Table S6

Table S6 Analysis of N-termini that were unmodified upon secretome harvest and chemically dimethylated in the TAILS procedure (replicate 2).
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
M	VQAWYMDDAPGDPR	MTND_HUMAN			1,2-dihydroxy-3-keto-5-methylthiopentene	0.86	0.05	63.30	1.39
M	VDREQLVQKAR	1433G_HUMAN			14-3-3 protein gamma;	-1.00	0.08	55.70	0.84
ALLRPGRLDR	KIHIDLPNEQAR	PRS10_HUMAN			26S protease regulatory	1.17	0.05	38.80	1.60
PGTGKTLLAK	AVANQTSATFLR	PRS4_HUMAN			26S protease regulatory subunit 4;	0.91	0.05	59.10	3.36
ARIMQIHSRK	MNVSPDVNYEELAR	PRS6A_HUMAN			26S protease regulatory subunit 6A;	0.67	0.06	52.30	6.54
IMQIHSRKMN	VSPDVNYEELAR	PRS6A_HUMAN			26S protease regulatory	0.42	0.04	37.80	1.33
QVKVIAATNR	VDILDPALLR	PRS6A_HUMAN			26S protease regulatory subunit 6A;	0.28	0.02	29.60	5.09
ATVWDEAEQD	GIGEEVLKMSTEEIIQR	PRS6A_HUMAN			26S protease regulatory subunit 6A;	-0.72	0.04	60.10	3.55
NVKVIMATNR	ADTLDPALLRPGR	PRS6B_HUMAN			26S protease regulatory	0.28	0.01	23.30	2.10
KCVAQASKNR	SLADFEKALTDYR	PSD11_HUMAN			26S proteasome non-ATPase regulatory subunit	1.12	0.08	25.60	3.82
M	VLESTMVCVDNSEYMR	PSMD4_HUMAN			26S proteasome non-ATPase regulatory subunit	0.74	0.08	89.30	6.07
TEDSDDALLK	MTISQQEFGR	PSMD4_HUMAN			26S proteasome non-	0.30	0.02	35.90	3.10
EDEEDDYQQK	RKGVEGLIDIENPNR	HAP28_HUMAN			28 kDa heat- and acid-	-0.62	0.05	52.20	3.31
PQLSPAGKRY	LLSSAYVDSHKWEAR	RT27_HUMAN			28S ribosomal protein S27, mitochondrial;	0.91	0.06	36.90	4.17
SGWMPQAAPC	LSGAPQASAADVVVVHGR	THIK_HUMAN			3-ketoacyl-CoA thiolase,	-1.24	0.12	48.90	6.16
GEADRDTYRR	SAVPPGADKKAEAGAGSATEFQFR	RS10_HUMAN			40S ribosomal protein	1.37	0.11	58.80	2.28
RGEADRDTYR	RSAVPPGADKKAEAGAGSATEFQF	RS10_HUMAN			40S ribosomal protein	1.05	0.06	41.30	2.43

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
GEFEIIDDHR	AGKIVVNLTGR	RS15A_HUMAN			40S ribosomal protein S15a;	1.74	0.13	34.90	-9.60
IVRFLTVMMK	HGYIGEFEIIDDHR	RS15A_HUMAN			40S ribosomal protein S15a;	0.79	0.07	42.70	-2.20
QKYVDEASKK	EIKDILIQYDR	RS16_HUMAN			40S ribosomal protein	0.59	0.04	40.30	0.81
MP	GVTVKDVNQQEFVR	RS19_HUMAN			40S ribosomal protein S19;	0.20	0.01	39.30	-1.07
MAFK	DTGKTPVEPEVAIHR	RS20_HUMAN			40S ribosomal protein	0.74	0.05	39.20	0.76
MAFKD	TGKTPVEPEVAIHR	RS20_HUMAN			40S ribosomal protein S20;	-0.55	0.02	33.60	0.50
MQN	DAGEFVDLYVPR	RS21_HUMAN			40S ribosomal protein S21;	-0.11	0.01	61.00	3.76
MQND	AGEFVDLYVPR	RS21_HUMAN			40S ribosomal protein S21;	-1.14	0.08	36.70	2.23
IIRNVKGPVR	EGDVLTLLESER	RS28_HUMAN			40S ribosomal protein S28;	0.50	0.12	51.80	3.02
M	GHQQLYWSHPR	RS29_HUMAN			40S ribosomal protein S29;	0.86	0.05	44.70	2.36
RKFVADGIFK	AELNEFLTR	RS3_HUMAN			40S ribosomal protein S3;	1.20	0.10	36.50	2.66
YEKRMATEVA	ADALGEEWKGYVVR	RS6_HUMAN			40S ribosomal protein S6;	-0.07	0.00	30.70	5.17
MNSDLKAQLR	ELNITAAKEIEVGGGR	RS7_HUMAN			40S ribosomal protein S7;	0.84	0.06	31.30	-0.46
RNTGQRAVLK	FAAATGATPIAGR	RSSA_HUMAN			40S ribosomal protein SA;	0.64	0.06	51.30	1.87
EMRMQNNSSP	SISPNTSFTSDGSPSPLGGIKR	XRN2_HUMAN			5'-3' exoribonuclease 2;	0.40	0.02	56.10	4.82
AAYEMRMQNN	SSPSISPNTSFTSDGSPSPLGGIKR	XRN2_HUMAN			5'-3' exoribonuclease 2;	-0.40	0.03	35.20	-0.75
LVIQQVFDNG	SIYNPEVLDITEETLHSR	RLA0_HUMAN			60S acidic ribosomal protein P0;	0.67	0.04	81.80	2.00

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
IQQVFDNGSI	YNPEVLDITEETLHSR	RLA0_HUMAN			60S acidic ribosomal protein P0;	-2.24	0.11	33.80	4.71
HISKKWGFTK	FNADEFEDMVAEKR	RL10_HUMAN			60S ribosomal protein L10;	-0.88	0.08	28.90	5.80
VGESGDRLTR	AAKVLEQLTGQTPVFSKAR	RL11_HUMAN			60S ribosomal protein	0.54	0.04	41.10	1.41
SGDRLTRAAK	VLEQLTGQTPVFSKAR	RL11_HUMAN			60S ribosomal protein	0.43	0.03	26.90	-0.98
KGDSSAEELK	LATQLTGPVMPVR	RL13_HUMAN			60S ribosomal protein L13;	0.46	0.04	44.20	2.96
ISVDPRRRNK	STESLQANVQR	RL13_HUMAN			60S ribosomal protein L13;	0.04	0.01	59.50	2.60
M	GAYKYIQELWR	RL15_HUMAN			60S ribosomal protein	1.09	0.03	41.90	1.47
KMKLPGRENK	TAVVVGTITDDVR	RL18_HUMAN			60S ribosomal protein L18;	0.54	0.05	72.10	3.84
GTHNMYREYR	DLTTAGAVTQCYR	RL18A_HUMAN			60S ribosomal protein L18a;	0.67	0.07	67.80	2.96
M	KFNPFVTSDR	RL26L_HUMAN	RL26_HUMAN		60S ribosomal protein L26-like 1;	0.33	0.02	32.00	0.64
QTRVNAAKNK	TGAAPIIDVVR	RL27A_HUMAN			60S ribosomal protein L27a;	0.61	0.06	47.30	6.37
FRYNGLIHRK	TVGVEPAADGKGVVVVIKR	RL28_HUMAN			60S ribosomal protein	1.03	0.04	45.90	0.40
RRALEKIDLK	FIDTTSKFGHGR	RL3L_HUMAN	RL3_HUMAN		60S ribosomal protein L3-	1.06	0.11	54.60	7.80
KKGGEKKKGR	SAINEVVTR	RL31_HUMAN			60S ribosomal protein L31;	0.30	0.03	40.60	1.17
AKKGGEKKKG	RSAINEVVTR	RL31_HUMAN			60S ribosomal protein	-0.49	0.05	32.40	2.46
RGKKKEELLK	QLDDLKVELSQLR	RL35_HUMAN			60S ribosomal protein	-0.04	0.00	24.70	5.90
KSNYNLPMHK	MINTDLSR	RL4_HUMAN			60S ribosomal protein L4;	0.86	0.09	23.70	0.51
FKKKKLRKPR	HQEGEIFDTEKEKYEITEQR	RL6_HUMAN			60S ribosomal protein L6;	0.18	0.01	38.00	3.63
RGYGKINKKR	IALTDNALIAR	RL7_HUMAN			60S ribosomal protein L7;	4.37	0.39	45.00	1.83
QRLLARAEKK	AAGKGDVPTKRPPVLR	RL7A_HUMAN			60S ribosomal protein	1.18	0.08	23.00	7.76
SKKVISSANR	AVVGVVAGGGR	RL8_HUMAN			60S ribosomal protein L8;	0.94	0.07	48.30	2.16
KPGDRGKLAR	ASGNYATVISHNPETKKTR	RL8_HUMAN			60S ribosomal protein L8;	0.67	0.05	46.30	3.29

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
M	KTILSNQTVDIPENVDITLKGR	RL9_HUMAN			60S ribosomal protein L9;	0.42	0.02	46.50	4.08
GTIAGLNVMR	IINEPTAAAIAYGLDKR	GRP78_HUMAN			78 kDa glucose-regulated protein;	4.35	0.34	47.90	3.15
EIIANDQGNR	ITPSYVAFTPEGER	GRP78_HUMAN			78 kDa glucose-regulated	0.68	0.06	50.10	4.57
SKELSESQVH	MMAAAVADGTR	AKA12_HUMAN			A-kinase anchor protein 12;	1.73	0.17	43.50	0.27
EPLEQVEAEA	ALLTEEVLER	AKA12_HUMAN			A-kinase anchor protein	1.41	0.10	40.00	1.57
ISASVTEPLE	QVEAEAALLTEEVLER	AKA12_HUMAN			A-kinase anchor protein	0.91	0.13	85.90	1.91
KDVPFFEGLE	GSIDTGITVSR	AKA12_HUMAN			A-kinase anchor protein 12;	0.66	0.06	52.30	1.67
QERRTQEVLQ	AVAEKVKEESQLPGTGGPEDVLQP	AKA12_HUMAN			A-kinase anchor protein	0.17	0.01	37.80	3.05
RTQEVLQAVA	EKVKEESQLPGTGGPEDVLQPVQ	AKA12_HUMAN			A-kinase anchor protein	-0.34	0.01	48.60	3.60
MN	AGSDPVVIVSAAR	THIC_HUMAN			Acetyl-CoA	0.97	0.04	46.90	-0.47
QEIRYVERSY	VSKPTLKEVVIVSATR	THIL_HUMAN			Acetyl-CoA acetyltransferase,	0.02	0.00	41.10	7.43
VEWIIIDPEG	FTENGEWEIVHRPAR	ACHD_HUMAN			Acetylcholine receptor subunit delta;	3.79	0.27	31.10	8.18
KTGVSKPIVK	STLSQTVPSKGELSR	ANLN_HUMAN			Actin-binding protein	1.70	0.08	32.80	3.58
DDGSTLMEID	GDKGKQGGPTYYIDTNALR	ACL6A_HUMAN			Actin-like protein 6A;	-0.88	0.08	48.30	1.90
M	ILLEVNNR	ARPC2_HUMAN			Actin-related protein 2/3 complex subunit 2;	0.13	0.01	37.20	1.85
VFPSIVGRPR	HQGVMVGMGQKDSYVGDEAQSK	ACTA_HUMAN	ACTB_HUMAN	ACTC_HUMAN	Actin, aortic smooth muscle;	0.96	0.09	66.60	1.88
AGFAGDDAPR	AVFPSIVGR	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	2.05	0.08	34.10	0.72
AGFAGDDAPR	AVFPSIVGRPR	ACTB_HUMAN	ACTA_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	1.64	0.04	22.40	5.05
WHHTFYNELR	VAPEEHPVLLTEAPLNPKANR	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	0.96	0.06	59.40	1.31
YPGIADRMQK	EITALAPSTMKIKIIAPPER	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.78	0.05	33.90	4.51

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
DYLMKILTER	GYSFTTTAER	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	0.61	0.06	36.90	1.88
DFEQEMATVA	SSSSLEKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.45	0.03	75.20	3.84
VIDNGSGMCK	AGFAGDDAPR	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.43	0.02	27.40	7.32
VDIRKDLYAN	TVLSGGTTMYPGIADR	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	0.43	0.04	85.30	6.03
FEQEMATVAS	SSSLEKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.38	0.02	62.90	3.65
LYANNVMSGG	TTMYPGIADR	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.35	0.03	27.30	2.50
TVASSSSLEK	SYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTBL_HUMAN	Actin, cytoplasmic 1;	0.30	0.01	93.40	3.45
VMDSGDGVTH	TVPIYEGYALPHAILR	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	0.30	0.01	67.30	2.16
QEMATVASSS	SLEKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.22	0.01	75.80	1.73
IRKDLYANNV	LSGGTTMYPGIADR	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.17	0.02	51.60	5.02
VALDFEQEMA	TAASSSSLEKSYELPDGQVITIGNE	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.15	0.01	86.80	5.23
VAPEEHPILL	TEAPLNPKANR	ACTB_HUMAN	ACTA_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	0.11	0.01	24.60	2.34
EMATVASSSS	LEKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.09	0.00	62.30	4.12
EQEMATVASS	SSLEKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	0.00	0.00	53.60	3.09
SGRTTGIVMD	SGDGVTHTVPIYEGYALPHAILR	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	-0.11	0.01	45.00	2.08
YANNVMSGGT	TMYPGIADR	ACTB_HUMAN	ACTA_HUMAN	ACTBL_HUMAN	Actin, cytoplasmic 1;	-0.26	0.02	28.00	4.75
LRVAPEEHPI	LLTEAPLNPKANR	ACTB_HUMAN	ACTA_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	-0.58	0.04	24.20	2.99
SLEKSYELPD	GQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTBL_HUMAN	Actin, cytoplasmic 1;	-0.69	0.07	40.90	1.52
DIRKDLYANN	VLSGGTTMYPGIADR	ACTB_HUMAN	ACTA_HUMAN	ACTC_HUMAN	Actin, cytoplasmic 1;	-1.29	0.13	38.30	6.93
SGDGVTHTVP	IYEGYALPHAILR	ACTB_HUMAN	ACTBL_HUMAN	ACTG_HUMAN	Actin, cytoplasmic 1;	-1.87	0.07	51.00	0.39

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MATVASSSSL	EKSYELPDGQVITIGNER	ACTB_HUMAN	ACTA_HUMAN	ACTBM_HUMAN	Actin, cytoplasmic 1;	-2.05	0.09	34.90	6.99
TTGIVMDSGD	GVTHTVPIYEGYALPHAILR	ACTB_HUMAN	ACTG_HUMAN		Actin, cytoplasmic 1;	-2.24	0.11	29.70	0.58
GAASQKKAFR	SSGFGLEFNSFQHQLR	TRIP4_HUMAN			Activating signal cointegrator 1;	1.06	0.07	35.90	6.00
IVEERADATN	VNNWHWTER	AHSA1_HUMAN			Activator of 90 kDa heat shock protein ATPase	0.81	0.02	28.50	0.39
PRWIVEERAD	ATNVNNWHWTER	AHSA1_HUMAN			Activator of 90 kDa heat	-1.14	0.05	34.40	0.70
GRVTQLCRQY	SDMPPLTLEGIQDR	ACPM_HUMAN			Acyl carrier protein, mitochondrial;	0.02	0.00	71.70	1.06
GQIIRVPARM	AATLILEPAGR	ACOT1_HUMAN	ACOT2_HUMAN		Acyl-coenzyme A thioesterase 1;	1.19	0.12	37.70	1.31
MERQVLL	SEPEEAAALYR	ACPH_HUMAN			Acylamino-acid-releasing enzyme;	0.76	0.04	48.20	10.07
NDSLSSLDFD	DDDVDLSR	APC_HUMAN			Adenomatous polyposis	-3.24	0.31	21.40	7.84
MSDKLPYK	VADIGLAAWGR	SAHH_HUMAN			Adenosylhomocysteinase;	0.63	0.05	39.40	2.59
DIGLAAWGRK	ALDIAENEMPGLMR	SAHH_HUMAN			Adenosylhomocysteinase;	0.60	0.05	67.40	3.14
RATDVMIAGK	VAVVAGYGDVGKGCAQALR	SAHH_HUMAN			Adenosylhomocysteinase;	0.40	0.04	30.60	6.48
M	APSVPAAEPEYPKGIR	KAD2_HUMAN			Adenylate kinase 2, mitochondrial;	-0.04	0.00	27.00	0.06
MAP	SVPAAEPEYPKGIR	KAD2_HUMAN			Adenylate kinase 2,	-1.00	0.08	21.50	2.59
IKKRLETYYK	ATEPVIAFYEKR	KAD1_HUMAN			Adenylate kinase	0.15	0.01	17.90	2.43
LALAVGCVFL	LEPELPGSALR	ADPGK_HUMAN			ADP-dependent glucokinase;	1.11	0.08	33.90	2.23
FLALAVGCVF	LLEPELPGSALR	ADPGK_HUMAN			ADP-dependent glucokinase;	0.72	0.07	33.40	2.34
AIQLVSLGGR	QLLTPEHVLR	AGRIN_HUMAN			Agrin;	7.32	0.57	28.20	-0.16
VGAGLRGCIR	LLDVNNQR	AGRIN_HUMAN			Agrin;	4.00	0.17	26.40	-0.50
IRLLDVNNQR	LELGIGPGAATR	AGRIN_HUMAN			Agrin;	3.54	0.30	41.00	2.28

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
DLGKGAAVIR	SREPVTLGAWTR	AGRIN_HUMAN			Agrin;	1.59	0.06	56.70	-0.14
PHCEKGLVEK	SAGDVDTLAFDGR	AGRIN_HUMAN			Agrin;	-1.59	0.10	52.30	-2.96
RRLDALSRGR	LLHQLADLVER	AL1A3_HUMAN			Aldehyde dehydrogenase family 1 member A3;	2.18	0.28	33.90	3.89
IKAIAAKHNK	TTAQVLIR	AK1BF_HUMAN	ALDR_HUMAN		Aldo-keto reductase family 1 member B15;	0.26	0.02	29.50	0.85
LGLRLQLSLG	IIPVEEENPDFWNR	PPB1_HUMAN	PPBN_HUMAN		Alkaline phosphatase,	0.00	0.00	73.00	6.04
AAGFCPAVLC	HPNSPLDEENLTQENQDR	AACT_HUMAN			Alpha-1-antichymotrypsin;	1.67	0.08	76.30	1.43
ILTLVVAACG	FVLWSSNGR	MGAT2_HUMAN			Alpha-1,6-mannosyl-glycoprotein 2-beta-N-	1.95	0.10	27.40	0.91
VTFGFIWGMM	LLHFTIQQR	MGT5A_HUMAN			Alpha-1,6-mannosylglycoprotein 6-	0.28	0.02	27.90	2.19
HTNYTMEHIR	VGWEQLLTTIAR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	4.67	0.70	48.80	1.41
WEQLLTTIAR	TINEVENQILTR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	2.37	0.24	67.30	0.21
HLMEDYEKLA	SDLLEWIR	ACTN1_HUMAN	ACTN4_HUMAN		Alpha-actinin-1;	-0.21	0.01	32.60	-0.19
QHLEQAEKGY	EEWLLNEIR	ACTN1_HUMAN	ACTN2_HUMAN	ACTN4_HUMAN	Alpha-actinin-1;	-5.06	1.69	35.10	6.79
LLNEIRRLER	LEHLAEKFR	ACTN2_HUMAN			Alpha-actinin-2;	6.64	0.75	29.50	1.83
TADQVIASFK	VLAGDKNFITAEELR	ACTN4_HUMAN			Alpha-actinin-4;	0.90	0.07	25.80	2.60
EIGRISIEMN	GTLEDQLSHLKQYER	ACTN4_HUMAN			Alpha-actinin-4;	-0.32	0.02	40.20	2.44
NIQNFTTSWR	DGLAFNALIHR	ACTN4_HUMAN	SPTN4_HUMAN		Alpha-actinin-4;	-0.65	0.04	48.00	0.55
NTRCQKICDQ	WDALGSLTHSR	ACTN4_HUMAN			Alpha-actinin-4;	-2.14	0.19	36.20	4.46
LAFNALIHRH	RPELIEYDKLR	ACTN4_HUMAN			Alpha-actinin-4;	-2.24	0.21	49.60	1.20
KAIMTYVSSF	YHAFSGAQKAETAANR	ACTN4_HUMAN	ACTN1_HUMAN		Alpha-actinin-4;	-3.24	0.31	34.70	3.01
GRLGVSLSKG	LHHKAVLAVR	AASS_HUMAN			Alpha-aminoadipic semialdehyde synthase,	8.88	1.39	26.20	7.66

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
DLYTAKGLFR	AAVPSGASTGIYEALELR	ENOA_HUMAN	ENOB_HUMAN	ENOG_HUMAN	Alpha-enolase;	0.92	0.05	107.80	5.89
FRAAVPSGAS	TGIYEALELR	ENOA_HUMAN	ENOB_HUMAN	ENOG_HUMAN	Alpha-enolase;	-0.09	0.00	32.90	4.58
WGAWQKFTAS	AGIQVVGDDLTVTNPKR	ENOA_HUMAN			Alpha-enolase;	-0.43	0.05	51.30	2.27
QDDWGAWQKF	TASAGIQVVGDDLTVTNPKR	ENOA_HUMAN			Alpha-enolase;	-0.55	0.03	79.50	1.10
DWGAWQKFTA	SAGIQVVGDDLTVTNPKR	ENOA_HUMAN			Alpha-enolase;	-0.58	0.03	70.00	2.37
KFGANAILGV	SLAVCKAGAVEKGVPLYR	ENOA_HUMAN			Alpha-enolase;	-0.80	0.06	25.90	2.92
WQKFTASAGI	QVVGDDLTVTNPKR	ENOA_HUMAN			Alpha-enolase;	-1.65	0.10	36.90	0.62
GAWQKFTASA	GIQVVGDDLTVTNPKR	ENOA_HUMAN			Alpha-enolase;	-2.05	0.42	28.30	1.46
KAGYTDKVVI	GMDVAASEFFR	ENOA_HUMAN			Alpha-enolase;	-3.72	0.49	44.10	1.42
SLLAAPPVAP	AEAPHLVHVDAAR	IDUA_HUMAN			Alpha-L-iduronidase;	0.15	0.01	72.60	0.28
NTWLSTGWFT	MTIALELCDR	SIA7E_HUMAN			Alpha-N-	-6.06	0.00	24.50	5.65
VILFALITIL	ILYSSNSANEVFHYGSLR	SIA7F_HUMAN			Alpha-N-	0.99	0.06	35.00	3.25
RALTPAATLS	AVQNLVVEGLR	STALP_HUMAN			AMSH-like protease;	-1.80	0.13	34.00	0.41
RALEVPTDGN	AGLLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	1.68	0.18	58.30	0.24
LLAAWTARAL	EVPTDGNAGLLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	1.62	0.10	98.60	1.39
LEVPTDGNAG	LLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	1.48	0.17	54.80	6.19
LLLAAWTARA	LEVPTDGNAGLLAEPQIAMFCGR	A4_HUMAN			Amyloid beta A4 protein;	0.74	0.12	101.70	5.18
LLLRAQPAIG	SLAGGSPGAAEAPGSAQVAGLCG	APLP1_HUMAN			Amyloid-like protein 1;	0.61	0.07	60.40	-1.15
AIMVKGVDEA	TIIDILTKR	ANXA1_HUMAN			Annexin A1;	-0.19	0.01	26.90	1.58
DADELRAAMK	GLGTDEDTLIEILASR	ANXA1_HUMAN			Annexin A1;	-0.46	0.07	55.20	2.30
AALHKAIMVK	GVDEATIIDILTKR	ANXA1_HUMAN			Annexin A1;	-0.65	0.06	43.90	3.59
KLMVALAKGR	RAEDGSVIDYELIDQDAR	ANXA2_HUMAN			Annexin A2;	2.58	0.11	44.50	1.29
STVHEILCKL	SLEGDHSTPPSAYGSVKAYTNFDA	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-0.34	0.02	29.50	1.99

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TPPSAYGSVK	AYTNFDAER	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-0.46	0.05	29.10	0.36
DALNIETAIK	TKGVDEVTIVNILTNR	ANXA2_HUMAN			Annexin A2;	-0.46	0.02	39.40	1.41
INRVYKEMYK	TDLEKDIISDTSGDFR	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-0.52	0.03	54.20	3.29
HEILCKLSLE	GDHSTPPSAYGSVKAYTNFDAER	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-0.69	0.07	37.90	0.24
HSTPPSAYGS	VKAYTNFDAER	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-0.69	0.06	38.60	-0.44
DHSTPPSAYG	SVKAYTNFDAER	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-1.14	0.10	33.40	0.48
ILTNRSNAQR	QDIAFAYQR	ANXA2_HUMAN			Annexin A2;	-1.59	0.05	29.50	3.95
VHEILCKLSL	EGDHSTPPSAYGSVKAYTNFDAER	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-1.80	0.13	48.40	2.92
ILCKLSLEGD	HSTPPSAYGSVKAYTNFDAER	ANXA2_HUMAN	AXA2L_HUMAN		Annexin A2;	-2.05	0.17	55.10	4.35
HTLIRVMVSR	SEIDLFNIR	ANXA5_HUMAN			Annexin A5;	2.05	0.08	48.40	4.49
TLRKAMKGLG	TDEESILTLLTSR	ANXA5_HUMAN			Annexin A5;	0.79	0.04	54.40	2.38
DAYELKHALK	GAGTNEKVLTEIIASR	ANXA5_HUMAN			Annexin A5;	-1.72	0.11	33.50	4.74
NRRLQTRKEK	AQALEELTGFR	KI67_HUMAN			Antigen KI-67;	0.22	0.01	43.80	-5.62
SGLLVDVFSD	SASVVAPLAPGSEDNFAR	AP2A2_HUMAN			AP-2 complex subunit alpha-2;	-1.80	0.19	62.70	3.35
LTRRSISQQK	SGVSITIDDPVR	ACINU_HUMAN			Apoptotic chromatin condensation inducer in	1.83	0.09	52.00	1.71
KESSLPKSFK	RKISVVSATKGVPAGNSDTEGGQP	ACINU_HUMAN			Apoptotic chromatin	0.68	0.04	39.10	3.88
KEKKSEKKEK	AQEEPPAKLLDDLFR	ACINU_HUMAN			Apoptotic chromatin condensation inducer in	0.50	0.05	33.00	2.81
KHHVEVVGVS	FHIGSGCPDPQAYAQSIADAR	ADC_HUMAN			Arginine decarboxylase;	6.02	0.63	31.30	3.18
M	VLAELYVSDR	SYNC_HUMAN			Asparagine--tRNA ligase,	-0.58	0.05	39.10	1.67
IGSARGQSTG	KGPPQSPVFEGVYNNSR	ATX2L_HUMAN			Ataxin-2-like protein;	0.57	0.02	53.80	2.62
KPQYVDQIPK	AAKGTVGSILDR	ABCE1_HUMAN			ATP-binding cassette sub-	6.38	0.22	45.90	1.75

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
ALGEAINEYK	GAVIVVSHDAR	ABCF1_HUMAN			ATP-binding cassette sub-family F member 1;	0.75	0.06	53.10	2.51
EEKELMERLK	KLSVPTSDEEDEVPAPKPR	ABCF1_HUMAN			ATP-binding cassette sub-family F member 1;	0.67	0.05	32.70	1.55
LGGIGQFLAK	AIEPPPLDAVIEAEHTLR	DHX9_HUMAN			ATP-dependent RNA helicase A;	1.04	0.03	67.00	2.25
VRFLVLDEAD	GLLSQGYSDFINR	DDX1_HUMAN			ATP-dependent RNA	-1.87	0.14	63.60	2.26
LLLLPCEAEA	AAAAAAVSGSAAAEAKECDRPCV	ATRN_HUMAN			Attractin;	0.63	0.06	55.00	0.82
PCEAEAAAAA	AAVSGSAAAEAKECDRPCVNGGR	ATRN_HUMAN			Attractin;	0.42	0.05	23.40	2.05
YSGRTQAQTR	QASTLIDRPAPHFER	E41L2_HUMAN			Band 4.1-like protein 2;	2.38	0.16	41.10	0.79
ITPLSLQTQG	SSHETLNIVEEKKR	E41L2_HUMAN			Band 4.1-like protein 2;	0.98	0.07	37.20	1.48
RHQVHGSRLR	LLQVTPADSGEYVCR	PGBM_HUMAN			Basement membrane-specific heparan sulfate	4.54	0.54	60.20	0.92
EETEDYRQFR	KSVLADQGKSFATASHR	BCLF1_HUMAN			Bcl-2-associated transcription factor 1;	1.09	0.09	43.20	2.52
ACLALAAALA	ALLLLPLPLPR	RFNG_HUMAN			Beta-1,3-N-	1.42	0.23	35.90	3.45
AGRDLSRLPQ	LVGVSTPLQGGSNSAAAIGQSSGE	B4GT1_HUMAN			Beta-1,4-galactosyltransferase 1;	-0.07	0.01	72.30	2.13
LVGSQLAVMM	YLSLGGFR	B4GT3_HUMAN			Beta-1,4-galactosyltransferase 3;	1.22	0.13	23.40	1.91
LLVGSQLAVM	MYLSLGGFR	B4GT3_HUMAN			Beta-1,4-galactosyltransferase 3;	0.81	0.03	26.50	1.21
PTEKDEYACR	VNHVTLSQPK	B2MG_HUMAN			Beta-2-microglobulin;	3.54	0.30	28.60	2.03
KDWSFYLLYY	TEFTPTEKDEYACR	B2MG_HUMAN			Beta-2-microglobulin;	1.12	0.10	35.50	0.94
SNFLNCYVSG	FHPSDIEVDLLKNGER	B2MG_HUMAN			Beta-2-microglobulin;	1.01	0.04	42.50	3.09
ALLSLSGLEA	IQRTPKIQVVYSR	B2MG_HUMAN			Beta-2-microglobulin;	0.97	0.05	26.60	2.39
ENGKSNFLNC	YVSGFHPSDIEVDLLKNGER	B2MG_HUMAN			Beta-2-microglobulin;	0.37	0.01	36.50	1.49

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
GPLLWGCALG	LQGGMLYPQESPSR	BGLR_HUMAN			Beta-glucuronidase;	2.53	0.21	51.50	5.82
AAAFAGRATA	LWPWPQNFQTSDQR	HEXA_HUMAN			Beta-hexosaminidase subunit alpha;	1.36	0.01	61.70	2.78
LALCGAGTTA	AELSYSLR	MANBA_HUMAN			Beta-mannosidase;	1.03	0.09	23.90	1.86
IPEDNADMAR	LDFNLIR	PUR9_HUMAN			Bifunctional purine biosynthesis protein	4.95	0.57	30.20	-0.87
KSLFSNVVTK	NKDLPESALR	PUR9_HUMAN			Bifunctional purine biosynthesis protein PURH;	0.37	0.01	34.20	5.66
CWVLVGYAKG	GLGDNHVHSSFIYR	BMP5_HUMAN			Bone morphogenetic	1.70	0.15	32.00	3.68
SYSNTLPVRK	SVTPKNSYATTENKTLPR	BAIP2_HUMAN			Brain-specific	0.56	0.06	34.10	1.75
ASRSKRRAVE	SGVPQPPDPPVQR	BCCIP_HUMAN			BRCA2 and CDKN1A-interacting protein;	0.31	0.01	31.70	1.92
EDEEWPTLEK	AATMTAAGHHAEVVVDPEDER	BYST_HUMAN			Bystin;	0.93	0.08	32.50	5.63
MIQYNNLNLK	TPVPSDIDISR	C1TC_HUMAN			C-1-tetrahydrofolate synthase, cytoplasmic;	0.53	0.05	36.00	1.38
MAP	AEILNGKEISAQIR	C1TC_HUMAN			C-1-tetrahydrofolate synthase, cytoplasmic;	0.37	0.03	24.20	2.06
LVYLTQPGNG	NEGSVTGSCYCGKR	CXL16_HUMAN			C-X-C motif chemokine	0.28	0.02	22.80	1.34
LTPPGPLASA	GPVSAVLTELR	CXCL6_HUMAN			C-X-C motif chemokine 6;	0.94	0.02	55.90	1.10
PPGPLASAGP	VSAVLTELR	CXCL6_HUMAN			C-X-C motif chemokine	0.53	0.05	28.60	5.71
RAPALSRVRR	AWVIPPISVSENHKR	CAD15_HUMAN			Cadherin-15;	2.31	0.13	28.80	4.63
FSLFDKDGDG	TITTKELGTVMR	CALM_HUMAN			Calmodulin;	0.53	0.04	32.40	3.20
AFRVFDKDGN	GYISAAELR	CALM_HUMAN			Calmodulin;	0.24	0.02	41.00	1.68
AMRILGGVIS	AISEAAAQYNPEPPPPR	CPNS1_HUMAN			Calpain small subunit 1;	0.43	0.01	43.80	2.87
AAEGLGSHDR	AIKYLNQDYEALR	CAN2_HUMAN			Calpain-2 catalytic subunit;	1.00	0.05	29.10	-1.98
SSKTRGIEWK	RPTEICADPQFIIGGATR	CAN2_HUMAN			Calpain-2 catalytic subunit;	0.81	0.03	52.30	3.97

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
FDQTTISLQM	GTNKGASQAGMLAPGTR	CNN3_HUMAN			Calponin-3;	0.90	0.08	38.40	3.28
LLGLLGLAVA	EPAVYFKEQFLDGDGWTSR	CALR_HUMAN			Calreticulin;	0.81	0.01	28.40	2.26
GDLHMTQFFR	GNLAGLTLR	CSTN1_HUMAN			Calsyntenin-1;	1.64	0.07	33.60	2.23
YHGIVTENDN	TVLLDPPLIALDKDAPLR	CSTN1_HUMAN			Calsyntenin-1;	1.42	0.13	33.30	4.73
FARAASEFES	SEGVFLFPELR	CSTN1_HUMAN			Calsyntenin-1;	1.29	0.15	33.10	-1.21
MTFTGVDTMA	SYEEVLHLLR	CSTN1_HUMAN			Calsyntenin-1;	1.29	0.11	32.50	-0.23
APVFKEKSYK	ATVIEGKQYDSILR	CSTN1_HUMAN			Calsyntenin-1;	0.85	0.08	26.20	5.17
NPVVKGRRRR	GAISAEVYTEEDAASYVR	KAP0_HUMAN			cAMP-dependent protein	0.30	0.02	72.00	3.31
ALLLAQTFLL	LFLVSRPGPSSPAGGEAR	CHST6_HUMAN			Carbohydrate sulfotransferase 6;	0.64	0.05	20.90	1.97
ALAAALVVHC	YSKSPSNKDAALLEAAR	CLPB_HUMAN			Caseinolytic peptidase B protein homolog;	-0.58	0.04	35.90	3.74
CLLVLANARS	RPSFHPLSDELVNYVNKR	CATB_HUMAN			Cathepsin B;	0.68	0.01	38.70	4.48
GGPKPPQRVM	FTEDLKLPASFDAR	CATB_HUMAN			Cathepsin B;	0.15	0.01	33.20	4.35
KPPQRVMFTE	DLKLPASFDAR	CATB_HUMAN			Cathepsin B;	-1.40	0.11	36.00	1.69
ADLPKSWDWR	NVDGVNYASITR	CATZ_HUMAN			Cathepsin Z;	3.37	0.22	41.40	4.04
TATACPMKSN	EHDDCQVTNPSTGHLFDLSSLSGR	MPRI_HUMAN			Cation-independent mannose-6-phosphate receptor;	1.42	0.11	33.90	2.74
AERFMEENEG	HIVDIHDFSLGSSPHVR	CD109_HUMAN			CD109 antigen;	2.38	0.12	66.30	3.34
YAERFMEENE	GHIVDIHDFSLGSSPHVR	CD109_HUMAN			CD109 antigen;	1.22	0.09	65.20	1.80

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
FMEENEGHIV	DIHDFSLGSSPHVR	CD109_HUMAN			CD109 antigen;	1.00	0.08	39.80	2.50
EYAERFMEEN	EGHIVDIHDFSLGSSPHVR	CD109_HUMAN			CD109 antigen;	0.87	0.04	37.20	0.98
SSPGPVEILT	TVTESVTGISR	CD109_HUMAN			CD109 antigen;	0.15	0.01	31.80	0.68
ERFMEENEGH	IVDIHDFSLGSSPHVR	CD109_HUMAN			CD109 antigen;	-0.43	0.03	48.00	2.97
SLNPSGEVTR	QIGDALPVSCTISASR	CD166_HUMAN			CD166 antigen;	2.24	0.24	40.70	5.69
GKWKYEKPDG	SPVFIAFR	CD166_HUMAN			CD166 antigen;	1.08	0.07	25.90	-0.41
SATVFRPGLG	WYTVNSAYGDTIIIPCR	CD166_HUMAN			CD166 antigen;	0.98	0.05	80.20	4.17
DSEQLPLRPK	SVDFDSLTVR	CD2AP_HUMAN			CD2-associated protein;	0.04	0.00	37.00	4.80
EASKSQEMVH	LVNKESSETPDQFMTADETR	CD44_HUMAN			CD44 antigen;	1.29	0.11	44.40	-3.65
GLCLVPLSLA	QIDLNITCR	CD44_HUMAN			CD44 antigen;	0.04	0.00	33.90	0.60
M	VGGEAAAAVEELVSGVR	C2AIL_HUMAN			CDKN2AIP N-terminal-like protein;	0.26	0.03	32.80	3.21
AVEELVSGVR	QAADFAEQFR	C2AIL_HUMAN			CDKN2AIP N-terminal-like protein;	-0.29	0.03	27.00	0.00
MHSLA	TAAPVPTTLAQVDR	RCD1_HUMAN			Cell differentiation	-0.24	0.02	44.00	4.20
TSDRGFQFVS	SSLPDICYR	CNBP_HUMAN			Cellular nucleic acid-binding protein;	0.11	0.01	40.40	3.58
SDRGFQFVSS	SLPDICYR	CNBP_HUMAN			Cellular nucleic acid-binding protein;	-0.52	0.03	22.90	4.06

Table S6

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;	2.62	0.23	42.40	2.98
IPEAFRGVHR	YLSNAYAR	CLIC1_HUMAN			Chloride intracellular channel protein 1;	4.07	0.37	24.30	3.85
EQPQVELFVK	AGSDGAKIGNCPFSQR	CLIC1_HUMAN			Chloride intracellular channel protein 1;	1.53	0.11	23.30	0.23
IVQVVCKKYR	GFTIPEAFR	CLIC1_HUMAN			Chloride intracellular	1.31	0.03	29.90	0.84
LLLGSRPARG	AGPEPPVLPIR	CHRD_HUMAN			Chordin;	0.33	0.02	37.30	2.71
MGKKQNGKSK	KVEEAEPEEFVVEKVLDRR	CBX3_HUMAN			Chromobox protein	0.20	0.00	34.00	2.20
MGKKTKR	TADSSSSEDEEEYVVEKVLDRR	CBX5_HUMAN			Chromobox protein homolog 5;	-2.46	0.14	51.10	2.64
VVESMVTATE	VAPPPPPVEVPIR	CHD4_HUMAN			Chromodomain-helicase-DNA-binding protein 4;	-0.72	0.06	30.90	4.63
PDLALRMAVR	NNLAGAEELFAR	CLH1_HUMAN			Clathrin heavy chain 1;	2.22	0.14	59.50	2.25
KDEEETVTTK	HIHITQATETTTTR	EPN4_HUMAN			Clathrin interactor 1;	1.40	0.13	32.40	2.50
RKQEAEWKEK	AIKELEEWYAR	CLCA_HUMAN			Clathrin light chain A;	-0.09	0.00	44.10	0.14
RLLRERAIFK	VHSDFTAAATR	K0664_HUMAN			Clustered mitochondria	0.66	0.06	31.50	3.22
LDVMQDHFSR	ASSIIDELFQDR	CLUS_HUMAN			Clusterin;	4.90	0.67	59.80	2.18
DVMQDHFSRA	SSIIDELFQDR	CLUS_HUMAN			Clusterin;	0.80	0.12	48.00	1.40
VTEVVVKLFD	SDPITVTVPVEVSR	CLUS_HUMAN			Clusterin;	0.79	0.07	48.70	4.58
AQQAMDIHFH	SPAFQHPPTEFIR	CLUS_HUMAN			Clusterin;	0.38	0.04	30.00	0.77
IDSLLENDRQ	QTHMLDVMQDHFSR	CLUS_HUMAN			Clusterin;	-3.05	0.25	24.70	2.13
M	VLLAAAVCTKAGKAIVSR	COPD_HUMAN			Coatomer subunit delta;	0.18	0.01	34.20	3.03
LLLLPGPAGS	EGAAPIAITCFTR	COCH_HUMAN			Cochlin;	7.84	0.81	66.60	1.81
LHARHKEQQR	QFGLTPPGSLR	CC153_HUMAN			Coiled-coil domain-containing protein 153;	2.08	0.08	27.40	3.73

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MRAAPRPAPV	AQPPAAAPPSAVGSSAAAPR	CHCH2_HUMAN	CHCH9_HUMAN		Coiled-coil-helix-coiled-	-0.26	0.02	46.90	1.27
PPASRAPQMR	AAPRPAPVAQPPAAAPPSAVGSSA	CHCH2_HUMAN	CHCH9_HUMAN		Coiled-coil-helix-coiled-coil-helix domain-	-0.40	0.03	48.60	1.60
AITPDHLEPR	LSIIATDHTYR	CO6A1_HUMAN			Collagen alpha-1(VI)	5.73	0.51	38.70	3.03
GRQVNEPHIR	VLVTGKTAEYDVAYGESHLFR	CO6A1_HUMAN			Collagen alpha-1(VI) chain;	5.36	0.31	40.60	3.89
GRTDPAHDVR	VAVVQYSGTGQQRPER	CO6A1_HUMAN			Collagen alpha-1(VI) chain;	4.24	0.54	31.00	0.66
RVPSYQALLR	GVFHQTVSR	CO6A1_HUMAN			Collagen alpha-1(VI) chain;	3.25	0.28	31.10	4.44
QLLPPSPNNR	IALVITDGR	CO6A1_HUMAN			Collagen alpha-1(VI)	1.89	0.33	35.80	0.41
LVWNAGALHY	SDEVEIIQGLTR	CO6A1_HUMAN			Collagen alpha-1(VI)	1.56	0.10	55.40	5.04
ESGTRRGIPK	VIVVITDGR	COEA1_HUMAN			Collagen alpha-1(XIV) chain;	7.54	1.08	30.10	2.40
LTESYCETWR	TEAPSATGQASSLLGGR	COIA1_HUMAN			Collagen alpha-1(XVIII) chain;	5.43	0.79	82.80	4.23
FAYGDHQSPN	TAITQMTFLR	CO5A2_HUMAN			Collagen alpha-2(V) chain;	-1.40	0.07	37.40	3.30
IGPKGDPGNR	GHPGPPGVLVTPPLPLK	CO4A4_HUMAN			Collagen alpha-4(IV) chain;	-2.24	0.11	22.50	4.41
VRLHWPTSLP	SGDAFSSVGTHR	C43BP_HUMAN			Collagen type IV alpha-3-binding protein;	0.45	0.04	26.70	0.72
SEKVRLHWPT	SLPSGDAFSSVGTHR	C43BP_HUMAN			Collagen type IV alpha-3-binding protein;	-1.59	0.05	36.80	-0.13
QVPDTESETR	ILLQGTPVAQMTEDAVDAER	CO3_HUMAN			Complement C3;	8.04	1.98	112.10	2.29
YTPGSTVLYR	IFTVNHKLLPVGR	CO3_HUMAN			Complement C3;	5.03	0.41	36.30	1.35
RISLPESLKR	IPIEDGSGEVVLSR	CO3_HUMAN			Complement C3;	4.83	0.32	55.90	5.00
PSRSSKITHR	IHWESASLLR	CO3_HUMAN			Complement C3;	4.02	0.29	29.90	-1.05

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
VVKSGQSEDR	QPVPGQQMTLKIEGDHGAR	CO3_HUMAN			Complement C3;	3.93	0.20	35.20	0.94
FDEYIMAIEQ	TIKSGSDEVQVGQQR	CO3_HUMAN			Complement C3;	3.88	0.45	45.90	2.07
ARASHLGLAR	SNLDEDIIAEENIVSR	CO3_HUMAN			Complement C3;	3.23	0.30	62.30	5.90
SDDKVTLEER	LDKACEPGVDYVYKTR	CO3_HUMAN			Complement C3;	2.74	0.18	51.20	-2.70
KGYTQQLAFR	QPSSAFAAFVKR	CO3_HUMAN			Complement C3;	2.61	0.19	20.00	0.73
GDGVAKLSIN	THPSQKPLSITVR	CO3_HUMAN			Complement C3;	1.73	0.13	29.80	2.89
LLTHLPLALG	SPMYSIITPNILR	CO3_HUMAN			Complement C3;	1.49	0.10	56.30	1.82
QALPYSTVGN	SNNYLHLSVLR	CO3_HUMAN			Complement C3;	1.38	0.09	39.80	0.59
PCACGCGCGS	LHTDGDKAFVDFLSDEIKEER	C1QBP_HUMAN			Complement component 1 Q subcomponent-binding	0.26	0.01	47.20	3.58
VLLCLPAVWG	DCGLPPDVPNAQPALEGR	DAF_HUMAN			Complement decay-	0.99	0.02	81.40	4.44
IVNHAGRRPD	SLQHVLLPVLDR	CFAD_HUMAN			Complement factor D;	0.74	0.04	41.20	-0.14
EVLKRLRLQK	RGTGGVDTAAVGGVFDVSNADR	KCRB_HUMAN			Creatine kinase B-type;	5.36	0.56	75.20	4.65
GDEESYEVFK	DLFDPIIEDR	KCRB_HUMAN			Creatine kinase B-type;	5.03	0.45	41.10	9.19
LSAHNNHMAK	VLTPELYAELR	KCRB_HUMAN			Creatine kinase B-type;	2.75	0.23	33.60	4.50
LQKRGTGGVD	TAAVGGVFDVSNADR	KCRB_HUMAN			Creatine kinase B-type;	1.45	0.19	49.50	-0.73
IQKRVPCAYD	KTALALEVGDIVKVTR	CRKL_HUMAN			Crk-like protein;	4.60	0.27	26.10	1.72
AARLPRGAEA	FEIALPR	CDCP1_HUMAN			CUB domain-containing protein 1;	5.79	0.49	23.30	-0.57
PHSAADDDTS	SELQRLADVDAPQQGR	CNGA2_HUMAN			Cyclic nucleotide-gated	2.77	0.29	47.50	9.76
IRHRPKAHYM	KKQPDITEGMR	CCNA1_HUMAN			Cyclin-A1;	7.47	1.03	32.90	1.23

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MMC	GAPSATQPATAETQHIADQVR	CYTB_HUMAN			Cystatin-B;	-0.52	0.05	42.50	1.83
MMCG	APSATQPATAETQHIADQVR	CYTB_HUMAN			Cystatin-B;	-0.69	0.07	32.30	3.48
MM	CGAPSATQPATAETQHIADQVR	CYTB_HUMAN			Cystatin-B;	-0.72	0.07	86.60	2.60
AGSSPGKPPR	LVGGPMDASVEEEGVR	CYTC_HUMAN			Cystatin-C;	4.97	0.60	84.30	-1.08
AGSSPGKPPR	LVGGPMDASVEEEGVRR	CYTC_HUMAN			Cystatin-C;	2.30	0.14	27.90	0.60
ASVEEEGVRR	ALDFAVGEYNKASNDMYHSR	CYTC_HUMAN			Cystatin-C;	1.56	0.07	43.30	2.73
LLLARSGTRA	LVCLPCDESKCEEPR	CRIM1_HUMAN			Cysteine-rich motor neuron 1 protein;	0.67	0.03	38.30	1.68
GSYIYEKPLA	EGPQVTGPIEVPAAR	CRIP2_HUMAN			Cysteine-rich protein 2;	0.72	0.07	69.20	5.59
MATAEASGSD	GKGQEVETSVTYYR	CYB5B_HUMAN			Cytochrome b5 type B;	-0.24	0.02	45.70	1.96
HTVEKGGKHK	TGPNLHGLFGR	CYC_HUMAN			Cytochrome c;	-0.37	0.01	30.00	1.66
MKLSPYYKVF	EEDALSWEDKLNR	DYHC1_HUMAN			Cytoplasmic dynein 1 heavy chain 1;	6.49	1.24	32.30	2.76
VPQIEVETHK	VAAPDVVVPTLDTVR	DYHC1_HUMAN			Cytoplasmic dynein 1 heavy chain 1;	0.71	0.05	50.20	0.57
HYDFGLRALK	SVLVSAGNVKR	DYHC1_HUMAN			Cytoplasmic dynein 1	0.60	0.06	36.00	2.69
TEEEKQQILH	SEEFLSFFDHSTR	DC1I2_HUMAN			Cytoplasmic dynein 1	0.02	0.00	32.30	0.61
HYLAGRRAMK	TVFGVEPDLTR	CNDP2_HUMAN			Cytosolic non-specific dipeptidase;	4.32	0.17	40.20	4.41
KGVRVVNCAR	GGIVDEGALLR	SERA_HUMAN			D-3-phosphoglycerate dehydrogenase;	2.16	0.09	47.80	1.06
WKLDVATDNF	FQNPELYIR	DCNL1_HUMAN			DCN1-like protein 1;	0.53	0.02	33.20	1.40
PSVIRHVRSW	SNIPFITVPLSR	P5CS_HUMAN			Delta-1-pyrroline-5-	-0.09	0.00	51.30	4.37
YPGLSISLRL	TGSSAQEEASGVALGEAPDHSYES	ECH1_HUMAN			Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase,	-1.04	0.09	82.70	3.84
EREAPAGALA	AVLKHSSTLPPESTQVR	DHYS_HUMAN			Deoxyhypusine synthase;	-0.21	0.01	33.40	3.02

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
ALRGSGEAAQ	RGLQYKYLDESSGGWR	DNS2A_HUMAN			Deoxyribonuclease-2-alpha;	-0.65	0.07	40.20	2.42
EKFEVKKGDR	IAQLICER	DUT_HUMAN			Deoxyuridine 5'-	3.50	0.26	30.70	0.10
ETPAISPSKR	ARPAEVGGMQLR	DUT_HUMAN			Deoxyuridine 5'-triphosphate	-0.04	0.00	57.60	-0.15
PKHPHLVRQK	RAWITAPVALR	DSG2_HUMAN			Desmoglein-2;	3.86	0.40	33.90	1.40
KHPHLVRQKR	AWITAPVALR	DSG2_HUMAN			Desmoglein-2;	0.57	0.02	33.90	2.38
CRKRRKRCMR	HAMCCPGNYCKNGICVSSDQNHF	DKK1_HUMAN			Dickkopf-related protein 1;	4.77	0.92	32.30	-8.18
TDEYCASPTR	GGDAGVQICLACR	DKK1_HUMAN			Dickkopf-related protein	2.15	0.18	67.90	3.90
EVCTKQRKKG	SHGLEIFQR	DKK1_HUMAN	DKK2_HUMAN		Dickkopf-related protein 1;	2.09	0.12	35.60	1.97
MCCPGNYCKN	GICVSSDQNHFR	DKK1_HUMAN			Dickkopf-related protein 1;	2.00	0.17	31.20	1.72
RGEIEETITE	SFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein 1;	1.94	0.14	25.70	0.82
LDGYSRRTTL	SSKMYHTKGQEGSVCLR	DKK1_HUMAN			Dickkopf-related protein 1;	1.76	0.06	36.50	1.80
NHFRGEIEET	ITESFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein	1.33	0.12	34.90	0.93
CVSSDQNHFR	GEIEETITESFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein	1.22	0.08	48.30	2.32
YSRRTTLSSK	MYHTKGQEGSVCLR	DKK1_HUMAN			Dickkopf-related protein	0.75	0.05	29.50	1.55
GEVCTKQRKK	GSHGLEIFQR	DKK1_HUMAN	DKK2_HUMAN		Dickkopf-related protein 1;	0.53	0.03	38.40	5.85
QNHFRGEIEE	TITESFGNDHSTLDGYSR	DKK1_HUMAN			Dickkopf-related protein 1;	0.42	0.03	32.30	2.41
RFFRTTAVCK	DDLVTVKTPAFAESVTEGDVR	ODO2_HUMAN			Dihydrolipoyllysine-residue	0.78	0.02	78.50	3.81

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MAP	VLSKDSADIESILALNPR	DPYD_HUMAN			Dihydropyrimidine dehydrogenase [NADP(+)];	0.60	0.03	50.10	2.93
M	APVLSKDSADIESILALNPR	DPYD_HUMAN			Dihydropyrimidine	0.26	0.01	56.90	4.86
KVTTYCNETM	TGWVHDVLGR	CATC_HUMAN			Dipeptidyl peptidase 1;	2.14	0.16	37.20	1.20
APLTAEIQQK	ILHLPTSWDWR	CATC_HUMAN			Dipeptidyl peptidase 1;	0.37	0.00	41.00	2.74
GSEHCYDIYR	LYHSCADPTGCGTGPDAR	DPP2_HUMAN			Dipeptidyl peptidase 2;	1.82	0.17	41.50	2.29
QDAPAIAFGG	SYGGMLSAYLR	DPP2_HUMAN			Dipeptidyl peptidase 2;	1.34	0.05	37.60	6.34
LWALGLLGAG	SPLPSWPLPNIGGTEEQQAESEKA	ADA15_HUMAN			Disintegrin and	1.76	0.03	56.50	6.33
QDDLPISLKK	VLQTSLPEPLR	ADA15_HUMAN			Disintegrin and	1.46	0.13	38.10	4.29
VLGTCPPARC	GQAGDASLMELEKR	ADA22_HUMAN			Disintegrin and	-1.24	0.23	40.40	1.46
PRPYSKQVSY	VIQAEGKEHIIHLER	ADAM9_HUMAN			Disintegrin and metalloproteinase domain-	1.32	0.08	34.90	0.11
LESFNYVLSK	STKADIGPNLDQLKDDEILR	ERC6L_HUMAN			DNA excision repair protein ERCC-6-like;	1.10	0.08	43.10	4.12
AHNLCYTTLL	RPGTAQKLGLTEDQFIR	DPOD1_HUMAN			DNA polymerase delta catalytic subunit;	0.15	0.01	31.10	4.83
MEQQSISISK	AGIVTSLQAR	MCM2_HUMAN			DNA replication licensing factor MCM2;	0.66	0.08	36.60	2.19
EEDQGIYQSK	VRELISDNQYR	MCM3_HUMAN			DNA replication licensing	1.09	0.10	42.40	1.61
LLGDKGQTAR	TQRPADVIFATVR	MCM7_HUMAN			DNA replication licensing	1.03	0.03	34.40	4.44
TSRSKEEFTK	LAASFQLR	RFX8_HUMAN			DNA-binding protein	2.09	0.15	21.40	0.86
ARWPVAGQIR	ATQQQHDFTLTQTADGR	PRKDC_HUMAN			DNA-dependent protein	2.32	0.25	45.10	2.31
AASQAVEEMR	SRVVLGEFGVR	RPAC1_HUMAN			DNA-directed RNA	0.11	0.01	45.60	1.20
M	GKDYYQTLGLAR	DNJB1_HUMAN			DnaJ homolog subfamily B member 1;	-0.14	0.01	46.50	1.10
M	VDYYEVLGVQR	DNJB6_HUMAN			DnaJ homolog subfamily B member 6;	-0.92	0.04	50.50	2.98
IVYMAILVGT	DQDFYSLLGVSKTASSR	DJC10_HUMAN			DnaJ homolog subfamily C member 10;	0.70	0.03	34.70	4.24

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
QQERQRLGQR	QPPPSEPTQGPEIVPR	DNJC4_HUMAN			DnaJ homolog subfamily	-4.47	0.00	32.40	-1.30
DRQSARKPLL	GLPSYMLQSEELR	DNMBP_HUMAN			Dynamin-binding protein;	-2.46	0.14	63.70	2.45
LLLSVVMAQS	HWPSEPSEAVR	DAG1_HUMAN			Dystroglycan;	1.31	0.03	38.30	2.56
SLPDIPPIQL	EDAGSSSLDNLLSR	TRI33_HUMAN			E3 ubiquitin-protein	1.66	0.13	32.10	0.60
DCELSAKLLR	RADLNQGIGEPQSPSR	EFHD2_HUMAN			EF-hand domain-containing protein D2;	1.01	0.08	71.20	2.90
LIAGTLVLEA	AVTGVPVKGQDTVKGR	ELAF_HUMAN			Elafin;	3.45	0.34	34.20	2.30
IKVSYARPSS	EVIKDANLYISGLPR	ELAV1_HUMAN			ELAV-like protein 1;	0.06	0.00	42.40	2.41
TIKVSYARPS	SEVIKDANLYISGLPR	ELAV1_HUMAN			ELAV-like protein 1;	-0.92	0.07	31.60	3.69
LQSKTIKVSY	ARPSSEVIKDANLYISGLPR	ELAV1_HUMAN			ELAV-like protein 1;	-1.09	0.05	45.70	2.45
SEWLDQKLTK	SDRPELTGAKVVVSGGR	ETFA_HUMAN			Electron transfer flavoprotein subunit alpha, mitochondrial;	0.24	0.02	35.30	2.22
LGRFAVRDMR	QTVAVGVIKAVDK	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	1.59	0.14	23.50	1.63
RPTDKPLRLP	LQDVYKIGGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha 1;	1.09	0.04	28.40	1.47
LGRFAVRDMR	QTVAVGVIKAVDKK	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	0.99	0.07	31.30	1.15
MVPGKPMCVE	SFSDYPPLGR	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	0.76	0.02	24.40	3.66
TDKPLRLPLQ	DVYKIGGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha 1;	0.37	0.03	38.90	3.02
LRLPLQDVYK	IGGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha	0.30	0.00	40.70	1.13
STEPPYSQKR	YEEIVKEVSTYIKK	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	0.02	0.00	29.00	3.36
RLPLQDVYKI	GGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha 1;	-0.09	0.01	43.70	1.17

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
KLEDGPKFLK	SGDAAIVDMVPGKPMCVESFSDY	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	-0.21	0.00	85.50	3.96
DKPLRLPLQD	VYKIGGIGTVPVGR	EF1A1_HUMAN	EF1A2_HUMAN	EF1A3_HUMAN	Elongation factor 1-alpha	-0.62	0.04	40.40	1.56
ISLWKFETSK	YYVTIIDAPGHR	EF1A1_HUMAN	EF1A3_HUMAN		Elongation factor 1-alpha 1;	-1.09	0.07	39.00	3.40
SGDHGELVVR	IASLEVENQSLR	EF1D_HUMAN			Elongation factor 1-delta;	1.36	0.08	50.50	2.02
VLEKSSPGHR	ATAPQTQHVSPMR	EF1D_HUMAN			Elongation factor 1-delta;	0.31	0.02	42.10	1.85
IARARENIQK	SLAGSSGPGASSGTSGDHGELVVR	EF1D_HUMAN			Elongation factor 1-delta;	-0.14	0.01	78.70	3.42
LRDIARAREN	IQKSLAGSSGPGASSGTSGDHGEL	EF1D_HUMAN			Elongation factor 1-delta;	-0.34	0.03	54.70	6.73
RARENIQKSL	AGSSGPGASSGTSGDHGELVVR	EF1D_HUMAN			Elongation factor 1-delta;	-0.37	0.04	37.80	0.84
DIARARENIQ	KSLAGSSGPGASSGTSGDHGELVV	EF1D_HUMAN			Elongation factor 1-delta;	-0.49	0.03	63.40	2.68
AKDPFAHLPK	STFVLDEFKR	EF1G_HUMAN			Elongation factor 1-	1.15	0.07	33.10	0.61
TYPENWRAFK	ALIAAQYSGAQVR	EF1G_HUMAN			Elongation factor 1-gamma;	0.78	0.06	77.50	2.69
SVIAHVDHGK	STLTDSLVCKAGIIASAR	EF2_HUMAN			Elongation factor 2;	0.63	0.02	32.60	2.50
M	VNFTVDQIR	EF2_HUMAN			Elongation factor 2;	0.13	0.01	32.30	1.15
GQIIPTARRC	LYASVLTAQPR	EF2_HUMAN			Elongation factor 2;	-2.24	0.32	40.50	3.19
M	VAPVLETSHVFCCPNR	ELP2_HUMAN			Elongator complex protein 2;	0.35	0.02	31.10	0.89
SCSLSPTSLA	ETVHCDLQPVGPER	EGLN_HUMAN			Endoglin;	1.31	0.11	36.90	1.14
MMKREYRGQR	SVKALADYIR	ERP44_HUMAN			Endoplasmic reticulum	-0.69	0.04	35.20	1.93
FYSNKEIFLR	ELISNASDALDKIR	ENPL_HUMAN	H90B2_HUMAN	H90B3_HUMAN	Endoplasmin;	1.68	0.12	38.30	2.00
VVLFETATLR	SGYLLPDTKAYGDR	ENPL_HUMAN			Endoplasmin;	0.87	0.07	22.70	2.58

Table S6

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change (log$_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
LLVPAHLVAA	WSNNYAVDCPQHCDSSECKSSPR	ESM1_HUMAN			Endothelial cell-specific	3.96	0.38	43.30	7.32
GLVRLVHQER	TLAFPLTIR	EPCR_HUMAN			Endothelial protein C receptor;	2.17	0.13	27.70	1.59
LAAGLVACLA	ALGIQYQTR	ECE1_HUMAN			Endothelin-converting enzyme 1;	1.68	0.12	35.70	3.34
LRRLLQEREL	VEPLTPSGEAPNQALLR	EGFR_HUMAN			Epidermal growth factor receptor;	3.22	0.26	50.40	6.09
FFPKEAKPNG	IFKGSTAENAEYLR	EGFR_HUMAN			Epidermal growth factor receptor;	1.24	0.11	41.80	4.47
SPSTSRTPLL	SSLSATSNNSTVACIDR	EGFR_HUMAN			Epidermal growth factor receptor;	1.03	0.12	81.30	3.92
VACIDRNGLQ	SCPIKEDSFLQR	EGFR_HUMAN			Epidermal growth factor receptor;	0.89	0.10	29.90	1.61
RYACCPGWKR	TSGLPGACGAAICQPPCR	EGFL7_HUMAN			Epidermal growth factor-like protein 7;	1.89	0.16	61.30	0.74
PRYACCPGWK	RTSGLPGACGAAICQPPCR	EGFL7_HUMAN			Epidermal growth factor-like protein 7;	1.64	0.16	70.10	4.86
ILQQIELDLK	ATQALVLAPTR	IF4A1_HUMAN			Eukaryotic initiation factor 4A-I;	0.68	0.06	41.60	-0.09
RRYLSPKWIK	MFVLDEADEMLSR	IF4A1_HUMAN	IF4A2_HUMAN		Eukaryotic initiation factor 4A-I;	0.38	0.05	67.80	5.22
PGYGAYDAFK	HAVSDPSILDSLDLNEDER	IF2A_HUMAN			Eukaryotic translation initiation factor 2 subunit	0.68	0.04	52.30	2.83
SEKPLRSIKR	IFHTVTTTDDPVIR	EIF3D_HUMAN			Eukaryotic translation	1.50	0.09	33.00	0.55
SVAYRYRRWK	LGDDIDLIVR	EIF3D_HUMAN			Eukaryotic translation initiation factor 3 subunit D;	0.60	0.04	27.40	4.92
M	KPILLQGHER	EIF3I_HUMAN			Eukaryotic translation initiation factor 3 subunit	0.38	0.01	51.50	2.25
SGELNQYSAK	SGEVLVNVKEHSR	EIF3I_HUMAN			Eukaryotic translation initiation factor 3 subunit	0.00	0.00	33.00	2.43
LAKETFGVNN	AVYGIDAMNPSSR	EIF3J_HUMAN			Eukaryotic translation initiation factor 3 subunit	0.04	0.00	56.50	1.06

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
RPIDTSRLTK	ITKPGSIDSNNQLFAPGGR	IF4G1_HUMAN			Eukaryotic translation initiation factor 4 gamma	0.89	0.08	38.50	0.64
QEEQRREMLE	TVKQLTGGVDVER	IF4G3_HUMAN			Eukaryotic translation	0.31	0.02	44.40	2.06
IVPAAATTVS	SPSAAITVQR	IF4G3_HUMAN			Eukaryotic translation initiation factor 4 gamma	-0.37	0.03	29.30	2.08
SSASTSQSTR	AASIFGGAKPVDTAAR	IF4B_HUMAN			Eukaryotic translation initiation factor 4B;	0.80	0.08	36.50	-0.31
RMDEISDHAK	VLTLSDDLER	IF5_HUMAN			Eukaryotic translation initiation factor 5;	1.39	0.04	39.40	3.95
IKRNDFQLIG	IQDGYLSLLQDSGEVR	IF5A1_HUMAN			Eukaryotic translation	0.20	0.02	85.50	1.10
DFQLIGIQDG	YLSLLQDSGEVR	IF5A1_HUMAN			Eukaryotic translation	-0.07	0.01	55.50	4.95
MADDLD	FETGDAGASATFPMQCSALR	IF5A1_HUMAN	IF5AL_HUMAN		Eukaryotic translation initiation factor 5A-1;	-1.00	0.04	98.20	3.25
ADDLDFETGD	AGASATFPMQCSALR	IF5A1_HUMAN	IF5AL_HUMAN		Eukaryotic translation initiation factor 5A-1;	-1.19	0.05	61.90	3.49
MAAGFK	TVEPLEYYR	EXOS8_HUMAN			Exosome complex component RRP43;	0.46	0.02	33.60	2.32
M	KETPLSNCER	EXOS9_HUMAN			Exosome complex component RRP45;	0.17	0.01	33.70	2.37
QQAREMPLLK	SEVAAGVKKSGPLPSAER	EXOSX_HUMAN			Exosome component 10;	0.78	0.07	34.80	0.26
VLLLVAGALT	ALLPSVKEDKMLMLR	EXTL2_HUMAN			Exostosin-like 2;	1.00	0.06	30.30	0.55
VLTYLAVASA	ASEGGFTATGQR	ECM1_HUMAN			Extracellular matrix protein 1;	1.54	0.04	46.60	2.23
MVFLVACALH	IALDLLPR	DMP4_HUMAN			Extracellular serine/threonine protein	-1.40	0.07	28.90	2.87
ASYVRSRSIR	SVAIEVDGR	SULF2_HUMAN			Extracellular sulfatase Sulf-2;	0.48	0.03	44.90	3.69
YEPVSYHVQE	SLQDEGAEPTGYSAELSSEGIR	EZRI_HUMAN			Ezrin;	-0.46	0.04	56.70	-1.33
EFNEVFNDVR	LLLNNDNLLR	CAZA1_HUMAN	CAZA2_HUMAN		F-actin-capping protein subunit alpha-1;	5.88	0.60	39.50	8.80
MLWLQTNKSG	SGTMNLGGSLTR	CAPZB_HUMAN			F-actin-capping protein	0.04	0.01	54.50	0.49

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
KVGGDACLLR	GSDPGGPGLLPPR	FXL19_HUMAN			F-box/LRR-repeat protein 19;	0.15	0.01	26.90	4.14
PVEAFAQNVL	SKADVIQATGDAICIFR	SSRP1_HUMAN			FACT complex subunit SSRP1;	0.97	0.04	60.30	1.76
KQLQERAGVK	MILIQDGSQNTNVDKPLR	FUBP2_HUMAN			Far upstream element-binding protein 2;	0.24	0.03	33.80	1.89
GGGIDVPVPR	HSVGVVIGR	FUBP2_HUMAN			Far upstream element-binding protein 2;	0.09	0.01	26.00	2.30
VQEIMIPAGK	AGLVIGKGGETIKQLQER	FUBP2_HUMAN	FUBP1_HUMAN		Far upstream element-	-0.09	0.01	40.60	-0.15
GAPESVQKAK	MMLDDIVSR	FUBP2_HUMAN			Far upstream element-	-0.52	0.05	39.80	0.81
APESVQKAKM	MLDDIVSR	FUBP2_HUMAN			Far upstream element-binding protein 2;	-0.55	0.06	29.40	2.95
ESKKLASQGD	SISSQLGPIHPPPR	FUBP2_HUMAN			Far upstream element-binding protein 2;	-1.52	0.04	44.50	1.05
PSVYGYGVQK	RPLDDGVGNQLGALVHQR	FUBP3_HUMAN			Far upstream element-binding protein 3;	0.57	0.04	29.80	2.27
FVQHFSQIVR	VLTEDEMGHPEIGDAIAR	FPPS_HUMAN			Farnesyl pyrophosphate synthase;	6.38	0.94	50.40	3.18
PEIPALLDGR	LQVVDQPLPVR	FAS_HUMAN			Fatty acid synthase;	2.59	0.26	37.50	3.64
VLHQATILPK	TGTVSLEVR	FAS_HUMAN			Fatty acid synthase;	2.17	0.18	36.40	-1.11
QTKVTQQGLK	MVVPGLDGAQIPR	FAS_HUMAN			Fatty acid synthase;	1.40	0.05	42.90	4.70
SKADEASELA	CPTPKEDGLAQQQTQLNLR	FAS_HUMAN			Fatty acid synthase;	0.59	0.04	63.60	1.29
NTEGSFRCQC	LGGLAVGTDGR	FBN3_HUMAN			Fibrillin-3;	5.16	0.49	26.90	4.31
FPESSLKLVS	STLFGNTKPR	FGFP1_HUMAN			Fibroblast growth factor-binding protein 1;	3.60	0.36	21.80	2.18
TSCLKLKDER	VYWKQVAR	FGFP1_HUMAN			Fibroblast growth factor-binding protein 1;	3.53	0.39	33.20	-0.09
RKDFPESSLK	LVSSTLFGNTKPR	FGFP1_HUMAN			Fibroblast growth factor-	-0.55	0.05	17.50	1.54

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
NEHLKCVSKR	IANLQTDLSDGLR	FLNA_HUMAN			Filamin-A;	7.52	1.10	59.00	3.39
QTGGPHVKAR	VANPSGNLTETYVQDR	FLNA_HUMAN			Filamin-A;	1.32	0.10	81.90	5.11
DVTYDGSPVP	SSPFQVPVTEGCDPSR	FLNA_HUMAN			Filamin-A;	0.99	0.07	55.80	6.06
LHSVDVTYDG	SPVPSSPFQVPVTEGCDPSR	FLNA_HUMAN			Filamin-A;	0.35	0.02	49.40	7.76
PVPGSPFPLE	AVAPTKPSKVKAFGPGLQGGSAGS	FLNA_HUMAN			Filamin-A;	-0.02	0.00	37.30	4.11
PGIEGQGVFR	EATTEFSVDAR	FLNA_HUMAN			Filamin-A;	-0.40	0.03	51.10	0.64
TQTVNYVPSR	EGPYSISVLYGDEEVPR	FLNA_HUMAN			Filamin-A;	-0.80	0.04	99.50	3.70
FNEEHIPDSP	FVVPVASPSGDAR	FLNA_HUMAN			Filamin-A;	-1.04	0.07	44.30	3.67
EPVDVVDNAD	GTQTVNYVPSR	FLNA_HUMAN			Filamin-A;	-1.52	0.09	42.50	2.47
SSSSRGSSYS	SIPKFSSDASKVVTR	FLNC_HUMAN			Filamin-C;	-0.32	0.02	45.50	3.59
VRVEESTQVG	GDPFPAVFGDFLGR	FLNC_HUMAN			Filamin-C;	-0.52	0.08	63.00	0.20
KSSSSRGSSY	SSIPKFSSDASKVVTR	FLNC_HUMAN			Filamin-C;	-0.65	0.02	53.70	1.54
SYAECSVPIG	VTAPSLQPVQAR	FNBP4_HUMAN			Formin-binding protein 4;	-0.76	0.05	31.30	5.15
GSLKTFRALL	TLAAGADGPPR	FJX1_HUMAN			Four-jointed box protein 1;	1.18	0.06	47.80	7.64
QSVYLMNLRK	SGTLGHPGSLDETTYER	FRDA_HUMAN			Frataxin, mitochondrial;	-0.96	0.07	58.80	1.29
IFLPLLRGHS	LFTCEPITVPR	FZD6_HUMAN			Frizzled-6;	5.78	0.36	26.40	7.53
KKELSDIAHR	IVAPGKGILAADESTGSIAKR	ALDOA_HUMAN			Fructose-bisphosphate aldolase A;	3.42	0.11	28.70	0.56

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
NTEENRRFYR	QLLLTADDR	ALDOA_HUMAN			Fructose-bisphosphate aldolase A;	2.87	0.13	35.60	0.65
MP	YQYPALTPEQKKELSDIAHR	ALDOA_HUMAN			Fructose-bisphosphate	0.15	0.01	30.80	2.75
WRCVLKIGEH	TPSALAIMENANVLAR	ALDOA_HUMAN			Fructose-bisphosphate aldolase A;	-0.07	0.00	34.40	1.05
ARYASICQQN	GIVPIVEPEILPDGDHDLKR	ALDOA_HUMAN	ALDOC_HUMAN		Fructose-bisphosphate aldolase A;	-0.46	0.02	38.80	2.86
MP	HSYPALSAEQKKELSDIALR	ALDOC_HUMAN			Fructose-bisphosphate	-0.37	0.03	33.30	3.54
TDPQTLKPSG	FHEDDPFFYDEHTLR	FXYD5_HUMAN			FXYD domain-containing ion transport regulator 5;	3.33	0.23	67.30	1.35
QTLKPSGFHE	DDPFFYDEHTLR	FXYD5_HUMAN			FXYD domain-containing	2.15	0.15	32.00	3.34
DPQTLKPSGF	HEDDPFFYDEHTLR	FXYD5_HUMAN			FXYD domain-containing	1.92	0.22	39.50	5.19
LCALLAPGGA	YVLDDSDGLGR	GALC_HUMAN			Galactocerebrosidase;	0.85	0.07	36.60	4.02
M	ACGLVASNLNLKPGECLR	LEG1_HUMAN			Galectin-1;	0.00	0.00	33.80	3.28
RSTHTLDLSR	ELSEALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding protein;	4.37	0.35	80.60	2.22
AGVVCTNETR	STHTLDLSR	LG3BP_HUMAN			Galectin-3-binding	3.86	0.36	31.80	1.61
QSRRGPLVKY	SSDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding	2.80	0.15	44.90	1.78
VEIFYRGQWG	TVCDNLWDLTDASVVCR	LG3BP_HUMAN			Galectin-3-binding protein;	2.11	0.17	31.20	-0.15
KKTLQALEFH	TVPFQLLAR	LG3BP_HUMAN			Galectin-3-binding protein;	1.62	0.07	25.00	2.59
SCWNYGFSCS	SDELPVLGLTKSGGSDR	LG3BP_HUMAN			Galectin-3-binding protein;	1.48	0.03	32.50	0.39
TIQSCWNYGF	SCSSDELPVLGLTKSGGSDR	LG3BP_HUMAN			Galectin-3-binding protein;	1.39	0.04	37.00	1.41
SRRGPLVKYS	SDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding	1.29	0.12	51.90	1.74
VTDSSWSARK	SQLVYQSR	LG3BP_HUMAN			Galectin-3-binding	1.19	0.05	28.00	3.84
RKSQLVYQSR	RGPLVKYSSDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding	1.16	0.05	33.10	5.20
QSCWNYGFSC	SSDELPVLGLTKSGGSDR	LG3BP_HUMAN			Galectin-3-binding protein;	1.08	0.02	47.90	0.96

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
YQSRRGPLVK	YSSDYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding protein;	1.08	0.16	63.70	2.95
ETRSTHTLDL	SRELSEALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding protein;	1.03	0.03	52.10	1.34
THTLDLSREL	SEALGQIFDSQR	LG3BP_HUMAN			Galectin-3-binding protein;	0.98	0.06	55.80	2.46
WKEPGSNVTM	SVDAECVPMVR	LG3BP_HUMAN			Galectin-3-binding protein;	0.75	0.05	48.20	2.63
RRGPLVKYSS	DYFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding protein;	-1.04	0.09	26.80	4.63
RGPLVKYSSD	YFQAPSDYR	LG3BP_HUMAN			Galectin-3-binding	-2.72	0.72	20.50	0.68
APAGPLIVPY	NLPLPGGVVPR	LEG3_HUMAN			Galectin-3;	4.34	0.35	31.90	-0.87
VVSSVNTVAT	KTVEEAENIAVTSGVVR	SYUG_HUMAN			Gamma-synuclein;	0.54	0.06	41.30	-0.80
VSEAVVSSVN	TVATKTVEEAENIAVTSGVVR	SYUG_HUMAN			Gamma-synuclein;	0.37	0.02	77.90	6.14
LLAAPAQAHL	KKPSQLSSFSWDNCDEGKDPAVIR	SAP3_HUMAN			Ganglioside GM2	0.45	0.02	52.00	6.65
HLKKPSQLSS	FSWDNCDEGKDPAVIR	SAP3_HUMAN			Ganglioside GM2 activator;	0.13	0.01	40.20	2.19
AHLKKPSQLS	SFSWDNCDEGKDPAVIR	SAP3_HUMAN			Ganglioside GM2 activator;	-0.02	0.00	39.40	5.95
KKGGVASGFK	HVVPNEVVVQR	GELS_HUMAN			Gelsolin;	0.51	0.05	48.10	1.75
ETLIKKRKAR	SLLPLSTSLDHR	GEMI5_HUMAN			Gem-associated protein 5;	1.72	0.03	43.90	1.10
RRKKYGIVLK	EFRPEDQPWLLR	T2FA_HUMAN			General transcription factor IIF subunit 1;	-0.26	0.01	27.90	0.68
IHQGTKMIPC	DFLIPVQTQHPIR	G6PI_HUMAN			Glucose-6-phosphate isomerase;	-0.52	0.02	33.20	4.38
EELPLGRELR	VPLIGSLPEAR	QPCTL_HUMAN			Glutaminyl-peptide cyclotransferase-like	-1.29	0.13	29.00	4.80

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
RHASSGSFLP	SANEHLKEDLNLR	GLRX3_HUMAN			Glutaredoxin-3;	-0.02	0.00	28.40	4.69
KNSQKIDRLD	GAHAPELTKKVQR	GLRX3_HUMAN			Glutaredoxin-3;	-0.32	0.01	26.80	4.86
MPP	YTVVYFPVR	GSTP1_HUMAN			Glutathione S-transferase P;	0.57	0.04	29.30	-0.42
QLPKFQDGDL	TLYQSNTILR	GSTP1_HUMAN			Glutathione S-transferase	-0.19	0.01	43.70	2.09
NGKLTGMAFR	VPTANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	1.60	0.11	68.20	3.65
KLTGMAFRVP	TANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	0.81	0.06	59.10	2.34
IIPASTGAAK	AVGKVIPELNGKLTGMAFR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	0.17	0.00	37.50	1.63
M	GKVKVGVNGFGR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	0.06	0.00	58.80	2.57
KAENGKLVIN	GNPITIFQER	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	0.04	0.00	44.50	-3.80
GMAFRVPTAN	VSVVDLTCR	G3P_HUMAN	G3PT_HUMAN		Glyceraldehyde-3-phosphate dehydrogenase;	0.04	0.00	23.30	2.12
KFHGTVKAEN	GKLVINGNPITIFQER	G3P_HUMAN			Glyceraldehyde-3-	-0.04	0.00	34.70	7.28
MAFRVPTANV	SVVDLTCR	G3P_HUMAN	G3PT_HUMAN		Glyceraldehyde-3-phosphate dehydrogenase;	-0.11	0.01	26.20	1.64
ELNGKLTGMA	FRVPTANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	-0.21	0.02	48.30	3.05
LNGKLTGMAF	RVPTANVSVVDLTCR	G3P_HUMAN			Glyceraldehyde-3-	-0.58	0.04	43.70	1.92
GIVEGLMTTV	HAITATQKTVDGPSGKLWR	G3P_HUMAN			Glyceraldehyde-3-phosphate dehydrogenase;	-1.09	0.07	27.90	-1.84
EKRKQISVRG	LAGLGDVAEVR	PYGB_HUMAN			Glycogen phosphorylase, brain form;	5.53	0.17	29.10	-1.94
SEKRKQISVR	GLAGLGDVAEVR	PYGB_HUMAN			Glycogen phosphorylase,	-1.04	0.09	63.40	-1.86
SGAISHLSLG	EIPAMAQPFVSSEER	GLYG_HUMAN			Glycogenin-1;	-0.32	0.02	43.90	0.00

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LAILLVIFIF	TKVFLIDNLDTSAANR	XYLK_HUMAN			Glycosaminoglycan xylosylkinase;	2.30	0.15	39.50	5.72
LVIFIFTKVF	LIDNLDTSAANR	XYLK_HUMAN			Glycosaminoglycan	1.19	0.09	47.20	3.89
QFWDTQPVPK	LGEVVNTHGPVEPDKDNIR	NMT1_HUMAN			Glycylpeptide N-	0.87	0.06	35.80	1.77
WDTQPVPKLG	EVVNTHGPVEPDKDNIR	NMT1_HUMAN			Glycylpeptide N-tetradecanoyltransferase	-0.34	0.04	34.00	2.16
KKLPAQRTNR	AVALSSSVMCPDAR	GRN_HUMAN			Granulins;	0.60	0.04	63.40	2.20
PAQRTNRAVA	LSSSVMCPDAR	GRN_HUMAN			Granulins;	0.20	0.01	39.10	0.72
LTKLPAHTVG	DVKCDMEVSCPDGYTCCR	GRN_HUMAN			Granulins;	-0.46	0.04	69.40	0.56
LVAAGRRAAG	ASVATELR	GROA_HUMAN			Growth-regulated alpha protein;	3.01	0.22	26.70	2.86
ALELRPRGEA	AEGPAAAAAAAAAAAAAGVGGE	GDF11_HUMAN			Growth/differentiation factor 11;	0.70	0.02	59.30	-2.75
GGHLHLRISR	AALPEGLPEASR	GDF15_HUMAN			Growth/differentiation factor 15;	2.01	0.15	33.40	5.24
GALSLAEASR	ASFPGPSELHSEDSR	GDF15_HUMAN			Growth/differentiation factor 15;	0.17	0.00	36.00	-0.18
AQGEPQVQFK	LVLVGDGGTGKTTFVKR	RAN_HUMAN			GTP-binding nuclear	0.67	0.06	30.40	2.32
TTACYFATIH	TDSSLLLADITDKFGQR	GUAD_HUMAN			Guanine deaminase;	-0.52	0.05	49.90	3.33
IVTPRFSLSC	SETLMGELGNIAKTR	GUAD_HUMAN			Guanine deaminase;	-0.55	0.02	36.60	-0.77
MCAA	QMPPLAHIFR	GUAD_HUMAN			Guanine deaminase;	-0.72	0.04	33.30	1.53
NKTVMAHGCY	LSAEELNVFHER	GUAD_HUMAN			Guanine deaminase;	-1.29	0.10	50.80	1.35
MCAAQ	MPPLAHIFR	GUAD_HUMAN			Guanine deaminase;	-1.80	0.06	15.60	2.59
TACYFATIHT	DSSLLLADITDKFGQR	GUAD_HUMAN			Guanine deaminase;	-2.24	0.21	45.00	2.54

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
FNESIVVDMK	SGFNLEELEKNNAQSIR	GNL3_HUMAN			Guanine nucleotide-binding protein-like 3;	0.72	0.04	40.60	2.49
M	FLQYYLNEQGDR	NOP10_HUMAN			H/ACA ribonucleoprotein complex subunit 3;	0.02	0.00	60.00	3.74
AKKEVVAEVV	KAPQVVAEAAKTAKR	DKC1_HUMAN			H/ACA ribonucleoprotein	-0.83	0.03	32.80	4.45
PSVEPVEEYD	YEDLKESSNSVSNHQLSGFDQAR	HBS1L_HUMAN			HBS1-like protein;	-3.24	0.61	37.00	-1.38
FNDSQRQATK	DAGVIAGLNVLR	HS71L_HUMAN	HSP71_HUMAN		Heat shock 70 kDa protein 1-like;	0.89	0.06	40.20	-0.49
GAIAGLNVLR	IINEPTAAAIAYGLDR	HSP71_HUMAN	HSP76_HUMAN		Heat shock 70 kDa protein 1A/1B;	4.25	0.55	42.10	1.46
TLEPVEKALR	DAKLDKAQIHDLVLVGGSTR	HSP71_HUMAN			Heat shock 70 kDa protein 1A/1B;	0.72	0.05	40.60	-0.27
KALRDAKLDK	AQIHDLVLVGGSTR	HSP71_HUMAN			Heat shock 70 kDa protein 1A/1B;	0.17	0.01	43.40	1.93
VPAYFNDSQR	QATKDAGTIAGLNVLR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	10.56	0.00	59.60	-4.21
SYVAFTDTER	LIGDAAKNQVAMNPTNTVFDAKR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	5.12	0.33	41.90	1.64
EIIANDQGNR	TTPSYVAFTDTER	HSP7C_HUMAN	HS71L_HUMAN	HSP71_HUMAN	Heat shock cognate 71	1.84	0.10	63.80	6.26
GTIAGLNVLR	IINEPTAAAIAYGLDKKVGAER	HSP7C_HUMAN			Heat shock cognate 71	1.38	0.04	56.40	7.98
DFYTSITRAR	FEELNADLFR	HSP7C_HUMAN	HSP72_HUMAN		Heat shock cognate 71 kDa protein;	1.27	0.07	29.40	2.03
GIDFYTSITR	ARFEELNADLFR	HSP7C_HUMAN	HSP72_HUMAN		Heat shock cognate 71 kDa protein;	1.10	0.07	50.70	1.59
EELNADLFRG	TLDPVEKALR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	0.93	0.06	20.30	2.97
FEELNADLFR	GTLDPVEKALR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	0.71	0.03	25.40	1.34
FNDSQRQATK	DAGTIAGLNVLR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	0.22	0.02	55.10	1.54

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
KALRDAKLDK	SQIHDIVLVGGSTR	HSP7C_HUMAN			Heat shock cognate 71	0.09	0.01	47.40	1.98
IGDAAKNQVA	MNPTNTVFDAKR	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	-0.04	0.00	29.50	-1.86
TIAGLNVLRI	INEPTAAAIAYGLDKKVGAER	HSP7C_HUMAN			Heat shock cognate 71 kDa protein;	-0.43	0.02	32.90	3.27
TTYSDNQPGV	LIQVYEGER	HSP7C_HUMAN	HS71L_HUMAN	HSP71_HUMAN	Heat shock cognate 71 kDa protein;	-2.24	0.21	36.00	2.98
APAYSRALSR	QLSSGVSEIR	HSPB1_HUMAN			Heat shock protein beta-1;	1.63	0.20	43.80	2.35
AAPAYSRALS	RQLSSGVSEIR	HSPB1_HUMAN			Heat shock protein beta-1;	-0.52	0.05	32.30	1.97
EFRALLFVPR	RAPFDLFENR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	3.26	0.28	21.30	2.86
LIPEYLNFIR	GVVDSEDLPLNISR	HS90A_HUMAN	H90B3_HUMAN	HS90B_HUMAN	Heat shock protein HSP 90-alpha;	2.60	0.19	75.50	2.72
QKHIYYITGE	TKDQVANSAFVER	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	2.25	0.17	55.60	2.54
WEDHLAVKHF	SVEGQLEFR	HS90A_HUMAN	H90B3_HUMAN	HS902_HUMAN	Heat shock protein HSP	0.48	0.03	37.30	1.18
MGYMAAKKHL	EINPDHSIIETLR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	0.15	0.01	35.30	2.48
NSTMGYMAAK	KHLEINPDHSIIETLR	HS90A_HUMAN			Heat shock protein HSP	0.06	0.00	37.30	2.74
RRIKEIVKKH	SQFIGYPITLFVEKER	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	0.02	0.00	48.90	4.84
STMGYMAAKK	HLEINPDHSIIETLR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.04	0.00	41.90	1.76
VKDLVILLYE	TALLSSGFSLEDPQTHANR	HS90A_HUMAN			Heat shock protein HSP	-0.19	0.01	52.90	2.94
VILLYETALL	SSGFSLEDPQTHANR	HS90A_HUMAN			Heat shock protein HSP	-0.32	0.03	33.50	0.00
TMGYMAAKKH	LEINPDHSIIETLR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-0.43	0.02	33.10	0.71
GYMAAKKHLE	INPDHSIIETLR	HS90A_HUMAN			Heat shock protein HSP	-0.46	0.03	32.50	3.74
HNDDEQYAWE	SSAGGSFTVR	HS90A_HUMAN	HS902_HUMAN	HS90B_HUMAN	Heat shock protein HSP 90-alpha;	-0.46	0.03	36.10	8.02

Table S6

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;	-1.04	0.07	32.80	4.06
ALLFVPRRAP	FDLFENR	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-1.65	0.10	20.40	1.54
ERRIKEIVKK	HSQFIGYPITLFVEKER	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-2.24	0.11	29.40	4.31
RMKENQKHIY	YITGETKDQVANSAFVER	HS90A_HUMAN			Heat shock protein HSP	-3.46	0.38	54.60	2.10
IMDSCDELIP	EYLNFIR	HS90A_HUMAN	HS904_HUMAN	HS90B_HUMAN	Heat shock protein HSP	-4.04	0.00	26.20	2.22
TRMKENQKHI	YYITGETKDQVANSAFVER	HS90A_HUMAN			Heat shock protein HSP 90-alpha;	-4.47	0.00	33.50	3.58
STMGYMMAKK	HLEINPDHPIVETLR	HS90B_HUMAN			Heat shock protein HSP 90-beta;	0.28	0.01	50.80	1.98
YVSRMKETQK	SIYYITGESKEQVANSAFVER	HS90B_HUMAN			Heat shock protein HSP 90-beta;	-0.09	0.01	78.60	1.34
FNDSQRQATK	DAGTITGLNVLR	HSP72_HUMAN			Heat shock-related 70 kDa protein 2;	1.74	0.10	40.00	-2.70
LSPADKTNVK	AAWGKVGAHAGEYGAEALER	HBA_HUMAN			Hemoglobin subunit alpha;	0.50	0.04	48.20	0.71
KTNVKAAWGK	VGAHAGEYGAEALER	HBA_HUMAN			Hemoglobin subunit alpha;	-0.04	0.00	59.20	1.28
QLSELHCDKL	HVDPENFR	HBB_HUMAN	HBD_HUMAN		Hemoglobin subunit beta;	-0.80	0.07	23.30	-0.38
VVAGSVCFML	ILYQYAGPGLSLGAPGGR	H6ST1_HUMAN			Heparan-sulfate 6-O-sulfotransferase 1;	0.54	0.07	41.40	4.34
DEDDEDRGVM	AVTAVTATAASDR	HDGR2_HUMAN			Hepatoma-derived growth factor-related protein 2;	-0.52	0.08	47.00	5.68
IQGHRVEVKK	AVPKEDIYSGGGGGGSR	ROA0_HUMAN			Heterogeneous nuclear ribonucleoprotein A0;	-0.02	0.00	50.20	6.14
ESPKEPEQLR	KLFIGGLSFETTDESLR	RA1L2_HUMAN	ROA1_HUMAN		Heterogeneous nuclear ribonucleoprotein A1-like	1.11	0.02	49.90	4.08
PGAHVTVKKL	FVGGIKEDTEEHHLR	RA1L2_HUMAN	ROA1_HUMAN	ROA2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2;	-0.52	0.04	27.00	2.99

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LRDYFEQYGK	IEVIEIMTDR	RA1L2_HUMAN	ROA1_HUMAN		Heterogeneous nuclear ribonucleoprotein A1-like	-1.40	0.15	26.70	5.18
HDPKEPEQLR	KLFIGGLSFETTDDSLR	ROA3_HUMAN			Heterogeneous nuclear ribonucleoprotein A3;	0.22	0.01	52.20	8.74
GGLSWDTSKK	DLTEYLSR	HNRDL_HUMAN			Heterogeneous nuclear	0.51	0.04	33.30	-0.68
EQIKEYFGAF	GEIENIELPMDTKTNER	HNRDL_HUMAN			Heterogeneous nuclear	-0.29	0.02	44.70	2.14
AMKTKEPVKK	IFVGGLSPDTPEEKIR	HNRPD_HUMAN			Heterogeneous nuclear ribonucleoprotein D0;	0.61	0.02	52.70	3.99
GPYDRPGTAR	RYIGIVKQAGLER	HNRPF_HUMAN			Heterogeneous nuclear ribonucleoprotein F;	0.28	0.02	43.30	3.18
MGHRYVEVFK	SNNVEMDWVLKHTGPNSPDTAN	HNRH1_HUMAN			Heterogeneous nuclear ribonucleoprotein H;	1.89	0.16	36.40	2.84
CVHMRGLPYK	ATENDIYNFFSPLNPVR	HNRH1_HUMAN	HNRPF_HUMAN		Heterogeneous nuclear ribonucleoprotein H;	0.68	0.12	58.10	3.01
NFFSPLNPVR	VHIEIGPDGR	HNRH1_HUMAN	HNRH2_HUMAN	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein H;	0.28	0.02	36.30	3.19
TEGGEGFVVK	VRGLPWSCSADEVQR	HNRH1_HUMAN			Heterogeneous nuclear ribonucleoprotein H;	-0.16	0.01	62.30	2.00
GGEGFVVKVR	GLPWSCSADEVQR	HNRH1_HUMAN			Heterogeneous nuclear	-0.19	0.01	48.10	5.02
NSVEMDWVLK	HTGPNSPDTANDGFVR	HNRH1_HUMAN	HNRH2_HUMAN		Heterogeneous nuclear	-0.40	0.04	58.00	3.60
VFKSNSVEMD	WVLKHTGPNSPDTANDGFVR	HNRH1_HUMAN	HNRH2_HUMAN		Heterogeneous nuclear	-1.52	0.09	52.30	4.58
TWSPSEWQMA	YEPQGGSGYDYSYAGGR	HNRPK_HUMAN			Heterogeneous nuclear	1.45	0.13	52.90	1.67
VELRILLQSK	NAGAVIGKGGKNIKALR	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	1.03	0.08	26.00	4.27
RGGRGGSRAR	NLPLPPPPPPR	HNRPK_HUMAN			Heterogeneous nuclear	1.00	0.01	33.40	3.25
VKGAKIKELR	ENTQTTIKLFQECCPHSTDR	HNRPK_HUMAN			Heterogeneous nuclear ribonucleoprotein K;	0.51	0.03	44.70	1.03
GNVEKVKFMK	SKPGAAMVEMADGYAVDR	HNRPL_HUMAN			Heterogeneous nuclear	0.30	0.01	60.60	2.84
LVKEKVGEVT	YVELLMDAEGKSR	HNRPM_HUMAN			Heterogeneous nuclear	0.51	0.03	36.30	6.07
RGNFGGSFAG	SFGGAGGHAPGVAR	HNRPM_HUMAN			Heterogeneous nuclear ribonucleoprotein M;	0.06	0.01	36.50	1.65

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
DYYGYEDYYD	YYGYDYHNYR	HNRPQ_HUMAN			Heterogeneous nuclear ribonucleoprotein Q;	-1.00	0.06	26.10	3.31
EFGKLERVKK	LKDYAFVHFEDR	HNRPR_HUMAN			Heterogeneous nuclear	0.30	0.03	39.40	3.38
MKINEEISVK	HLPSTEPDPHVVR	HNRL1_HUMAN			Heterogeneous nuclear ribonucleoprotein U-like	0.64	0.02	32.90	3.55
AEPGGYSGPD	GHYAMDNITR	HNRL1_HUMAN			Heterogeneous nuclear ribonucleoprotein U-like	-2.58	0.16	24.60	3.13
RGAAKEAAGK	SSGPTSLFAVTVAPPGAR	HNRPU_HUMAN			Heterogeneous nuclear ribonucleoprotein U;	0.83	0.02	54.70	3.14
GKSSGPTSLF	AVTVAPPGAR	HNRPU_HUMAN			Heterogeneous nuclear	0.56	0.02	28.20	4.55
RKKREKEQFR	KLFIGGLSFETTEESLR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	0.83	0.02	46.90	-0.55
MEK	TLETVPLER	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	0.48	0.04	23.70	-0.55
LRDYFEEYGK	IDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	0.15	0.01	26.00	6.24
TEEHHLRDYF	EEYGKIDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	-0.21	0.01	37.00	1.73
DTEEHHLRDY	FEEYGKIDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear ribonucleoproteins A2/B1;	-0.49	0.03	38.50	1.85
HLRDYFEEYG	KIDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear	-0.65	0.05	37.40	2.16
EHHLRDYFEE	YGKIDTIEIITDR	ROA2_HUMAN			Heterogeneous nuclear	-0.88	0.03	51.70	0.62
YYDRMYSYPA	RVPPPPPIAR	HNRPC_HUMAN			Heterogeneous nuclear ribonucleoproteins C1/C2;	-1.80	0.19	37.50	4.08
TGVRGGQVRG	AAGVTDGNEVAKAQQATPGGAAP	HINT2_HUMAN			Histidine triad nucleotide-	0.31	0.03	92.60	6.78
FTDVKRPGYR	VKEIGSTMSGR	SAP18_HUMAN			Histone deacetylase complex subunit SAP18;	0.13	0.01	26.20	-1.31
VGMSLVALKK	ALAAAGYDVEKNNSR	H11_HUMAN	H12_HUMAN	H13_HUMAN	Histone H1.1;	-0.07	0.01	42.10	-1.15
ARKSAGAAKR	KASGPPVSELITKAVAASKER	H12_HUMAN	H13_HUMAN	H14_HUMAN	Histone H1.2;	0.33	0.01	44.40	3.64

Table S6

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change (log$_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
RKSAGAAKRK	ASGPPVSELITKAVAASKER	H12_HUMAN	H13_HUMAN	H14_HUMAN	Histone H1.2;	-1.04	0.02	52.00	1.80
AAGAGAAKRK	ATGPPVSELITKAVAASKER	H15_HUMAN			Histone H1.5;	0.18	0.00	37.00	2.30
RNGLSLAALK	KALAAGGYDVEKNNSR	H15_HUMAN			Histone H1.5;	0.00	0.00	30.30	3.00
KAAGAGAAKR	KATGPPVSELITKAVAASKER	H15_HUMAN			Histone H1.5;	-0.21	0.01	29.50	4.23
YMAAVLEYLT	AEILELAGNAAR	H2A1B_HUMAN	H2A1C_HUMAN	H2A1D_HUMAN	Histone H2A type 1-B/E;	-1.72	0.23	47.90	4.51
ISSKAMGIMN	SFVNDIFER	H2B1B_HUMAN	H2B1C_HUMAN	H2B1D_HUMAN	Histone H2B type 1-B;	-0.19	0.01	33.10	5.60
RLARRGGVKR	ISGLIYEETR	H4_HUMAN			Histone H4;	2.40	0.13	40.20	1.82
SRPGRGEPRF	IAVGYVDDTQFVR	1A01_HUMAN	1A02_HUMAN	1A03_HUMAN	HLA class I	1.13	0.07	62.90	2.84
SRPGAGEPRF	ISVGYVDDTQFVR	1B07_HUMAN	1B08_HUMAN	1B14_HUMAN	HLA class I	1.52	0.12	47.30	5.28
RPGAGEPRFI	SVGYVDDTQFVR	1B07_HUMAN	1B08_HUMAN	1B14_HUMAN	HLA class I histocompatibility	1.48	0.09	72.30	-0.77
AGEPRFISVG	YVDDTQFVR	1B07_HUMAN	1A01_HUMAN	1A02_HUMAN	HLA class I	0.11	0.01	32.40	1.44
PGAGEPRFIS	VGYVDDTQFVR	1B07_HUMAN	1A01_HUMAN	1A02_HUMAN	HLA class I histocompatibility	-0.07	0.00	35.60	3.07
SVGYVDDTQF	VRFDSDAASPR	1C06_HUMAN	1B07_HUMAN	1B08_HUMAN	HLA class I histocompatibility	0.37	0.02	37.70	5.52
DYIALNEDLR	SWTAADTAAQITQR	1C07_HUMAN	1B07_HUMAN	1B08_HUMAN	HLA class I histocompatibility antigen, Cw-7 alpha	0.71	0.09	63.30	-1.29
GDGTFQKWAA	VVVPSGQEQR	1C07_HUMAN	1A02_HUMAN	1A25_HUMAN	HLA class I	0.02	0.00	30.90	7.18
LLMLGMGCWA	REVLVPEGPLYR	IGSF8_HUMAN			Immunoglobulin superfamily member 8;	-0.43	0.02	37.10	1.50
EAAMFDSLLM	DSYVSSTTGESVITR	IMA7_HUMAN			Importin subunit alpha-7;	-0.14	0.01	68.30	1.71
LPTFLVELSR	VLANPGNSQVAR	IMB1_HUMAN			Importin subunit beta-1;	3.31	0.35	48.10	7.01
LLPLLGGTQT	AIVFIKQPSSQDALQGR	PTK7_HUMAN			Inactive tyrosine-protein kinase 7;	0.00	0.00	70.00	1.82
ANEILQRSKK	GKLPIVNEDDELVAIIAR	IMDH2_HUMAN			Inosine-5'-monophosphate	1.01	0.04	49.80	2.52

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LTVQVGVTAG	APWQCAPCSAEKLALCPPVSASCS	IBP1_HUMAN			Insulin-like growth factor-binding protein 1;	0.18	0.00	54.20	4.73
FRCPPCTPER	LAACGPPPVAPPAAVAAVAGGAR	IBP2_HUMAN			Insulin-like growth factor-	6.58	0.72	47.90	7.82
PKKLRPPPAR	TPCQQELDQVLER	IBP2_HUMAN			Insulin-like growth factor-	2.80	0.28	55.30	3.71
GGGGARAEVL	FRCPPCTPER	IBP2_HUMAN			Insulin-like growth factor-binding protein 2;	2.47	0.12	30.90	2.22
GGSAGRKPLK	SGMKELAVFR	IBP2_HUMAN			Insulin-like growth factor-binding protein 2;	0.92	0.06	20.70	2.90
LLRGPPVARA	GASSAGLGPVVR	IBP3_HUMAN			Insulin-like growth factor-binding protein 3;	3.60	0.30	55.50	1.82
LRGPPVARAG	ASSAGLGPVVR	IBP3_HUMAN			Insulin-like growth factor-binding protein 3;	3.53	0.32	43.40	-0.48
PPCSEEKLAR	CRPPVGCEELVR	IBP4_HUMAN			Insulin-like growth factor-binding protein 4;	1.03	0.06	49.40	1.60
LAAGPGPSLG	DEAIHCPPCSEEKLAR	IBP4_HUMAN			Insulin-like growth factor-	0.48	0.03	45.80	-0.35
QDTEMGPCRR	HLDSVLQQLQTEVYR	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	3.62	0.13	58.30	2.04
EMGPCRRHLD	SVLQQLQTEVYR	IBP6_HUMAN			Insulin-like growth factor-	2.61	0.20	67.30	1.60
LQQLQTEVYR	GAQTLYVPNCDHR	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	2.34	0.16	37.50	-1.03
LAASPGGALA	RCPGCGQGVQAGCPGGCVEEEDG	IBP6_HUMAN			Insulin-like growth factor-	2.25	0.21	69.10	5.68
LAASPGGALA	RCPGCGQGVQAGCPGGCVEEEDG	IBP6_HUMAN			Insulin-like growth factor-binding protein 6;	2.24	0.14	81.60	9.65
RETIKGIQKR	EASNCFAIR	ITM2B_HUMAN			Integral membrane protein	0.46	0.04	43.60	1.63
ETIKGIQKRE	ASNCFAIR	ITM2B_HUMAN			Integral membrane protein	-1.72	0.11	26.10	1.45
QGQRIGHFEF	HGDHALLCVR	GP180_HUMAN			Integral membrane protein	-2.05	0.17	27.80	4.45
GGGQGPPPVT	LAAAKKAKSETVLTCATGR	ITA3_HUMAN			Integrin alpha-3;	1.26	0.11	32.90	1.72
GQGPPPVTLA	AAKKAKSETVLTCATGR	ITA3_HUMAN			Integrin alpha-3;	0.46	0.02	32.80	3.88
PFLVDGLTLG	AQHLEAGGSLTR	ITB4_HUMAN			Integrin beta-4;	0.63	0.05	41.00	1.25
LDRSFTSQML	SSQPPPHGDLGAPQNPNAKAAGS	ITB4_HUMAN			Integrin beta-4;	0.53	0.02	63.30	3.01

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
RSFTSQMLSS	QPPPHGDLGAPQNPNAKAAGSR	ITB4_HUMAN			Integrin beta-4;	-0.09	0.01	68.40	4.13
DRSFTSQMLS	SQPPPHGDLGAPQNPNAKAAGSR	ITB4_HUMAN			Integrin beta-4;	-0.21	0.01	52.30	0.81
IVDTVLMAPR	SAKPALLKLTEKQVEQR	ITB4_HUMAN			Integrin beta-4;	-0.26	0.01	22.50	1.59
VEQRAFHDLK	VAPGYYTLTADQDAR	ITB4_HUMAN			Integrin beta-4;	-0.65	0.06	64.30	6.17
EPVHPASLPD	SSLATSAPLCCTLCHER	I2BP2_HUMAN			Interferon regulatory	-0.24	0.01	36.10	3.55
EPCPQPLRSP	SLDNPTPFPNLGPSENPLKR	IRF3_HUMAN			Interferon regulatory factor 3;	1.94	0.06	30.90	2.39
PSDKVLIQEK	TQLKGSELEITLTR	SYIC_HUMAN			Isoleucine--tRNA ligase,	1.25	0.09	46.00	3.13
PLAGFVSQRA	HSLLPVDDAINGLSEEQR	IVD_HUMAN			Isovaleryl-CoA dehydrogenase, mitochondrial;	-0.37	0.02	64.30	4.34
VMAEAPPGVE	TDLIDVGFTDDVKKGGPGR	IST1_HUMAN			IST1 homolog;	0.92	0.05	53.50	3.76
AILLCSLALG	SVTVHSSEPEVR	JAM1_HUMAN			Junctional adhesion molecule A;	-0.76	0.04	25.70	4.62
QLRLALLVAA	GAPEVLVSAPR	KDEL2_HUMAN			KDEL motif-containing protein 2;	0.15	0.01	49.10	3.89
GGGGVSSLRI	SSSKGSLGGGFSSGGFSGGSFSR	K1C10_HUMAN			Keratin, type I	1.78	0.17	74.60	-1.25
GYGSSFGGVD	GLLAGGEKATMQNLNDR	K1C17_HUMAN			Keratin, type I cytoskeletal 17;	-1.14	0.10	59.80	1.94
HYFKIIEDLR	AQIFANTVDNAR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	4.33	0.51	51.20	2.82
ILGATIENSR	IVLQIDNAR	K1C18_HUMAN	K1C19_HUMAN		Keratin, type I cytoskeletal 18;	2.71	0.18	32.60	0.56
MQTIQKTTTR	RIVDGKVVSETNDTKVLR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.75	0.07	34.00	0.98
LGSVQAPSYG	ARPVSSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.70	0.06	83.90	2.23
TFSTNYRSLG	SVQAPSYGARPVSSAASVYAGAG	K1C18_HUMAN			Keratin, type I	0.67	0.06	71.80	2.70

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
STTVVTTQSA	EVGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.64	0.06	64.30	3.51
SLGSVQAPSY	GARPVSSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.37	0.03	100.40	2.05
VQAPSYGARP	VSSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.35	0.04	99.00	5.49
TRSTFSTNYR	SLGSVQAPSYGAR	K1C18_HUMAN			Keratin, type I	0.28	0.06	63.70	3.18
GSVQAPSYGA	RPVSSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	0.06	0.01	49.50	3.78
APSYGARPVS	SAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I	-0.21	0.01	85.10	4.50
IEESTTVVTT	QSAEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.24	0.02	84.80	4.79
QIEESTTVVT	TQSAEVGAAETTLTELRR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.24	0.02	38.20	0.36
IEESTTVVTT	QSAEVGAAETTLTELRR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.29	0.02	28.20	0.59
QAPSYGARPV	SSAASVYAGAGGSGSR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.32	0.02	80.30	1.13
SVENDIHGLR	KVIDDTNITR	K1C18_HUMAN			Keratin, type I	-0.37	0.06	18.90	5.15
TTVVTTQSAE	VGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.40	0.04	34.10	5.56
TGIAGGLAGM	GGIQNEKETMQSLNDR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.49	0.04	49.70	5.87
LATGIAGGLA	GMGGIQNEKETMQSLNDR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.52	0.03	44.30	3.71
EESTTVVTTQ	SAEVGAAETTLTELRR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.80	0.06	34.90	1.61
EESTTVVTTQ	SAEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-0.80	0.07	81.00	3.73
QIEESTTVVT	TQSAEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I	-0.80	0.08	84.90	4.42
ESTTVVTTQS	AEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I	-0.88	0.08	81.60	3.21
GMGSGGLATG	IAGGLAGMGGIQNEKETMQSLND	K1C18_HUMAN			Keratin, type I	-1.00	0.08	51.00	-0.35

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
DLAKIMADIR	AQYDELAR	K1C18_HUMAN			Keratin, type I	-1.14	0.05	29.90	2.70
VVTTQSAEVG	AAETTLTELR	K1C18_HUMAN			Keratin, type I	-1.19	0.11	43.80	2.81
YWSQQIEEST	TVVTTQSAEVGAAETTLTELR	K1C18_HUMAN			Keratin, type I	-1.19	0.11	79.90	2.35
NEKETMQSLN	DRLASYLDR	K1C18_HUMAN			Keratin, type I	-1.34	0.07	35.70	2.18
YWSQQIEEST	TVVTTQSAEVGAAETTLTELRR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-1.34	0.10	25.00	5.40
GIAGGLAGMG	GIQNEKETMQSLNDR	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-1.52	0.13	36.50	0.00
SGLTVEVDAP	KSQDLAKIMADIR	K1C18_HUMAN			Keratin, type I	-1.65	0.05	38.30	4.51
RGGMGSGGLA	TGIAGGLAGMGGIQNEKETMQSL	K1C18_HUMAN			Keratin, type I cytoskeletal 18;	-1.72	0.11	72.40	3.09
GYGGVLTASD	GLLAGNEKLTMQNLNDR	K1C19_HUMAN			Keratin, type I cytoskeletal 19;	3.32	0.25	33.10	3.70
INQSLLAPLR	LDADPSLQR	K2C7_HUMAN			Keratin, type II cytoskeletal 7;	-1.80	0.13	23.70	-1.72
AQEREQIKVL	NDKFASFIDKVR	K2C74_HUMAN			Keratin, type II cytoskeletal 74;	3.85	0.21	29.40	3.04
YMNKVELESR	LEGLTDEINFLR	K2C8_HUMAN			Keratin, type II	4.27	0.32	66.70	4.90
NKVELESRLE	GLTDEINFLR	K2C8_HUMAN			Keratin, type II	2.32	0.14	39.80	4.37
AEIEGLKGQR	ASLEAAIADAEQR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	0.74	0.06	59.40	-1.23
ISEMNRNISR	LQAEIEGLKGQR	K2C8_HUMAN			Keratin, type II	0.51	0.03	22.20	2.86
TAVTVNQSLL	SPLVLEVDPNIQAVR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	0.22	0.01	75.90	3.75
SSFSRTSSSR	AVVVKKIETR	K2C8_HUMAN			Keratin, type II	0.11	0.01	51.80	3.01
ITAVTVNQSL	LSPLVLEVDPNIQAVR	K2C8_HUMAN			Keratin, type II	0.09	0.01	84.80	5.23
YGGLTSPGLS	YSLGSSFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II	-0.04	0.00	103.20	3.55
TSPGLSYSLG	SSFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.19	0.01	80.90	0.30
SPGLSYSLGS	SFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.46	0.04	39.80	-3.94
VNQSLLSPLV	LEVDPNIQAVR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.49	0.06	37.00	4.03

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
PGLSYSLGSS	FGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.58	0.06	29.20	1.61
VTVNQSLLSP	LVLEVDPNIQAVR	K2C8_HUMAN			Keratin, type II	-0.58	0.05	48.60	10.13
FLEQQNKMLE	TKWSLLQQQKTAR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-0.65	0.05	26.10	2.60
QSLLSPLVLE	VDPNIQAVR	K2C8_HUMAN			Keratin, type II cytoskeletal 8;	-1.00	0.10	30.90	1.82
TVNQSLLSPL	VLEVDPNIQAVR	K2C8_HUMAN			Keratin, type II	-1.00	0.10	47.50	6.08
GGLTSPGLSY	SLGSSFGSGAGSSSFSR	K2C8_HUMAN			Keratin, type II	-1.14	0.08	89.00	4.98
AARMSRSSGR	SGSMDPSGAHPSVR	KHDR1_HUMAN			KH domain-containing,	-1.40	0.07	28.80	2.89
RQNEELNLLK	AQLNETLTKLR	KTN1_HUMAN			Kinectin;	0.20	0.02	20.60	2.43
SCYLKQGKFK	QAETLYKEILTR	KLC1_HUMAN			Kinesin light chain 1;	2.54	0.15	30.60	1.38
KILDTSVAYV	RGEENLAGWRPR	KIF1A_HUMAN	KIF1B_HUMAN		Kinesin-like protein KIF1A;	4.32	0.41	27.50	9.72
WKISGLPVTR	VIGSGCNLDSAR	LDH6A_HUMAN	LDHA_HUMAN	LDHB_HUMAN	L-lactate dehydrogenase	4.66	0.41	55.50	-1.33
IGPSKERTLS	ADASVNTLPVVVSR	LAR4B_HUMAN			La-related protein 4B;	0.40	0.04	55.10	5.95
LLCAPSLLVA	LDICSKNPCHNGGLCEEISQEVR	MFGM_HUMAN			Lactadherin;	2.32	0.15	55.30	3.66
VRGRELTGLK	ALYETELADAR	LMNB1_HUMAN			Lamin-B1;	-0.04	0.00	46.30	5.36
VISESTPIAE	TIMASSNESLVVNR	LAP2B_HUMAN			Lamina-associated polypeptide 2, isoforms	2.06	0.15	67.80	-0.26
NRVTGNFKHA	SPILPITEFSDIPR	LAP2B_HUMAN			Lamina-associated polypeptide 2, isoforms	1.08	0.08	54.90	7.62
VNRVTGNFKH	ASPILPITEFSDIPR	LAP2B_HUMAN			Lamina-associated polypeptide 2, isoforms beta/gamma;	0.66	0.07	35.40	1.42
VAYVLIKFAN	SPRPDLWVLER	LAMA3_HUMAN	LAMA5_HUMAN		Laminin subunit alpha-3;	1.55	0.06	24.30	3.93
ERLLWEMRAR	DLGAPQAAAEAELAAAQR	LAMA5_HUMAN			Laminin subunit alpha-5;	5.54	0.67	58.60	1.63
VVEYANEDAR	QEVGVAVHTPQR	LAMA5_HUMAN			Laminin subunit alpha-5;	4.41	0.28	26.30	2.59

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
SMHVLPRSSR	GLLLFTAR	LAMA5_HUMAN			Laminin subunit alpha-5;	2.59	0.31	30.90	-1.30
GLALLGAARA	REEAGGGFSLHPPYFNLAEGAR	LAMA5_HUMAN			Laminin subunit alpha-5;	1.51	0.01	48.80	3.45
FGKTWRVYQY	LAADCTSTFPR	LAMB3_HUMAN			Laminin subunit beta-3;	-6.06	0.00	11.80	9.11
FLPNTEGFSR	AALPFGLVR	LPHN2_HUMAN			Latrophilin-2;	1.90	0.08	30.10	2.45
DVYQGVPKDY	TGEDVTPQNFLAVLR	LGMN_HUMAN			Legumain;	1.33	0.18	50.40	4.26
LKSTGDGTLG	RASEVEVKNEIVANVGKR	LRRF1_HUMAN			Leucine-rich repeat flightless-interacting protein 1;	0.09	0.01	31.60	6.85
KGSRNMPGLS	AATLASLGGTSSR	LRRF1_HUMAN			Leucine-rich repeat flightless-interacting protein 1;	-0.40	0.04	63.20	1.23
YLRSCRAHSV	VPISCFLR	YV012_HUMAN			Leucine-rich repeat-	2.18	0.15	32.20	-5.88
VKPKTLPLDK	SINHQIESPSER	LIMC1_HUMAN			LIM and calponin	-1.14	0.05	27.10	3.77
QPVAQSYGGY	KEPAAPVSIQR	LASP1_HUMAN			LIM and SH3 domain	0.79	0.07	29.70	3.79
MVADTPENLR	LKQQSELQSQVR	LASP1_HUMAN			LIM and SH3 domain	0.45	0.04	29.70	7.59
SAPVYQQPQQ	QPVAQSYGGYKEPAAPVSIQR	LASP1_HUMAN			LIM and SH3 domain protein 1;	0.35	0.03	21.10	1.51
QQPQQQPVAQ	SYGGYKEPAAPVSIQR	LASP1_HUMAN			LIM and SH3 domain protein 1;	0.22	0.02	30.40	3.63
PQQQPVAQSY	GGYKEPAAPVSIQR	LASP1_HUMAN			LIM and SH3 domain protein 1;	0.00	0.00	32.30	0.84
LCGCPAPAAA	SPLLLFANR	LRP5_HUMAN			Low-density lipoprotein receptor-related protein 5;	1.34	0.06	43.30	1.13
LLQLQHLAAA	AADPLLGGQGPAKDCEKDQFQCR	LRP8_HUMAN			Low-density lipoprotein	0.17	0.01	32.40	0.15
LLLQLQHLAA	AAADPLLGGQGPAKDCEKDQFQC	LRP8_HUMAN			Low-density lipoprotein receptor-related protein 8;	0.02	0.00	35.90	2.37
M	DGLQASAGPLR	NO66_HUMAN			Lysine-specific demethylase NO66;	3.80	0.15	21.90	0.45

Table S6

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;	1.69	0.03	44.50	4.15
ATAALLGHIL	LHDFLLVPR	LYAG_HUMAN			Lysosomal alpha-glucosidase;	1.43	0.07	26.00	-0.09
TAALLGHILL	HDFLLVPR	LYAG_HUMAN			Lysosomal alpha-	1.22	0.06	29.90	6.69
LLHDFLLVPR	ELSGSSPVLEETHPAHQQGASRPGI	LYAG_HUMAN			Lysosomal alpha-	0.48	0.02	44.90	1.41
APQPIPRRSW	SPALTIENEHIR	MA2B1_HUMAN			Lysosomal alpha-mannosidase;	-0.24	0.02	29.70	0.71
PTPHQTPYQL	DPANITLEPMEIR	MA2B1_HUMAN			Lysosomal alpha-	-0.88	0.05	40.30	3.85
VPSHFRYEKD	TVVVQDLGNIFTR	PPGB_HUMAN			Lysosomal protective protein;	1.50	0.17	67.50	4.36
SPDGPSRFRK	AYKPEQPLVR	LOXL2_HUMAN			Lysyl oxidase homolog 2;	-0.46	0.03	25.20	0.31
VCLLASRSIT	EEVSEYCSHMIGSGHLQSLQR	CSF1_HUMAN			Macrophage colony-stimulating factor 1;	1.31	0.11	41.50	1.86
IGKIGGAQNR	SYSKLLCGLLAER	MIF_HUMAN			Macrophage migration inhibitory factor;	2.58	0.05	42.00	3.19
MAFGGSSEPC	ALCSLHSIGKIGGAQNR	MIF_HUMAN			Macrophage migration inhibitory factor;	0.67	0.03	30.40	4.75
VPDQLMAFGG	SSEPCALCSLHSIGKIGGAQNR	MIF_HUMAN			Macrophage migration inhibitory factor;	-0.02	0.00	34.60	0.08
KIGGAQNRSY	SKLLCGLLAER	MIF_HUMAN			Macrophage migration inhibitory factor;	-0.19	0.01	37.00	-1.88
GGSSEPCALC	SLHSIGKIGGAQNR	MIF_HUMAN			Macrophage migration	-0.49	0.04	23.80	4.28
YMLGSAMSRP	IIHFGSDYEDR	PRIO_HUMAN			Major prion protein;	-0.72	0.06	48.00	6.56
DPLADRGEKD	TAKSLQPLAPR	MVP_HUMAN			Major vault protein;	0.71	0.04	28.40	3.36
QPSRHMSTMR	SAQILASALAEMQR	MMP15_HUMAN			Matrix metalloproteinase-15;	1.36	0.09	30.60	3.61
PPPLPRLKRR	DFTPAELR	PGRC1_HUMAN			Membrane-associated progesterone receptor	1.31	0.07	29.60	4.88
GSLLSEADVR	ALGGLACDLPGR	MSLN_HUMAN			Mesothelin;	5.74	0.42	52.70	-1.06

Table S6

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;	4.70	0.61	39.40	2.22
AESAEVLLPR	LVSCPGPLDQDQQEAAR	MSLN_HUMAN			Mesothelin;	3.73	0.33	62.80	0.63
PPNISSLSPR	QLLGFPCAEVSGLSTER	MSLN_HUMAN			Mesothelin;	2.92	0.30	71.00	3.01
GGLACDLPGR	FVAESAEVLLPR	MSLN_HUMAN			Mesothelin;	1.62	0.04	60.10	1.18
CTRFFSRITK	ANVDLLPR	MSLN_HUMAN			Mesothelin;	0.02	0.00	33.00	2.48
QSRHLACLPR	EPGLCTWQSLR	TIMP1_HUMAN			Metalloproteinase inhibitor 1;	2.86	0.15	35.70	-0.07
WLIAPSRACT	CVPPHPQTAFCNSDLVIR	TIMP1_HUMAN			Metalloproteinase	1.44	0.14	46.80	3.36
QDGLLHITTC	SFVAPWNSLSLAQR	TIMP1_HUMAN			Metalloproteinase	1.38	0.09	66.70	5.86
GDAADIRFVY	TPAMESVCGYFHR	TIMP1_HUMAN			Metalloproteinase inhibitor 1;	1.33	0.07	34.10	0.57
LLWLIAPSRA	CTCVPPHPQTAFCNSDLVIR	TIMP1_HUMAN			Metalloproteinase inhibitor 1;	1.18	0.02	71.30	3.83
ACTCVPPHPQ	TAFCNSDLVIR	TIMP1_HUMAN			Metalloproteinase inhibitor 1;	0.93	0.07	54.90	1.13
AFCNADVVIR	AKAVSEKEVDSGNDIYGNPIKR	TIMP2_HUMAN			Metalloproteinase inhibitor 2;	5.59	0.61	58.40	4.55
AKAVSEKEVD	SGNDIYGNPIKR	TIMP2_HUMAN			Metalloproteinase inhibitor 2;	1.56	0.10	32.70	0.86
LLRPADACSC	SPVHPQQAFCNADVVIR	TIMP2_HUMAN			Metalloproteinase	1.33	0.09	79.80	2.79
LATLLRPADA	CSCSPVHPQQAFCNADVVIR	TIMP2_HUMAN			Metalloproteinase inhibitor 2;	1.10	0.01	72.90	2.57
ATLLRPADAC	SCSPVHPQQAFCNADVVIR	TIMP2_HUMAN			Metalloproteinase	0.90	0.08	47.30	2.57

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
KLDGEKAVLE	NNLGAAVLR	MAT2B_HUMAN			Methionine adenosyltransferase 2 subunit beta;	1.75	0.08	33.10	8.47
MSP	ALQDLSQPEGLKKTLR	METH_HUMAN			Methionine synthase;	2.26	0.24	32.20	5.04
MRK	ETPPPLVPPAAR	MEP50_HUMAN			Methylosome protein 50;	1.46	0.12	31.00	6.12
M	RKETPPPLVPPAAR	MEP50_HUMAN			Methylosome protein 50;	0.91	0.05	39.30	5.82
FALGPVSGPQ	AFPKLVR	C2TA_HUMAN			MHC class II	10.56	0.00	15.90	9.24
LPLRGPRARR	SASPHDVDLCLVSPCEFEHR	MAP1S_HUMAN			Microtubule-associated protein 1S;	-0.02	0.00	52.70	4.47
MAVNVY	STSVTSDNLSR	MARE1_HUMAN			Microtubule-associated protein RP/EB family	-0.34	0.02	32.00	3.91
ELMQQVNVLK	LTVEDLEKER	MARE1_HUMAN			Microtubule-associated	-0.46	0.04	22.60	3.07
MAP	KFPDSVEELR	TOM34_HUMAN			Mitochondrial import	3.78	0.29	23.00	-1.63
M	APKFPDSVEELR	TOM34_HUMAN			Mitochondrial import	-1.80	0.06	26.10	4.15
SKPVEAAVVA	AAVPSSGSGVGGGGTAGPGTGGL	TOM70_HUMAN			Mitochondrial import receptor subunit TOM70;	0.24	0.02	40.80	5.89
EESLKTDHPE	IGEGKPTPALSEEASSSSIR	IMMT_HUMAN			Mitochondrial inner membrane protein;	-1.29	0.10	62.60	5.40
M	VGGGGVGGGLLENANPLIYQR	MIP18_HUMAN			Mitotic spindle-associated	1.04	0.07	73.10	3.33
DMKLVWPSAK	LLQAAAGASAR	MMS19_HUMAN			MMS19 nucleotide excision repair protein	1.62	0.07	33.00	2.65
YGDFNKEVHK	SGYLAGDKLLPQR	MOES_HUMAN			Moesin;	2.18	0.13	28.10	7.45
KEVYELLDSP	GKVLLQSKDQITAGNAAR	PUR6_HUMAN			Multifunctional protein ADE2;	-0.76	0.06	42.90	0.46
SVPAPPRQFR	ELPDSVPQECTVR	MYOF_HUMAN			Myoferlin;	0.48	0.03	37.20	0.96
FTEDQTAEFK	EAFQLFDR	MYL6_HUMAN			Myosin light polypeptide	-0.76	0.05	36.30	1.04
MERELEKSQR	SQISSVNSDVEALRR	MPRIP_HUMAN			Myosin phosphatase Rho-interacting protein;	0.30	0.03	33.20	3.54
RCIIPNHEKK	AGKLDPHLVLDQLR	MYH10_HUMAN	MYH9_HUMAN		Myosin-10;	0.43	0.02	36.80	4.96

Table S6

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
VRCIIPNHEK	KAGKLDPHLVLDQLR	MYH9_HUMAN			Myosin-9;	0.51	0.03	30.70	7.02
EVSSLKNKLR	RGDLPFVVPR	MYH9_HUMAN			Myosin-9;	-0.02	0.00	34.70	2.19
EAEELRARLT	AKKQELEEICHDLEAR	MYH9_HUMAN			Myosin-9;	-0.62	0.03	36.80	2.33
GWDRTAQLTS	LAMLMLDSFYR	MTM1_HUMAN			Myotubularin;	8.88	1.12	32.60	5.25
GGPAPAGAAK	MKVVEEPNAFGVNNPFLPQASR	GNPTG_HUMAN			N-acetylglucosamine-1-	1.71	0.05	66.70	7.03
SAGGPAPAGA	AKMKVVEEPNAFGVNNPFLPQAS	GNPTG_HUMAN			N-acetylglucosamine-1-phosphotransferase	1.56	0.01	59.00	2.64
PAPAGAAKMK	VVEEPNAFGVNNPFLPQASR	GNPTG_HUMAN			N-acetylglucosamine-1-phosphotransferase	0.74	0.02	50.40	2.80
KHKKEVGKLK	SMDLSEYIIR	NAT10_HUMAN			N-acetyltransferase 10;	0.02	0.00	48.20	0.64
M	TSALENYINR	NAA38_HUMAN			N-alpha-acetyltransferase 38, NatC auxiliary	2.85	0.14	25.20	5.59
EKGKLGQYIR	LVEPGSPAEKAGLLAGDR	NHRF1_HUMAN			Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	1.31	0.07	39.50	1.90
IQKENSREAL	AEAALESPRPALVR	NHRF1_HUMAN			Na(+)/H(+) exchange	0.54	0.03	26.40	-1.52
EKELEQLELR	GSKVQTLFLSK	NALP6_HUMAN			NACHT, LRR and PYD domains-containing	4.75	0.80	24.70	7.42
MVGRR	ALIVLAHSER	NQO1_HUMAN			NAD(P)H dehydrogenase [quinone] 1;	-0.02	0.00	32.80	3.23
WYRQHPQPYI	FPDSPGGTSYER	NDUB9_HUMAN			NADH dehydrogenase	2.21	0.21	24.60	0.67
LMKLFQRSTP	AITLESPDIKYPLR	NB5R3_HUMAN			NADH-cytochrome b5	1.13	0.05	30.70	0.84
QDSTQATTQQ	AQLAAAAEIDEEPVSKAKQSR	NACA_HUMAN			Nascent polypeptide-associated complex	1.03	0.09	57.10	1.73
TQATTQQAQL	AAAAEIDEEPVSKAKQSR	NACA_HUMAN			Nascent polypeptide-associated complex subunit alpha;	0.63	0.08	48.70	1.60
STQATTQQAQ	LAAAAEIDEEPVSKAKQSR	NACA_HUMAN			Nascent polypeptide-associated complex	0.51	0.03	26.40	3.00
IKNVNTALNT	TQIPSSIEDIFNDDR	ULA1_HUMAN			NEDD8-activating enzyme E1 regulatory	-1.34	0.17	29.90	-1.90
LEKETLKSLG	EEIQESLKTLENQSHETLER	NEST_HUMAN			Nestin;	0.92	0.08	30.80	3.62
AKRVQGLEGP	RKDLEEAGGLGTEFSELPGKSR	NEST_HUMAN			Nestin;	0.91	0.05	69.10	-0.81

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
GEFLESDSVS	VSVPWDDSLR	NEST_HUMAN			Nestin;	0.60	0.04	44.30	1.41
GVLFCPRPDG	TADMHIIINGEDMGPSAR	NEUL2_HUMAN			Neuralized-like protein 2;	2.52	0.09	32.50	-3.17
WVQREISNFE	YLMQLNTIAGR	NBEL2_HUMAN			Neurobeachin-like protein 2;	-5.06	0.00	28.40	7.99
FALLAAGVAP	LSWDLPEPR	NMB_HUMAN			Neuromedin-B;	1.19	0.07	36.20	4.03
RVSQGLNGDL	YFSNVLPEDTR	NRCAM_HUMAN			Neuronal cell adhesion molecule;	-6.06	0.00	26.10	3.42
ESPGPERVWR	ASWGEFQAR	VGF_HUMAN			Neurosecretory protein VGF;	2.22	0.13	29.60	2.85
IDELEPRRPR	YRVPDVLVADPPIAR	GANAB_HUMAN			Neutral alpha-glucosidase AB;	0.60	0.01	37.00	3.16
FEYEYAMRWK	ALIEMEKQQQDQVDR	NONO_HUMAN			Non-POU domain-containing octamer-binding protein;	1.13	0.10	42.40	1.22
AFSQFGPIER	AVVIVDDR	NONO_HUMAN	SFPQ_HUMAN		Non-POU domain-containing octamer-	0.78	0.06	30.60	0.22
VLSTSSPAQQ	AENEAKASSSILIDESEPTTNIQIR	NSF1C_HUMAN			NSFL1 cofactor p47;	-0.52	0.04	67.90	3.41
LKATLVESST	SGFTPGGGGSSVSMIASR	NASP_HUMAN			Nuclear autoantigenic sperm protein;	0.17	0.01	97.70	1.19
ELALKATLVE	SSTSGFTPGGGGSSVSMIASR	NASP_HUMAN			Nuclear autoantigenic	0.00	0.00	89.80	1.78
IPARSQAPLE	SSLDSLGDVFLDSGR	NUMA1_HUMAN			Nuclear mitotic apparatus	1.41	0.12	59.10	8.20
LRRASMQPIQ	IAEGTGITTR	NUMA1_HUMAN			Nuclear mitotic apparatus protein 1;	-0.43	0.04	23.30	5.32
RYMTQFADQN	FSDFLFR	NU133_HUMAN			Nuclear pore complex	2.41	0.09	22.50	0.00
TSVPPGFKVF	GAPNVVEDEIDQYLSKQDGKIYR	NPL4_HUMAN			Nuclear protein	-0.52	0.02	38.60	3.49
VSDSHFQRVS	AAVLPLVHPLPEGLR	NCOR1_HUMAN			Nuclear receptor corepressor 1;	-0.19	0.01	41.80	0.87
GETVEFDVVE	GEKGAEAANVTGPGGVPVQGSKY	YBOX1_HUMAN			Nuclease-sensitive element-binding protein 1;	-0.69	0.04	46.00	4.38
SQGRLEAQKR	ELQQAVLHMEQR	NUCB1_HUMAN			Nucleobindin-1;	0.33	0.02	42.70	0.13

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MVATTKPKAT	AKAALSLPAKQAPQGSR	NOLC1_HUMAN			Nucleolar and coiled-body phosphoprotein 1;	0.61	0.03	27.00	4.00
QKSTWKKKVK	SLPNILTDDR	NOL10_HUMAN			Nucleolar protein 10;	1.12	0.05	30.90	4.26
RKPYVLNDLE	AEASLPEKKGNTLSR	NOP16_HUMAN			Nucleolar protein 16;	-0.16	0.01	26.80	3.46
EEKGAVEALA	AALAHISGATSVDQR	DDX21_HUMAN			Nucleolar RNA helicase 2;	0.38	0.03	52.90	-0.65
ARSQPSKTLF	VKGLSEDTTEETLKESFDGSVR	NUCL_HUMAN			Nucleolin;	1.13	0.07	35.00	3.54
KNLPYKVTQD	ELKEVFEDAAEIR	NUCL_HUMAN			Nucleolin;	0.26	0.01	38.80	0.68
NFNKSAPELK	TGISDVFAKNDLAVVDVR	NUCL_HUMAN			Nucleolin;	-0.19	0.01	54.70	3.09
NLPYKVTQDE	LKEVFEDAAEIR	NUCL_HUMAN			Nucleolin;	-0.37	0.02	43.90	-0.13
TLLAKNLPYK	VTQDELKEVFEDAAEIR	NUCL_HUMAN			Nucleolin;	-0.37	0.04	43.40	2.00
FNKSAPELKT	GISDVFAKNDLAVVDVR	NUCL_HUMAN			Nucleolin;	-1.29	0.10	51.50	7.20
MSVQPTVSLG	GFEITPPVVLR	NPM_HUMAN			Nucleophosmin;	1.14	0.04	30.80	4.22
M	AICQFFLQGR	NUPL2_HUMAN			Nucleoporin-like protein 2;	0.87	0.04	44.10	-5.26
ERPSTSTAVF	GTVSATPSSSLPKR	TPR_HUMAN			Nucleoprotein TPR;	1.26	0.11	24.60	5.95
EGLNVVKTGR	VMLGETNPADSKPGTIR	NDKA_HUMAN	NDK8_HUMAN	NDKB_HUMAN	Nucleoside diphosphate kinase A;	4.00	0.41	29.50	-2.60
QNPQILAALQ	ERLDGLVETPTGYIESLPR	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	2.41	0.15	57.30	0.69
ARQLTVQMMQ	NPQILAALQER	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	1.95	0.16	47.70	0.62
ALQERLDGLV	ETPTGYIESLPR	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	1.61	0.08	40.10	5.25
LKARQLTVQM	MQNPQILAALQER	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	1.53	0.10	68.90	4.27

Table S6

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change (log$_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
KARQLTVQMM	QNPQILAALQER	NP1L1_HUMAN			Nucleosome assembly	1.41	0.11	51.50	9.58
YEEVHDLERK	YAVLYQPLFDKR	NP1L1_HUMAN			Nucleosome assembly	1.01	0.05	28.70	1.90
ILAALQERLD	GLVETPTGYIESLPR	NP1L1_HUMAN			Nucleosome assembly protein 1-like 1;	-0.49	0.03	81.40	3.48
RTRSSTCGPP	AFLGVFGR	MACD1_HUMAN			O-acetyl-ADP-ribose	4.71	0.17	20.80	5.58
LLLSGRPTRA	DSKVFGDLDQVR	OLM2A_HUMAN			Olfactomedin-like protein 2A;	2.19	0.16	40.90	1.18
RGVHSSVASA	TSVATKKTVQGPPTSDDIFER	OAT_HUMAN			Ornithine aminotransferase,	0.94	0.07	40.50	2.35
VDSEWFGFYR	SGQAKETIPLQETSLYTQDR	PPT1_HUMAN			Palmitoyl-protein	0.20	0.02	77.30	3.55
SMPQDFRPVS	SIIDVDILPETHR	PAR6B_HUMAN			Partitioning defective 6 homolog beta;	-0.52	0.02	35.20	1.55
YSGSVAPANS	ALGQTQPSDQDTLVQR	PDLI5_HUMAN			PDZ and LIM domain protein 5;	0.13	0.01	50.70	2.12
TYSGSVAPAN	SALGQTQPSDQDTLVQR	PDLI5_HUMAN			PDZ and LIM domain	-0.04	0.00	30.90	1.97
RISNSATYSG	SVAPANSALGQTQPSDQDTLVQR	PDLI5_HUMAN			PDZ and LIM domain protein 5;	-0.19	0.02	62.90	5.83
TGRISNSATY	SGSVAPANSALGQTQPSDQDTLVQ	PDLI5_HUMAN			PDZ and LIM domain protein 5;	-0.43	0.04	71.20	3.39
CAPGAPAEAR	LTSALDELLQATR	PTX3_HUMAN			Pentraxin-related protein PTX3;	4.13	0.58	59.80	5.48
APGAPAEARL	TSALDELLQATR	PTX3_HUMAN			Pentraxin-related protein PTX3;	3.72	0.28	61.90	8.09
MLENSQMRER	MLLQATDDVLR	PTX3_HUMAN			Pentraxin-related protein PTX3;	2.48	0.19	41.70	5.91
LQRLREELGR	LAESLARPCAPGAPAEAR	PTX3_HUMAN			Pentraxin-related protein	2.22	0.10	34.50	3.16
LLVFPSSCLA	FRSPLSVFKR	AMD_HUMAN			Peptidyl-glycine alpha-	1.26	0.03	31.80	3.17
FGYKGSCFHR	IIPGFMCQGGDFTR	PAL4A_HUMAN	PPIA_HUMAN		Peptidyl-prolyl cis-trans isomerase A-like 4A/B/C;	2.88	0.19	33.50	3.69
AVDGEPLGRV	SFELFADKVPKTAENFR	PPIA_HUMAN			Peptidyl-prolyl cis-trans isomerase A;	0.24	0.00	30.30	1.76

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LDGKHVVFGK	VKEGMNIVEAMER	PPIA_HUMAN			Peptidyl-prolyl cis-trans isomerase A;	-0.55	0.02	24.40	4.28
M	GVQVETISPGDGR	FKB1A_HUMAN			Peptidyl-prolyl cis-trans isomerase FKBP1A;	-0.16	0.01	60.20	-0.97
DSNNEKGLFR	RGEAHLAVNDFELAR	FKBP4_HUMAN			Peptidyl-prolyl cis-trans	0.42	0.05	52.10	0.64
VTGQAAPVAG	LGSDAELQIER	FKBP9_HUMAN			Peptidyl-prolyl cis-trans isomerase FKBP9;	1.22	0.09	35.40	5.61
TGKVSASFTS	TAMVPETTHEAAAIDEDVLR	PPIL2_HUMAN			Peptidyl-prolyl cis-trans isomerase-like 2;	-0.72	0.06	61.90	4.26
MSADGAEAD	GSTQVTVEEPVQQPSVVDR	PLIN3_HUMAN			Perilipin-3;	0.00	0.00	60.00	4.73
VSSGVASVVD	VAKGVVQGGLDTTR	PLIN4_HUMAN			Perilipin-4;	0.72	0.08	44.30	1.85
FIIDGKGVLR	QITVNDLPVGR	PRDX1_HUMAN	PRDX2_HUMAN		Peroxiredoxin-1;	5.10	0.50	32.70	3.39
NIPLVSDPKR	TIAQDYGVLKADEGISFR	PRDX1_HUMAN			Peroxiredoxin-1;	0.87	0.07	37.30	4.85
YLEDSGHTLR	GLFIIDDKGILR	PRDX1_HUMAN	PRDX4_HUMAN		Peroxiredoxin-1;	0.68	0.06	30.80	2.17
VSDPKRTIAQ	DYGVLKADEGISFR	PRDX1_HUMAN			Peroxiredoxin-1;	0.63	0.02	31.20	2.38
HLAWVNTPKK	QGGLGPMNIPLVSDPKR	PRDX1_HUMAN			Peroxiredoxin-1;	0.20	0.01	42.20	3.30
CHLAWVNTPK	KQGGLGPMNIPLVSDPKR	PRDX1_HUMAN			Peroxiredoxin-1;	0.00	0.00	39.50	2.34
VVFFFYPLDF	TFVCPTEIIAFSDR	PRDX1_HUMAN			Peroxiredoxin-1;	-0.32	0.02	50.70	0.59
EDSGHTLRGL	FIIDDKGILR	PRDX1_HUMAN	PRDX4_HUMAN		Peroxiredoxin-1;	-5.06	1.69	23.20	2.30
FIIDDKGILR	QITLNDLPVGR	PRDX4_HUMAN			Peroxiredoxin-4;	8.40	1.63	29.40	4.06
MPGGLLLG	DVAPNFEANTTVGR	PRDX6_HUMAN			Peroxiredoxin-6;	1.26	0.11	63.40	8.55

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
KKKVEKGVLN	VHPAASASKPSADQIR	PHF3_HUMAN			PHD finger protein 3;	0.78	0.04	30.30	2.05
MPTVSVKR	DLLFQALGR	SYFB_HUMAN			Phenylalanine--tRNA	1.25	0.09	44.30	3.86
MAERGGAGG	GPGGAGGGSGQR	PACS1_HUMAN			Phosphofurin acidic cluster sorting protein 1;	3.06	0.24	22.70	0.61
FTDGSRIVFR	LSGTGSAGATIR	PGM1_HUMAN			Phosphoglucomutase-1;	1.90	0.11	36.00	5.00
AEPDKIEAFR	ASLSKLGDVYVNDAFGTAHR	PGK1_HUMAN	PGK2_HUMAN		Phosphoglycerate kinase 1;	0.50	0.03	46.90	3.58
EKACANPAPG	SVILLENLR	PGK1_HUMAN	PGK2_HUMAN		Phosphoglycerate kinase 1;	-0.26	0.01	40.70	2.11
IEAFRASLSK	LGDVYVNDAFGTAHR	PGK1_HUMAN	PGK2_HUMAN		Phosphoglycerate kinase 1;	-0.80	0.04	53.70	2.39
ISKDRRYADL	TEDQLPSCESLKDTIAR	PGAM1_HUMAN			Phosphoglycerate mutase 1;	0.38	0.04	33.10	2.26
GISVLEMSHR	SSDFAKIINNTENLVR	SERC_HUMAN			Phosphoserine	2.28	0.10	49.20	3.62
KVIFLQGGGC	GQFSAVPLNLIGLKAGR	SERC_HUMAN			Phosphoserine	0.06	0.00	37.70	1.82
VGSAGVTVVI	VRDDLLGFALR	SERC_HUMAN			Phosphoserine aminotransferase;	-2.05	0.17	48.00	5.04
LTGESDHVKK	SLDKDPLLLSGTHVMEGSGR	AT2B1_HUMAN			Plasma membrane	0.86	0.05	35.40	1.52
GGGVGGPGAK	SAAQAAAQTNSNAAGKQLR	PAIRB_HUMAN			Plasminogen activator inhibitor 1 RNA-binding	0.75	0.07	59.60	1.76
MPG	HLQEGFGCVVTNR	PAIRB_HUMAN			Plasminogen activator inhibitor 1 RNA-binding protein;	-0.07	0.01	48.20	1.68
LGLALVFGEG	SAVHHPPSYVAHLASDFGVR	PAI1_HUMAN			Plasminogen activator	0.64	0.03	50.40	-1.29
KRPLPIRRKR	SIEEAVPAVCKTR	PDGFA_HUMAN			Platelet-derived growth factor subunit A;	2.37	0.08	42.90	1.57
KRPLPIRRKR	SIEEAVPAVCK	PDGFA_HUMAN			Platelet-derived growth	2.18	0.23	26.80	1.35

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LCCYLRLVSA	EGDPIPEELYEMLSDHSIR	PDGFB_HUMAN			Platelet-derived growth factor subunit B;	-3.24	0.31	41.10	2.56
SRSSSVGSSS	SYPISPAVSR	PLEC_HUMAN			Plectin;	0.13	0.00	26.40	1.72
EAAVDAQQQK	RSIQEELQQLR	PLEC_HUMAN			Plectin;	0.11	0.01	31.10	4.60
LLPLSEKAAR	ARQEELYSELQAR	PLEC_HUMAN			Plectin;	0.09	0.01	56.70	0.98
LLQETQALQQ	SFLSEKDSLLQR	PLEC_HUMAN			Plectin;	0.02	0.00	27.70	2.55
CAQRIAEQQK	AQAEVEGLGKGVAR	PLEC_HUMAN			Plectin;	-0.19	0.02	36.10	-2.08
RSRSSSVGSS	SSYPISPAVSR	PLEC_HUMAN			Plectin;	-0.76	0.05	33.70	5.53
VAQVTLQSVQ	RRPELEDSTLR	PLEC_HUMAN			Plectin;	-0.83	0.03	24.20	0.92
ILALKASFEK	AAAGKAELELELGR	PLEC_HUMAN			Plectin;	-0.96	0.06	25.90	1.80
LPSDMAVALL	EAQAGTGHIIDPATSAR	PLEC_HUMAN			Plectin;	-1.14	0.08	39.30	1.04
PSDMAVALLE	AQAGTGHIIDPATSAR	PLEC_HUMAN			Plectin;	-1.19	0.05	25.50	1.75
LQQRCRPDQL	TGLSLLPLSEKAAR	PLEC_HUMAN			Plectin;	-1.40	0.15	26.80	3.80
ILSPWGAEVK	AEPVEVVAPR	PARP1_HUMAN			Poly [ADP-ribose]	-0.14	0.01	41.10	1.92
LDAYSIQGQH	TISPLDLAKLNQVAR	PCBP1_HUMAN			Poly(rC)-binding protein 1;	1.47	0.11	33.90	2.24
PEVKGYWGLD	ASAQTTSHELTIPNDLIGCIIGR	PCBP2_HUMAN			Poly(rC)-binding protein 2;	0.72	0.06	66.10	1.64
TNLQMAAVTM	GFGDPLSPLQSMAAQR	PUF60_HUMAN			Poly(U)-binding-splicing factor PUF60;	0.24	0.01	89.20	1.70
LTKVVQNDAY	TAPALPSSIR	PDIP3_HUMAN			Polymerase delta-interacting protein 3;	0.92	0.08	33.70	1.24
AFLWVLGIAY	YMYSGGGSALAGGAGGGAGR	GALT2_HUMAN			Polypeptide N-	0.98	0.10	123.50	3.44
FAFLWVLGIA	YYMYSGGGSALAGGAGGGAGR	GALT2_HUMAN			Polypeptide N-acetylgalactosaminyltrans	0.98	0.06	128.70	-0.10

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LWVLGIAYYM	YSGGGSALAGGAGGGAGR	GALT2_HUMAN			Polypeptide N-acetylgalactosaminyltransferase 2;	0.91	0.08	84.00	5.83
FLWVLGIAYY	MYSGGGSALAGGAGGGAGR	GALT2_HUMAN			Polypeptide N-acetylgalactosaminyltransferase 2;	0.85	0.11	128.30	2.09
LTVAYIFVEL	LVSTFHASAGAGR	GALT4_HUMAN			Polypeptide N-acetylgalactosaminyltransferase 4;	1.31	0.13	35.70	1.53
AASAAAVDAG	MAMAGQSPVLR	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	1.72	0.11	47.00	-1.00
QTMAAAFGLS	VPNVHGALAPLAIPSAAAAAAAA(	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	0.04	0.00	69.50	0.88
PNVHGALAPL	AIPSAAAAAAAAGR	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	-0.09	0.00	51.50	4.59
AGRIAIPGLA	GAGNSVLLVSNLNPER	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	-0.52	0.03	63.00	4.24
MD	GIVPDIAVGTKR	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	-0.80	0.04	36.20	1.09
AFGLSVPNVH	GALAPLAIPSAAAAAAAAGR	PTBP1_HUMAN			Polypyrimidine tract-	-0.83	0.03	89.70	6.74
MDG	IVPDIAVGTKR	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	-0.96	0.06	21.30	1.13
ALAASAAAVD	AGMAMAGQSPVLR	PTBP1_HUMAN			Polypyrimidine tract-binding protein 1;	-1.04	0.07	59.60	2.64
MRSEK	SLTLAAPGEVR	KCNA6_HUMAN			Potassium voltage-gated channel subfamily A member 6;	6.26	0.83	27.10	3.33
QTDVGITHFR	SGMSHEEDQLIPNLYR	PRP8_HUMAN			Pre-mRNA-processing-splicing factor 8;	0.46	0.02	42.10	-1.87
KAPAPRPSLL	GLDLLASLKR	PRP16_HUMAN			Pre-mRNA-splicing factor ATP-dependent RNA	-0.96	0.09	30.30	-4.41
EDEEGQKVTI	HDKTEINLVSFR	CWC22_HUMAN			Pre-mRNA-splicing factor	6.89	0.96	38.70	-7.59

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MAENSGRAGK	SSGSGAGKGAVSAEQVIAGFNR	PFD2_HUMAN			Prefoldin subunit 2;	-0.09	0.01	69.80	-2.37
ALSTALSEKR	TLEGELHDLR	LMNA_HUMAN			Prelamin-A/C;	2.68	0.25	29.20	6.18
NTWGCGNSLR	TALINSTGEEVAMR	LMNA_HUMAN			Prelamin-A/C;	1.64	0.08	49.80	5.06
LDNARQSAER	NSNLVGAAHEELQQSR	LMNA_HUMAN			Prelamin-A/C;	1.47	0.10	42.40	2.75
ETPSQRRATR	SGAQASSTPLSPTR	LMNA_HUMAN			Prelamin-A/C;	0.15	0.01	72.40	1.29
DNARQSAERN	SNLVGAAHEELQQSR	LMNA_HUMAN			Prelamin-A/C;	-0.11	0.01	35.30	0.00
ARQSAERNSN	LVGAAHEELQQSR	LMNA_HUMAN			Prelamin-A/C;	-0.52	0.05	36.30	0.20
PSQRRATRSG	AQASSTPLSPTR	LMNA_HUMAN			Prelamin-A/C;	-0.76	0.01	44.70	8.44
TEVVAPFMAN	IPLLLYPQDGPR	SAP_HUMAN			Proactivator polypeptide;	0.97	0.04	29.10	2.98
PRSKPQPKDN	GDVCQDCIQMVTDIQTAVR	SAP_HUMAN			Proactivator polypeptide;	0.38	0.04	75.80	2.81
EEIMAEKENK	TIIFVETKR	DDX17_HUMAN			Probable ATP-dependent RNA helicase DDX17;	1.37	0.06	29.70	0.09
WVLNEFKHGK	APILIATDVASR	DDX17_HUMAN	DDX5_HUMAN		Probable ATP-dependent RNA helicase DDX17;	0.57	0.05	39.80	7.85
ERDWVLNEFR	SGKAPILIATDVASR	DDX17_HUMAN			Probable ATP-dependent	0.15	0.01	43.60	1.59
QREFALSNLK	AGAKDILVATDVAGR	DDX23_HUMAN			Probable ATP-dependent RNA helicase DDX23;	0.61	0.04	52.50	-1.19
QSEAQINTAK	RLLEKGKEAVVQEPER	DDX27_HUMAN			Probable ATP-dependent	0.45	0.04	43.60	3.93
QKAEGKIIKK	SSGFSGKGFKFDETEQALANER	DDX46_HUMAN			Probable ATP-dependent RNA helicase DDX46;	0.61	0.04	39.60	3.39
QKNLGIESQD	VMQQATNAILR	DDX46_HUMAN			Probable ATP-dependent	-1.52	0.18	39.40	5.94
ERDWVLNEFK	HGKAPILIATDVASR	DDX5_HUMAN			Probable ATP-dependent	0.64	0.05	46.20	1.49
HILGDPNLTK	FSVIILDEAHER	DHX40_HUMAN			Probable ATP-dependent RNA helicase DHX40;	2.29	0.13	65.10	0.21
M	KDSLVLLGR	CIAO1_HUMAN			Probable cytosolic iron-	0.48	0.03	41.90	0.67
DKPISLQNWK	RGLDILSPMER	EXO5_HUMAN			Probable exonuclease V;	4.62	0.43	36.80	6.76

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
SPQSSAGGKP	AMSYASALR	HELZ_HUMAN			Probable helicase with zinc finger domain;	3.24	0.16	24.40	0.90
GWLLLAEAKG	DAKPEDNLLVLTVATKETEGFRR	PLOD1_HUMAN			Procollagen-lysine,2-oxoglutarate 5-	1.18	0.02	41.20	0.11
PSVWAAVPGK	TFVNITPAEVGVLVGKDR	PROF1_HUMAN			Profilin-1;	0.06	0.00	47.10	4.99
VWAAVPGKTF	VNITPAEVGVLVGKDR	PROF1_HUMAN			Profilin-1;	-0.88	0.05	24.80	3.57
MYPVFNELER	VNLSAAQTLR	PDC10_HUMAN			Programmed cell death	2.47	0.18	30.00	3.81
PGYIKLRKIR	AAQNISKTIATSQNR	PHB2_HUMAN			Prohibitin-2;	1.37	0.12	37.60	2.21
SGPFEPDLYK	SEMEVQDAELKALLQSSASR	PA2G4_HUMAN			Proliferation-associated protein 2G4;	0.04	0.00	53.60	3.05
VESEAGWGMV	TPDLLFAEGTAAYAR	P3H1_HUMAN			Prolyl 3-hydroxylase 1;	1.11	0.07	21.60	1.53
HGAGWQLFCR	TVWSAHSGPTR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	4.57	0.25	24.20	2.03
AELRQRLIHF	SAKDVINEAWFPEDQR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	2.74	0.12	38.50	0.10
PEEDGTRFHR	QASKCDSHGTHLAGVVSGR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	1.19	0.08	58.70	3.88
RFHRQASKCD	SHGTHLAGVVSGR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	0.54	0.03	35.70	4.66
GGKLVCRAHN	AFGGEGVYAIAR	PCSK9_HUMAN			Proprotein convertase subtilisin/kexin type 9;	0.37	0.02	50.70	0.16
IEEDSSVFAQ	SIPWNLER	PCSK9_HUMAN			Proprotein convertase	-0.02	0.00	22.90	1.25
GVAAPRRLRR	AADHDVGSELPPEGVLGALLR	PCSK1_HUMAN			ProSAAS;	1.31	0.11	61.50	4.19
ETGAPRRFRR	SVPRGEAAGAVQELAR	PCSK1_HUMAN			ProSAAS;	1.31	0.10	42.50	1.40
LLGVLGDLQA	APEAQVSVQPNFQQDKFLGR	PTGDS_HUMAN			Prostaglandin-H2 D-	8.85	0.99	29.10	2.33
GVLGDLQAAP	EAQVSVQPNFQQDKFLGR	PTGDS_HUMAN			Prostaglandin-H2 D-isomerase;	6.58	1.40	38.40	4.61
EEPGIEMLHG	TTTLAFKFR	PSB5_HUMAN			Proteasome subunit beta	0.22	0.02	15.40	2.60
RDGSSGGVIR	LAAIAESGVER	PSB6_HUMAN			Proteasome subunit beta type-6;	3.83	0.45	48.10	1.66
YKLPKVRKTG	TTIAGVVYKDGIVLGADTR	PSB7_HUMAN			Proteasome subunit beta type-7;	0.13	0.01	70.90	2.53

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LPSKCEVCKL	LSTELQAELSR	CNPY4_HUMAN			Protein canopy homolog 4;	0.92	0.09	35.70	2.82
PPTQPSPASD	SGSGYVPGSVSAAFVTCPNEKVAK	CUTA_HUMAN			Protein CutA;	-1.65	0.16	41.90	1.71
MEDQDGLLGK	ELGFDASEVELTR	CYR61_HUMAN			Protein CYR61;	-0.58	0.05	59.90	1.40
IAVGKGSSLK	RLPVFGMEPR	CYR61_HUMAN			Protein CYR61;	-0.96	0.02	51.20	2.75
LLHLTRLALS	TCPAACHCPLEAPKCAPGVGLVR	CYR61_HUMAN			Protein CYR61;	-1.00	0.04	47.50	1.74
LLAAARLAAA	SDVLELTDDNFESR	PDIA3_HUMAN			Protein disulfide-	0.37	0.02	85.10	2.33
WVVLPSWLSS	AKVSSLIER	PDIA5_HUMAN			Protein disulfide-isomerase A5;	0.89	0.10	24.60	1.89
SCTFFLAVNG	LYSSSDDVIELTPSNFNR	PDIA6_HUMAN			Protein disulfide-isomerase A6;	0.20	0.01	77.60	5.27
CLAVAALVRA	DAPEEEDHVLVLR	PDIA1_HUMAN			Protein disulfide-	0.28	0.02	44.70	1.74
M	AVTGWLESLR	DPCD_HUMAN			Protein DPCD;	0.61	0.03	44.10	1.63
LLSLGRFVRG	DGVGGDPAVALPHR	LMAN1_HUMAN			Protein ERGIC-53;	0.70	0.02	56.80	3.08
PETPAPAARS	AAPSSVPAAPPGPEPRVVR	F110C_HUMAN			Protein FAM110C;	0.20	0.01	35.30	2.22
TFYVISQVFE	IKMDASLGNLFAR	FAM3C_HUMAN			Protein FAM3C;	0.70	0.02	37.60	2.01
VISQVFEIKM	DASLGNLFAR	FAM3C_HUMAN			Protein FAM3C;	0.53	0.03	47.20	2.11
YVISQVFEIK	MDASLGNLFAR	FAM3C_HUMAN			Protein FAM3C;	0.30	0.02	43.00	2.20
RRLIADLGST	SITNLGFR	FAM3C_HUMAN			Protein FAM3C;	-2.34	0.24	33.70	1.49
RDAEKKDQMK	ADLTALFLPR	FLII_HUMAN			Protein flightless-1 homolog;	0.84	0.07	48.30	4.34
M	FGCLVAGR	CK073_HUMAN			Protein Hikeshi;	0.33	0.03	25.70	0.19
IMALMNTLLY	LCLDHFFIAPR	SG196_HUMAN			Protein kinase-like protein	1.13	0.07	29.90	1.83
MALMNTLLYL	CLDHFFIAPR	SG196_HUMAN			Protein kinase-like protein SgK196;	0.31	0.01	44.10	0.31

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
LLLPASLTGG	VGSLNLEELSEMR	OS9_HUMAN			Protein OS-9;	1.37	0.06	54.90	1.79
RSRQARQSRR	STQGVTLTDLQEAEKTIGR	MYPT1_HUMAN			Protein phosphatase 1	-0.96	0.07	49.60	3.45
GGKRAARPAT	AGKAGGAAVVITEPEHTKER	RCC2_HUMAN			Protein RCC2;	0.22	0.02	39.20	-0.80
RSSRTNPETK	SKVEDPEINSIQDIKEGQLLR	RRP5_HUMAN			Protein RRP5 homolog;	1.15	0.07	49.90	2.78
GLQPLKLDYR	ALAAVPSAGSVQR	SCRIB_HUMAN			Protein scribble homolog;	1.23	0.12	32.30	5.34
VTTFVNHPQV	SALLGEEDEEALHYLTR	SET_HUMAN			Protein SET;	-1.04	0.07	33.00	0.66
SLVISQGADG	RGKPEVVSVVGR	TUTLA_HUMAN			Protein turtle homolog A;	0.18	0.01	23.50	1.70
NIPPIQRVPR	DIPAMLPAAR	YIPF3_HUMAN			Protein YIPF3;	0.45	0.02	31.40	1.56
MAWK	SGGASHSELIHNLR	PIMT_HUMAN			Protein-L-isoaspartate(D-aspartate) O-methyltransferase;	0.18	0.02	62.50	1.86
PLQLCALVHC	APPAAGQQQPPREPPAAPGAWR	LYOX_HUMAN			Protein-lysine 6-oxidase;	4.53	0.20	48.70	1.62
SPWQVMLFRK	SPQELLCGASLISDR	THRB_HUMAN			Prothrombin;	-0.07	0.00	68.30	-0.65
MSPWQVMLFR	KSPQELLCGASLISDR	THRB_HUMAN			Prothrombin;	-0.21	0.01	60.40	1.25
DTSSEITTKD	LKEKKEVVEEAENGR	PTMA_HUMAN			Prothymosin alpha;	-0.21	0.02	34.80	1.95
GRLAHEVGWK	YQAVTATLEEKR	R13AX_HUMAN	RL13A_HUMAN		Putative 60S ribosomal	-0.24	0.02	35.20	2.23
YVSHMKETQK	STYYITGESKEQVANSAFVER	H90B3_HUMAN			Putative heat shock protein HSP 90-beta-3;	2.51	0.13	48.40	-4.45
AKVNDTTPNN	FPLLYEEALR	MA13P_HUMAN	MAGB4_HUMAN		Putative MAGE domain-containing protein	1.78	0.14	26.00	1.09
MSAQAQMR	ALLDQLMGTAR	LUC7L_HUMAN			Putative RNA-binding protein Luc7-like 1;	-0.11	0.01	48.20	4.82

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MSAQAQMR	AMLDQLMGTSR	LC7L2_HUMAN			Putative RNA-binding protein Luc7-like 2;	0.09	0.01	36.60	-1.19
EGLMKVEAAR	LSAQDPVVAVAEDGR	S38AA_HUMAN			Putative sodium-coupled neutral amino acid transporter 10;	0.75	0.04	54.50	7.36
MA	ASGSPGPTPSPGPGR	YJ017_HUMAN			Putative uncharacterized protein LOC439951;	2.94	0.21	27.90	2.96
RVVDDELATR	FLKSFKANLENPIR	ODPX_HUMAN			Pyruvate dehydrogenase protein X component,	6.45	0.49	24.30	1.93
ADTFLEHMCR	LDIDSPPITAR	KPYM_HUMAN			Pyruvate kinase isozymes	8.04	0.56	52.20	3.18
DIDSPPITAR	NTGIICTIGPASR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	1.39	0.09	60.70	3.01
SPLSYRPVAI	ALDTKGPEIR	KPYM_HUMAN	KPYR_HUMAN		Pyruvate kinase isozymes M1/M2;	0.93	0.06	25.10	2.42
YHAETIKNVR	TATESFASDPILYR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	0.59	0.05	67.40	4.50
GTAFIQTQQL	HAAMADTFLEHMCR	KPYM_HUMAN			Pyruvate kinase isozymes	0.37	0.02	39.50	6.66
VLGEKGKNIK	IISKIENHEGVR	KPYM_HUMAN			Pyruvate kinase isozymes	0.35	0.04	54.80	8.06
SKIENHEGVR	RFDEILEASDGIMVAR	KPYM_HUMAN			Pyruvate kinase isozymes	0.22	0.01	50.90	6.40
YHAETIKNVR	TATESFASDPILYRPVAVALDTKGPE	KPYM_HUMAN			Pyruvate kinase isozymes	0.17	0.00	36.40	1.14
TAFIQTQQLH	AAMADTFLEHMCR	KPYM_HUMAN			Pyruvate kinase isozymes	-0.16	0.01	35.20	5.85
TQQLHAAMAD	TFLEHMCR	KPYM_HUMAN			Pyruvate kinase isozymes	-0.24	0.01	27.70	2.48
QTQQLHAAMA	DTFLEHMCR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	-0.26	0.02	29.20	1.12
GAVEASFKCC	SGAIIVLTKSGR	KPYM_HUMAN			Pyruvate kinase isozymes M1/M2;	-1.72	0.23	32.10	4.56
KPIEEIIVQN	GKVIGVKSEGEIAR	GDIB_HUMAN			Rab GDP dissociation	-0.69	0.07	30.30	2.91
QDQTTVRTVA	SATTAIEIR	REPS1_HUMAN			RalBP1-associated Eps domain-containing protein	0.04	0.01	33.40	2.41
LFKMRAKLFR	FASENDLPEWKER	RANG_HUMAN			Ran-specific GTPase-	0.30	0.02	35.40	2.14
SDRAWVWNTH	ADFADECPKPELLAIR	RANG_HUMAN			Ran-specific GTPase-	-1.29	0.10	29.00	-1.42
SAADEVDGLG	VARPHYGSVLDNER	IQGA1_HUMAN			Ras GTPase-activating-like protein IQGAP1;	0.17	0.01	34.80	1.88

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
MSAADEVD	GLGVARPHYGSVLDNER	IQGA1_HUMAN			Ras GTPase-activating-like protein IQGAP1;	-0.40	0.04	55.50	1.23
WDTAGQERFW	TITSSYYR	RAB1A_HUMAN	RAB1B_HUMAN	RAB1C_HUMAN	Ras-related protein Rab-	0.87	0.10	34.80	3.92
VNKKFSNQYK	ATIGADFLTKEVMVDDR	RAB7A_HUMAN			Ras-related protein Rab-7a;	0.31	0.01	37.40	7.12
LQDLREQILR	VKDTDDVPMILVGNKCDLEDER	RAP1B_HUMAN	RP1BL_HUMAN		Ras-related protein Rap-1b;	0.59	0.04	54.70	1.95
LALLPPGAAS	TQVCTGTDMKLR	ERBB2_HUMAN			Receptor tyrosine-protein	0.85	0.08	42.40	-2.09
TKEDEMPVGR	NVLELSNVVR	PTPRF_HUMAN			Receptor-type tyrosine-	2.17	0.24	47.70	5.97
GGLGGSGGLR	LLLCLLLLSSR	PTPRN_HUMAN			Receptor-type tyrosine-protein phosphatase-like N;	6.01	0.52	23.00	0.60
VPGKVELQEK	VVQVSAGDSHTAALTDDGR	RCC1_HUMAN			Regulator of chromosome condensation;	0.57	0.06	71.10	0.52
AASGASSALE	AGGSSGLEDVLPLLQQADELHR	RMD3_HUMAN			Regulator of microtubule dynamics protein 3;	-1.00	0.12	70.70	5.81
VEKITTKLLK	AGAKPDQIGIITPYEGQR	RENT1_HUMAN			Regulator of nonsense	1.02	0.08	30.40	5.63
LLALVAGVLG	NEFSILKSPGSVVFR	RENR_HUMAN			Renin receptor;	0.90	0.01	34.00	7.31
LALVAGVLGN	EFSILKSPGSVVFR	RENR_HUMAN			Renin receptor;	0.60	0.02	29.40	8.37
MLPRDERRFK	AADLNGDLTATR	RCN1_HUMAN			Reticulocalbin-1;	-0.07	0.00	48.00	0.00
LLLCAAAAGA	GKAEELHYPLGER	RCN2_HUMAN			Reticulocalbin-2;	1.26	0.09	44.80	1.72
SVNYKPPAQK	SIQEIQELDKDDESLR	GDIR1_HUMAN			Rho GDP-dissociation inhibitor 1;	0.13	0.01	47.10	-0.05
KDDESLIKYK	KTLLGDGPVVTDPKAPNVVVTR	GDIR2_HUMAN			Rho GDP-dissociation	-0.24	0.01	34.10	-1.81
MWDQ	RLVKLALLQHLR	RHGBB_HUMAN			Rho GTPase-activating protein 11B;	4.19	0.53	14.70	9.02

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
EKEEDARPNA	AAPALGPVGLESDLSKVR	RHG27_HUMAN			Rho GTPase-activating protein 27;	-0.26	0.01	26.40	3.41
FQEPTEPKTK	AAAPGVEDEPLLR	RIR2_HUMAN			Ribonucleoside-diphosphate reductase	1.85	0.19	55.30	7.76
EKAQEQQQQM	AELHSKLQSSEAEVR	RRBP1_HUMAN			Ribosome-binding protein 1;	-0.83	0.09	33.30	2.05
KQGQEVEPPR	RGPAVPPAR	REXO1_HUMAN			RNA exonuclease 1 homolog;	-1.40	0.11	22.00	7.74
M	VKLFIGNLPR	RBM4B_HUMAN	RBM4_HUMAN		RNA-binding protein 4B;	0.93	0.02	41.10	1.65
SAKAAIDWFD	GKEFSGNPIKVSFATR	FUS_HUMAN			RNA-binding protein	-1.65	0.05	30.80	1.74
ARQRSRAWLK	EGGGDEPLNFLDPKVAQR	RRP12_HUMAN			RRP12-like protein;	1.04	0.03	28.80	1.99
M	KIEEVKSTTKTQR	RUVB1_HUMAN			RuvB-like 1;	0.76	0.06	24.70	3.52
LGLDDALEPR	QASQGMVGQLAAR	RUVB2_HUMAN			RuvB-like 2;	1.04	0.08	40.80	4.83
LKNLFSKYGK	VVGAKVVTNAR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	0.43	0.04	40.80	3.08
ESTAHAQSSK	ADSLLAVVKR	SAFB1_HUMAN	SAFB2_HUMAN		Scaffold attachment factor B1;	0.26	0.02	30.50	2.30
KHDKKGNKED	YDLSKMR	SCG3_HUMAN			Secretogranin-3;	-6.06	0.00	18.60	2.55
VIQHRPSRQY	ATLDVYNPFETR	SCAM3_HUMAN			Secretory carrier-associated membrane	0.15	0.01	48.00	2.53
VKGSSQPQAR	VYLTFDELR	SEM3C_HUMAN			Semaphorin-3C;	2.96	0.18	34.10	2.62
AARLWGLGIG	AEVWWNLVPR	SEM4C_HUMAN			Semaphorin-4C;	0.86	0.04	45.00	3.08
LLLLLGGAHG	LFPEEPPPLSVAPR	SEM6B_HUMAN			Semaphorin-6B;	2.51	0.04	44.50	4.94
KRENIRSLTM	SGHVGFESLPDQLVNR	SEP10_HUMAN			Septin-10;	-1.00	0.08	42.60	-2.79
INPETPGYVG	FANLPNQVHR	SEPT2_HUMAN			Septin-2;	-0.07	0.01	37.70	2.84
EERSVNSSTM	VAQQKNLEGYVGFANLPNQVYR	SEPT7_HUMAN			Septin-7;	-0.02	0.00	75.80	3.00

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
PAPVSQLQSR	LEPKPQPPVAEATPR	SEPT9_HUMAN			Septin-9;	1.18	0.04	39.70	2.41
AIGPSRFGLK	RAEVLGHKTPEPAPR	SEPT9_HUMAN			Septin-9;	0.57	0.02	31.40	3.82
SVAAALSPLG	IEVDIDVEHGGKR	SQSTM_HUMAN			Sequestosome-1;	0.64	0.06	32.20	2.73
AIGSPFSLQN	TVTTGIVSTTQR	HTRA1_HUMAN			Serine protease HTRA1;	1.83	0.29	68.10	-4.10
ASAQLSRAGR	SAPLAAGCPDR	HTRA1_HUMAN			Serine protease HTRA1;	0.81	0.03	48.80	-1.92
IRETQEKRFK	DPGLVDQLVKADSEWR	SYSC_HUMAN			Serine--tRNA ligase, cytoplasmic;	0.80	0.03	41.90	2.58
M	VLDLDLFR	SYSC_HUMAN			Serine--tRNA ligase, cytoplasmic;	0.18	0.00	25.90	0.78
ISGHTSGIKK	ALWCSEDKQILSADDKTVR	STRAP_HUMAN			Serine-threonine kinase receptor-associated protein;	0.51	0.04	35.90	1.67
LPVQPEVALK	RVPSPTPAPKEAVR	SRRM2_HUMAN			Serine/arginine repetitive matrix protein 2;	1.02	0.08	33.90	1.40
AAAMNLASPR	TAVAPSAVNLADPR	SRRM2_HUMAN			Serine/arginine repetitive	0.33	0.03	36.70	3.18
DERGGEGDGR	IYVGNLPTDVR	SRSF9_HUMAN			Serine/arginine-rich splicing factor 9;	3.70	0.18	35.80	2.67
DEIKAHPFFK	TIDFSSDLR	LATS1_HUMAN			Serine/threonine-protein kinase LATS1;	-0.26	0.01	27.20	1.20
LLNAPTKRPR	SSTVTEAPIAVVTSR	NEK9_HUMAN			Serine/threonine-protein kinase Nek9;	1.42	0.15	72.10	4.77
LPYEELQGLK	VASEAPLEHKPQVEASSPR	NEK9_HUMAN			Serine/threonine-protein kinase Nek9;	0.86	0.07	47.50	1.72
YEELQGLKVA	SEAPLEHKPQVEASSPR	NEK9_HUMAN			Serine/threonine-protein kinase Nek9;	0.22	0.03	33.10	-0.26
EPAKTAQALS	SGSGSQETKIPISLVLR	OXSR1_HUMAN			Serine/threonine-protein kinase OSR1;	0.60	0.03	32.70	4.97
LPVTPTRDVA	TSPISPTENNTTPPDALTR	PAK1_HUMAN			Serine/threonine-protein	-0.26	0.03	55.00	8.06
AAYFDSARLR	AAGIGKDFKENPNLR	PRP4B_HUMAN			Serine/threonine-protein kinase PRP4 homolog;	0.81	0.06	27.20	4.73
ILYQTVTGLK	KDLSGVQKVPALLENQVEER	RIOK1_HUMAN			Serine/threonine-protein	0.94	0.03	38.00	1.50
SHEPEFDYLK	SLEIEEKINKIR	2ABA_HUMAN	2ABB_HUMAN	2ABD_HUMAN	Serine/threonine-protein	-0.04	0.00	26.60	4.44

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
MAP	LDLDKYVEIAR	PPP6_HUMAN			Serine/threonine-protein phosphatase 6 catalytic	0.96	0.06	21.20	1.01
M	APLDLDKYVEIAR	PPP6_HUMAN			Serine/threonine-protein phosphatase 6 catalytic	0.35	0.03	13.90	0.89
MFWK	FDLHSSSHIDTLLER	PP6R3_HUMAN			Serine/threonine-protein	0.48	0.02	30.20	2.83
NKCVPNSNER	YYGYTGAFR	TRFE_HUMAN	TRFL_HUMAN		Serotransferrin;	2.28	0.14	25.10	2.57
AEGHSEASLA	SALVEGEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-response protein;	1.10	0.05	55.10	3.94
SNHQKISSGK	SSPFKVSPLTFGR	SDPR_HUMAN			Serum deprivation-response protein;	1.00	0.05	29.90	-1.49
FAEGHSEASL	ASALVEGEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-	0.59	0.04	43.70	1.62
EESFAEGHSE	ASLASALVEGEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-response protein;	0.45	0.03	43.50	6.69
EGHSEASLAS	ALVEGEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-	0.38	0.03	35.10	3.50
EEESFAEGHS	EASLASALVEGEIAEEAAEKATSR	SDPR_HUMAN			Serum deprivation-response protein;	-0.40	0.05	47.70	2.16
INGSAPRDLF	DMKPFEDALR	SHC1_HUMAN			SHC-transforming protein 1;	-0.11	0.01	28.60	0.70
DMKPFEDALR	VPPPPQSVSMAEQLR	SHC1_HUMAN			SHC-transforming protein 1;	-0.43	0.04	31.60	3.11
RLISLFTANS	HLGPLQISLGR	TRPC4_HUMAN	TRPC5_HUMAN		Short transient receptor	4.16	0.47	25.10	5.65
RHITLDKTWK	GSDHSASLEPGELAELVR	SIAS_HUMAN			Sialic acid synthase;	0.04	0.00	41.40	4.15
SEQDLEKLGG	KSPPPPPPPPR	SKT_HUMAN			Sickle tail protein homolog;	8.47	1.37	49.00	3.76
M	VLLESEQFLTELTR	SRP14_HUMAN			Signal recognition particle 14 kDa protein;	0.02	0.00	76.40	3.57
EVNSDAGAFK	NSLKDLPDVQELITQVR	SRP68_HUMAN			Signal recognition particle	1.51	0.14	49.20	8.04
EQRQQSTTLS	TLYPSTSSLLTNHQHEGR	STAM1_HUMAN			Signal transducing adapter molecule 1;	-0.72	0.06	36.70	2.26

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
LQVLRQFVRH	ESETTTSLVLER	SSBP_HUMAN			Single-stranded DNA-binding protein,	0.20	0.02	54.70	3.50
PGKSSILQHE	RPASLYQSSIDR	SRBS2_HUMAN			Sorbin and SH3 domain-	-6.06	0.00	32.60	5.18
IAPRIESKSM	SAPVIFDR	SNX2_HUMAN			Sorting nexin-2;	-0.40	0.03	33.60	2.13
VKKIHENEKR	LEAGDHPVELLAR	SPRC_HUMAN			SPARC;	0.45	0.03	41.70	1.52
FGQLDQHPID	GYLSHTELAPLR	SPRC_HUMAN			SPARC;	-0.52	0.03	34.60	-0.86
IAALQAFADQ	LIAAGHYAKGDISSR	SPTA2_HUMAN			Spectrin alpha chain, non-	-0.62	0.05	32.50	2.70
VQEEKIAALQ	AFADQLIAAGHYAKGDISSR	SPTA2_HUMAN			Spectrin alpha chain, non-erythrocytic 1;	-0.76	0.06	55.20	1.30
AALQAFADQL	IAAGHYAKGDISSR	SPTA2_HUMAN			Spectrin alpha chain, non-	-0.88	0.08	23.10	2.99
ETDIAAYEER	VQAVVAVAR	SPTB2_HUMAN			Spectrin beta chain, non-	1.36	0.15	25.80	2.76
PSPTSDRKAK	TALPAQSAATLPAR	SPTB2_HUMAN			Spectrin beta chain, non-erythrocytic 1;	0.13	0.01	63.10	2.07
EEYWNSSKFK	AFTFDDEDDELSQLKESKR	VIPAR_HUMAN			Spermatogenesis-defective protein 39	0.72	0.07	44.80	-0.88
ATPTPGHIMS	MTPEQLQAWR	SF3B1_HUMAN			Splicing factor 3B subunit 1;	-0.88	0.05	40.60	1.24
KEHELLEQQK	RAAVLLEQER	SF3B2_HUMAN			Splicing factor 3B subunit 2;	0.81	0.06	32.10	4.53
QAKSQRTKQS	TVLAPVIDLKR	SPF45_HUMAN			Splicing factor 45;	1.55	0.12	32.30	1.09
LPTMTPDGLA	VTPTPVPVVGSQMTR	U2AF2_HUMAN			Splicing factor U2AF 65 kDa subunit;	-0.14	0.01	42.60	2.37
TALLPTMTPD	GLAVTPTPVPVVGSQMTR	U2AF2_HUMAN			Splicing factor U2AF 65 kDa subunit;	-1.29	0.10	71.30	3.69
GEKTYTQRCR	LFVGNLPADITEDEFKR	SFPQ_HUMAN			Splicing factor, proline- and glutamine-rich;	2.03	0.12	31.90	4.30
VKASFAPISF	AIKAKENDLLPLEKNR	SFSWA_HUMAN			Splicing factor, suppressor	-1.04	0.13	39.00	2.31
YGVQADRVDK	SAVGFDYQGKTEKHESQR	SRC8_HUMAN			Src substrate cortactin;	0.68	0.05	29.30	3.27
RPAKPPVVDR	SLKPGALSNSESIPTIDGLR	STABP_HUMAN			STAM-binding protein;	-1.00	0.06	40.40	3.15

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
KLNVCSIAKR	NPEAITEVVQLPNHFSNR	STC1_HUMAN			Stanniocalcin-1;	4.68	0.44	47.90	5.06
ELEKRASGQA	FELILSPR	STMN1_HUMAN			Stathmin;	-0.80	0.03	26.70	2.58
FNDSQRQATK	DAGQISGLNVLR	GRP75_HUMAN			Stress-70 protein, mitochondrial;	1.28	0.14	54.70	2.03
YTKAMDVYQK	ALDLDSSCKEAADGYQR	STIP1_HUMAN			Stress-induced-	0.11	0.01	32.80	1.84
AGLTVANEAD	SLTYDIANNKDALR	STRN_HUMAN			Striatin;	-1.96	0.23	33.20	-0.97
FSNNHPGAGG	AKGLGPLAEAAAAGDGAAAAGA	STRN_HUMAN			Striatin;	-3.46	0.00	36.70	-0.34
SQHKGVAVRR	VLNTEANVVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	10.56	0.00	47.50	2.19
KRQKRNKIPY	SFFKTALDDR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	3.08	0.22	29.20	1.27
PLGQWHLSKR	DTGAALLAESR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	2.13	0.16	55.60	2.47
GPLEVRRVGR	SSKQLVDIPEGQLEAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	2.03	0.19	61.40	1.75
ANAAPRSALY	SPSDPLTLLQADTVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.72	0.07	42.10	-2.38
AVPGANAAPR	SALYSPSDPLTLLQADTVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.48	0.21	113.30	4.24
LAVPGANAAP	RSALYSPSDPLTLLQADTVR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.35	0.05	80.90	3.49
VRRVGRSSKQ	LVDIPEGQLEAR	QSOX1_HUMAN			Sulfhydryl oxidase 1;	1.24	0.12	43.10	3.21
GFHVHEFGDN	TAGCTSAGPHFNPLSR	SODC_HUMAN			Superoxide dismutase [Cu-Zn];	1.03	0.05	28.80	-1.81
LLLGALSGWA	ASDDPIEKVIEGINR	SBSN_HUMAN			Suprabasin;	3.69	0.18	34.80	-0.35
SEDVSNKVSM	SSTVQGSNIFER	SDC4_HUMAN			Syndecan-4;	1.50	0.09	47.60	1.99
LFFVGGVAES	IRETEVIDPQDLLEGR	SDC4_HUMAN			Syndecan-4;	1.25	0.07	69.20	3.49
GLSLNEEEIR	ANVAVVSGAPLQGQLVAR	SDCB1_HUMAN			Syntenin-1;	3.53	0.36	41.60	6.74
LVARPSSINY	MVAPVTGNDVGIR	SDCB1_HUMAN			Syntenin-1;	0.50	0.06	53.50	5.43
FARSLLVIPN	TLAVNAAQDSTDLVAKLR	TCPA_HUMAN			T-complex protein 1 subunit alpha;	0.96	0.07	47.30	-1.13
MASLS	LAPVNIFKAGADEER	TCPB_HUMAN			T-complex protein 1	0.00	0.00	33.20	2.94

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
NKLVIEEAER	SIHDALCVIR	TCPD_HUMAN			T-complex protein 1 subunit delta;	0.20	0.01	35.60	1.24
DTEPLIQTAK	TTLGSKVVNSCHR	TCPE_HUMAN			T-complex protein 1 subunit epsilon;	0.79	0.07	33.70	2.55
MTGVEQWPYR	AVAQALEVIPR	TCPG_HUMAN			T-complex protein 1 subunit gamma;	0.87	0.06	52.30	5.16
LVCCSAKNLR	DIDEVSSLLR	TCPQ_HUMAN			T-complex protein 1 subunit theta;	2.42	0.23	48.00	4.68
KAPGFAQMLK	EGAKHFSGLEEAVYR	TCPQ_HUMAN			T-complex protein 1	0.57	0.05	29.60	0.40
VGDTQVVVFK	HEKEDGAISTIVLR	TCPQ_HUMAN			T-complex protein 1 subunit theta;	0.50	0.04	47.90	1.22
TVSRTPCDPD	LPYICTAQNPVSQR	LY9_HUMAN			T-lymphocyte surface	4.69	0.39	26.40	-0.18
TMLEDSVSPK	KSTVLQQQYNR	TLN1_HUMAN			Talin-1;	0.59	0.05	31.20	1.60
IVISAKTMLE	SAGGLIQTAR	TLN1_HUMAN			Talin-1;	0.30	0.02	39.60	0.69
LREAAEGLRM	ATNAAAQNAIKKKLVQR	TLN1_HUMAN			Talin-1;	0.24	0.01	25.50	3.61
VANSTANLVK	TIKALDGAFTEENR	TLN1_HUMAN			Talin-1;	-0.14	0.01	39.50	-5.93
ASGPENFQVG	SMPPAQQQITSGQMHR	TLN1_HUMAN			Talin-1;	-0.62	0.02	43.90	-0.38
LEAVDNLSAF	ASNPEFSSIPAQISPEGR	TLN1_HUMAN			Talin-1;	-1.24	0.12	79.70	6.50
AVAHALHSLL	GCDKSTCTKR	TS1R2_HUMAN			Taste receptor type 1 member 2;	5.85	0.24	14.80	3.01
PSRTAPGALT	AKPPLAPKPGTTVASGVTAR	TB10B_HUMAN			TBC1 domain family member 10B;	-0.07	0.00	27.30	-0.35
QYKDRDGQPQ	VVPVEGSLR	TENX_HUMAN			Tenascin-X;	6.85	0.67	24.10	2.84
VKGCTAMIGC	RLMSGILAVGPMFVR	TX101_HUMAN			Testis-expressed sequence 101 protein;	-1.87	0.14	25.70	-0.06
PAACAGDMAD	AASPCSVVNDLR	THOP1_HUMAN			Thimet oligopeptidase;	-0.88	0.05	60.80	-0.08
M	VGVKPVGSDPDFQPELSGAGSR	TXNL1_HUMAN			Thioredoxin-like protein	0.15	0.01	89.10	2.97
RTIYTTRISL	TTFNIQDGPDFQDR	THIOM_HUMAN			Thioredoxin,	-0.19	0.02	71.50	2.84

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
M	SPTPPLFSLPEAR	THOC1_HUMAN			THO complex subunit 1;	-0.52	0.03	44.70	0.55
RLADFGVLHR	NELSGALTGLTR	SYTC_HUMAN			Threonine--tRNA ligase, cytoplasmic;	1.96	0.11	36.70	7.61
IKALKIHKNS	STYWEGKADMETLQR	SYTC_HUMAN			Threonine--tRNA ligase,	-1.09	0.07	28.70	-2.07
SMVLELRGLR	TIVTTLQDSIR	TSP1_HUMAN			Thrombospondin-1;	1.15	0.10	40.10	5.64
VLFLMHVCGT	NRIPESGGDNSVFDIFELTGAAR	TSP1_HUMAN			Thrombospondin-1;	-0.88	0.08	76.80	2.00
LLLLCFFTSA	SQDLQVIDLLTVGESR	TSP3_HUMAN			Thrombospondin-3;	4.63	0.90	90.60	2.55
GAKGDFPTGK	SSFSITR	TR150_HUMAN			Thyroid hormone receptor-	0.04	0.00	21.00	0.36
RMGATPTPFK	STGDIAGTVVPETNKEPR	ZO2_HUMAN			Tight junction protein ZO-	0.20	0.01	40.60	4.43
GEGGAYTDNE	LDEPAEEPLVSSITR	ZO2_HUMAN			Tight junction protein ZO-2;	-0.34	0.03	51.40	4.20
TRDNANRIIK	TTLQQEKPDFCFLEEDPGICR	TFPI1_HUMAN			Tissue factor pathway inhibitor;	0.98	0.05	67.60	0.53
IHARFRRGAR	SYQVICR	TPA_HUMAN			Tissue-type plasminogen activator;	1.76	0.10	31.10	0.94
ISKKTVRSIQ	EAPVSEDLVIR	TOIP1_HUMAN			Torsin-1A-interacting	1.53	0.17	37.50	1.59
SQTISKKTVR	SIQEAPVSEDLVIR	TOIP1_HUMAN			Torsin-1A-interacting protein 1;	-0.21	0.03	58.20	6.47
LLGLVSAAAA	AWDLASLR	TOR2A_HUMAN	TOR2X_HUMAN		Torsin-2A;	2.69	0.19	29.30	2.81
PSQMDVELVS	GSPVALSPQPR	TOX4_HUMAN			TOX high mobility group box family member 4;	0.06	0.01	45.20	0.62
M	QLTHQLDLFPECR	TPRKB_HUMAN			TP53RK-binding protein;	0.51	0.01	44.40	1.05
LELNQMRAFK	SSATGSVFTGKAVR	PRCM_HUMAN			Trans-L-3-hydroxyproline dehydratase;	1.20	0.09	29.60	1.32
RGGTRGQEPQ	MKETIMNQEKLAKLQAQVR	BTF3_HUMAN			Transcription factor	1.08	0.08	35.40	0.80

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
TLPGGLLAPG	GNSMASGVGVGAGLGAGVNQR	SOX2_HUMAN			Transcription factor SOX-	0.33	0.02	37.20	1.64
FAQDVGRMFK	QFNKLTEDKADVQSIIGLQR	TIF1B_HUMAN			Transcription intermediary factor 1-beta;	0.35	0.01	45.50	2.66
TADSQPPVFK	VFPGSTTEDYNLIVIER	TIF1B_HUMAN			Transcription intermediary factor 1-	-0.37	0.01	55.70	3.22
EGPETKPVLM	ALAEGPGAEGPR	TIF1B_HUMAN			Transcription	-0.43	0.02	37.20	0.52
AASASASAAA	SSPAGGGAEALELLEHCGVCR	TIF1B_HUMAN			Transcription intermediary factor 1-	-0.83	0.03	49.20	3.99
LTADSQPPVF	KVFPGSTTEDYNLIVIER	TIF1B_HUMAN			Transcription	-1.00	0.02	67.80	3.53
PSGSTSSGLE	VVAPEGTSAPGGGPGTLDDSATIC	TIF1B_HUMAN			Transcription	-1.00	0.10	37.50	8.34
EAAIGAPPTA	TEGPETKPVLMALAEGPGAEGPR	TIF1B_HUMAN			Transcription intermediary factor 1-	-1.14	0.03	73.10	2.99
AAASASASAA	ASSPAGGGAEALELLEHCGVCR	TIF1B_HUMAN			Transcription	-1.19	0.11	43.60	0.92
EKRSTAPSAA	ASASASAAASSPAGGGAEALELLE	TIF1B_HUMAN			Transcription intermediary factor 1-beta;	-1.40	0.07	95.90	4.35
KRSTAPSAAA	SASASAAASSPAGGGAEALELLEH	TIF1B_HUMAN			Transcription intermediary factor 1-	-1.46	0.12	75.80	6.31
RSTAPSAAAS	ASASAAASSPAGGGAEALELLEHC	TIF1B_HUMAN			Transcription intermediary factor 1-	-1.80	0.19	40.30	4.90
QHLQSSRHRR	ALDTNYCFSSTEKNCCVR	TGFB1_HUMAN			Transforming growth	1.21	0.11	35.30	3.27
LALGPAATLA	GPAKSPYQLVLQHSR	BGH3_HUMAN			Transforming growth	-0.40	0.01	30.50	2.34
EGKNMACVQR	TLMNLGGLAVAR	TAGL2_HUMAN			Transgelin-2;	3.65	0.41	64.00	2.89
HVGADLAALC	SEAALQAIR	TERA_HUMAN			Transitional endoplasmic reticulum ATPase;	-1.52	0.18	30.60	3.22
YKVGDKIATR	KAYGQALAKLGHASDR	TKT_HUMAN			Transketolase;	2.08	0.11	36.80	1.13
KVGDKIATRK	AYGQALAKLGHASDR	TKT_HUMAN			Transketolase;	0.57	0.05	32.70	4.91
ATRNRTVPFC	STFAAFFTR	TKT_HUMAN			Transketolase;	0.38	0.02	30.60	4.43
IIQEIYSQIQ	SKKKILATPPQEDAPSVDIANIR	TKT_HUMAN			Transketolase;	0.17	0.01	45.40	1.96

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm
KKILATPPQE	DAPSVDIANIR	TKT_HUMAN			Transketolase;	-0.26	0.01	39.70	3.32
YEGGIGEAVS	SAVVGEPGITVTHLAVNR	TKT_HUMAN			Transketolase;	-1.14	0.05	49.90	4.90
TRNRTVPFCS	TFAAFFTR	TKT_HUMAN			Transketolase;	-1.96	0.08	26.60	0.60
YLPSVTPGLK	ASLLDPVPEVR	GCN1L_HUMAN			Translational activator	-0.92	0.05	35.90	2.78
EIVLCGIQLV	NATIGVFCGDCR	T4S5_HUMAN			Transmembrane 4 L6 family member 5;	5.38	0.67	25.40	0.43
FLLGPRLVLA	ISFHLPINSR	TMEDA_HUMAN			Transmembrane emp24 domain-containing protein 10;	1.54	0.16	32.70	1.90
MQGPAGNASR	GLPGGPPSTVASGAGR	TM110_HUMAN			Transmembrane protein	6.34	0.38	27.20	2.98
PSVVKRMPAM	LTGLCQGCGTR	TMEM2_HUMAN			Transmembrane protein 2;	-1.52	0.13	38.70	0.32
QVVFTSDPHK	SYLPVQFQSPDKAETQR	TMEM2_HUMAN			Transmembrane protein 2;	-2.88	0.21	37.80	4.21
EAPAAVTSAQ	VIKPPLIFVDPNR	TCOF_HUMAN			Treacle protein;	0.59	0.02	23.90	1.46
EPVWAIGTGK	TATPQQAQEVHEKLR	TPIS_HUMAN			Triosephosphate isomerase;	1.21	0.08	33.20	3.49
VHEKLRGWLK	SNVSDAVAQSTR	TPIS_HUMAN			Triosephosphate isomerase;	0.94	0.08	59.90	2.22
DVDGFLVGGA	SLKPEFVDIINAK	TPIS_HUMAN			Triosephosphate isomerase;	0.91	0.05	27.10	2.46
YEPVWAIGTG	KTATPQQAQEVHEKLR	TPIS_HUMAN			Triosephosphate isomerase;	-0.24	0.01	37.20	2.44
SPGMIKDCGA	TWVVLGHSER	TPIS_HUMAN			Triosephosphate	-0.69	0.04	38.00	3.44
RPPLGFLNPR	LYQQHGAGLFDVTR	TPP1_HUMAN			Tripeptidyl-peptidase 1;	3.86	0.18	35.80	1.10
EADRKYEEVA	RKLVIIEGDLER	TPM3_HUMAN			Tropomyosin alpha-3 chain;	0.51	0.03	43.70	0.40
FVDPWTVQTS	SAKGIDYDKLIVR	SYWC_HUMAN			Tryptophan--tRNA ligase,	0.79	0.06	27.60	1.85

Table S6

Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change (log$_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
VDEVRAGTYR	QLFHPEQLITGKEDAANNYAR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	2.30	0.08	48.40	1.50
QPDGQMPSDK	TIGGGDDSFNTFFSETGAGKHVPR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.83	0.03	50.10	2.38
GKHVPRAVFV	DLEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.78	0.07	52.50	0.68
VVDEVRAGTY	RQLFHPEQLITGKEDAANNYAR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.66	0.03	38.10	3.52
VDWCPTGFKV	GINYQPPTVVPGGDLAKVQR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.56	0.04	20.00	2.25
FVDWCPTGFK	VGINYQPPTVVPGGDLAKVQR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.42	0.03	43.70	-1.50
GAGKHVPRAV	FVDLEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.28	0.01	43.80	3.59
FEGPLNVDLI	EFQTNLVPYPR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.20	0.01	43.80	2.29
PTGFKVGINY	QPPTVVPGGDLAKVQR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.13	0.01	22.10	1.33
ETGAGKHVPR	AVFVDLEPTVIDEVR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	0.04	0.00	66.90	5.87
DEVRAGTYRQ	LFHPEQLITGKEDAANNYAR	TBA1A_HUMAN	TBA1B_HUMAN	TBA1C_HUMAN	Tubulin alpha-1A chain;	-0.29	0.01	38.90	1.36
LTSRGSQQYR	ALTVPELTQQVFDAKNMMAACDP	TBB5_HUMAN			Tubulin beta chain;	0.53	0.06	41.10	0.36
GDSDLQLDRI	SVYYNEATGGKYVPR	TBB5_HUMAN			Tubulin beta chain;	0.48	0.05	29.80	2.31
QSGAGNNWAK	GHYTEGAELVDSVLDVVR	TBB5_HUMAN	TBB2A_HUMAN	TBB2B_HUMAN	Tubulin beta chain;	0.38	0.03	48.70	1.41
EATGGKYVPR	AILVDLEPGTMDSVR	TBB2A_HUMAN	TBB2B_HUMAN	TBB3_HUMAN	Tubulin beta-2A chain;	1.31	0.08	40.30	0.30
AGNNWAKGHY	TEGAELVDSVLDVVR	TBB4B_HUMAN	TBB2A_HUMAN	TBB2B_HUMAN	Tubulin beta-4B chain;	0.51	0.09	71.90	3.80

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
GDSDLQLERI	NVYYNEATGGKYVPR	TBB4B_HUMAN			Tubulin beta-4B chain;	0.45	0.03	26.50	3.16
SGGRYVPRAV	LVDLEPGTMDSVR	TBB4B_HUMAN	TBB2A_HUMAN	TBB2B_HUMAN	Tubulin beta-4B chain;	0.42	0.04	30.30	-0.21
EASGGRYVPR	AVLVDLEPGTMDSVR	TBB4B_HUMAN	TBB4A_HUMAN	TBB8_HUMAN	Tubulin beta-4B chain;	0.38	0.02	63.90	5.31
LKMASTFIGN	STAIQELFKR	TBB4B_HUMAN	TBB2A_HUMAN	TBB2B_HUMAN	Tubulin beta-4B chain;	0.30	0.02	21.70	0.16
GNNWAKGHYT	EGAELVDSVLDVVR	TBB4B_HUMAN	TBB2A_HUMAN	TBB2B_HUMAN	Tubulin beta-4B chain;	0.28	0.04	55.70	5.40
GRYVPRAVLV	DLEPGTMDSVR	TBB4B_HUMAN	TBB2A_HUMAN	TBB2B_HUMAN	Tubulin beta-4B chain;	0.22	0.02	30.80	5.58
GAGNNWAKGH	YTEGAELVDSVLDVVR	TBB4B_HUMAN	TBB2A_HUMAN	TBB2B_HUMAN	Tubulin beta-4B chain;	-0.37	0.05	48.20	4.11
LTSRGSQQYR	ALTVPELTQQMFDAR	TBB6_HUMAN			Tubulin beta-6 chain;	0.98	0.09	58.30	1.31
RGPERRPAER	SSPGQTPEEGAQALAEFAALHGPA	TTL12_HUMAN			Tubulin--tyrosine ligase-like protein 12;	-0.16	0.01	37.30	8.82
APFFYMPQQV	AYTLLWPLR	TTL12_HUMAN			Tubulin--tyrosine ligase-	-0.19	0.02	33.10	0.00
PGSAASPRLR	EGPELSPDDPAGLLDLR	TNFL9_HUMAN			Tumor necrosis factor	1.51	0.11	72.10	5.16
ASPGSAASPR	LREGPELSPDDPAGLLDLR	TNFL9_HUMAN			Tumor necrosis factor ligand superfamily	0.96	0.06	63.00	4.44
GTAPCSRGSS	WSADLDKCMDCASCR	TNR12_HUMAN			Tumor necrosis factor	-1.09	0.12	29.70	6.05
CDEWGRRARR	GVEVAAGASSGGETR	TR19L_HUMAN			Tumor necrosis factor receptor superfamily member 19L;	1.31	0.07	72.20	4.27
STTTAQPEQK	ASNLIGTYR	TNR21_HUMAN			Tumor necrosis factor receptor superfamily	-0.76	0.04	40.30	1.17
QDISIKRLQR	LLQALEAPEGWGPTPR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily member 6B;	6.03	0.94	84.70	4.25
AALQLKLRRR	LTELLGAQDGALLVR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily	2.35	0.15	89.30	2.32

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**
ALLPVPAVRG	VAETPTYPWR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily member 6B;	1.70	0.02	23.70	1.91
RAALQLKLRR	RLTELLGAQDGALLVR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily	1.33	0.07	42.80	-1.54
ALQLKLRRRL	TELLGAQDGALLVR	TNF6B_HUMAN			Tumor necrosis factor receptor superfamily	1.16	0.14	67.50	0.40
TLSQAGQKTS	AALSTVGSAISR	TPD54_HUMAN			Tumor protein D54;	0.70	0.08	40.20	-0.52
DSAGQDINLN	SPNKGLLSDSMTDVPVDTGVAAR	TPD54_HUMAN			Tumor protein D54;	0.61	0.05	52.80	8.33
PYEAVTPLTK	AADISLDNLVEGKR	TP53B_HUMAN			Tumor suppressor p53-binding protein 1;	1.35	0.11	35.50	3.12
AAAGPSDGLD	ASSPGNSFVGLR	TP53B_HUMAN			Tumor suppressor p53-	-1.24	0.06	42.70	-0.08
QIKINEVQTD	VGVDTKHQTLQGVAFPISR	TWF1_HUMAN			Twinfilin-1;	-1.46	0.04	35.90	-1.51
LQQIRINEVK	TEISVESKHQTLQGLAFPLQPEAQ	TWF2_HUMAN			Twinfilin-2;	-0.55	0.02	45.80	4.90
SVLLPLGLRK	AHSGAQGLLAAQKAR	SYYM_HUMAN			Tyrosine--tRNA ligase, mitochondrial;	0.38	0.04	35.70	3.45
VPLAWCLALC	GWACMAPR	UFO_HUMAN			Tyrosine-protein kinase	8.39	1.12	25.40	1.84
HNAKGVTTSR	TATITVLPQQPR	UFO_HUMAN			Tyrosine-protein kinase receptor UFO;	3.98	0.34	27.10	6.57
ASCAWSGVAG	EEELQVIQPDKSVLVAAGETATLR	SHPS1_HUMAN			Tyrosine-protein phosphatase non-receptor	-1.46	0.08	77.70	7.43
M	VKLTAELIEQAAQYTNAVR	RU2A_HUMAN			U2 small nuclear ribonucleoprotein A';	-0.65	0.01	43.90	5.30

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
VLEQRGRLQK	LVAKEIQAPASADIR	U3IP2_HUMAN			U3 small nucleolar RNA-interacting protein 2;	0.24	0.02	33.20	3.41
TARSLQYEYK	ANSNLVLQADR	U520_HUMAN			U5 small nuclear ribonucleoprotein 200 kDa helicase;	0.46	0.05	55.20	1.38
NKMKGYTLLS	EGIDEMVGIIYKPKTKETR	U520_HUMAN			U5 small nuclear	-0.52	0.03	30.50	2.98
INKMKGYTLL	SEGIDEMVGIIYKPKTKETR	U520_HUMAN			U5 small nuclear ribonucleoprotein 200	-0.52	0.02	48.50	-0.12
VKRQRHELLL	GAGSGPGAGQQQATPGALLQAGP	SNR40_HUMAN			U5 small nuclear	-0.40	0.03	46.90	3.42
GSGPGAGQQQ	ATPGALLQAGPPR	SNR40_HUMAN			U5 small nuclear ribonucleoprotein 40 kDa	-1.29	0.19	55.30	4.60
MADDVDQQQ	TTNTVEEPLDLIR	LSM3_HUMAN			U6 snRNA-associated Sm-like protein LSm3;	-0.88	0.05	44.00	7.81
QDGIAPRMFK	ALIGKGHPEFSTNR	UBP5_HUMAN			Ubiquitin carboxyl-terminal hydrolase 5;	1.10	0.05	28.30	3.15
LFAQTVRVLK	KINKPGNMIMAFSNLAER	UBE4A_HUMAN			Ubiquitin conjugation factor E4 A;	-0.96	0.06	24.80	3.74
SVSESLDEFD	YSVAEISR	UBE4A_HUMAN			Ubiquitin conjugation factor E4 A;	-1.09	0.09	25.60	2.61
YDEAIMAQQD	RIQQEIAVQNPLVSER	OTUB1_HUMAN			Ubiquitin thioesterase	-6.06	0.00	44.00	1.10
TKIFTASNVS	SVPLPAENVTITAGQR	UBP2L_HUMAN			Ubiquitin-associated	1.37	0.09	64.70	3.02
DPKFVERTLR	LAGTQPLEVLEAVQR	UBA1_HUMAN			Ubiquitin-like modifier-activating enzyme 1;	1.84	0.10	79.90	0.97
SVQVPEFTPK	SGVKIHVSDQELQSANASVDDSR	UBA1_HUMAN			Ubiquitin-like modifier-	0.37	0.03	51.10	3.96
GSALLYAAGW	SPEKQAQHLPLR	UBA7_HUMAN			Ubiquitin-like modifier-activating enzyme 7;	6.67	0.82	31.80	-2.46
M	IEVVCNDR	UBL5_HUMAN			Ubiquitin-like protein 5;	0.81	0.07	30.10	0.17
GAPKRRRPAR	SIFDGFR	UBXN7_HUMAN			UBX domain-containing	0.89	0.03	27.30	4.14
APDGNGGLYR	ALAAQNIVEDMEQR	UAP1_HUMAN			UDP-N-acetylhexosamine pyrophosphorylase;	0.85	0.07	72.30	1.48
SGGVNLFAND	GSFLELFKR	CS043_HUMAN			Uncharacterized protein C19orf43;	-1.34	0.10	21.90	0.34
DQSLLLTLRH	LHSVLEELR	CT202_HUMAN			Uncharacterized protein C20orf202;	7.31	0.60	31.00	1.69

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
SNKIAEMMFG	FVLDIPER	CE025_HUMAN			Uncharacterized protein	0.28	0.03	27.00	2.44
QFSAGRWGSA	AAVSAAAAAATR	CI041_HUMAN			UPF0586 protein	-1.65	0.10	47.20	5.35
FSAGRWGSAA	AVSAAAAAATR	CI041_HUMAN			UPF0586 protein C9orf41;	-2.24	0.11	44.20	1.01
EVQFSAGRWG	SAAAVSAAAAAATR	CI041_HUMAN			UPF0586 protein C9orf41;	-2.46	0.27	76.30	0.90
QDLSKAMSQD	GASQFQEVIR	UGPA_HUMAN			UTP--glucose-1-phosphate	-1.29	0.16	47.10	3.51
HGSVQESQVS	EQPATEAAGENPLEFLR	RD23A_HUMAN			UV excision repair	-0.88	0.05	90.10	6.82
AATTTATTTT	TSSGGHPLEFLR	RD23B_HUMAN			UV excision repair protein RAD23 homolog	0.66	0.03	32.90	3.14
ATTTATTTTT	SSGGHPLEFLR	RD23B_HUMAN			UV excision repair	0.13	0.01	33.80	2.27
AVAAAAATTT	ATTTTTSSGGHPLEFLR	RD23B_HUMAN			UV excision repair protein RAD23 homolog B;	-0.21	0.02	45.70	1.05
VAAAAATTTA	TTTTTSSGGHPLEFLR	RD23B_HUMAN			UV excision repair protein RAD23 homolog	-0.26	0.02	34.70	-0.34
LRAMRGIVNG	AAPELPVPTGGPAVGAR	VATB2_HUMAN			V-type proton ATPase	-0.58	0.03	56.20	1.20
SLAAAAAAAA	AEQQVPLVLWSSDR	VAS1_HUMAN			V-type proton ATPase subunit S1;	0.91	0.06	58.60	3.62
LAAAAAAAAA	EQQVPLVLWSSDR	VAS1_HUMAN			V-type proton ATPase subunit S1;	0.60	0.04	58.60	3.97
FLSLAAAAAA	AAAEQQVPLVLWSSDR	VAS1_HUMAN			V-type proton ATPase	0.59	0.03	71.40	4.82
LSLAAAAAAA	AAEQQVPLVLWSSDR	VAS1_HUMAN			V-type proton ATPase subunit S1;	0.28	0.02	58.70	3.70
RPHVKKATPR	MIGLTVGFDKK	VP13A_HUMAN			Vacuolar protein sorting-associated protein 13A;	9.67	1.50	23.40	8.57
M	VLESVVADLLNR	VP13C_HUMAN			Vacuolar protein sorting-	-0.16	0.01	55.00	1.32
VNKKFSVRYF	LNLVLVDEEDR	VP26A_HUMAN			Vacuolar protein sorting-	-6.06	0.00	30.60	4.44
KNSTTLPRMK	SSSSVTTSETQPCTPSSSDYSDLQR	VASP_HUMAN			Vasodilator-stimulated	0.17	0.01	64.30	2.70
PRPGPARRPY	AGGAAQLALDKSDSHPSDALTR	ACADV_HUMAN			Very long-chain specific	0.60	0.04	42.60	-0.09
LRPSTSRSLY	ASSPGGVYATR	VIME_HUMAN			Vimentin;	1.63	0.07	29.60	5.21
LPLVDTHSKR	TLLIKTVETR	VIME_HUMAN			Vimentin;	0.59	0.05	20.60	3.08

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
NLQEAEEWYK	SKFADLSEAANR	VIME_HUMAN			Vimentin;	0.24	0.02	40.90	3.92
FLEQQNKILL	AELEQLKGQGKSR	VIME_HUMAN			Vimentin;	0.13	0.01	24.80	1.76
QEAEEWYKSK	FADLSEAANR	VIME_HUMAN			Vimentin;	0.04	0.00	32.20	0.89
LLQDSVDFSL	ADAINTEFKNTR	VIME_HUMAN			Vimentin;	-0.09	0.01	27.30	-1.66
GVRLLQDSVD	FSLADAINTEFKNTR	VIME_HUMAN			Vimentin;	-0.11	0.01	23.80	-1.22
QAKQESTEYR	RQVQSLTCEVDALKGTNESLER	VIME_HUMAN			Vimentin;	-0.80	0.04	66.30	0.46
EYRRQVQSLT	CEVDALKGTNESLER	VIME_HUMAN			Vimentin;	-0.83	0.09	36.40	4.41
ESTEYRRQVQ	SLTCEVDALKGTNESLER	VIME_HUMAN			Vimentin;	-1.00	0.08	28.70	4.88
DKVRFLEQQN	KILLAELEQLKGQGKSR	VIME_HUMAN			Vimentin;	-1.19	0.05	27.90	5.12
VRLLQDSVDF	SLADAINTEFKNTR	VIME_HUMAN			Vimentin;	-1.59	0.14	34.30	3.52
QEQHVQIDVD	VSKPDLTAALR	VIME_HUMAN			Vimentin;	-1.87	0.07	36.50	1.69
QDSVDFSLAD	AINTEFKNTR	VIME_HUMAN			Vimentin;	-2.05	0.17	22.20	5.51
EQHVQIDVDV	SKPDLTAALR	VIME_HUMAN	DESM_HUMAN		Vimentin;	-2.34	0.12	33.20	4.64
M	KLTDSVLR	WDR82_HUMAN			WD repeat-containing	-0.69	0.07	33.70	3.39
WQQHQGLLPP	GMTIDLFR	SMU1_HUMAN			WD40 repeat-containing	-1.00	0.10	23.90	-1.01
PPPAPQPQAR	SRLNATASLEQER	WFS1_HUMAN			Wolframin;	-0.34	0.04	33.80	1.59
TKIPNPRFQR	LFQCLLHR	XRCC5_HUMAN			X-ray repair cross-complementing protein 5;	4.35	0.33	24.20	1.97
EQGGAHFSVS	SLAEGSVTSVGSVNPAENFR	XRCC5_HUMAN			X-ray repair cross-complementing protein 5;	-0.46	0.04	84.70	6.18
GGAHFSVSSL	AEGSVTSVGSVNPAENFR	XRCC5_HUMAN			X-ray repair cross-complementing protein 5;	-0.80	0.08	63.40	3.23
AHFSVSSLAE	GSVTSVGSVNPAENFR	XRCC5_HUMAN			X-ray repair cross-complementing protein 5;	-1.14	0.10	84.80	2.17
ALAILLLQGL	VVWSFSGLEEDEAGEKGR	XYLT2_HUMAN			Xylosyltransferase 2;	0.66	0.05	24.00	3.56

Table S6

Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
HSSPASLQLG	AVSPGTLTPTGVVSGPAATPTAQHI	YAP1_HUMAN			Yorkie homolog;	0.17	0.01	68.90	5.07
STDFSSSSQE	AFAASAVGSGERR	ZBT22_HUMAN			Zinc finger and BTB	-1.34	0.07	27.50	-0.08
ILKTLRQQTS	SRPPASVGELSSSGLGDPR	ZC3H4_HUMAN			Zinc finger CCCH domain-containing protein	-0.88	0.05	40.50	4.57
TLPAARSSLG	SLQTPEAVTTR	ZCCHV_HUMAN			Zinc finger CCCH-type	0.76	0.05	39.60	3.41
TPSPDQISHR	ASLEDAPVDDLTR	ZCCHV_HUMAN			Zinc finger CCCH-type antiviral protein 1;	0.56	0.06	44.40	5.64
IECGQAFIQK	AHLIVHQR	ZN175_HUMAN			Zinc finger protein 175;	-9.97	0.00	26.20	5.95
RGGPSRRAPR	AAQPPAQPCQLCGR	ZN428_HUMAN			Zinc finger protein 428;	0.56	0.11	41.00	2.27
ISASVAVKQS	SVTQVTEQSPKVQSR	ZN638_HUMAN			Zinc finger protein 638;	1.42	0.10	43.10	3.52
PARSPPLQLS	EAELLNQLQR	ZN646_HUMAN			Zinc finger protein 646;	-0.29	0.03	32.70	5.87
IVKNTVCPEQ	SEALAGGSAGDGAQAAGVTKEGP	ZN687_HUMAN			Zinc finger protein 687;	0.24	0.02	55.30	-0.15
LKKEGLISQD	GSSLEALLR	REQU_HUMAN			Zinc finger protein ubi-d4;	3.71	0.23	40.50	0.82
RNSPDVSYER	SIIKCEKNGNLK	FOG2_HUMAN			Zinc finger protein	1.96	0.14	27.50	7.04
TLAEKSRGLF	SANDWQCKTCSNVNWAR	ZRAB2_HUMAN			Zinc finger Ran-binding domain-containing protein	-0.58	0.06	36.90	3.23
LRHARWFQAR	ASGLQPCVIVIR	ZFR2_HUMAN			Zinc finger RNA-binding	-0.02	0.00	32.60	1.94
VTPASLAALQ	SDVQPVGHDYVEEVR	ZFR_HUMAN			Zinc finger RNA-binding	-0.14	0.01	61.80	2.10
SEPVTPASLA	ALQSDVQPVGHDYVEEVR	ZFR_HUMAN			Zinc finger RNA-binding protein;	-0.21	0.02	46.90	5.01
SLELGLQVMR	MTLSTLNWRR	ZSWM5_HUMAN	ZSWM6_HUMAN		Zinc finger SWIM domain-containing protein	0.42	0.02	19.70	2.82
EGELRHTRKR	EAPHVKNNAIISLR	S39AA_HUMAN			Zinc transporter ZIP10;	2.68	0.16	35.70	1.17
LLEMCVSGDL	VCEVDLGDLSPEGR	ZADH2_HUMAN			Zinc-binding alcohol dehydrogenase domain-containing protein 2;	-6.06	0.00	24.00	-2.15
QVQLHVQSQT	QPVSLANTQPR	ZYX_HUMAN			Zyxin;	0.56	0.04	42.60	6.53
YYKMKGDYHR	YLAEFATGNDR	1433E_HUMAN				3.21	0.21	41.00	9.33

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Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm
SEIQDRCCRK	AALLDQALSNAR	MACF4_HUMAN				2.96	0.13	30.20	0.63
EKKGEKKEKK	QQSIAGSADSKPIDVSR	AIMP1_HUMAN				1.05	0.08	37.90	-0.22

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Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm

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Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**

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Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm

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Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log$_2$)	Fc standard deviation	X! Tandem hyperscore	ppm

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Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change (log_2)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**

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Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change (log_2)	Fc standard deviation	X! Tandem hyperscore	ppm

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Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm

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Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm

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Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**

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Non-prime	**Prime**	**Id 1**	**Id 2**	**Id 3**	**Protein (Id1)**	**Fold-change ($\log_2$)**	**Fc standard deviation**	**X! Tandem hyperscore**	**ppm**

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Non-prime	Prime	Id 1	Id 2	Id 3	Protein (Id1)	Fold-change ($\log_2$)	Fc standard deviation	X! Tandem hyperscore	ppm

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