGGAYTDNEL	DEPAEEPLVSSITR	ZO2_HUMAN			Tight junction protein ZO-2;	-0.55	0.02	45.10	-1.20
GEGGAYTDNE	LDEPAEEPLVSSITR	ZO2_HUMAN			Tight junction protein ZO-	-0.76	0.05	35.90	3.86
RMGATPTPFK	STGDIAGTVVPETNKEPR	ZO2_HUMAN			Tight junction protein ZO-2;	-1.00	0.06	39.80	-2.01
TDGEGGAYTD	NELDEPAEEPLVSSITR	ZO2_HUMAN			Tight junction protein ZO-2;	-1.04	0.06	62.80	0.83
ELRLEIPGSR	LEQEEPLTDAER	TJAP1_HUMAN			Tight junction-associated	0.72	0.07	33.10	-1.98
WNSKDVGPHR	DLVGELGTALR	FUCO_HUMAN			Tissue alpha-L-	2.69	0.17	48.40	-6.48
TRDNANRIIK	TTLQQEKPDFCFLEEDPGICR	TFPI1_HUMAN			Tissue factor pathway	0.85	0.05	43.90	-1.89
VPSCSTCGLR	QYSQPQFR	TPA_HUMAN			Tissue-type plasminogen activator;	3.91	0.28	25.00	-0.74
AGKCCEIDTR	ATCYEDQGISYR	TPA_HUMAN			Tissue-type plasminogen	3.11	0.25	56.30	-1.14
IHARFRRGAR	SYQVICR	TPA_HUMAN			Tissue-type plasminogen activator;	0.11	0.00	30.60	-6.25
HRGENVKSAA	NLIVEEEDLR	TITIN_HUMAN			Titin;	3.84	0.42	33.60	-2.38
TRGSCRLSWK	MPDDDGGDR	TITIN_HUMAN			Titin;	3.43	0.06	14.80	-6.66
LAKGNKSILD	ADPEAQALLEISGHSR	K1609_HUMAN			TLD domain-containing	-0.42	0.02	32.20	-0.52
TRMQNDSILK	SELGNQSPSTSSR	TOIP1_HUMAN			Torsin-1A-interacting	1.45	0.14	58.90	1.02
ISKKTVRSIQ	EAPVSEDLVIR	TOIP1_HUMAN			Torsin-1A-interacting protein 1;	0.51	0.04	41.30	-9.11
AIVGFQVLNA	IENLDDNAQR	CI167_HUMAN			Torsin-4A;	0.62	0.05	30.50	-3.68
PSQMDVELVS	GSPVALSPQPR	TOX4_HUMAN			TOX high mobility group box family member 4;	1.27	0.12	37.60	-0.35
M	QLTHQLDLFPECR	TPRKB_HUMAN			TP53RK-binding protein;	0.14	0.00	42.90	-5.01
ITTPQYHQLQ	ASTTPQSAQAQPQPSSSSR	SPT6H_HUMAN			Transcription elongation	0.37	0.03	84.90	0.92
VTLDDILSLK	SGPPEGGSVAVQDADIEKR	TCF20_HUMAN			Transcription factor 20;	0.65	0.03	24.40	-1.97

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LPSSTAAENK	ASPAGTAGGPGAGAAAGGTGPLA	TAF10_HUMAN			Transcription initiation factor TFIID subunit 10;	0.04	0.00	60.80	-1.00
LTADSQPPVF	KVFPGSTTEDYNLIVIER	TIF1B_HUMAN			Transcription	-0.12	0.00	44.20	0.98
EAAIGAPPTA	TEGPETKPVLMALAEGPGAEGPR	TIF1B_HUMAN			Transcription intermediary factor 1-	-0.12	0.00	63.10	-0.38
IVAERPGTNS	TGPAPMAPPR	TIF1B_HUMAN			Transcription	-0.16	0.01	29.60	-1.27
MAASAAAASA	AAASAASGSPGPGEGSAGGEKR	TIF1B_HUMAN			Transcription intermediary factor 1-	-0.20	0.02	43.00	-4.94
EGPETKPVLM	ALAEGPGAEGPR	TIF1B_HUMAN			Transcription intermediary factor 1-	-0.20	0.01	56.10	-2.50
EGPRLASPSG	STSSGLEVVAPEGTSAPGGGPGTL	TIF1B_HUMAN			Transcription intermediary factor 1-beta;	-0.27	0.03	33.00	0.03
STAPSAAASA	SASAAASSPAGGGAEALELLEHCG	TIF1B_HUMAN			Transcription	-0.34	0.02	33.60	-4.47
PSGSTSSGLE	VVAPEGTSAPGGGPGTLDDSATIC	TIF1B_HUMAN			Transcription intermediary factor 1-beta;	-0.44	0.04	48.10	1.98
AASASASAAA	SSPAGGGAEALELLEHCGVCR	TIF1B_HUMAN			Transcription	-0.55	0.03	35.10	-1.00
AAASASASAA	ASSPAGGGAEALELLEHCGVCR	TIF1B_HUMAN			Transcription	-0.58	0.03	38.50	-2.02
TAPSAAASAS	ASAAASSPAGGGAEALELLEHCG	TIF1B_HUMAN			Transcription intermediary factor 1-	-0.63	0.05	48.30	-0.97
KRSTAPSAAA	SASASAAASSPAGGGAEALELLEH	TIF1B_HUMAN			Transcription intermediary factor 1-	-0.69	0.05	47.40	-0.46
ERTVYCNVHK	HEPLVLFCESCDTLTCR	TIF1B_HUMAN			Transcription	-0.76	0.03	44.80	-1.47
ASAAASSPAG	GGAEALELLEHCGVCR	TIF1B_HUMAN			Transcription intermediary factor 1-	-0.89	0.03	28.00	-2.93
AEPHVSGVKR	SRSGEGEVSGLMR	TIF1B_HUMAN			Transcription intermediary factor 1-	-1.08	0.09	33.80	-2.29
TADSQPPVFK	VFPGSTTEDYNLIVIER	TIF1B_HUMAN			Transcription	-1.25	0.03	65.60	-0.96
SGISPCFSSR	RSSEASQAEGR	GLI3_HUMAN			Transcriptional activator GLI3;	6.21	0.30	29.60	2.07
QSSGDEALSK	SVPVTVDDDDDDNDPENR	ATRX_HUMAN			Transcriptional regulator	0.11	0.01	93.60	0.49
FNHTQFPPSR	SSGLPNIPVQTISR	TFR1_HUMAN			Transferrin receptor	2.80	0.19	32.30	1.87
RLAGTESPVR	EEPGEDFPAAR	TFR1_HUMAN			Transferrin receptor	0.56	0.03	34.60	-0.80

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
QHLQSSRHRR	ALDTNYCFSSTEKNCCVR	TGFB1_HUMAN			Transforming growth factor beta-1;	1.15	0.13	26.00	-2.28
EGKNMACVQR	TLMNLGGLAVAR	TAGL2_HUMAN			Transgelin-2;	4.39	0.48	63.50	-4.74
GKNMACVQRT	LMNLGGLAVAR	TAGL2_HUMAN			Transgelin-2;	-1.55	0.14	26.40	3.83
ESEIRRERER	QTNPSAMEVEEDDPVPEIR	TERA_HUMAN			Transitional endoplasmic reticulum ATPase;	3.09	0.21	53.20	5.49
ALRRFGRFDR	EVDIGIPDATGR	TERA_HUMAN			Transitional endoplasmic reticulum ATPase;	2.16	0.11	23.40	-1.10
ELLKMFGIDR	DAIAQAVR	TKT_HUMAN			Transketolase;	3.56	0.09	40.30	-3.44
RSGKPAELLK	MFGIDRDAIAQAVR	TKT_HUMAN			Transketolase;	3.23	0.20	32.90	-1.82
IYSQIQSKKK	ILATPPQEDAPSVDIANIR	TKT_HUMAN			Transketolase;	0.20	0.02	80.60	1.41
ATRNRTVPFC	STFAAFFTR	TKT_HUMAN			Transketolase;	-0.76	0.03	29.30	-2.22
KKILATPPQE	DAPSVDIANIR	TKT_HUMAN			Transketolase;	-0.86	0.08	48.10	-1.24
YSQIQSKKKI	LATPPQEDAPSVDIANIR	TKT_HUMAN			Transketolase;	-1.55	0.09	62.60	5.25
AMAFASIYKL	DNLVAILDINR	TKT_HUMAN			Transketolase;	-2.92	0.22	43.70	0.00
ASEFDPQYNK	DATSRPTDNILIPQLIR	SEC63_HUMAN			Translocation protein	0.35	0.02	39.80	-1.08
MAGVGDAA	APGEGGGGGVDGPQR	TAPT1_HUMAN			Transmembrane anterior	-6.27	0.00	30.60	0.67
FLLGPRLVLA	ISFHLPINSR	TMEDA_HUMAN			Transmembrane emp24 domain-containing protein	0.34	0.02	32.80	-2.06
DQPEGTPVEL	YYTVHPGGER	T132D_HUMAN			Transmembrane protein 132D;	0.53	0.04	28.50	1.65
LQVAAYVWFC	YAVLVSLR	TM145_HUMAN			Transmembrane protein 145;	-0.37	0.02	19.90	-1.15
LQAKASGKTS	QVGAASAPAKESPR	TCOF_HUMAN			Treacle protein;	2.43	0.23	31.60	-2.38
IETFHKYASE	DSNGATLTGR	TCHL1_HUMAN			Trichohyalin-like protein	5.58	0.22	28.70	-5.19
ELIGTLNAAK	VPADTEVVCAPPTAYIDFAR	TPIS_HUMAN			Triosephosphate	3.90	0.33	72.30	-0.36
VHEKLRGWLK	SNVSDAVAQSTR	TPIS_HUMAN			Triosephosphate	2.37	0.15	73.00	-3.17

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TGEISPGMIK	DCGATWVVLGHSER	TPIS_HUMAN			Triosephosphate isomerase;	1.85	0.09	39.90	-3.65
HEKLRGWLKS	NVSDAVAQSTR	TPIS_HUMAN			Triosephosphate	-1.34	0.10	42.80	-3.47
QEVHEKLRGW	LKSNVSDAVAQSTR	TPIS_HUMAN			Triosephosphate isomerase;	-1.55	0.14	41.90	-2.52
LFALILSGKC	SYSPEPDQR	TPP1_HUMAN			Tripeptidyl-peptidase 1;	1.47	0.09	33.30	-0.36
LFALILSGKC	SYSPEPDQRR	TPP1_HUMAN			Tripeptidyl-peptidase 1;	0.80	0.02	27.80	-7.12
QRNVGSSQFK	TIEDDLVSALVR	TRUA_HUMAN			tRNA pseudouridine	3.97	0.25	28.10	-2.86
ESPSLHKRKR	EAPDQDPGGPR	DUS2L_HUMAN			tRNA-dihydrouridine(20) synthase [NAD(P)+]-like;	-0.16	0.01	34.30	-1.11
HHSLALTSFK	RQQEESFQEQSALAAEAR	SEN34_HUMAN			tRNA-splicing endonuclease subunit	-0.73	0.07	52.10	0.00
LSETELKQLE	TVLDDLDPENALLPAGFR	TMOD3_HUMAN			Tropomodulin-3;	0.96	0.14	84.60	-2.07
TELKQLETVL	DDLDPENALLPAGFR	TMOD3_HUMAN			Tropomodulin-3;	0.32	0.01	51.00	4.54
AEGDVAALNR	RIQLVEEELDR	TPM1_HUMAN	TPM2_HUMAN	TPM3_HUMAN	Tropomyosin alpha-1 chain;	3.45	0.18	40.50	-1.82
EGDVAALNRR	IQLVEEELDRAQER	TPM1_HUMAN	TPM2_HUMAN	TPM3_HUMAN	Tropomyosin alpha-1 chain;	1.51	0.12	33.50	1.02
QEKLELAEKK	AADAEAEVASLNR	TPM3_HUMAN			Tropomyosin alpha-3 chain;	3.37	0.62	32.30	-2.60
EGDVAALNRR	IQLVEEELDR	TPM3_HUMAN	TPM1_HUMAN	TPM2_HUMAN	Tropomyosin alpha-3 chain;	2.51	0.17	47.70	4.87
RKYEEVARKL	VIIEGDLER	TPM3_HUMAN			Tropomyosin alpha-3	0.98	0.09	33.30	0.28
PWTVQTSSAK	GIDYDKLIVR	SYWC_HUMAN			Tryptophan--tRNA ligase,	3.68	0.30	25.30	-1.11
RTDIQCLIPC	AIDQDPYFR	SYWC_HUMAN			Tryptophan--tRNA ligase,	-0.14	0.01	24.00	-1.64
KHVPRAVFVD	LEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	2.72	0.19	35.90	-3.40
AGKHVPRAVF	VDLEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	1.72	0.14	51.30	-2.97
PTGFKVGINY	QPPTVVPGGDLAKVQR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	1.37	0.14	26.70	-3.18

Table S5

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
GKHVPRAVFV	DLEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.94	0.07	45.50	-1.14
YRQLFHPEQL	ITGKEDAANNYAR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.84	0.09	33.00	0.95
ETGAGKHVPR	AVFVDLEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.76	0.06	59.70	-0.52
MYAKRAFVHW	YVGEGMEEGEFSEAR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.55	0.05	34.00	5.24
GAGKHVPRAV	FVDLEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.53	0.05	37.90	0.64
FEGPLNVDLI	EFQTNLVPYPR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.45	0.03	43.80	-2.29
SETGAGKHVP	RAVFVDLEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.09	0.00	43.30	-4.01
NNWAKGHYTE	GAELVDSVLDVVR	TBB2A_HUMAN	TBB2B_HUMAN	TBB3_HUMAN	Tubulin beta-2A chain;	0.42	0.02	47.80	-4.27
AKGHYTEGAE	LVDSVLDVVR	TBB2A_HUMAN	TBB2B_HUMAN	TBB3_HUMAN	Tubulin beta-2A chain;	0.31	0.02	24.20	-2.96
GRYVPRAVLV	DLEPGTMDSVR	TBB2A_HUMAN	TBB2B_HUMAN	TBB3_HUMAN	Tubulin beta-2A chain;	0.18	0.02	36.80	-2.23
SGGRYVPRAV	LVDLEPGTMDSVR	TBB2A_HUMAN	TBB2B_HUMAN	TBB3_HUMAN	Tubulin beta-2A chain;	0.14	0.01	33.20	-0.34
QSGAGNNWAK	GHYTEGAELVDSVLDVVR	TBB2A_HUMAN	TBB2B_HUMAN	TBB3_HUMAN	Tubulin beta-2A chain;	0.13	0.01	47.00	1.95
GHYTEGAELV	DSVLDVVR	TBB2A_HUMAN	TBB2B_HUMAN	TBB3_HUMAN	Tubulin beta-2A chain;	-0.10	0.01	26.70	-5.97
EATGGKYVPR	AILVDLEPGTMDSVR	TBB2A_HUMAN	TBB2B_HUMAN	TBB3_HUMAN	Tubulin beta-2A chain;	-0.29	0.03	60.50	-2.37
IGAKFWEVIS	DEHGIDPTGTYHGDSDLQLER	TBB4A_HUMAN	TBB4B_HUMAN		Tubulin beta-4A chain;	0.64	0.05	29.40	-1.42
EASGGRYVPR	AVLVDLEPGTMDSVR	TBB4B_HUMAN	TBB4A_HUMAN	TBB8_HUMAN	Tubulin beta-4B chain;	2.01	0.13	63.90	-1.10
LQLDRISVYY	NEATGGKYVPR	TBB4B_HUMAN	TBB5_HUMAN		Tubulin beta-4B chain;	1.47	0.14	50.20	0.72
GNNWAKGHYT	EGAELVDSVLDVVR	TBB4B_HUMAN	TBB2A_HUMAN	TBB2B_HUMAN	Tubulin beta-4B chain;	-0.23	0.03	56.20	-0.59
ESSSQKYVPR	AALVDLEPGTMDSVR	TBB6_HUMAN			Tubulin beta-6 chain;	4.42	0.52	43.10	-0.62
APFFYMPQQV	AYTLLWPLR	TTL12_HUMAN			Tubulin--tyrosine ligase-like protein 12;	0.34	0.02	39.40	-5.82
SRMMIPDCQR	RLEAAYLDLQR	TBCA_HUMAN			Tubulin-specific chaperone A;	4.94	0.76	32.70	-0.07

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
PGSAASPRLR	EGPELSPDDPAGLLDLR	TNFL9_HUMAN			Tumor necrosis factor ligand superfamily	1.05	0.06	51.10	7.68
LLLAAACAVF	LACPWAVSGAR	TNFL9_HUMAN			Tumor necrosis factor	0.34	0.01	33.20	-1.81
LLLVSAESAL	ITQQDLAPQQR	TR10B_HUMAN			Tumor necrosis factor	1.24	0.11	37.00	0.60
AVLLLVSAES	ALITQQDLAPQQR	TR10B_HUMAN			Tumor necrosis factor receptor superfamily	0.11	0.01	40.60	-2.85
GTAPCSRGSS	WSADLDKCMDCASCR	TNR12_HUMAN			Tumor necrosis factor	0.78	0.09	23.60	-1.45
WLALLRSVAG	EQAPGTAPCSR	TNR12_HUMAN			Tumor necrosis factor receptor superfamily	0.06	0.00	43.90	0.08
CDEWGRRARR	GVEVAAGASSGGETR	TR19L_HUMAN			Tumor necrosis factor	0.34	0.03	68.30	-2.17
GTFVQRPCRR	DSPTTCGPCPPR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily member 6B;	6.07	0.58	43.00	-1.89
AALQLKLRRR	LTELLGAQDGALLVR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily	5.51	0.45	89.40	1.69
RAALQLKLRR	RLTELLGAQDGALLVR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily member 6B;	5.43	0.47	61.90	-0.80
QDISIKRLQR	LLQALEAPEGWGPTPR	TNF6B_HUMAN			Tumor necrosis factor	5.02	0.52	75.80	1.30
QFWNYLERCR	YCNVLCGEREEEAR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily member 6B;	3.98	0.39	36.80	-2.59
PGTFVQRPCR	RDSPTTCGPCPPR	TNF6B_HUMAN			Tumor necrosis factor	1.62	0.06	41.30	-2.61
ALLPVPAVRG	VAETPTYPWR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily member 6B;	1.20	0.01	29.70	-4.38
ISIKRLQRLL	QALEAPEGWGPTPR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily	0.96	0.07	34.20	-1.04
ALPALLPVPA	VRGVAETPTYPWR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily	0.90	0.05	38.30	-4.53
AEECERAVID	FVAFQDISIKR	TNF6B_HUMAN			Tumor necrosis factor	0.24	0.02	24.60	-3.23
FQDISIKRLQ	RLLQALEAPEGWGPTPR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily	0.02	0.00	31.40	-2.13

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LCTSCTGFPL	STRVPGAEECER	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily	-0.60	0.04	22.60	-2.31
LNSPNKGLLS	DSMTDVPVDTGVAAR	TPD54_HUMAN			Tumor protein D54;	1.35	0.14	38.80	-0.06
NLVEGKRKRR	SNVSSPATPTASSSSSTTPTR	TP53B_HUMAN			Tumor suppressor p53-binding protein 1;	0.13	0.01	85.60	1.21
LRQIKINEVQ	TDVGVDTKHQTLQGVAFPISR	TWF1_HUMAN			Twinfilin-1;	1.21	0.13	43.20	-2.79
QAFVHWQEPR	APLQGTLLGYR	UFO_HUMAN			Tyrosine-protein kinase receptor UFO;	6.07	0.74	49.70	-1.31
PLQGTLLGYR	LAYQGQDTPEVLMDIGLR	UFO_HUMAN			Tyrosine-protein kinase receptor UFO;	6.00	0.62	50.50	-0.29
HNAKGVTTSR	TATITVLPQQPR	UFO_HUMAN			Tyrosine-protein kinase receptor UFO;	4.63	0.34	36.30	-2.36
GARGLTGTLR	CQLQVQGEPPEVHWLR	UFO_HUMAN			Tyrosine-protein kinase	4.25	0.23	44.20	-0.60
GPPEPVDLLW	LQDAVPLATAPGHGPQR	UFO_HUMAN			Tyrosine-protein kinase	-0.76	0.04	43.90	-3.06
FVSQPGYVGL	EGLPYFLEEPEDR	UFO_HUMAN			Tyrosine-protein kinase receptor UFO;	-3.66	0.00	27.90	1.90
LASEHNTPVR	SEWSELQSQER	PTN12_HUMAN			Tyrosine-protein phosphatase non-receptor	0.31	0.03	40.80	-1.63
DAFKTLFVAR	VNYDTTESKLR	RU17_HUMAN			U1 small nuclear ribonucleoprotein 70 kDa;	-0.32	0.02	29.80	-2.82
ATKKAVQGGG	ATPVVGAVQGPVPGMPPMTQAPR	SNRPA_HUMAN			U1 small nuclear	-0.39	0.02	67.30	-2.66
MPKFYCDYCD	TYLTHDSPSVR	RU1C_HUMAN			U1 small nuclear	-0.12	0.01	26.70	-3.58
RKPGMRPDWK	AGAGPGGPPQKPAPSSQR	UTP18_HUMAN			U3 small nucleolar RNA-associated protein 18	0.16	0.01	27.30	-1.40
AQEKKLRLAK	LYLEQLR	U3IP2_HUMAN			U3 small nucleolar RNA-interacting protein 2;	0.13	0.01	19.90	-0.93
VRADDLLPLG	DQTQDGDFGSR	SNUT1_HUMAN			U4/U6.U5 tri-snRNP-associated protein 1;	1.36	0.02	35.90	2.14
EKEVVVRADD	LLPLGDQTQDGDFGSR	SNUT1_HUMAN			U4/U6.U5 tri-snRNP-	-2.16	0.19	28.60	-1.71
KSNSLISIKR	LTLQQKAK	U520_HUMAN			U5 small nuclear	14.30	2.38	26.40	-0.59
TARSLQYEYK	ANSNLVLQADR	U520_HUMAN			U5 small nuclear	-0.34	0.03	49.10	4.07
KRQRHELLLG	AGSGPGAGQQQATPGALLQAGPPI	SNR40_HUMAN			U5 small nuclear ribonucleoprotein 40 kDa protein;	-0.76	0.05	43.70	2.65

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
VKRQRHELLL	GAGSGPGAGQQQATPGALLQAGP	SNR40_HUMAN			U5 small nuclear	-0.79	0.07	35.30	0.48
GMDTEAETVA	TEAPARPVNCLEAEAAAGAAAED	UBFD1_HUMAN			Ubiquitin domain-containing protein	0.84	0.06	53.40	-2.47
APARPVNCLE	AEAAAGAAAEDSGAAR	UBFD1_HUMAN			Ubiquitin domain-	0.00	0.00	95.20	0.91
ENGKISRLRR	ECPSDECGAGVFMASHFDR	RS27A_HUMAN			Ubiquitin-40S ribosomal protein S27a;	1.86	0.08	38.80	0.55
TKIFTASNVS	SVPLPAENVTITAGQR	UBP2L_HUMAN			Ubiquitin-associated	0.79	0.06	63.10	-0.30
QSTTYTSQNN	AQGPLYEQR	UBP2L_HUMAN			Ubiquitin-associated protein 2-like;	0.66	0.07	25.60	-3.10
MLQTRFPLDY	YSIPFPTPTTPLTGR	UBP2L_HUMAN			Ubiquitin-associated	0.23	0.01	34.80	-3.40
IQSTTYTSQN	NAQGPLYEQR	UBP2L_HUMAN			Ubiquitin-associated protein 2-like;	-1.04	0.09	33.90	-1.00
LKNMTVEQLL	TGSPTSPTVEPEKPTR	UBE2O_HUMAN			Ubiquitin-conjugating	1.05	0.09	50.00	-3.33
ADDEAADDTD	DTSSVTSSASSTTSSQSGSGTSR	UBE2O_HUMAN			Ubiquitin-conjugating	-0.63	0.09	45.20	-2.32
DPKFVERTLR	LAGTQPLEVLEAVQR	UBA1_HUMAN			Ubiquitin-like modifier-	3.37	0.31	62.40	-0.36
AQHGRPPRPR	NEEDAAELVALAQAVNAR	UBA1_HUMAN			Ubiquitin-like modifier-	1.44	0.07	62.40	2.87
DFIVAASNLR	AENYDIPSADR	UBA1_HUMAN			Ubiquitin-like modifier-activating enzyme 1;	1.32	0.05	36.70	-2.19
LSAMVSMVTK	DNPGVVTCLDEAR	UBA1_HUMAN			Ubiquitin-like modifier-activating enzyme 1;	0.91	0.07	61.70	-2.03
VLGPYTFSIC	DTSNFSDYIR	UBA1_HUMAN			Ubiquitin-like modifier-	-6.27	0.00	27.50	-7.34
M	IEVVCNDR	UBL5_HUMAN			Ubiquitin-like protein 5;	0.69	0.02	33.10	0.94
ESSVSTPSAS	FEPNNTCENSQSR	UBXN4_HUMAN			UBX domain-containing	0.67	0.09	48.00	-0.93
LHIYDPKVPR	EQIVVDLSHPGVSEDDQVSR	UGDH_HUMAN			UDP-glucose 6-dehydrogenase;	-0.04	0.00	40.50	-7.22
APDGNGGLYR	ALAAQNIVEDMEQR	UAP1_HUMAN			UDP-N-acetylhexosamine	1.26	0.12	68.00	-2.34
SGGVNLFAND	GSFLELFKR	CS043_HUMAN			Uncharacterized protein C19orf43;	-0.16	0.01	21.90	-1.97
KIQNFLNEFK	NIPEIVAVYSR	CX038_HUMAN			Uncharacterized protein	1.93	0.10	35.40	-2.48
TSEAAMETDI	TEQQQAAMQQEER	MYO9A_HUMAN			Unconventional myosin-IXa;	4.59	0.55	29.40	-1.18
NSGRAVTYSR	SRYLECISCGSSDMSCER	UPAR_HUMAN			Urokinase plasminogen activator surface receptor;	0.92	0.11	66.40	-1.53
VQRGFDSFLG	RYQAVQEAVEDR	UTRO_HUMAN			Utrophin;	-0.27	0.02	35.90	-4.89

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
ASPTAAPESS	TSFPPAPTSGMSHPPPAAR	RD23A_HUMAN			UV excision repair	0.26	0.00	27.80	-2.01
ATTTATTTTT	SSGGHPLEFLR	RD23B_HUMAN			UV excision repair protein RAD23 homolog	0.67	0.03	27.00	-7.08
VAAAAATTTA	TTTTTSSGGHPLEFLR	RD23B_HUMAN			UV excision repair	0.55	0.05	34.50	-2.54
AVAAAAATTT	ATTTTTSSGGHPLEFLR	RD23B_HUMAN			UV excision repair protein RAD23 homolog	0.48	0.03	56.50	-1.61
TGAPQSSAVA	AAAATTTATTTTTSSGGHPLEFLR	RD23B_HUMAN			UV excision repair protein RAD23 homolog	0.20	0.02	33.20	-1.71
LRAMRGIVNG	AAPELPVPTGGPAVGAR	VATB2_HUMAN			V-type proton ATPase	-0.06	0.00	57.60	-4.72
LAAAAAAAAA	EQQVPLVLWSSDR	VAS1_HUMAN			V-type proton ATPase subunit S1;	-0.04	0.00	62.40	-0.63
ATLQDRHERI	TKLAGVHALLR	FFR_HUMAN			Vacuolar protein sorting-	10.36	0.00	25.70	-5.91
SPEEVEQQKR	QQPGPSEHIER	VASP_HUMAN			Vasodilator-stimulated	2.17	0.09	23.30	-3.67
RMKSSSSVTT	SETQPCTPSSSDYSDLQR	VASP_HUMAN			Vasodilator-stimulated	0.85	0.06	81.70	-0.76
PRPGPARRPY	AGGAAQLALDKSDSHPSDALTR	ACADV_HUMAN			Very long-chain specific acyl-CoA dehydrogenase,	0.37	0.03	41.50	-2.95
M	VLLTMIAR	SC22B_HUMAN			Vesicle-trafficking protein SEC22b;	0.35	0.03	25.90	-3.28
AKQESTEYRR	QVQSLTCEVDALKGTNESLER	VIME_HUMAN			Vimentin;	4.99	0.43	39.90	-1.40
VDQLTNDKAR	VEVERDNLAEDIMR	VIME_HUMAN			Vimentin;	4.77	0.28	35.50	-3.03
EQLKGQGKSR	LGDLYEEEMR	VIME_HUMAN			Vimentin;	4.54	0.22	48.10	-4.99
ALDIEIATYR	KLLEGEESR	VIME_HUMAN	DESM_HUMAN	K2C7_HUMAN	Vimentin;	3.89	0.20	25.00	-1.16
KVELQELNDR	FANYIDKVR	VIME_HUMAN			Vimentin;	3.81	0.43	36.50	0.93
AANYQDTIGR	LQDEIQNMKEEMAR	VIME_HUMAN			Vimentin;	3.08	0.27	40.80	-3.18
EKLQEEMLQR	EEAENTLQSFRQDVDNASLAR	VIME_HUMAN			Vimentin;	2.31	0.18	35.70	-1.07
EAENTLQSFR	QDVDNASLAR	VIME_HUMAN			Vimentin;	2.04	0.06	39.70	-2.42
RKLLEGEESR	ISLPLPNFSSLNLR	VIME_HUMAN			Vimentin;	1.55	0.16	45.80	-2.38
EYRRQVQSLT	CEVDALKGTNESLER	VIME_HUMAN			Vimentin;	1.31	0.12	24.80	0.22

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EKLQEEMLQR	EEAENTLQSFR	VIME_HUMAN			Vimentin;	1.02	0.07	47.00	-0.22
NTEFKNTRTN	EKVELQELNDR	VIME_HUMAN	DESM_HUMAN		Vimentin;	1.01	0.02	42.70	-2.59
LQDSVDFSLA	DAINTEFKNTR	VIME_HUMAN			Vimentin;	0.88	0.09	33.80	-1.39
LPNFSSLNLR	ETNLDSLPLVDTHSK	VIME_HUMAN			Vimentin;	0.87	0.03	28.40	1.04
AINTEFKNTR	TNEKVELQELNDR	VIME_HUMAN	DESM_HUMAN		Vimentin;	0.53	0.05	50.70	-2.35
LLQDSVDFSL	ADAINTEFKNTR	VIME_HUMAN			Vimentin;	0.51	0.04	23.90	-1.25
LRPSTSRSLY	ASSPGGVYATR	VIME_HUMAN			Vimentin;	0.47	0.03	44.60	-0.82
YRRQVQSLTC	EVDALKGTNESLER	VIME_HUMAN			Vimentin;	0.29	0.02	33.60	-4.23
TNESLERQMR	EMEENFAVEAANYQDTIGR	VIME_HUMAN			Vimentin;	0.21	0.02	94.60	-1.35
EFKNTRTNEK	VELQELNDR	VIME_HUMAN	DESM_HUMAN		Vimentin;	0.18	0.01	30.00	-0.70
QREEAENTLQ	SFRQDVDNASLAR	VIME_HUMAN			Vimentin;	0.13	0.01	49.70	-1.99
IQEQHVQIDV	DVSKPDLTAALR	VIME_HUMAN			Vimentin;	0.00	0.00	39.30	-1.03
GVRLLQDSVD	FSLADAINTEFKNTR	VIME_HUMAN			Vimentin;	-0.06	0.00	89.40	-2.62
QVQSLTCEVD	ALKGTNESLER	VIME_HUMAN			Vimentin;	-0.16	0.02	44.20	1.09
EAEEWYKSKF	ADLSEAANR	VIME_HUMAN			Vimentin;	-0.18	0.02	37.20	0.41
LPLVDTHSKR	TLLIKTVETR	VIME_HUMAN			Vimentin;	-0.25	0.02	22.40	-2.44
NLQEAEEWYK	SKFADLSEAANR	VIME_HUMAN			Vimentin;	-0.32	0.02	54.00	-2.76
GSALRPSTSR	SLYASSPGGVYATR	VIME_HUMAN			Vimentin;	-0.47	0.03	41.20	-2.05
DQLTNDKARV	EVERDNLAEDIMR	VIME_HUMAN			Vimentin;	-0.60	0.04	46.40	0.74
QEQHVQIDVD	VSKPDLTAALR	VIME_HUMAN			Vimentin;	-0.63	0.05	39.90	-2.66
QDSVDFSLAD	AINTEFKNTR	VIME_HUMAN			Vimentin;	-0.69	0.03	51.70	-2.30
ERQMREMEEN	FAVEAANYQDTIGR	VIME_HUMAN			Vimentin;	-0.79	0.05	40.40	1.96
VRLLQDSVDF	SLADAINTEFKNTR	VIME_HUMAN			Vimentin;	-0.79	0.05	32.40	-3.94

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EMEENFAVEA	ANYQDTIGR	VIME_HUMAN			Vimentin;	-0.89	0.03	27.70	-2.80
QEAEEWYKSK	FADLSEAANR	VIME_HUMAN			Vimentin;	-0.89	0.08	29.20	-4.52
AENTLQSFRQ	DVDNASLAR	VIME_HUMAN			Vimentin;	-1.20	0.06	41.00	-1.21
RLREKLQEEM	LQREEAENTLQSFR	VIME_HUMAN			Vimentin;	-1.25	0.12	40.00	-0.23
ELEQLKGQGK	SRLGDLYEEEMR	VIME_HUMAN			Vimentin;	-1.44	0.08	45.10	-2.22
KLNQAKGWLR	DPSASPGDAGEQAIR	VINC_HUMAN			Vinculin;	5.75	1.05	67.50	0.60
PYRQDLLAKC	DRVDQLTAQLADLAAR	VINC_HUMAN			Vinculin;	0.86	0.05	50.30	-0.28
VRPGYPKLIR	DVWGIEGPIDAAFTR	VTNC_HUMAN			Vitronectin;	3.13	0.31	76.00	-2.80
EDFLGRTLLA	DDLFAAYFGPGSSRR	VWA7_HUMAN			von Willebrand factor A domain-containing protein	3.17	0.11	27.30	-4.44
MQSRL	LLLGAPGGHGGPASR	K0564_HUMAN			von Willebrand factor A	3.31	0.15	24.10	-8.10
CWLLGAGAEA	DFSILDEAQVLASQMR	CAHD1_HUMAN			VWFA and cache domain-containing protein 1;	0.38	0.06	63.90	0.32
MQHSLAGQTY	AVPLIQPDLR	WASH2_HUMAN	WASH3_HUMAN		WAS protein family	0.62	0.06	28.50	-1.30
MA	VETLSPDWEFDR	WASH7_HUMAN			WASH complex subunit	1.43	0.13	26.50	-6.24
GSIHNLPLVT	SQRPFYDGPMPTPR	WDHD1_HUMAN			WD repeat and HMG-box DNA-binding protein 1;	0.68	0.02	40.60	-5.90
SVLGGQDQLR	VRVTELEDEVR	WDR18_HUMAN			WD repeat-containing	-0.58	0.03	31.90	-1.67
M	KLTDSVLR	WDR82_HUMAN			WD repeat-containing protein 82;	0.26	0.02	29.10	-0.80
QDITMRKAFR	SSTIQDQQLFDR	WASF1_HUMAN			Wiskott-Aldrich syndrome protein family	0.65	0.04	35.30	1.49
PPPAPQPQAR	SRLNATASLEQER	WFS1_HUMAN			Wolframin;	-0.89	0.07	38.80	-2.58
EQGGAHFSVS	SLAEGSVTSVGSVNPAENFR	XRCC5_HUMAN			X-ray repair cross-complementing protein 5;	0.06	0.00	40.20	-3.06
GGFDISLFYR	DIISIAEDEDLR	XRCC6_HUMAN			X-ray repair cross-complementing protein 6;	6.38	0.90	59.10	-3.81

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
IVEKLRFTYR	SDSFENPVLQQHFR	XRCC6_HUMAN			X-ray repair cross-complementing protein 6;	1.74	0.08	50.70	-3.75
IGKELQKQGR	QEALEWLIR	XPP1_HUMAN			Xaa-Pro aminopeptidase 1;	3.09	0.18	25.90	-4.38
HSSPASLQLG	AVSPGTLTPTGVVSGPAATPTAQHL	YAP1_HUMAN			Yorkie homolog;	0.28	0.02	69.40	0.48
IITDFKEKTK	SPPASSAASADQHSQSGSSSDNTEF	YAF2_HUMAN			YY1-associated factor 2;	0.23	0.01	43.40	2.96
GGQAQSAASG	AEQTEKADAPR	ZBT17_HUMAN			Zinc finger and BTB	5.86	0.44	29.80	-4.16
IKLEKALRVQ	QSSESSTSSPSQHEATPGAR	ZC11A_HUMAN			Zinc finger CCCH	1.03	0.09	36.60	-6.02
STSAITISTS	ATPTNTTNNTFANEDSHR	ZC3HD_HUMAN			Zinc finger CCCH domain-containing protein 13;	0.21	0.02	26.60	-2.57
PTSKPEGSLH	SSPVGPSSSKGSGPPPTEEEEGER	ZC3H4_HUMAN			Zinc finger CCCH domain-containing protein	0.34	0.02	27.40	0.94
ILKTLRQQTS	SRPPASVGELSSSGLGDPR	ZC3H4_HUMAN			Zinc finger CCCH domain-containing protein	-0.25	0.02	48.50	-1.90
TLPAARSSLG	SLQTPEAVTTR	ZCCHV_HUMAN			Zinc finger CCCH-type antiviral protein 1;	0.21	0.01	29.00	-0.65
TPSPDQISHR	ASLEDAPVDDLTR	ZCCHV_HUMAN			Zinc finger CCCH-type antiviral protein 1;	-0.18	0.01	48.90	1.26
IECGQAFIQK	AHLIVHQR	ZN175_HUMAN			Zinc finger protein 175;	-9.97	0.00	25.70	1.29
IFRTASQRCR	DPPSNPVAASPR	Z280C_HUMAN			Zinc finger protein 280C;	0.95	0.03	37.10	-6.28
ANTSSNVSND	FQEDNLCQSER	ZN292_HUMAN			Zinc finger protein 292;	4.37	0.37	26.50	-2.06
LSASTSSSCS	TAATPGPVGLALPYAIPAR	ZN598_HUMAN			Zinc finger protein 598;	0.32	0.02	41.70	-4.91
NPHLSRHRKI	HAGENSLR	ZN610_HUMAN			Zinc finger protein 610;	-2.25	0.11	24.00	-0.11

Table S5

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TLAEKSRGLF	SANDWQCKTCSNVNWAR	ZRAB2_HUMAN			Zinc finger Ran-binding domain-containing protein	1.05	0.10	30.70	0.60
LRHARWFQAR	ASGLQPCVIVIR	ZFR2_HUMAN			Zinc finger RNA-binding protein 2;	0.34	0.02	25.20	-0.82
VTPASLAALQ	SDVQPVGHDYVEEVR	ZFR_HUMAN			Zinc finger RNA-binding protein;	0.79	0.08	58.20	-3.41
SEPVTPASLA	ALQSDVQPVGHDYVEEVR	ZFR_HUMAN			Zinc finger RNA-binding	0.04	0.01	50.50	1.30
LMQDMEHPQR	QNVAVNELCGR	ZYX_HUMAN			Zyxin;	4.65	0.26	29.80	-1.63
QVQLHVQSQT	QPVSLANTQPR	ZYX_HUMAN			Zyxin;	0.57	0.04	30.50	-8.39
EEAKGQVEAR	RESLDPVQEPGGQAEADGDVPGP	CGRE1_HUMAN				3.92	0.41	61.90	2.31
AVIQHFQEKV	ESLEQEAANER	A4_HUMAN				0.16	0.01	43.70	-3.20
EKRSTAPSAA	ASASASAAASSPAGGGAEALELLE	TIF1B_HUMAN				-0.66	0.04	75.10	-1.18