

2301_LCM_CTRvsMCD

Experiment: 2301_LCM_CTRvsMCD

















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Proteins

Protein building options




















Protein grouping Group similar proteins
























Protein quantitation Absolute Quantitation using Hi-3





























Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
P13645	72 (72)	543.78	0.53	1.85		Keratin_ type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6	15.19	8.19
P02768	53 (53)	479.23	0.03	4.87		Albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2	2.95	0.61
P04264	74 (74)	477.72	0.19	1.14		Keratin_ type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6	20.21	17.66
P08670	56 (56)	477.06	0.50	1.52		Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4	3.55	2.33
P00330	91 (91)	394.51	6.30e-004	3.09		Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH1 PE=1 SV=5	21.67	67.00
P35908	45 (45)	372.42	0.07	1.32		Keratin_ type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2	7.74	10.19
P63261	46 (46)	360.87	0.64	1.12		Actin_ cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1	4.44	4.95
P35579	51 (51)	354.00	0.16	1.15		Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4	0.29	0.33
O43707	36 (36)	295.37	0.44	1.93		Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2	2.10	1.09
P35527	35 (35)	254.07	3.25e-003	2.42		Keratin_ type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3	3.04	7.36
P02545	29 (29)	226.95	3.19e-004	2.55		Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1	1.54	3.93
P11047	29 (29)	192.47	0.02	1.61		Laminin subunit gamma-1 OS=Homo sapiens OX=9606 GN=LAMC1 PE=1 SV=3	1.11	1.79
O00468	23 (23)	173.21	5.71e-004	2.78		Agrin OS=Homo sapiens OX=9606 GN=AGRN PE=1 SV=6	3.42	9.49
P68871	23 (23)	167.29	0.03	1.51		Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2	3.19	4.81
P55268	25 (25)	158.98	0.05	1.36		Laminin subunit beta-2 OS=Homo sapiens OX=9606 GN=LAMB2 PE=1 SV=2	0.40	0.55
P48681	24 (24)	149.14	5.70e-004	2.67		Nestin OS=Homo sapiens OX=9606 GN=NES PE=1 SV=2	0.27	0.10
P13647	22 (22)	148.49	0.90	1.35		Keratin_ type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3	1.41	1.04
P07355	17 (17)	143.55	2.07e-005	2.76		Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2	0.30	0.84
P11142	20 (20)	139.40	4.70e-003	1.39		Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1	0.35	0.26
P02533	16 (16)	130.29	0.68	1.14		Keratin_ type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4	1.32	1.16
P18206	19 (19)	125.27	1.37e-005	2.83		Vinculin OS=Homo sapiens OX=9606 GN=VCL PE=1 SV=4	0.52	1.48
P12883	18 (18)	117.16	5.76e-004	3.02			3.21	9.69



























Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
						Myosin-7 OS=Homo sapiens OX=9606 GN=MYH7 PE=1 SV=5		
P14543	21 (21)	114.53	2.68e-004	8.25		Nidogen-1 OS=Homo sapiens OX=9606 GN=NID1 PE=1 SV=3	0.54	4.49
P08572	18 (18)	112.46	8.94e-005	2.74		Collagen alpha-2(IV) chain OS=Homo sapiens OX=9606 GN=COL4A2 PE=1 SV=4	0.67	1.83
P02538	12 (12)	105.02	3.53e-003	2.18		Keratin_ type II cytoskeletal 6A OS=Homo sapiens OX=9606 GN=KRT6A PE=1 SV=3	1.32	2.87
P00738	16 (16)	103.39	0.04	3.47		Haptoglobin OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1	0.18	0.05
Q96JY6	13 (13)	103.16	0.76	1.07		PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 PE=1 SV=1	0.32	0.30
P33778	13 (13)	102.12	2.52e-004	2.67		Histone H2B type 1-B OS=Homo sapiens OX=9606 GN=H2BC3 PE=1 SV=2	8.96	23.93
P68363	12 (12)	101.83	1.11e-004	1.64		Tubulin alpha-1B chain OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1	0.49	0.81
P26038	16 (16)	99.21	1.49e-004	1.98		Moesin OS=Homo sapiens OX=9606 GN=MSN PE=1 SV=3	0.76	1.50
P01024	17 (17)	98.56	0.44	1.17		Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2	0.46	0.54
P53420	18 (18)	92.91	1.93e-003	1.89		Collagen alpha-4(IV) chain OS=Homo sapiens OX=9606 GN=COL4A4 PE=1 SV=3	0.77	1.46
P69905	17 (17)	91.74	4.72e-004	1.75		Hemoglobin subunit alpha OS=Homo sapiens OX=9606 GN=HBA1 PE=1 SV=2	4.27	7.46
P11021	15 (15)	90.27	0.93	1.09		Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2	0.88	0.80
P02787	12 (12)	79.58	4.41e-005	2.13		Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3	0.14	0.30
P02462	13 (13)	78.69	0.03	1.53		Collagen alpha-1(IV) chain OS=Homo sapiens OX=9606 GN=COL4A1 PE=1 SV=4	0.50	0.33
P15311	13 (13)	74.44	0.90	2.08		Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=4	3.04	1.46
P62805	9 (9)	73.27	0.70	1.05		Histone H4 OS=Homo sapiens OX=9606 GN=H4C1 PE=1 SV=2	1.54	1.47
P01860	11 (11)	70.03	0.01	2.30		Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2	0.60	0.26
P68431	6 (6)	69.54	0.18	1.33		Histone H3.1 OS=Homo sapiens OX=9606 GN=H3C1 PE=1 SV=2	0.53	0.70
Q15599	9 (9)	68.86	0.30	1.44		Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens OX=9606 GN=SLC9A3R2 PE=1 SV=2	0.08	0.06
P0CG47	8 (8)	67.42	8.55e-005	1.90		Polyubiquitin-B OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1	1.22	2.32
P07911	10 (10)	67.19	0.01	7.31		Uromodulin OS=Homo sapiens OX=9606 GN=UMOD PE=1 SV=1	0.41	0.06
P07437	10 (10)	66.31	1.39e-003	1.65		Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2	0.45	0.27
Q02413	10 (10)	64.26	0.09	6.84		Desmoglein-1 OS=Homo sapiens OX=9606 GN=DSG1 PE=1 SV=2	0.27	0.04
P67936	9 (9)	62.57	0.24	1.62		Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=3	0.75	0.46
P06396	10 (10)	61.80	1.85e-003	4.18		Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1	0.37	0.09
P08779	10 (10)	60.94	0.15	1.51		Keratin_ type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4	0.21	0.32
Q01955	12 (12)	59.01	0.28	1.22		Collagen alpha-3(IV) chain OS=Homo sapiens OX=9606 GN=COL4A3 PE=1 SV=3	0.88	0.72
P32119	8 (8)	57.47	5.53e-003	1.95		Peroxisiredoxin-2 OS=Homo sapiens OX=9606 GN=PRDX2 PE=1 SV=5	0.57	0.29
P0DMV8	7 (7)	56.30	1.07e-006	1.80		Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1	0.27	0.15
























Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
P01876	6 (6)	55.01	0.05	3.77		Immunoglobulin heavy constant alpha 1 OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=2	0.39	0.10
P02679	8 (8)	54.79	0.03	1.53		Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=3	0.18	0.12
P04406	7 (7)	54.62	0.14	1.32		Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3	0.70	0.53
P00761	14 (14)	53.64	2.95e-003	2.16		Trypsin OS=Sus scrofa OX=9823 PE=1 SV=1	13.26	28.70
P07195	8 (8)	53.25	0.40	1.23		L-lactate dehydrogenase B chain OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=2	0.29	0.24
P08238	8 (8)	52.77	7.27e-003	1.63		Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4	0.22	0.14
P00558	10 (10)	52.47	2.40e-005	5.13		Phosphoglycerate kinase 1 OS=Homo sapiens OX=9606 GN=PGK1 PE=1 SV=3	4.66	23.89
P02675	8 (8)	52.36	0.86	1.03		Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2	0.18	0.17
P50895	8 (8)	52.33	5.27e-003	3.62		Basal cell adhesion molecule OS=Homo sapiens OX=9606 GN=BCAM PE=1 SV=2	0.10	0.03
P04083	7 (7)	52.15	0.74	1.04		Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2	0.12	0.12
P12036	10 (10)	50.14	0.19	1.00		Neurofilament heavy polypeptide OS=Homo sapiens OX=9606 GN=NEFH PE=1 SV=4	3.50	3.50
P61981	7 (7)	49.90	1.07e-004	2.80		14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2	0.45	0.16
Q5TZA2	10 (10)	49.77	0.13	1.81		Rootletin OS=Homo sapiens OX=9606 GN=CROCC PE=1 SV=1	0.71	0.39
Q06830	6 (6)	49.59	1.67e-003	2.24		Peroxisomal protein 1 OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1	0.24	0.11
Q05682	8 (8)	49.06	0.36	1.20		Caldesmon OS=Homo sapiens OX=9606 GN=CALD1 PE=1 SV=3	0.11	0.09
Q03252	9 (9)	47.61	9.47e-003	1.42		Lamin-B2 OS=Homo sapiens OX=9606 GN=LMNB2 PE=1 SV=4	0.18	0.13
P02671	8 (8)	47.30	0.92	1.03		Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA PE=1 SV=2	0.18	0.18
P04004	8 (8)	47.00	0.01	2.01		Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1	0.79	1.60
P08758	7 (7)	46.24	5.85e-004	1.77		Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=2	0.33	0.58
P14618	8 (8)	46.11	8.60e-005	2.23		Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4	0.49	1.08
P09467	9 (9)	45.83	1.80e-004	3.07		Fructose-1,6-bisphosphatase 1 OS=Homo sapiens OX=9606 GN=FBP1 PE=1 SV=5	1.29	3.95
Q07157	9 (9)	45.36	5.63e-004	3.21		Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=3	0.15	0.05
Q14745	7 (7)	45.19	0.28	1.39		Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens OX=9606 GN=SLC9A3R1 PE=1 SV=4	0.46	0.33
P25705	7 (7)	44.43	0.38	1.45		ATP synthase subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1	0.18	0.13
P04792	6 (6)	42.82	0.03	1.82		Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2	0.37	0.20
Q5T749	7 (7)	42.72	0.09	1.56		Keratinocyte proline-rich protein OS=Homo sapiens OX=9606 GN=KPRP PE=1 SV=1	0.56	0.87
Q8N3V7	8 (8)	41.05	0.06	1.94		Synaptopodin OS=Homo sapiens OX=9606 GN=SYNPO PE=1 SV=2	0.10	0.05
P19012	7 (7)	40.32	0.04	2.88		Keratin type I cytoskeletal 15 OS=Homo sapiens OX=9606 GN=KRT15 PE=1 SV=3	0.16	0.06
























Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
P35749	8 (8)	39.99	1.31e-003	2.61		Myosin-11 OS=Homo sapiens OX=9606 GN=MYH11 PE=1 SV=3	0.32	0.12
P02042	5 (5)	39.04	4.88e-007	2.75		Hemoglobin subunit delta OS=Homo sapiens OX=9606 GN=HBD PE=1 SV=2	2.01	5.54
P08473	7 (7)	38.63	4.65e-004	1.54		Neprilysin OS=Homo sapiens OX=9606 GN=MME PE=1 SV=2	0.22	0.34
Q9NZN3	7 (7)	38.59	6.41e-006	3.72		EH domain-containing protein 3 OS=Homo sapiens OX=9606 GN=EHD3 PE=1 SV=2	0.65	2.41
P60660	6 (6)	38.41	1.11e-005	1.88		Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=2	0.37	0.69
Q93088	6 (6)	38.30	1.36e-003	2.25		Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens OX=9606 GN=BHMT PE=1 SV=2	1.11	2.50
Q03154	7 (7)	37.97	0.08	3.88		Aminoacylase-1 OS=Homo sapiens OX=9606 GN=ACY1 PE=1 SV=1	0.34	0.09
P62937	5 (5)	36.84	1.21e-003	4.17		Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=2	0.23	0.05
P05556	6 (6)	36.80	0.15	1.49		Integrin beta-1 OS=Homo sapiens OX=9606 GN=ITGB1 PE=1 SV=2	0.31	0.20
P30086	6 (6)	36.41	0.08	1.36		Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PEBP1 PE=1 SV=3	0.40	0.55
P10909	7 (7)	36.35	0.01	1.24		Clusterin OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1	0.15	0.12
P59665	4 (4)	35.90	5.02e-006	3.98		Neutrophil defensin 1 OS=Homo sapiens OX=9606 GN=DEFA1 PE=1 SV=1	0.39	0.10
Q6S8J3	9 (9)	35.86	0.32	1.03		POTE ankyrin domain family member E OS=Homo sapiens OX=9606 GN=POTEE PE=2 SV=3	1.40	1.44
Q14847	6 (6)	35.54	0.26	1.40		LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1 PE=1 SV=2	0.18	0.13
B9A064	5 (5)	35.39	0.02	3.77		Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2	0.30	0.08
P02649	6 (6)	35.35	2.99e-003	2.04		Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1	0.21	0.10
P12109	6 (6)	35.16	0.27	1.42		Collagen alpha-1(VI) chain OS=Homo sapiens OX=9606 GN=COL6A1 PE=1 SV=3	0.09	0.07
P60174	5 (5)	34.53	6.25e-003	3.16		Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=4	0.17	0.05
P0C0L4	6 (6)	34.43	0.01	2.36		Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=2	0.08	0.03
P37802	6 (6)	34.36	0.13	1.32		Transgelin-2 OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=3	0.28	0.21
P19440	5 (5)	33.95	0.31	1.21		Glutathione hydrolase 1 proenzyme OS=Homo sapiens OX=9606 GN=GGT1 PE=1 SV=2	0.36	0.44
P63104	4 (4)	33.48	8.99e-005	3.39		14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1	0.14	0.04
Q16555	6 (6)	33.05	6.92e-003	2.95		Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=DPYSL2 PE=1 SV=1	0.07	0.02
P06576	6 (6)	32.91	0.13	1.27		ATP synthase subunit beta_mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=3	0.23	0.29
P81605	3 (3)	32.30	0.52	2.07		Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2	1.19	0.58
Q14950	5 (5)	32.28	8.41e-003	1.94		Myosin regulatory light chain 12B OS=Homo sapiens OX=9606 GN=MYL12B PE=1 SV=2	0.12	0.06
P14625	5 (5)	31.66	0.39	1.11		Endoplasmic reticulum protein OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1	0.11	0.10
Q75083	6 (6)	31.38	1.07e-003	4.45			0.05	0.01



























Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
						WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=WDR1 PE=1 SV=4		
P68133	4 (4)	31.12	0.66	2.47		Actin_ alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1	2.02	0.82
P01871	5 (5)	30.72	2.13e-003	8.08		Immunoglobulin heavy constant mu OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=4	0.07	8.51e-003
P10412	4 (4)	30.69	9.52e-004	2.74		Histone H1.4 OS=Homo sapiens OX=9606 GN=H1-4 PE=1 SV=2	7.08	19.42
P08729	6 (6)	30.35	0.92	1.06		Keratin_ type II cytoskeletal 7 OS=Homo sapiens OX=9606 GN=KRT7 PE=1 SV=5	0.46	0.44
Q6UXI9	5 (5)	30.17	7.49e-003	2.06		Nephronectin OS=Homo sapiens OX=9606 GN=NPNT PE=2 SV=3	0.10	0.05
P09210	5 (5)	30.15	1.13e-005	1.84		Glutathione S-transferase A2 OS=Homo sapiens OX=9606 GN=GSTA2 PE=1 SV=4	0.37	0.20
P39060	5 (5)	29.76	2.45e-003	1.90		Collagen alpha-1(XVIII) chain OS=Homo sapiens OX=9606 GN=COL18A1 PE=1 SV=5	0.14	0.07
P06733	5 (5)	29.55	0.05	2.40		Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2	0.30	0.13
Q86Y46	8 (8)	29.33	0.02	1.72		Keratin_ type II cytoskeletal 73 OS=Homo sapiens OX=9606 GN=KRT73 PE=1 SV=1	1.62	2.79
P01009	5 (5)	29.17	0.02	2.77		Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3	0.07	0.03
P00915	5 (5)	29.08	1.85e-005	2.85		Carbonic anhydrase 1 OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=2	0.45	1.29
P22626	4 (4)	28.61	0.28	1.21		Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1 PE=1 SV=2	0.15	0.12
P01857	4 (4)	28.60	9.26e-003	2.99		Immunoglobulin heavy constant gamma 1 OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1	0.15	0.05
P01834	3 (3)	28.42	1.92e-003	8.91		Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2	0.26	0.03
P30101	5 (5)	28.34	1.25e-004	1.85		Protein disulfide-isomerase A3 OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=4	0.11	0.06
P59998	4 (4)	28.31	0.02	2.08		Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens OX=9606 GN=ARPC4 PE=1 SV=3	0.07	0.03
P06702	3 (3)	28.05	0.04	7.83		Protein S100-A9 OS=Homo sapiens OX=9606 GN=S100A9 PE=1 SV=1	0.36	0.05
Q99798	6 (6)	27.77	0.19	1.65		Aconitate hydratase_ mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=2	0.05	0.03
P35580	6 (6)	27.70	2.93e-004	2.56		Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3	0.18	0.07
P05062	4 (4)	27.64	0.08	3.96		Fructose-bisphosphate aldolase B OS=Homo sapiens OX=9606 GN=ALDOB PE=1 SV=2	0.26	0.07
O00592	4 (4)	27.56	5.79e-003	2.79		Podocalyxin OS=Homo sapiens OX=9606 GN=PODXL PE=1 SV=2	0.21	0.07
P01833	4 (4)	25.93	0.04	2.84		Polymeric immunoglobulin receptor OS=Homo sapiens OX=9606 GN=PIGR PE=1 SV=4	0.47	0.17
P68104	5 (5)	25.89	2.70e-003	1.84		Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1	0.66	1.21
Q04695	10 (10)	25.77	0.76	1.90		Keratin_ type I cytoskeletal 17 OS=Homo sapiens OX=9606 GN=KRT17 PE=1 SV=2	4.55	2.39
P00918	5 (5)	25.59	4.45e-005	2.96		Carbonic anhydrase 2 OS=Homo sapiens OX=9606 GN=CA2 PE=1 SV=2	1.42	4.21
P05787	5 (5)	24.94	0.70	1.19		Keratin_ type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=7	1.22	1.02





























Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
P55290	5 (5)	24.69	2.99e-003	4.15		Cadherin-13 OS=Homo sapiens OX=9606 GN=CDH13 PE=1 SV=1	0.06	0.02
P0DP25	5 (5)	24.13	0.01	2.20		Calmodulin-3 OS=Homo sapiens OX=9606 GN=CALM3 PE=1 SV=1	0.17	0.08
Q7Z406	4 (4)	24.08	0.05	2.38		Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=2	0.13	0.05
P09382	4 (4)	23.67	0.03	2.18		Galectin-1 OS=Homo sapiens OX=9606 GN=LGALS1 PE=1 SV=2	0.08	0.04
P00338	4 (4)	23.64	0.10	3.62		L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=2	1.20	0.33
P01591	3 (3)	23.31	0.06	9.51		Immunoglobulin J chain OS=Homo sapiens OX=9606 GN=JCHAIN PE=1 SV=4	0.23	0.02
P04075	4 (4)	22.64	0.11	1.41		Fructose-bisphosphate aldolase A OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=2	0.13	0.09
P05783	4 (4)	22.40	0.16	1.49		Keratin_ type I cytoskeletal 18 OS=Homo sapiens OX=9606 GN=KRT18 PE=1 SV=2	0.21	0.31
Q01995	4 (4)	22.33	0.03	2.61		Transgelin OS=Homo sapiens OX=9606 GN=TAGLN PE=1 SV=4	0.07	0.03
P06703	3 (3)	22.03	2.55e-004	2.18		Protein S100-A6 OS=Homo sapiens OX=9606 GN=S100A6 PE=1 SV=1	0.46	0.21
P29400	5 (5)	21.75	0.56	1.70		Collagen alpha-5(IV) chain OS=Homo sapiens OX=9606 GN=COL4A5 PE=1 SV=2	0.94	0.55
Q15365	4 (4)	21.62	3.22e-004	2.11		Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2	0.09	0.04
Q00159	4 (4)	21.56	2.51e-004	2.75		Unconventional myosin-Ic OS=Homo sapiens OX=9606 GN=MYO1C PE=1 SV=4	0.04	0.10
Q12931	3 (3)	21.54	7.71e-005	2.97		Heat shock protein 75 kDa_ mitochondrial OS=Homo sapiens OX=9606 GN=TRAP1 PE=1 SV=3	0.78	2.31
P23526	4 (4)	21.15	0.01	1.57		Adenosylhomocysteinase OS=Homo sapiens OX=9606 GN=AHCY PE=1 SV=4	0.09	0.14
Q76013	4 (4)	20.46	0.01	1.68		Keratin_ type I cuticular Ha6 OS=Homo sapiens OX=9606 GN=KRT36 PE=1 SV=1	0.18	0.11
Q3LXA3	5 (5)	20.35	1.06e-004	2.77		Triokinase/FMN cyclase OS=Homo sapiens OX=9606 GN=TKFC PE=1 SV=2	0.20	0.55
P26006	3 (3)	20.12	2.25e-004	3.22		Integrin alpha-3 OS=Homo sapiens OX=9606 GN=ITGA3 PE=1 SV=5	0.09	0.03
P02743	3 (3)	19.87	1.06e-003	2.24		Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2	0.12	0.05
P23396	3 (3)	19.71	3.98e-003	2.70		40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=2	0.05	0.02
Q9NP85	3 (3)	19.48	9.06e-003	9.32		Podocin OS=Homo sapiens OX=9606 GN=NPHS2 PE=1 SV=1	0.03	3.07e-003
P68371	3 (3)	19.33	2.64e-003	2.46		Tubulin beta-4B chain OS=Homo sapiens OX=9606 GN=TUBB4B PE=1 SV=1	0.28	0.12
Q96KP4	3 (3)	19.26	0.18	1.82		Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=2	0.12	0.07
Q9HC38	4 (4)	19.05	0.55	2.26		Glyoxalase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GLOD4 PE=1 SV=1	2.23	0.99
P17661	4 (4)	18.74	4.48e-004	2.31		Desmin OS=Homo sapiens OX=9606 GN=DES PE=1 SV=3	1.41	3.26
Q08554	3 (3)	18.71	0.12	3.94		Desmocollin-1 OS=Homo sapiens OX=9606 GN=DSC1 PE=1 SV=2	0.34	0.09
P12110	4 (4)	18.49	0.02	2.73		Collagen alpha-2(VI) chain OS=Homo sapiens OX=9606 GN=COL6A2 PE=1 SV=4	0.15	0.05
P00966	3 (3)	18.24	0.02	3.13		Argininosuccinate synthase OS=Homo sapiens OX=9606 GN=ASS1 PE=1 SV=2	0.16	0.05
P30041	3 (3)	18.23	0.02	2.01		Peroxisomal oxidoreductase OS=Homo sapiens OX=9606 GN=PRDX6 PE=1 SV=3	0.03	0.02
P09493	3 (3)	18.19	0.04	2.28		Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=2	0.07	0.03















Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
P07900	3 (3)	17.95	0.01	2.27		Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5	0.07	0.03
Q13885	2 (2)	17.38	4.65e-005	4.70		Tubulin beta-2A chain OS=Homo sapiens OX=9606 GN=TUBB2A PE=1 SV=1	0.08	0.02
P05023	3 (3)	17.36	3.36e-004	3.73		Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 PE=1 SV=1	0.05	0.01
P01040	3 (3)	17.17	0.22	2.42		Cystatin-A OS=Homo sapiens OX=9606 GN=CSTA PE=1 SV=1	0.18	0.07
P14550	3 (3)	17.00	0.10	1.52		Aldo-keto reductase family 1 member A1 OS=Homo sapiens OX=9606 GN=AKR1A1 PE=1 SV=3	0.10	0.16
P07737	3 (3)	16.73	0.02	3.53		Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2	0.03	7.72e-003
P17066	3 (3)	16.54	0.02	1.99		Heat shock 70 kDa protein 6 OS=Homo sapiens OX=9606 GN=HSPA6 PE=1 SV=2	0.09	0.05
Q9BR76	3 (3)	16.01	0.31	1.32		Coronin-1B OS=Homo sapiens OX=9606 GN=CORO1B PE=1 SV=1	0.06	0.04
P01011	3 (3)	15.90	1.66e-005	2.30		Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2	0.24	0.56
Q08380	3 (3)	15.73	0.03	2.76		Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1	0.09	0.03
Q5D862	3 (3)	15.40	0.10	3.58		Filaggrin-2 OS=Homo sapiens OX=9606 GN=FLG2 PE=1 SV=1	0.36	0.10
Q9NSB2	3 (3)	15.28	0.96	2.11		Keratin_type II cuticular Hb4 OS=Homo sapiens OX=9606 GN=KRT84 PE=2 SV=2	2.67	1.27
Q9BSE5	3 (3)	15.17	0.10	1.92		Agmatinase_mitochondrial OS=Homo sapiens OX=9606 GN=AGMAT PE=1 SV=2	0.36	0.19
P52566	3 (3)	15.12	0.04	2.18		Rho GDP-dissociation inhibitor 2 OS=Homo sapiens OX=9606 GN=ARHGDIB PE=1 SV=3	0.11	0.05
Q43809	2 (2)	15.03	5.20e-004	3.03		Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens OX=9606 GN=NUDT21 PE=1 SV=1	4.67	14.17
P04040	3 (3)	14.95	7.50e-003	2.17		Catalase OS=Homo sapiens OX=9606 GN=CAT PE=1 SV=3	0.15	0.07
P01859	3 (3)	14.94	1.03e-003	5.70		Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2	0.17	0.03
Q13642	3 (3)	14.77	0.14	2.79		Four and a half LIM domains protein 1 OS=Homo sapiens OX=9606 GN=FHL1 PE=1 SV=4	0.02	6.61e-003
P50395	2 (2)	14.64	2.53e-004	4.56		Rab GDP dissociation inhibitor beta OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=2	0.13	0.03
P06727	3 (3)	14.56	2.54e-005	4.77		Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=4	1.68	8.03
Q14240	3 (3)	14.42	2.75e-006	1.85		Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=2	0.09	0.05
P55060	2 (2)	14.24	0.21	1.64		Exportin-2 OS=Homo sapiens OX=9606 GN=CSE1L PE=1 SV=3	0.19	0.11
P22061	2 (2)	14.11	0.07	3.00		Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=4	4.25	12.73
P20700	3 (3)	13.75	0.03	1.58		Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2	0.12	0.19
P04899	2 (2)	13.45	8.93e-003	2.24		Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAI2 PE=1 SV=3	0.06	0.03
P52943	2 (2)	13.22	0.31	1.76		Cysteine-rich protein 2 OS=Homo sapiens OX=9606 GN=CRIP2 PE=1 SV=1	0.03	0.02
P04439	2 (2)	13.21	6.32e-003	2.64			0.06	0.02






Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
						HLA class I histocompatibility antigen_A alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2		
Q7Z794	3 (3)	13.10	5.55e-006	6.22		Keratin_type II cytoskeletal 1b OS=Homo sapiens OX=9606 GN=KRT77 PE=1 SV=3	2.20	13.69
Q9BW30	2 (2)	12.91	0.08	2.46		Tubulin polymerization-promoting protein family member 3 OS=Homo sapiens OX=9606 GN=TPPP3 PE=1 SV=1	0.04	0.02
P61626	2 (2)	12.54	0.03	1.72		Lysozyme C OS=Homo sapiens OX=9606 GN=LYZ PE=1 SV=1	0.24	0.14
P21291	2 (2)	12.41	0.03	19.10		Cysteine and glycine-rich protein 1 OS=Homo sapiens OX=9606 GN=CSRP1 PE=1 SV=3	0.02	8.04e-004
P61224	2 (2)	12.40	2.21e-005	3.25		Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1	0.43	1.41
P05109	2 (2)	12.06	0.04	3.45		Protein S100-A8 OS=Homo sapiens OX=9606 GN=S100A8 PE=1 SV=1	0.20	0.06
P31946	2 (2)	11.91	4.16e-003	5.97		14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=3	0.04	6.06e-003
P02760	2 (2)	11.68	0.01	2.20		Protein AMBP OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1	0.18	0.08
P13646	2 (2)	11.67	0.60	1.61		Keratin_type I cytoskeletal 13 OS=Homo sapiens OX=9606 GN=KRT13 PE=1 SV=4	6.60	4.11
Q9UN36	2 (2)	11.65	0.01	57.51		Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 PE=1 SV=2	0.02	3.71e-004
P05089	2 (2)	11.62	0.04	10.11		Arginase-1 OS=Homo sapiens OX=9606 GN=ARG1 PE=1 SV=2	0.17	0.02
P00403	2 (2)	11.44	0.20	1.45		Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1	0.20	0.14
Q562R1	2 (2)	11.43	6.57e-005	2.05		Beta-actin-like protein 2 OS=Homo sapiens OX=9606 GN=ACTBL2 PE=1 SV=2	0.47	0.23
P06753	2 (2)	11.28	5.09e-004	1.87		Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=2	0.07	0.04
P42765	2 (2)	11.19	0.74	1.25		3-ketoacyl-CoA thiolase_mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1 SV=2	0.07	0.09
Q9NZT1	2 (2)	11.13	0.23	1.55		Calmodulin-like protein 5 OS=Homo sapiens OX=9606 GN=CALML5 PE=1 SV=2	0.47	0.30
P52758	2 (2)	11.09	1.73e-004	2.63		2-iminobutanoate/2-iminopropanoate deaminase OS=Homo sapiens OX=9606 GN=RIDA PE=1 SV=1	1.13	2.99
Q13228	2 (2)	11.08	6.28e-003	3.80		Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=2	0.12	0.03
P61978	2 (2)	11.00	0.08	1.96		Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1	0.03	0.01
P13797	3 (3)	10.86	0.07	2.15		Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4	0.15	0.07
P54652	2 (2)	10.80	0.16	2.39		Heat shock-related 70 kDa protein 2 OS=Homo sapiens OX=9606 GN=HSPA2 PE=1 SV=1	0.04	0.01
P37837	2 (2)	10.77	0.28	1.35		Transaldolase OS=Homo sapiens OX=9606 GN=TALDO1 PE=1 SV=2	0.06	0.05
P09496	2 (2)	10.73	0.05	5.56		Clathrin light chain A OS=Homo sapiens OX=9606 GN=CLTA PE=1 SV=1	0.42	0.08
Q7Z4W1	2 (2)	10.72	0.05	2.03		L-xylulose reductase OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=2	0.16	0.08
P30038	2 (2)	10.70	0.33	1.94		Delta-1-pyrroline-5-carboxylate dehydrogenase_mitochondrial OS=Homo sapiens OX=9606 GN=ALDH4A1 PE=1 SV=3	0.04	0.02
Q9UBI6	2 (2)	10.69	3.36e-003	3.80		Guanine nucleotide-binding protein G (I)/G(S)/G(O) subunit gamma-12	0.09	0.02

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
						OS=Homo sapiens OX=9606 GN=GNG12 PE=1 SV=3		
P10809	2 (2)	10.69	0.55	1.19		60 kDa heat shock protein_ mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=2	0.16	0.19
P14923	2 (2)	10.67	0.05	3.27		Junction plakoglobin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3	0.23	0.07
P38646	2 (2)	10.50	1.52e-006	3.28		Stress-70 protein_ mitochondrial OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=2	0.20	0.67
P12277	2 (2)	10.39	3.81e-004	2.83		Creatine kinase B-type OS=Homo sapiens OX=9606 GN=CKB PE=1 SV=1	0.05	0.02
P23246	2 (2)	10.28	0.05	2.60		Splicing factor_ proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2	0.02	7.72e-003
P61313	2 (2)	10.23	7.35e-004	1.84		60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=2	0.10	0.05
P62424	2 (2)	10.12	0.09	1.75		60S ribosomal protein L7a OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=2	0.09	0.05
Q15366	2 (2)	9.98	0.02	2.17		Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1	0.29	0.13
P50995	2 (2)	9.84	0.01	1.90		Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 PE=1 SV=1	0.03	0.02
Q14195	2 (2)	9.60	0.03	1.97		Dihydropyrimidinase-related protein 3 OS=Homo sapiens OX=9606 GN=DPYSL3 PE=1 SV=1	0.05	0.02
P07196	2 (2)	9.46	0.03	1.94		Neurofilament light polypeptide OS=Homo sapiens OX=9606 GN=NEFL PE=1 SV=3	0.05	0.03
O95571	2 (2)	9.45	0.12	1.97		Persulfide dioxygenase ETHE1_ mitochondrial OS=Homo sapiens OX=9606 GN=ETHE1 PE=1 SV=2	0.01	5.73e-003
P09211	2 (2)	9.32	0.01	4.63		Glutathione S-transferase P OS=Homo sapiens OX=9606 GN=GSTP1 PE=1 SV=2	0.04	7.67e-003
Q96AC1	2 (2)	8.82	0.84	1.17		Fermitin family homolog 2 OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1	0.01	9.77e-003
P16104	3 (3)	8.52	0.52	1.11		Histone H2AX OS=Homo sapiens OX=9606 GN=H2AX PE=1 SV=2	0.54	0.60
Q99456	2 (2)	8.33	8.20e-005	3.05		Keratin_ type I cytoskeletal 12 OS=Homo sapiens OX=9606 GN=KRT12 PE=1 SV=1	0.78	2.39
Q2TBA0	1 (1)	7.77	2.20e-006	5.92		Kelch-like protein 40 OS=Homo sapiens OX=9606 GN=KLHL40 PE=1 SV=2	0.99	5.83
P08590	1 (1)	7.69	0.31	13.85		Myosin light chain 3 OS=Homo sapiens OX=9606 GN=MYL3 PE=1 SV=3	0.01	0.16
P16520	1 (1)	7.30	2.00e-003	2.67		Guanine nucleotide-binding protein G (I)/G(S)/G(T) subunit beta-3 OS=Homo sapiens OX=9606 GN=GNB3 PE=1 SV=1	0.11	0.04
A0A0A0MRZ8	1 (1)	7.25	5.30e-003	4.92		Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6	0.15	0.03
A0A0B4J1V1	1 (1)	7.23	5.80e-004	4.36		Immunoglobulin heavy variable 3-21 OS=Homo sapiens OX=9606 GN=IGHV3-21 PE=1 SV=1	0.09	0.02
P48741	1 (1)	7.21	1.42e-004	3.57		Putative heat shock 70 kDa protein 7 OS=Homo sapiens OX=9606 GN=HSPA7 PE=5 SV=2	3.15	11.26
P52565	1 (1)	7.17	1.33e-003	4.16		Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDI1A PE=1 SV=3	0.09	0.02
Q14103	1 (1)	7.15	0.35	1.36		Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=1	0.11	0.08
P16444	1 (1)	6.75	0.01	5.39		Dipeptidase 1 OS=Homo sapiens OX=9606 GN=DPEP1 PE=1 SV=3	0.12	0.02
P51153	1 (1)	6.75	0.42	1.14		Ras-related protein Rab-13 OS=Homo sapiens OX=9606 GN=RAB13 PE=1 SV=1	0.05	0.04

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
P27348	1 (1)	6.61	3.34e-003	29.31		14-3-3 protein theta OS=Homo sapiens OX=9606 GN=YWHAQ PE=1 SV=1	0.02	5.27e-004
Q9BVC6	1 (1)	6.58	0.24	1.35		Transmembrane protein 109 OS=Homo sapiens OX=9606 GN=TMEM109 PE=1 SV=1	0.08	0.06
P01619	1 (1)	6.58	5.36e-003	3.26		Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2	0.07	0.02
Q9BVQ7	1 (1)	6.56	0.83	1.04		Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens OX=9606 GN=SPATA5L1 PE=1 SV=2	0.08	0.08
Q9NVA2	1 (1)	6.54	0.02	3.24		Septin-11 OS=Homo sapiens OX=9606 GN=SEPTIN11 PE=1 SV=3	0.11	0.03
Q15517	1 (1)	6.54	0.17	1.98		Corneodesmosin OS=Homo sapiens OX=9606 GN=CDSN PE=1 SV=3	0.35	0.18
P01889	1 (1)	6.51	2.00e-003	6.23		HLA class I histocompatibility antigen_ B alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=3	0.07	0.01
P31944	1 (1)	6.45	0.05	2.26		Caspase-14 OS=Homo sapiens OX=9606 GN=CASP14 PE=1 SV=2	0.44	0.20
Q86UL8	1 (1)	6.37	6.81e-003	4.65		Membrane-associated guanylate kinase_ WW and PDZ domain-containing protein 2 OS=Homo sapiens OX=9606 GN=MAGI2 PE=1 SV=3	0.05	0.01
Q02252	1 (1)	6.32	0.84	1.16		Methylmalonate-semialdehyde dehydrogenase [acylating]_ mitochondrial OS=Homo sapiens OX=9606 GN=ALDH6A1 PE=1 SV=2	0.08	0.07
P52209	1 (1)	6.22	0.02	4.53		6-phosphogluconate dehydrogenase_ decarboxylating OS=Homo sapiens OX=9606 GN=PGD PE=1 SV=3	0.03	6.80e-003
P47755	1 (1)	6.18	0.90	1.02		F-actin-capping protein subunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 PE=1 SV=3	0.10	0.10
P01877	1 (1)	6.13	0.03	3.55		Immunoglobulin heavy constant alpha 2 OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=4	0.04	9.85e-003
P02748	1 (1)	6.11	8.34e-003	2.71		Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=2	0.05	0.02
P18124	1 (1)	6.10	0.03	2.06		60S ribosomal protein L7 OS=Homo sapiens OX=9606 GN=RPL7 PE=1 SV=1	0.06	0.03
Q969L2	1 (1)	6.07	0.05	2.78		Protein MAL2 OS=Homo sapiens OX=9606 GN=MAL2 PE=1 SV=1	0.07	0.03
Q9BVM4	1 (1)	6.06	0.06	4.09		Gamma-glutamylaminocyclotransferase OS=Homo sapiens OX=9606 GN=GGACT PE=1 SV=2	0.04	0.01
Q00796	1 (1)	6.05	0.18	2.50		Sorbitol dehydrogenase OS=Homo sapiens OX=9606 GN=SORD PE=1 SV=4	0.06	0.02
P14649	1 (1)	6.03	0.93	1.02		Myosin light chain 6B OS=Homo sapiens OX=9606 GN=MYL6B PE=1 SV=1	0.68	0.69
P13489	1 (1)	6.00	2.44e-003	3.61		Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=2	0.04	0.01
Q9H299	1 (1)	5.98	2.70e-005	3.74		SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens OX=9606 GN=SH3BGL3 PE=1 SV=1	0.06	0.02
P62942	1 (1)	5.94	0.11	1.74		Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens OX=9606 GN=FKBP1A PE=1 SV=2	0.05	0.03
P35237	1 (1)	5.94	1.11e-003	22.01		Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=3	0.03	1.28e-003
P61158	1 (1)	5.92	1.97e-007	6.96		Actin-related protein 3 OS=Homo sapiens OX=9606 GN=ACTR3 PE=1 SV=3	0.08	0.01
P50453	1 (1)	5.83	3.26e-004	14.53		Serpin B9 OS=Homo sapiens OX=9606 GN=SERPINB9 PE=1 SV=1	0.02	1.50e-003
Q92597	1 (1)	5.82	0.04	1.32		Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1	0.07	0.09
Q96A08	1 (1)	5.82	0.19	2.01			0.18	0.09

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
						Histone H2B type 1-A OS=Homo sapiens OX=9606 GN=H2BC1 PE=1 SV=3		
P45880	1 (1)	5.79	2.50e-003	2.99		Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606 GN=VDAC2 PE=1 SV=2	0.08	0.03
P07858	1 (1)	5.72	0.22	1.97		Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=3	0.61	0.31
P02766	1 (1)	5.72	0.08	2.58		Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1	0.04	0.01
P59910	1 (1)	5.66	2.44e-004	2.95		DnaJ homolog subfamily B member 13 OS=Homo sapiens OX=9606 GN=DNAJB13 PE=1 SV=1	0.88	2.60
P61604	1 (1)	5.62	0.87	1.09		10 kDa heat shock protein_ mitochondrial OS=Homo sapiens OX=9606 GN=HSPE1 PE=1 SV=2	0.10	0.10
P12035	1 (1)	5.62	0.04	5.22		Keratin_ type II cytoskeletal 3 OS=Homo sapiens OX=9606 GN=KRT3 PE=1 SV=3	0.12	0.02
P61106	1 (1)	5.57	8.90e-003	39.83		Ras-related protein Rab-14 OS=Homo sapiens OX=9606 GN=RAB14 PE=1 SV=4	9.15e-003	2.30e-004
P51148	1 (1)	5.55	0.04	2.77		Ras-related protein Rab-5C OS=Homo sapiens OX=9606 GN=RAB5C PE=1 SV=2	0.03	9.60e-003
A0A075B6P5	1 (1)	5.55	3.55e-004	3.95		Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=1	0.11	0.03
P22528	1 (1)	5.53	0.04	5.87		Cornifin-B OS=Homo sapiens OX=9606 GN=SPRR1B PE=1 SV=2	0.16	0.03
Q9BQI9	1 (1)	5.49	0.14	3.38		Nuclear receptor-interacting protein 2 OS=Homo sapiens OX=9606 GN=NRIP2 PE=1 SV=3	0.01	4.39e-003
Q14894	1 (1)	5.47	2.39e-004	3.51		Ketimine reductase mu-crystallin OS=Homo sapiens OX=9606 GN=CRYM PE=1 SV=1	0.07	0.02
P07339	1 (1)	5.47	0.31	1.49		Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1	0.08	0.06
P28072	1 (1)	5.44	1.49e-004	2.83		Proteasome subunit beta type-6 OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=4	0.25	0.71
P62750	1 (1)	5.40	0.60	1.15		60S ribosomal protein L23a OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1	0.06	0.06
P62258	1 (1)	5.39	7.96e-009	4.71		14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1	0.17	0.04
Q2M2I5	1 (1)	5.38	5.72e-004	3.29		Keratin_ type I cytoskeletal 24 OS=Homo sapiens OX=9606 GN=KRT24 PE=1 SV=1	10.23	33.64
P14136	1 (1)	5.37	5.08e-003	31.51		Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1	0.02	7.45e-004
Q75971	1 (1)	5.36	5.59e-004	3.27		snRNA-activating protein complex subunit 5 OS=Homo sapiens OX=9606 GN=SNAPC5 PE=1 SV=1	24.20	79.12
P19013	1 (1)	5.34	0.22	1.76		Keratin_ type II cytoskeletal 4 OS=Homo sapiens OX=9606 GN=KRT4 PE=1 SV=5	0.63	0.36
P47914	1 (1)	5.28	0.42	1.41		60S ribosomal protein L29 OS=Homo sapiens OX=9606 GN=RPL29 PE=1 SV=2	0.03	0.02
P04259	1 (1)	5.28	0.04	8.17		Keratin_ type II cytoskeletal 6B OS=Homo sapiens OX=9606 GN=KRT6B PE=1 SV=5	0.33	0.04
P07305	1 (1)	5.27	4.71e-004	2.34		Histone H1.0 OS=Homo sapiens OX=9606 GN=H1-0 PE=1 SV=3	0.21	0.09
P29401	1 (1)	5.24	2.22e-003	6.17		Transketolase OS=Homo sapiens OX=9606 GN=TKT PE=1 SV=3	0.03	5.15e-003
P02792	1 (1)	5.17	0.51	1.46		Ferritin light chain OS=Homo sapiens OX=9606 GN=FTL PE=1 SV=2	0.10	0.07
Q9H0W9	1 (1)	5.04	0.04	6.14		Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1	0.13	0.02
P69892	3 (3)	5.04	0.11	4.03			0.11	0.03





































Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTR	MCD
						Hemoglobin subunit gamma-2 OS=Homo sapiens OX=9606 GN=HBG2 PE=1 SV=2		
P02008	1 (1)	5.00	2.39e-004	4.04		Hemoglobin subunit zeta OS=Homo sapiens OX=9606 GN=HBZ PE=1 SV=2	17.83	72.07
Q9H082	1 (1)	4.91	8.57e-003	2.81		Ras-related protein Rab-33B OS=Homo sapiens OX=9606 GN=RAB33B PE=1 SV=1	0.05	0.02
P08311	1 (1)	4.90	0.05	2.26		Cathepsin G OS=Homo sapiens OX=9606 GN=CTSG PE=1 SV=2	0.06	0.03
P04350	1 (1)	4.83	0.10	17.38		Tubulin beta-4A chain OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=2	0.02	9.68e-004
Q58FF8	1 (1)	4.77	9.45e-003	2.70		Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens OX=9606 GN=HSP90AB2P PE=1 SV=2	0.16	0.06
A0A075B6H7	1 (1)	4.63	0.01	4.34		Probable non-functional immunoglobulin kappa variable 3-7 OS=Homo sapiens OX=9606 GN=IGKV3-7 PE=1 SV=1	0.02	4.00e-003
P21695	1 (1)	4.62	3.17e-003	2.72		Glycerol-3-phosphate dehydrogenase [NAD(+)]_ cytoplasmic OS=Homo sapiens OX=9606 GN=GPD1 PE=1 SV=4	0.13	0.05
Q9NZ72	1 (1)	4.38	0.14	2.55		Stathmin-3 OS=Homo sapiens OX=9606 GN=STMN3 PE=1 SV=3	0.19	0.07
P78417	1 (1)	4.29	0.03	3.31		Glutathione S-transferase omega-1 OS=Homo sapiens OX=9606 GN=GSTO1 PE=1 SV=2	0.06	0.02
Q3MJ62	1 (1)	4.17	8.11e-008	7.09		Zinc finger and SCAN domain-containing protein 23 OS=Homo sapiens OX=9606 GN=ZSCAN23 PE=1 SV=1	0.30	2.15
Q9BUT1	1 (1)	4.13	2.45e-006	7.32		3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens OX=9606 GN=BDH2 PE=1 SV=2	0.39	2.86
P12882	1 (1)	3.84	0.64	1.25		Myosin-1 OS=Homo sapiens OX=9606 GN=MYH1 PE=1 SV=3	0.17	0.21
Q9H2M3	1 (1)	3.53	8.77e-007	4.77		S-methylmethionine--homocysteine S-methyltransferase BHMT2 OS=Homo sapiens OX=9606 GN=BHMT2 PE=1 SV=1	0.64	3.06
Q8N257	2 (2)	0.00	0.12	1.42		Histone H2B type 3-B OS=Homo sapiens OX=9606 GN=H2BU1 PE=1 SV=3	0.10	0.07
Q5TEC6	2 (2)	0.00	0.91	1.02		Histone HIST2H3PS2 OS=Homo sapiens OX=9606 GN=H3-2 PE=1 SV=1	0.25	0.24
P48668	2 (2)	0.00	0.10	4.88		Keratin_ type II cytoskeletal 6C OS=Homo sapiens OX=9606 GN=KRT6C PE=1 SV=3	0.31	0.06










































Tags	
	reverse
	no peptides
	one unique peptide
	Anova p-value ≤ 0.05
	Max fold change ≥ 1.5

P13645

Keratin_ type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
72 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
ADINGLRR	729	0.00	1	913.5076	2		0		no	3.95
ADLEMQIESLTEELAYLK	4212	8.12	1	2095.0314	3		0		no	5.33
ADLEMQIESLTEELAYLK	12271	---	---	2095.0292	2		0		no	8.17
ADLEMQIESLTEELAYLKK	706	9.29	10	2223.1341	3		0		no	5.61
A ¹⁶ LEMQIESLTEELAYLKK	1019	6.87	1	2239.1253	3		0	[2] Hydroxyl DKNP	no	5.61
A ¹⁶ LEMQIESLTEELAYLKK	1276	7.16	3	2239.1250	3		0	[2] Hydroxyl DKNP	no	5.61
AEQNRK	3405	0.00	1	744.3876	1		0		no	8.24
AETE ¹⁶ QNTHEYQQLLDIK	257	9.42	16	2081.9627	3		0	[5] Carbamidomethyl C	no	4.85
AETE ¹⁶ QNTHEYQQLLDIK	248	9.42	16	2081.9579	2		0	[5] Carbamidomethyl C	no	7.55
+AETE ¹⁶ QNTHEYQQLLDIK	3561	0.00	1	2064.9369	3		0	[N-term] Ammonia-loss [5] Carbamidomethyl C	no	4.50
ALEESNYELEGK	105	9.43	16	1380.6461	2		0		no	5.47
AWFNEK	555	0.00	1	793.3756	1		0		no	8.73
DAAEFNEK	3744	7.65	1	1108.4891	2		0		no	4.29
D ¹⁶ AEFNEK	5010	7.34	1	1124.4881	2		0	[1] Hydroxyl DKNP	no	4.43
DAAEFNE ¹⁶ K	2303	7.64	1	1124.4822	2		0	[9] Hydroxyl DKNP	no	4.43
DELTLTK	163	0.00	10	818.4396	1		0		no	9.14
EADINGLRR	576	0.00	1	1042.5523	2		0		no	4.22
ELTLTK	1897	0.00	1	703.4109	1		0		no	8.03
ELTTEIDNNIEQISSYK	920	9.62	8	1995.9650	3		0		no	4.71
ELTTEIDNNIEQISSYK	527	9.62	12	1995.9622	2		0		no	7.41
ENEVALR	3020	0.00	1	829.4277	1		0		no	8.86
GSLGGGFSSGGFSGGSFSR	5548	9.17	2	1706.7647	3		0		no	4.50
GSLGGGFSSGGFSGGSFSR	242	9.17	14	1706.7659	2		0		no	6.37
GSSGGG ¹⁶ FGSSGGYGGLGGFGGSFR	1362	9.06	2	2341.9734	3		0	[7] Carbamidomethyl C	no	6.09
GSSGGG ¹⁶ FGSSGGYGGLGGFGGSFR	3471	9.06	2	2341.9761	2		0	[7] Carbamidomethyl C	no	8.10
IKEWYEK	1884	8.89	2	994.5190	3		0		no	2.91
IQTYR	1089	0.00	1	679.3656	1		0		no	7.89
IQTYR	2318	0.00	1	679.3656	2		0		no	3.39
IRLEN	6284	---	---	625.3542	2		0		no	3.05
IRLEN	904	0.00	1	625.3555	1		0		no	7.41
IRLENEI	489	0.00	2	867.4804	2		0		no	3.88
IRLENEI	1055	---	---	867.4814	1		0		no	9.90
IRLENEIQ	888	0.00	1	995.5400	2		0		no	4.16
IRLENEIQTYR	237	8.60	14	1433.7643	2		0		no	5.75
IRLENEIQTYR	158	8.60	14	1433.7714	3		0		no	3.74
KDAEAWFNEK	1947	9.39	2	1236.5760	3		0		no	3.46
KDAEAWFNEK	744	9.39	5	1236.5801	2		0		no	4.92
LAADDFR	57	9.19	16	806.3969	2		0		no	3.67

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
										
LAADDFR	267	9.19	11	806.3930	1		0		no	9.00
LAADDRLK	770	6.78	1	1047.5757	2		0		no	4.50
LASYLDK	674	8.92	7	808.4332	2		0		no	3.46
LASYLDK	7420	---	---	808.4345	1		0		no	9.70
LASYLDKVR	3753	---	---	1063.6024	3		0		no	3.32
LASYLDKVR	2291	8.15	2	1063.6030	2		0		no	4.78
LDELTLTK	338	0.00	4	931.5217	1		0		no	10.80
LDELTLTK	3253	---	---	931.5217	2		0		no	3.88
LENEIQTYR	5586	---	---	1164.5761	1		0		no	11.98
LENEIQTYR	138	9.30	16	1164.5794	2		0		no	4.85
+LENEIQTYR	4139	0.00	1	1147.5334	2		0	[N-term] Ammonia-loss	no	4.64
LKYEN	2778	---	---	647.3276	2		0		no	3.12
LKYEN	717	0.00	1	647.3281	1		0		no	7.55
LKYENE	595	0.00	2	776.3709	2		0		no	3.39
LKYENE	179	0.00	3	776.3702	1		0		no	8.73
LKYENEVALR	153	8.07	15	1233.6767	2		0		yes	5.12
LKYENEVALR	135	8.07	15	1233.6796	3		0		yes	3.74
+LKYENEVALR	308	0.00	3	1216.6498	3		0	[N-term] Ammonia-loss	no	3.74
NEIQTYR	3145	0.00	1	922.4487	1		0		no	9.76
NEVALR	1532	0.00	2	700.3868	1		0		no	7.96
NHEEEMKDLR	3323	8.08	1	1299.5879	2		0		no	5.33
NHEEEMKDLR	285	8.36	15	1299.5945	3		0		no	3.74
+NHEEEMKDLR	3352	0.00	1	1282.5602	3		0	[N-term] Ammonia-loss	no	3.67
NHEEEMKDLR	1668	6.81	1	1315.5845	3		0	[1] Hydroxyl DKNP	no	3.74
NHEEEMKDLR	835	7.91	2	1315.5849	3		0	[6] Oxidation M	no	3.74
NHEEEMKDLR	968	7.97	1	1315.5843	3		0	[8] Hydroxyl DKNP	no	3.74
NVQALEIELQSQLALK	2388	8.74	3	1796.0033	3		0		no	4.64
NVQALEIELQSQLALK	5006	8.74	2	1795.9882	2		0		no	6.99
NVSTGDVNVMNAAFGVDLTQLLNMR	3933	7.65	1	2887.3644	3		0	[15] Hydroxyl DKNP	no	7.55
NVSTGDVNVMNAAFGVDLTQLLNMR	451	7.47	1	2903.3651	3		0	[1] Hydroxyl DKNP [24] Hydroxyl DKNP	no	7.34
QSLEASLAETEGR	98	9.37	15	1389.6784	2		0		yes	5.33
QSLEASLAETEGR	1548	9.37	1	1389.6763	3		0		yes	3.95
QSVEADINGLR	360	9.28	14	1200.6123	2		0		no	4.78
QSVEADINGLR+	3470	0.00	1	1182.5986	2		0	[C-term] Dehydrated	no	4.71
QSVEADINGLRR	145	8.52	15	1356.7198	3		0		no	3.74
QSVEADINGLRR	204	8.52	7	1356.7137	2		0		no	5.61
RVLDELTLTK	6318	---	---	1186.6922	3		0		no	3.39
RVLDELTLTK	716	7.75	6	1186.6914	2		0		no	4.85
SEITELR	892	8.74	3	846.4448	2		0		no	3.81
SEITELRR	800	8.33	7	1002.5508	3		0		no	3.05
SEITELRR	136	8.79	15	1002.5509	2		0		no	4.29

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
SGGGGGGGGGC ⁺ GGGGGVSSLR	4219	8.58	2	1548.6674	2		0	[10] Carbamidomethyl C	no	5.61
SKELTTEIDNNIEQISSYK	2441	9.26	2	2211.0881	2		0		no	8.03
SKELTTEIDNNIEQISSYK	222	9.26	16	2211.0984	3		0		no	4.78
SLLEGEGSSGGGGGR	126	9.22	16	1261.5945	2		0		no	4.71
SQYEQLAEQNR	410	9.43	16	1364.6342	2		0		no	5.26
SQYEQLAEQNR	4116	9.43	2	1364.6364	3		0		no	3.53
SQYEQLAEQNRK	479	9.29	16	1492.7287	2		0		no	6.02
SQYEQLAEQNRK	104	9.29	16	1492.7402	3		0		yes	3.88
+SQYEQLAEQNRK	832	0.00	2	1475.7025	3		0	[N-term] Ammonia-loss	no	3.81
TELRR	1489	0.00	1	673.3882	2		0		no	3.19
TELRR	2439	0.00	1	673.3880	1		0		no	7.83
TIDDLKNQJLNLTDDNANILLQIDNAR	3568	8.65	2	3051.6207	3		0		no	6.37
VLDELTLTK	861	8.63	2	1030.5903	1		0		no	11.70
VLDELTLTKADLEMQIESLTEELAYLK	2179	8.63	2	3107.6170	3		0		no	6.86
VLDELTLTKADLEMQIESLTEELAYLK	5159	---	---	3107.6018	4		0		no	5.68
VLDELTLTKADLEMQIESLTEELAYLK	10660	---	---	3123.5993	4		0	[9] Hydroxyl DKNP	no	5.68
VLDELTLTKADLEMQIESLTEELAYLK	4567	7.35	1	3123.6012	3		0	[9] Hydroxyl DKNP	no	6.72
VRALLESNYELEGK	4068	6.69	2	1635.8140	3		0		no	4.16
VTMQNLNDR	2842	8.48	2	1089.5278	2		0		no	4.43
VT ⁺ MQNLNDR	2058	6.84	4	1105.5180	2		0	[3] Oxidation M	no	4.43
VT ⁺ MQNLNDR	619	8.72	7	1105.5192	2		0	[3] Oxidation M	no	4.43
WFNEK	705	0.00	1	722.3395	1		0		no	7.89
YC ⁺ VQLSQIQAQISALEEQLQQIR	588	9.52	4	2745.4067	3		0	[2] Carbamidomethyl C	no	6.99
YENEVALR	3109	0.00	1	992.4920	1		0		no	10.25
YENEVALR	1338	0.00	1	992.4987	2		0		no	4.36
YENEVALR	202	9.22	16	992.4955	2		0		no	4.36
YEQLAEQNRK	12458	0.00	6	1277.6330	2		0		no	3.88
YEQLAEQNRK	488	0.00	8	1277.6385	2		0		no	5.19





























Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02768

Albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2
53 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Av Nc Ab CT
AA ¹ LLPK	1774	7.72	2	771.4313	1		0	[3] Carbamidomethyl C	no	9.35	
AA ¹ LLPK	482	7.72	4	771.4315	2		0	[3] Carbamidomethyl C	no	3.67	
AAFT ¹ CCQAADK	1353	8.81	4	1370.5608	2		0	[6] Carbamidomethyl C [7] Carbamidomethyl C	no	5.26	
ADDKET ¹ FAEEGK	2821	8.02	4	1498.6245	3		0	[7] Carbamidomethyl C	no	3.88	
AEFAEVSK	4888	8.74	1	879.4331	1		0		no	9.76	
AEFAEVSK	407	8.87	6	879.4357	2		0		no	3.67	
AEFAEVSKLVDTLK	7168	6.70	1	1649.8880	3		0		no	4.50	
AVMD ¹ FFAFVEK	689	8.05	2	1357.6238	2		0	[5] Hydroxyl DKNP	no	5.19	
AVM ¹ DDFAAFVEK	3116	7.11	3	1373.6206	2		0	[4] Hydroxyl DKNP [5] Hydroxyl DKNP	no	5.19	
AVM ¹ DDFAAFVEK ¹ CC ¹ K	7221	6.79	1	1819.7946	3		0	[4] Hydroxyl DKNP [13] Carbamidomethyl C [14] Carbamidomethyl C [15] Methyl K	no	4.57	
¹ CCAAADPHE ¹ YAK	11052	---	---	1551.5907	2		0	[1] Carbamidomethyl C [2] Carbamidomethyl C [10] Carbamidomethyl C	no	5.89	
¹ CCAAADPHE ¹ YAK	1114	8.34	4	1551.5924	3		0	[1] Carbamidomethyl C [2] Carbamidomethyl C [10] Carbamidomethyl C	no	4.22	
¹ CCAAAD ¹ PHE ¹ YAK ¹	12025	6.83	1	1583.5838	2		0	[1] Carbamidomethyl C [2] Carbamidomethyl C [7] Hydroxyl DKNP [10] Carbamidomethyl C [13] Hydroxyl DKNP	no	5.82	
¹ CTESLVNR	207	9.20	8	1137.4968	2		0	[1] Carbamidomethyl C [2] Carbamidomethyl C	yes	4.64	1.1
¹ CTVATLR	3674	0.00	1	819.4266	1		0	[1] Carbamidomethyl C	no	9.14	
DDNPNLPR	1171	8.28	4	939.4436	2		0		no	4.09	
DELRDEGK	437	0.00	1	960.4555	2		0		no	3.95	
DVFLG ¹ MFLYEYAR	3021	7.91	2	1638.7736	2		0	[6] Oxidation M	no	6.44	
E ¹ CC ¹ EKP ¹ LEK	1220	7.69	4	1304.6111	3		0	[2] Carbamidomethyl C [3] Carbamidomethyl C	no	3.81	

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Av Nc Ab
								Carbamidomethyl C			CT
ECC ² EKP ³ LP ³ LEK	4171	7.69	2	1304.6103	2		0	[2] Carbamidomethyl C [3] Carbamidomethyl C	no	5.40	
EFAEVSK	4759	0.00	1	808.3949	1		0		no	8.80	
ETYGEMADCCAK	10321	7.40	1	1433.5392	2		0	[9] Carbamidomethyl C [10] Carbamidomethyl C	no	5.47	
ETYGEMADCCAK	664	8.18	4	1449.5211	2		0	[6] Oxidation M [9] Carbamidomethyl C [10] Carbamidomethyl C	no	5.40	
FAEVSK	906	0.00	3	679.3545	1		0		no	7.96	
FQNALLVR	765	8.25	4	959.5553	2		0		no	4.16	
KECC ² EKP ³ LP ³ LEK	5126	0.00	1	1432.7057	3		0	[3] Carbamidomethyl C [4] Carbamidomethyl C	no	4.09	
KLVAASQAALGL	4164	6.73	2	1140.6788	2		0		no	4.71	
KLVAASQAALGL	4666	6.62	1	1154.6968	2		0	[1] Methyl K	no	4.64	
KQTALVELVK	2489	7.54	3	1127.6921	2		0		no	4.64	
KVPQVSTPTLVEVSR	357	8.71	4	1638.9299	3		0		no	3.95	
KVPQVSTPTLVEVSR	4300	8.71	3	1638.9249	2		0		no	6.37	
+KVPQVSTPTLVEVSR	6689	7.50	1	1666.9066	2		0	[N-term] Formyl K N-TERM	no	6.51	
LAKTYETTLEK	2905	6.48	2	1295.6945	3		0		no	3.67	
LAKTYETTLEK	10928	---	---	1295.6946	2		0		no	5.26	
LCTVATLR	359	8.69	4	932.5167	2		0	[2] Carbamidomethyl C	no	4.02	
LDELRDEGK	828	8.97	4	1073.5428	3		0		yes	3.25	
LDELRDEGK	344	8.97	6	1073.5392	2		0		yes	4.50	
LKECC ² EKP ³ LP ³ LEK	3386	8.16	1	1545.7960	4		0	[4] Carbamidomethyl C [5] Carbamidomethyl C	no	3.39	
LKECC ² EKP ³ LP ³ LEK	970	8.29	3	1545.7908	3		0	[4] Carbamidomethyl C [5] Carbamidomethyl C	no	4.29	
LKECC ² EKP ³ LP ³ LEK	1052	8.16	1	1545.7945	3		0	[4] Carbamidomethyl C [5] Carbamidomethyl C	no	4.29	
LKECC ² EKP ³ LP ³ LEK	2624	8.29	3	1545.7922	4		0	[4] Carbamidomethyl C [5] Carbamidomethyl C	no	3.39	
LVAASQAALGL	680	8.53	4	1012.5910	1		0		no	11.43	
LVNEVTEFAK	144	9.23	8	1148.6144	2		0		yes	4.57	1.

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Av No Ab CT
LVNEVTEFAK	4458	9.17	1	1148.6093	1		0		yes	12.74	
LVNEVTEFAK	4704	7.08	2	1162.6095	2		0	[10] Methyl K	no	4.64	
LVTDLTK	2106	8.87	2	788.4638	1		0		no	9.21	
LVTDLTK	440	8.87	6	788.4649	2		0		no	3.46	
QEPERNECFLQHK	12502	6.94	1	1713.7830	4		0	[8] Carbamidomethyl C	no	3.39	
QEPERNECFLQHK	6826	6.94	1	1713.7809	3		0	[8] Carbamidomethyl C	no	4.09	
QNCLEFEQLGEYK	3008	8.34	4	1656.7480	2		0	[3] Carbamidomethyl C	no	6.23	
QTALVELVK	307	8.95	6	999.6009	2		0		no	4.29	
QTALVELVK+	1228	0.00	3	981.5865	2		0	[C-term] Dehydrated	no	4.16	
RPCFSALEVDETYVPK	4210	8.62	4	1909.9163	2		0	[3] Carbamidomethyl C	no	7.27	
RPCFSALEVDETYVPK	368	8.62	4	1909.9272	3		0	[3] Carbamidomethyl C	no	4.85	
SHCIAEVENDEMPADLP SLAADFVESK	8021	7.24	1	2989.3184	3		0	[3] Carbamidomethyl C [9] Hydroxyl DKNP	no	5.89	
SLHTLFGDKLC TVATLR	1213	6.61	1	1931.0237	3		0	[11] Carbamidomethyl C	no	5.06	
SLHTLFGDKLC TVATLR	792	6.61	1	1931.0192	2		0	[11] Carbamidomethyl C	no	7.34	
TCVADESAENC DK	335	8.95	4	1497.5742	2		0	[2] Carbamidomethyl C [11] Carbamidomethyl C	no	5.40	
TDLTK	403	0.00	3	576.3128	1		0		no	6.86	
TYETTLEK	5500	9.12	1	983.4820	1		0		no	11.22	
TYETTLEK	380	9.12	4	983.4866	2		0		no	4.16	
VFDEFKPLVEEPQNLIK	487	9.07	5	2044.0930	3		0		no	4.57	
VFDEFKPLVEEPQNLIK	5787	9.07	1	2044.0807	2		0		no	7.69	
VPQVSTPTLVEVSR	405	9.11	4	1510.8366	2		0		no	5.75	
VPQVSTPTLVEVSR	3499	9.11	4	1510.8348	3		0		no	4.02	
VTKCC TESLVNR	6280	6.86	1	1465.7028	3		0	[4] Carbamidomethyl C [5] Carbamidomethyl C	no	3.67	
YEIAR	829	0.00	4	650.3393	1		0		no	7.83	
YETTLEK	7987	0.00	1	882.4320	1		0		no	10.11	
YICENQDISSK	616	8.76	6	1442.6362	2		0	[3] Carbamidomethyl C	no	5.54	
YKAAFTECCQAADK	2826	7.93	4	1675.7414	3		0	[2] Methyl K [8] Carbamidomethyl C [9] Carbamidomethyl C	no	4.02	
LYIEIAR	4632	8.84	1	926.4846	1		0		no	10.80	




































Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Av Nc Ab
YLYEIAR	364	8.84	6	926.4873	2		0		no	4.22	CT




































Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04264

Keratin_ type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
74 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation
AEAESLYQSK	342	8.97	16	1124.5362	2		0		no
AEAESLYQSKYEELQITAGR	1143	8.42	4	2285.1154	3		0		no
AENEFVTIKK	140	0.00	2	1177.6238	2		0		no
AENEFVTIKK	14999	0.00	2	1177.6471	2		0		no
AQYEDIAQK	63	8.89	15	1064.5212	2		0		yes
AQYEDIAQK	1395	8.46	2	1064.5135	1		0		no
+AQYEDIAQK	1145	0.00	1	1047.4915	2		0	[N-term] Ammonia-loss	no
AQYEDIAQK	2678	5.44	2	1080.4991	2		0	[9] Hydroxyl DKNP	no
DGAYMTK	1820	0.00	3	800.3361	1		0	[7] Hydroxyl DKNP	no
DLDSIIAEVK	627	0.00	4	1101.5915	1		0		no
DLDSIIAEVK	4950	---	---	1101.5934	2		0		no
DVDGAYMTK	406	8.55	15	998.4419	2		0		no
DVDGAYMTK	11583	---	---	998.4413	1		0		no
DVDGAYMTK	542	7.85	1	1014.4365	2		0	[1] Hydroxyl DKNP	no
DVDGAYMTK	412	8.36	15	1014.4357	2		0	[9] Hydroxyl DKNP	no
DYQELMNTK	1129	8.85	3	1140.5234	2		0		no
DYQELMNTK	5118	5.71	1	1156.4997	2		0	[1] Hydroxyl DKNP	no
DYQELMNTK	2629	7.02	3	1156.5086	2		0	[6] Oxidation M	no
DYQELMNTK	1513	7.45	3	1154.5339	2		0	[9] Methyl K	no
EDIAQK	1420	0.00	1	702.3541	1		0		no
EDLAR	1634	7.74	2	602.3037	1		0		no
EELQITAGR	4007	0.00	2	1015.5304	1		0		no
EGEESR	320	0.00	8	705.2939	1		0		no
ELQITAGR	1295	0.00	1	886.4830	1		0		no
ENEFVTIKK	986	0.00	2	1106.5959	2		0		no
FLEQQNQVLQTK	362	9.00	13	1474.7776	2		0		no
FSSGGGGGSFGAGGGFGSR	3840	9.06	2	1764.7326	3		0		no

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation
								[4] Carbamidomethyl C	
FSSGGGGGSFGAGGGFGR	691	9.06	13	1764.7274	2		0	[4] Carbamidomethyl C	no
FVTIKK	5747	---	---	734.4676	2		0		no
FVTIKK	1646	0.00	2	734.4687	1		0		no
GEESR	510	0.00	1	576.2521	1		0		no
GGGGGGYGSGGSSYGSGGGGGGGR	2659	7.83	9	2382.9353	3		0		no
GGGGGGYGSGGSSYGSGGGGGGGR	9499	---	---	2382.9455	2		0		no
IEISELNR	547	8.50	9	972.5230	2		0		no
ISVAR	1204	0.00	2	544.3342	1		0		no
KVDGAYMTK	3535	7.82	2	1126.5293	2		0		no
LALDLEIATYR	1342	8.46	8	1276.7021	2		0		no
LDSELKNMQDMVEDYR	2772	8.61	2	1984.8879	3		0		no
LDSELKNMQDMVEDYR	4324	6.86	1	2000.8820	3		0	[10] Hydroxyl DKNP	no
LDSELKNMQDMVEDYR	4980	6.57	1	2000.8815	3		0	[10] Hydroxyl DKNP	no
LDSELKNMQDMVEDYR	1150	7.67	4	2016.8764	3		0	[6] Hydroxyl DKNP [7] Hydroxyl DKNP	no
LDSIAEVK	2095	0.00	1	986.5649	1		0		no
LEGEESR	170	0.00	10	818.3780	1		0		no
LEGEESR	1425	---	---	818.3790	2		0		no
LLRDYQELMNTK	871	8.78	3	1522.7841	3		0		no
LLRDYQELMNTK	4247	8.78	2	1522.7765	2		0		no
LLRDYQELMNTK	560	7.91	7	1538.7772	3		0	[9] Oxidation M	no
LLRDYQELMNTK	4363	7.91	2	1538.7700	2		0	[9] Oxidation M	no
LLRDYQELMNTK	6155	---	---	1536.7924	2		0	[12] Methyl K	no
LLRDYQELMNTK	633	7.34	1	1536.7955	3		0	[12] Methyl K	no
LNDLEDALQQAEDLAR	2693	7.75	2	1940.9741	3		0		no
LYQSK	1704	0.00	2	637.3430	1		0		no
LYQSK	5307	---	---	637.3432	2		0		no
MSGECAPNVSVSVSTHTTISGGGSR	2440	8.02	2	2564.1534	3		0	[5] Carbamidomethyl C	no
MSGECAPNVSVSVSTHTTISGGGSR	5011	7.29	1	2580.1417	3		0	[1] Oxidation M [5] Carbamidomethyl C	no
NAENEFVTIKK	1199	0.00	1	1274.6511	2		0		no
NEFVTIKK	3997	0.00	1	977.5534	1		0		no
NEFVTIKK	2018	0.00	2	977.5514	2		0		no
NKLNDLEDALQQAQ	2625	7.94	2	1598.8255	3		0		no
NKLNDLEDALQQAQ	4186	7.94	2	1598.8213	2		0		no
NLGGSK	293	0.00	3	574.3089	1		0		no
NMQDMVEDYR	773	8.88	11	1299.5248	2		0		no
NMQDMVEDYR	1622	7.74	1	1315.5180	2		0	[4] Hydroxyl DKNP	no
NMQDMVEDYR	1343	6.67	3	1315.5177	2		0	[4] Hydroxyl DKNP	no

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation
NMQDMVEDYR	1064	7.89	4	1315.5181	2		0	[4] Hydroxyl DKNP	no
QITAGR	1732	0.00	2	644.3594	1		0		no
SDQSRLDSELK	1975	7.51	2	1276.6256	3		0		no
SGGGFSSGSAGIINYQR	3566	---	---	1656.7975	3		0		no
SGGGFSSGSAGIINYQR	1036	8.60	12	1656.7834	2		0		no
SGYRSGGGFSSGSAGIINYQR	1377	6.11	1	2120.0011	3		0		no
SISISVAR	1400	8.74	2	831.4816	1		0		no
SISISVAR	278	8.74	12	831.4828	2		0		no
SISVAR	4487	---	---	631.3642	2		0		no
SISVAR	169	0.00	8	631.3666	1		0		no
SKAEAE	1267	0.00	2	615.2870	1		0		no
SKAEAE	2368	---	---	615.2856	2		0		no
SKAEAES	887	0.00	1	702.3186	1		0		no
SKAEAES	2695	---	---	702.3183	2		0		no
SKAEAES	3205	0.00	2	684.3074	1		0		no
SKAEAES	9789	---	---	684.3069	2		0		no
SKAEAESL	4086	0.00	1	815.4013	1		0		no
SKAEAESL	1852	---	---	815.4088	2		0		no
SKAEAESLYQSK	281	8.66	16	1339.6622	2		0		no
SKAEAESLYQSK	274	8.66	16	1339.6630	3		0		no
SKAEAESLYQSK ⁺	585	0.00	7	1321.6503	3		0	[C-term] Dehydrated	no
SLDLDSIIAEVK	3986	8.13	1	1301.7055	3		0		no
SLDLDSIIAEVK	9900	---	---	1301.7132	1		0		no
SLDLDSIIAEVK	32	8.70	15	1301.7150	2		0		no
SLDLDSIIAEVKAQYEDIAQK	1958	7.95	4	2348.2035	3		0		no
SLNNQFASFDK	3027	8.51	4	1382.6751	2		0		no
SLVNLGGSK	83	8.61	15	873.4962	2		0		no
SLVNLGGSK	788	8.61	3	873.4914	1		0		no
SLYQSK	1119	0.00	2	724.3755	1		0		no
SLYQSK	2286	0.00	2	724.3748	2		0		no
TLLEGEESR	39	8.66	14	1032.5181	2		0		yes
TLLEGEESR	880	8.72	3	1032.5093	1		0		yes
TLLEGEESR ⁺	1698	0.00	1	1014.5078	2		0	[C-term] Dehydrated	no
TNAENE	8479	---	---	658.2558	2		0		no
TNAENE	930	0.00	2	658.2563	1		0		no
TNAENEF	1804	0.00	2	805.3236	1		0		no
TNAENEFVTIK	106	9.15	16	1264.6349	2		0		no
TNAENEFVTIKK	42	9.18	15	1392.7412	3		0		yes
TNAENEFVTIKK	137	9.18	15	1392.7280	2		0		yes
VTIKK	6780	---	---	587.3987	2		0		no
VTIKK	810	0.00	2	587.4010	1		0		no
WELLQQVDTSTR	1164	8.92	4	1474.7384	2		0		no
YEDEINKR	1658	8.40	2	1065.5082	3		0		no
YEDEINKR	1238	8.40	3	1065.5093	2		0		no






































Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation
YEELQITAGR	80	9.30	16	1178.5996	2		0		no
YEELQITAGR	3360	9.30	2	1178.5917	1		0		no

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08670

Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4
56 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	A
DGQVINETSQHDDLE	3243	7.74	3	1835.7923	3		0		no	4.02	
EEAENTLQSFR	3990	8.53	2	1322.6119	2		0		no	5.06	
EGEESR	2140	0.00	1	705.2932	1		0		no	7.48	
EKLQEMLQR	4046	5.61	1	1302.6467	2		0		no	5.06	
EMEE ^N FAVEAANYQDTIGR	6152	8.31	2	2201.9489	2		0	[5] Hydroxyl DKNP	no	7.83	
EMEE ^N FAVEAANYQDTIGR	3295	8.31	2	2201.9503	3		0	[5] Hydroxyl DKNP	no	5.61	
EQQNK	3700	0.00	1	645.3088	1		0		no	7.13	
ETNLDLPLVDTHSKR	7945	7.67	1	1823.9317	4		0		no	3.60	
ETNLDLPLVDTHSKR	3034	7.68	2	1823.9327	3		0		no	4.50	
EYQDLLNVK	474	8.58	8	1120.5767	2		0		no	4.71	
FADLSEAANR	312	8.77	12	1092.5262	2		0		no	4.36	
FADLSEAANRNNDALR	8837	8.62	2	1775.8500	2		0		no	7.20	
FANYIDK	1277	8.40	2	869.4272	2		0		no	3.67	
FANYIDKVR	2357	8.36	2	1124.5998	3		0		no	3.39	
FLEQQNK	581	8.60	9	905.4622	2		0		no	3.88	
FLEQQNK	8474	7.93	1	905.4548	1		0		no	10.25	
ILLAELEQLK	2288	8.23	1	1168.7088	2		0		no	5.06	
ILLAELEQLK	2884	8.16	1	1168.7072	2		0		no	5.06	
ILLAELEQLKGQ GK	630	8.54	7	1538.9077	3		0		no	4.09	
ILLAELEQLKGQ GK	2961	8.54	2	1538.8999	2		0		no	6.51	
ISLPLPNFSSLNLR	4451	8.08	2	1569.8856	2		0		no	6.09	
ISLPLPNFSSLNLR ^{ETNLDLPLVDTHSK}	2345	5.91	1	3235.6931	3		0	[29] Hydroxyl DKNP	yes	8.17	
ISLPLPNFSSLNLR ^{ETNLDLPLVDTHSK}	319	5.91	1	3235.7105	4		0	[29] Hydroxyl DKNP	yes	5.61	1
ISLPLPNFSSLNLR ^{ETNLDLPLVDTHSK}	6574	---	---	3235.7039	5		0	[29] Hydroxyl DKNP	yes	5.19	
KLLEGESR	972	8.22	3	1059.5530	2		0		no	4.71	
KVESLQEEIAFLK	1406	9.12	4	1532.8450	2		0		no	6.16	
KVESLQEEIAFLK	1158	9.12	5	1532.8503	3		0		no	4.02	

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	A
LDLER	1636	8.39	1	644.3495	1		0		no	7.83	
LDLER	1951	8.39	1	644.3507	2		0		no	3.19	
LEGEESR	5849	0.00	1	818.3757	1		0		no	9.07	
LEQQNK	6577	0.00	1	758.3927	1		0		no	8.52	
LGDLYYYYMR	1781	8.11	3	1269.5613	2		0	[9] Oxidation M	no	4.92	
LGDLYYYYMRELRL	2412	6.75	1	1683.7954	3		0	[3] Hydroxyl DKNP [9] Oxidation M	no	4.16	
LLEGEESR	11149	---	---	931.4581	1		0		no	10.32	
LLEGEESR	535	8.62	10	931.4629	2		0		no	3.95	
LQDEIQNMKEEMAR	1056	7.81	2	1765.7994	3		0	[9] Hydroxyl DKNP [12] Oxidation M	no	4.22	
LQDEIQNMKEEMAR	2024	7.71	2	1781.7925	3		0	[7] Hydroxyl DKNP [8] Oxidation M [9] Hydroxyl DKNP	no	4.22	
LQEEMLQREEAEITLQSFRL	4856	7.15	2	2366.1144	3		0	[13] Hydroxyl DKNP	no	4.92	
IMALDIEIATYR	2416	8.36	2	1310.6543	2		0	[1] Oxidation M	no	5.12	
IMALDIEIATYRK	2461	7.72	1	1438.7487	3		0	[1] Oxidation M	no	4.02	
IMFGGPGTASRPSSSR	3039	7.17	2	1509.7003	3		0	[1] Oxidation M	no	4.16	
NLQEAEEWYK	758	9.03	11	1308.6022	2		0		no	5.06	
QVDVNASLAR	466	8.71	12	1087.5290	2		0		no	4.29	
QIMREMEENFAVEAANITQDTIGRL	1860	6.94	2	2633.1502	3		0	[2] Oxidation M [15] Hydroxyl DKNP	no	5.33	
QQYESVAAK	5094	8.94	1	1022.5018	1		0		no	12.19	
QQYESVAAK	431	8.94	9	1022.5071	2		0		no	4.50	
+QQYESVAAK	1823	0.00	1	1005.4851	2		0	[N-term] Ammonia-loss	no	4.36	
QQYESVAAKNLQEAEEWYK	452	5.77	1	2313.0812	4		0		yes	4.57	
QQYESVAAKNLQEAEEWYK	2217	5.85	1	2329.0963	3		0	[10] Hydroxyl DKNP	no	5.19	
QQYESVAAKNLQEAEEWYK	5018	5.85	1	2329.0927	2		0	[10] Hydroxyl DKNP	no	8.59	
QVDQLTNDK	950	8.32	4	1059.5216	2		0		no	4.29	
QVDQLTNDKAR	4480	8.13	2	1286.6586	2		0		no	5.19	
QVDQLTNDKAR	881	8.13	8	1286.6603	3		0		no	3.67	
QQVSLTICEVDALKGTNESLER	2594	8.12	3	2376.1529	3		0	[7] Carbamidomethyl C	no	6.02	
RQVDQLTNDK	2132	8.16	2	1215.6199	2		0		no	4.78	
RQVDQLTNDK	678	5.36	1	1229.6370	2		0	[10] Methyl K	no	5.06	
SEAAAR	4108	0.00	1	646.3057	1		0		no	7.06	
SKFADLSEAAAR	6241	---	---	1307.6449	2		0		yes	5.12	
SKFADLSEAAAR	528	5.10	2	1307.6495	3		0		yes	3.53	2
SSVPGVR	2813	7.94	1	700.3859	1		0		no	7.96	
SSVPGVR	3685	7.94	1	700.3867	2		0		no	3.25	
SYVTTSTR	5979	4.52	1	913.4665	2		0		no	3.81	
SYVTTSTR	2156	8.81	2	913.4511	1		0		no	10.25	
SYVTTSTR	481	8.81	7	913.4532	2		0		no	3.95	
TLLIK	827	6.95	1	586.4065	1		0		no	7.41	
































Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	A
TNEKVELQELNDR	5858	8.73	2	1586.7874	2		0		no	6.16	A
TNEKVELQELNDR	769	8.73	7	1586.7924	3		0		no	3.95	
TTSTR	1112	0.00	1	564.2878	1		0		no	6.44	
TYSLGSALRPSTSR	7326	7.88	1	1494.7779	2		0		no	6.30	
VERDNLAEI M R	3414	0.00	1	1475.7023	2		0	[11] Oxidation M	no	5.82	
VEVERDNLAEIDMR	6098	6.90	1	1687.8201	3		0		no	3.95	
VEVERDNLAEI D MR	292	6.35	8	1703.8209	3		0	[11] Hydroxyl DKNP	no	3.88	
VEVERDNLAEI M R	2800	8.46	2	1703.8131	2		0	[13] Oxidation M	no	6.44	
VEVER D NLAEI D MR	12727	7.26	1	1719.8086	2		0	[6] Hydroxyl DKNP [11] Hydroxyl DKNP	no	6.58	









































Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05










































P00330







Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292
GN=ADH1 PE=1 SV=5
91 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
ALDFFAR	174	0.00	7	838.4341	1		0		no	9.56
ALDFFAR	667	0.00	6	838.4341	2		0		no	3.81
ANELL	334	0.00	12	540.2922	1		0		no	6.44
ANELLI	436	0.00	1	653.3757	1		0		no	7.83
ANELLINVK	91	9.37	13	1012.5921	1		0		no	11.91
+ ANELLINVK	101	0.00	8	995.5700	2		0	[N-term] Ammonia-loss	no	4.09
ANGTTVLVGMPAGAK	128	8.93	16	1385.7345	2		0		no	5.47
ANGTTVLVGM P AGAK	343	7.76	6	1401.7270	2		0	[11] Hydroxyl DKNP	no	5.54
ANGTTVLVGM P AGAK	363	7.58	10	1401.7270	2		0	[11] Hydroxyl DKNP	no	5.61
ATDGGAHGVINVSVSEA	2992	0.00	1	1564.7427	2		0		no	5.75
ATDGGAHGVINVSVSEAA	3138	0.00	2	1635.7830	2		0		no	5.96
ATDGGAHGVINVSVSEAAIEASTR	2889	---	---	2311.1383	4		0		no	4.78
ATDGGAHGVINVSVSEAAIEASTR	925	9.24	7	2311.1385	2		0		no	8.66
ATDGGAHGVINVSVSEAAIEASTR	38	9.24	16	2311.1475	3		0		no	6.23
ATDGGAHGVINVSVSEAAIEASTR +	938	0.00	4	2293.1257	3		0	[C-term] Dehydrated	no	6.02
ATDGGAHGVINVSVSEAAIEASTRYVR	2708	7.90	3	2729.3648	3		0		no	7.20
ATDGGAHGVINVSVSEAAIEASTRYVR	355	7.90	10	2729.3706	4		0		no	5.33
CC SDVFNQVVK	8	9.52	16	1354.6131	2		0	[1] Carbamidomethyl	yes	5.33

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
								C [2] Carbamidomethyl C		
CCSDVFNQVVK	4356	---	---	1354.6067	1		0	[1] Carbamidomethyl C [2] Carbamidomethyl C	yes	13.57
CCSDVFNQVVK	955	7.32	5	1370.5970	2		0	[1] Carbamidomethyl C [2] Carbamidomethyl C [4] Hydroxyl DKNP	no	5.19
CCSDVFNQVVKISIVGSYVGNR	2578	7.81	8	2587.2392	3		0	[1] Carbamidomethyl C [2] Carbamidomethyl C	no	6.79
CCSDVFNQVVKISIVGSYVGNR	1555	7.81	8	2587.2398	3		0	[1] Carbamidomethyl C [2] Carbamidomethyl C	no	5.54
DFFAR	3296	0.00	6	654.3155	1		0		no	4.16
DFFAR	26	0.00	6	654.3154	1		0		no	7.62
DGGEGK	233	0.00	9	561.2410	1		0		no	6.37
DGGEGKEELFR	252	0.00	6	1235.5804	2		0		no	5.33
DGGEGKEELFR	1139	0.00	4	1235.5776	1		0		no	12.60
DIPVPPKPK	27	8.49	11	892.5482	2		0		no	3.95
DIPVPPKPK	1960	---	---	892.5343	1		0		no	10.11
DIVGAVLK	513	0.00	11	813.4951	1		0		no	9.21
DIVGAVLK	45	9.36	16	813.5057	2		0		no	3.67
DIVGAVLK	18	9.36	16	813.4985	1		0		no	9.14
DIVGAVLK	13196	8.54	3	813.4979	1		0		no	1.80
DYAGIK	8013	---	---	665.3358	2		0		no	3.12
DYAGIK	49	0.00	9	665.3397	1		0		no	7.89
EALDF	221	0.00	3	557.2501	1		0		no	6.44
EALDFFAR	92	9.34	7	967.4768	1		0		no	10.73
EALDFFAR	7	9.34	5	967.4906	2		0		yes	4.16
EALDFFAR ⁺	36	0.00	5	949.4707	2		0	[C-term] Dehydrated	no	4.02
EELFR	151	8.75	13	692.3501	1		0		no	7.96
EELFR	230	8.75	13	692.3529	2		0		no	3.53
EELFR ⁺	550	0.00	9	674.3395	2		0	[C-term] Dehydrated	no	3.19
EKDIV	583	0.00	6	584.3175	1		0		no	6.72
EKDIVGAVLK	20	9.31	16	1070.6453	2		0		no	4.50
EKDIVGAVLK	397	9.31	16	1070.6373	3		0		no	3.46
EKDIVGAVLK	3946	---	---	1070.6341	1		0		no	12.33
EKDIVGAVLK ⁺	1328	---	---	1052.6224	3		0	[C-term] Dehydrated	no	3.19
ESHGK	288	0.00	9	556.2628	1		0		no	6.37
ESHGKLEYK	2079	0.00	1	1089.5507	2		0		no	4.50
FYESHGK	102	0.00	1	866.3924	1		0		no	9.70
FYESHGKLEYK	389	0.00	7	1399.6786	2		0		no	5.61

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
FYESHGKLEYK	373	0.00	7	1399.6792	3		0		no	3.74
GAVLK	51	0.00	15	486.3185	1		0		no	6.16
GAVLK	37	0.00	13	486.3189	1		0		no	6.09
GAVLK	2065	---	---	486.3171	2		0		no	2.63
GDYAGIK	2	0.00	2	722.3644	1		0		no	8.38
G ^D YAGIK	688	0.00	1	738.3529	1		0	[2] Hydroxyl DKNP	no	8.45
GGEKKEELFR	1006	0.00	6	1120.5533	2		0		no	4.92
GGEKKEELFR	2375	---	---	1120.5519	1		0		no	11.77
GGEVFIDFTK	1000	0.00	10	1111.5545	1		0		no	12.47
GIDGGEGK	25	0.00	4	731.3476	1		0		no	8.10
GIDGGEGKEELFR	33	0.00	2	1405.6923	2		0		no	6.23
GIDGGEGKEELFR	2963	0.00	2	1405.6894	2		0		no	4.36
GIDGGEGKEELFR	8681	---	---	1405.6813	3		0		no	3.81
GSYVGNR	54	0.00	5	751.3629	1		0		no	8.31
GSYVGNR	14842	0.00	5	751.3631	1		0		no	0.97
GSYVGNR	7294	0.00	5	751.3634	1		0		no	1.73
GVIFYESHG ^K	10759	---	---	1151.5560	3		0	[10] Hydroxyl DKNP	no	3.12
GVIFYESHG ^K	1773	6.96	1	1151.5581	2		0	[10] Hydroxyl DKNP	no	4.64
GVIFYESHGKLEYK	95	8.87	16	1668.8592	3		0		no	4.16
GVIFYESHGKLEYK	1839	---	---	1668.8418	2		0		no	6.58
IDGGEGKEELFR	721	0.00	6	1348.6631	2		0		no	5.96
IFYESHGKLEYK	193	0.00	8	1512.7670	3		0		no	3.95
IGDYAGI	693	0.00	1	689.3387	1		0		no	7.48
IGDYAGIK	15	9.28	2	835.4558	2		0		no	3.67
IGDYAGIK	35	9.62	15	835.4451	1		0		no	9.56
IGDYAGI ^K	239	6.73	2	851.4364	2		0	[8] Hydroxyl DKNP	no	3.88
IG ^D YAGI ^K	597	6.89	1	867.4313	2		0	[3] Hydroxyl DKNP [8] Hydroxyl DKNP	no	3.95
IVGAVLK	1468	---	---	698.4688	1		0		no	7.96
IVGAVLK	738	0.00	2	698.4686	2		0		no	3.46
IVGSYVGNR	480	0.00	2	963.5125	1		0		no	10.87
KDIVGAVLK	1350	0.00	2	941.5900	2		0		no	4.02
LDFFAR	236	0.00	5	767.3980	2		0		no	3.53
LDFFAR	8096	0.00	3	767.3855	2		0		no	4.16
LDFFAR	34	0.00	5	767.3983	1		0		no	9.07
LEYKDIPVPPKPK	2089	7.48	3	1425.8146	3		0		no	3.81
LGIDGGEGK	483	0.00	2	844.4292	2		0		no	3.53
LGIDGGEGK	116	0.00	2	844.4293	1		0		no	9.07
LGIDGGEGKEELFR	99	0.00	4	1518.7700	2		0		no	6.58
LGIDGGEGKEELFR	651	0.00	4	1518.7715	3		0		no	4.02
LINVK	68	0.00	2	585.3871	1		0		no	7.20
LLINVK	74	0.00	1	698.4702	1		0		no	8.52
LPLVGGHEGAGVVVGMGENVK	7458	---	---	2018.0516	2		0		no	8.31
LPLVGGHEGAGVVVGMGENVK	173	8.85	16	2018.0655	3		0		no	4.64























Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
LPLVGGHEGAGVVVG ⁺ MGENVK	476	7.80	8	2034.0556	3		0	[16] Oxidation M	no	4.64
LPLVGGHEGAGVVVG ⁺ MGENVK	603	6.47	1	2034.0552	3		0	[16] Oxidation M	no	4.57
LPLVGGHEGAGVVVGMGEN ⁺ NVK	559	7.56	4	2034.0553	3		0	[19] Hydroxyl DKNP	no	4.64
LPLVGGHEGAGVVVGMGEN ⁺ NVK	1137	7.56	3	2034.0566	3		0	[19] Hydroxyl DKNP	no	5.75
LPLVGGHEGAGVVVGMGEN ⁺ NVK	1611	6.84	1	2034.0535	3		0	[19] Hydroxyl DKNP	no	4.64
LPLVGGHEGAGVVVGMGENV ⁺ K	610	7.10	3	2032.0785	4		0	[21] Methyl K	no	4.64
LPLVGGHEGAGVVVGMGENV ⁺ K	582	7.10	3	2032.0744	3		0	[21] Methyl K	no	5.47
NELLINVK	272	0.00	1	941.5557	2		0		no	4.02
NELLINVK	423	---	---	941.5528	1		0		no	11.08
SANLMAGHWWAISGAAGGLGSLAVQYAK	849	8.28	10	2699.3750	3		0		no	7.83
SA ⁺ NLMAGHWWAISGAAGGLGSLAVQYAK	2116	6.30	1	2715.3644	3		0	[3] Hydroxyl DKNP	no	7.83
SDVFNQVVK	671	0.00	13	1034.5386	1		0		no	11.29
SEAAIEASTR	2103	0.00	1	1033.5045	1		0		no	11.50
SIGGEVFIDFTK	47	9.64	16	1311.6775	2		0		no	5.19
SIGGEVFIDFTKEK	3804	---	---	1568.8063	2		0		no	6.72
SIGGEVFIDFTKEK	820	7.94	9	1568.8093	3		0		no	4.29
SISIV	322	0.00	7	499.2998	1		0		no	6.16
SISIVGSYVGNR	3	9.32	9	1250.6738	2		0		yes	5.06
SISIVGSYVGNR	660	9.18	7	1250.6614	1		0		no	13.43
SISIVGSYVG ⁺ N ⁺ R	1186	7.16	2	1266.6509	2		0	[11] Hydroxyl DKNP	no	4.92
SISIVGSYVGNR ⁺	600	0.00	5	1232.6479	2		0	[C-term] Dehydrated	no	4.85
SISIVGSYVGNRADTR	2166	7.02	5	1693.8598	3		0		no	4.43
SIVGSYVGNR	514	0.00	1	1050.5453	2		0		no	4.29
SIVGSYVGNR	112	0.00	2	1050.5462	1		0		no	11.77
SPIKVVGLSTLPEIYEK	772	6.72	13	1872.0561	3		0		no	4.43
SYVGNR	444	0.00	5	694.3410	1		0		no	7.83
VDTSK	71	0.00	7	548.2828	1		0		no	6.37
VGAVLK	759	---	---	585.3850	2		0		no	3.05
VGAVLK	569	0.00	8	585.3851	1		0		no	7.13
VGAVLK	9	0.00	9	585.3899	1		0		no	7.06
VGAVLK	2092	---	---	585.3804	2		0		no	2.98
VGSYVGNR	87	0.00	3	850.4309	1		0		no	9.49
VLGIDGGEGK	19	9.30	16	943.5098	2		0		no	3.95
VLGIDGGEGK	271	9.30	13	943.4965	1		0		no	10.11
VLGIDGGEGKEELFR	53	9.42	16	1617.8403	2		0		no	7.06
VLGIDGGEGKEELFR	12712	9.42	16	1617.8042	2		0		no	6.02
VPKPK	206	0.00	8	567.3756	1		0		no	6.79
VVDTSK	147	0.00	9	647.3499	1		0		no	7.55
VVGLSTL ⁺ PEIYEK	1788	7.42	7	1462.7854	2		0	[8] Hydroxyl DKNP	no	5.75
VVGLSTLPEIYE ⁺ K	531	7.55	2	1462.7861	2		0	[13] Hydroxyl DKNP	no	6.02
YAGIK	287	0.00	9	550.3127	1		0		no	6.58
YESHGK	653	0.00	4	719.3259	2		0		no	3.25




































Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
YESHGKLEYK	2145	---	---	1252.6060	3		0		no	3.46
YESHGKLEYK	493	0.00	5	1252.6098	2		0		no	4.99
YVGNR	754	0.00	1	607.3087	1		0		no	7.13
YVVDTSK	89	9.33	16	810.4202	2		0		no	3.60
YVVDTSK	156	9.33	11	810.4129	1		0		no	9.07
YVVDTSK	249	8.37	5	810.4126	1		0		no	9.07








Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05




P35908

Keratin_ type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2
45 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation
AENDFVTLKK	323	0.00	6	1163.6207	2		0		no
AQYEEIAQR	133	8.51	15	1106.5413	2		0		no
AQYEEIAQR	6344	---	---	1106.5361	1		0		no
DNAYMIK	3292	0.00	2	853.4003	1		0		no
DPEIQNVK	3000	0.00	1	941.4849	2		0		no
DVDNAYMIK	520	8.68	9	1067.4984	2		0		no
DVDNAYMIK	2020	7.67	1	1083.4935	2		0	[4] Hydroxyl DKNP	no
DVDNAYMIK	683	8.46	6	1083.4932	2		0	[9] Hydroxyl DKNP	no
DVDNAYMIK	933	7.44	1	1083.4940	2		0	[9] Hydroxyl DKNP	no
GFSSGSAAVSGGSR	629	8.99	10	1253.5999	2		0		no
GGGFGGGSSFGGGSGFGGGFGGGFGGGR	3812	7.91	2	2398.0071	3		0		no
GGGFGGGSSFGGGSGFGGGFGGGFGGGR	13962	---	---	2398.0157	2		0		no
GGGGFGSR	6580	---	---	693.3218	2		0		no
GGGGFGSR	3527	0.00	2	693.3200	1		0		no
GGISGGGYSGGGK	564	9.07	12	1196.5434	2		0		no
GLGGTK	544	0.00	3	531.3019	1		0		no
GSSSGGGYSSGSSYGSGGR	3083	8.20	2	1739.6935	2		0		no
HGGGGGGFGGGFGSR	3967	8.63	2	1319.5763	2		0		no
HGGGGGGFGGGFGSR	1979	8.63	2	1319.5749	3		0		no
HGGGGGGFGGGFGSR	6130	0.00	1	1301.5685	3		0	[C-term] Dehydrated	no
KLLEGEECR	870	8.44	3	1132.5573	2		0	[8] Carbamidomethyl C	no
LLEGEECR	10169	---	---	1004.4545	1		0		no


















Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitati
								[7] Carbamidomethyl C	
LLEGEETCR	317	8.54	16	1004.4646	2		0	[7] Carbamidomethyl C	no
LLRDYQELMNVK	4450	8.75	2	1520.7901	2		0		no
LLRDYQELMNVK	912	8.75	3	1520.8043	3		0		no
LLRDYQELMNVK	3040	7.07	1	1536.7959	3		0	[10] Hydroxyl DKNP	no
LNDLEEALQQAK	3632	8.08	2	1370.6940	2		0		no
LNDLEEALQQAKEDLAR	6043	7.61	1	1954.9998	3		0		no
LQGEIAHVK	3022	7.68	2	993.5589	2		0		no
LQGEIAHVK	8489	---	---	993.5611	3		0		no
NKLNDLEEALQQAK	3172	8.23	2	1612.8448	3		0		no
NKLNDLEEALQQAK	4191	8.23	2	1612.8381	2		0		no
NQEIEFLK	4636	0.00	1	1019.5275	1		0		no
NVQDAIADAEQR	863	8.84	9	1328.6307	2		0		no
NVQDAIADAEQRGEHALK	1725	7.82	2	1963.9759	4		0		no
NVQDAIADAEQRGEHALK	1504	7.82	2	1963.9749	3		0		no
PEIQNVK	1105	0.00	1	826.4538	1		0		no
PEIQNVK	473	0.00	1	826.4462	2		0		no
SKEEAEALYHSK	700	8.61	14	1390.6755	3		0		no
SKEEAEALYHSK	13299	---	---	1390.6695	2		0		no
SLVGLGGTK	280	8.65	16	830.4875	2		0		no
SLVGLGGTK	1919	8.65	2	830.4852	1		0		no
SSFSTLSR	2808	0.00	2	942.4219	1		0	[5] Carbamidomethyl C	no
STSSFSSTLSR	276	8.68	15	1130.5099	2		0	[7] Carbamidomethyl C	no
STSSFSSTLSR	8803	---	---	1130.5063	1		0	[7] Carbamidomethyl C	no
TAAENDFVTLK	330	8.98	16	1207.6109	2		0		no
TAAENDFVTLKK	186	9.04	16	1335.7115	3		0		yes
TAAENDFVTLKK	422	9.04	16	1335.7052	2		0		yes
TAAENDFVTLKK+	1453	0.00	2	1317.6882	3		0	[C-term] Dehydrated	no
TSQNSELNNMQDLVEDYKK	404	9.06	11	2255.0415	3		0		no
TSQNSELNNMQDLVEDYKK	842	7.60	3	2271.0297	3		0	[4] Hydroxyl DKNP	no
TSQNSELNNMQDLVEDYKK	4562	7.31	1	2271.0257	3		0	[8] Hydroxyl DKNP	no
VDLLNQEIEFLK	4609	8.89	2	1459.7946	3		0		yes
VDLLNQEIEFLK	111	8.89	16	1459.7962	2		0		yes
VDLLNQEIEFLKVLVDAEISQIHQSVTDNTVILSMDNSR	1043	---	---	4519.2616	4		0	[12] Hydroxyl DKNP [12] Methyl K	yes
VDLLNQEIEFLKVLVDAEISQIHQSVTDNTVILSMDNSR	232	6.21	1	4519.2507	5		0	[12] Hydroxyl DKNP [12] Methyl K	yes
VDPEIQNVK	187	8.80	16	1040.5524	2		0		no
VELQSKVDLLNQEIEFLK	3488	7.87	1	2144.1721	3		0		no





















Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitati
VLYDAEISQIHQSVTDTNVILSMDNSR	2747	8.23	2	3047.4785	3		0		no
VLYDAEISQIHQSVTDTNVILSMDNSR	8444	8.23	1	3047.4724	4		0		no
VLYDAEISQIHQSVTDTNVILSM ^D NSR	2756	7.74	2	3063.4650	4		0	[24] Hydroxyl DKNP	no
VLYDAEISQIHQSVTDTNVILSM ^D NSR	1692	7.74	2	3063.4745	3		0	[24] Hydroxyl DKNP	no
YEELQVTVGR	730	9.11	5	1192.6003	2		0		no
YEELQVTVGR	923	4.84	1	1192.5881	2		0		no
YEELQVTVGR	1678	5.85	1	1192.5858	3		0		no
YLDGLTAER	516	8.59	9	1036.5214	2		0		no
YLDGLTAER	781	5.09	5	1036.5081	2		0		no

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P63261

Actin_ cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1
46 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
AGFAGDDAPR	175	9.00	16	975.4459	2		0		yes	4.09
ALAPSTM ^K	4121	0.00	1	833.4305	1		0	[8] Hydroxyl DKNP	no	9.28
APEEHPVLLTEAPLNPK	7383	0.00	1	1853.9755	2		0		no	7.34
APPER	4412	---	---	568.2976	2		0		no	2.91
APPER	235	0.00	8	568.2984	1		0		no	6.37
APSTM ^K	2277	0.00	1	649.3116	1		0	[6] Hydroxyl DKNP	no	7.48
AVFPSIVGRPR	1742	8.35	2	1197.6975	2		0		no	5.19
AVFPSIVGRPR	1717	8.35	2	1197.6988	3		0		no	3.67
^C DVDIR	2185	8.16	2	776.3481	2		0	[1] Carbamidomethyl C	no	3.67
DLTDYLM ^K	733	8.19	4	1013.4763	2		0	[8] Hydroxyl DKNP	no	4.16
DLTDYLM ^K	13980	---	---	1013.4846	1		0	[8] Hydroxyl DKNP	no	11.43
DLTDYL ^{MK}	5264	7.53	1	1029.4747	2		0	[7] Oxidation M [8] Hydroxyl DKNP	no	4.22
DLYANTVLSGGTTMYPGIA ^{DR}	1286	---	---	2230.0519	2		0	[20] Hydroxyl DKNP	no	8.24
DLYANTVLSGGTTMYPGIA ^{DR}	796	6.12	1	2230.0562	3		0	[20] Hydroxyl DKNP	no	4.99
DSYVGDEAQS ^K	837	8.72	8	1197.5176	2		0		no	4.64
DSYVGDEAQS ^K	945	9.05	6	1353.6158	2		0		no	5.61
DSYVGDEAQS ^K	822	9.05	8	1353.6216	3		0		no	3.60

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
DSYVGDEAQS K R	3434	7.78	3	1367.6311	3		0	[11] Methyl K	no	3.60
DSYVGDEAQS K R	6535	7.62	1	1367.6302	2		0	[11] Methyl K	no	5.61
EITALAPSTM K	3219	7.69	1	1160.5989	2		0		no	4.71
EITALAPSTM K	5680	8.70	1	1176.6077	1		0	[11] Hydroxyl DKNP	no	13.30
EITALA P STM K	3402	7.17	1	1190.6032	2		0	[7] Hydroxyl DKNP [11] Methyl K	no	4.71
EITALAPST MK	594	8.49	3	1192.5928	2		0	[10] Oxidation M [11] Hydroxyl DKNP	no	4.85
EITALAPSTM K IK	5370	7.16	1	1417.7800	2		0	[11] Hydroxyl DKNP	no	6.09
EITALAPSTM K IK	2599	7.16	1	1417.7816	3		0	[11] Hydroxyl DKNP	no	4.09
EITALAPSTM K IK ⁺	6390	0.00	1	1399.7566	3		0	[11] Hydroxyl DKNP [C-term] Dehydrated	no	3.88
EIVRDIK	1848	7.59	3	871.5098	2		0		no	3.81
FTTTAER	4213	0.00	1	824.4010	1		0		no	9.42
GILTLK	3899	8.29	1	643.4275	2		0		no	3.12
GILTLK	429	8.46	5	643.4278	1		0		no	7.89
GYSFTTTAER	210	8.98	16	1131.5243	2		0		no	4.57
GYSFTTTAER	4140	8.98	2	1131.5171	1		0		no	12.47
GYSFTTTAEREIVR	1544	8.22	3	1628.8181	3		0		no	4.09
GYSFTTTAEREIVRDIK	2562	6.08	1	1985.0330	2		0		no	7.69
GYSFTTTAEREIVRDIK	2003	6.06	1	1985.0377	3		0		no	5.06
GYSFTTTAEREIVRDIK	2393	6.06	1	1985.0298	2		0		no	7.55
IAPPER	5139	---	---	681.3814	2		0		no	3.25
IAPPER	814	0.00	2	681.3805	1		0		no	7.69
IIAPPER	7598	---	---	794.4651	1		0		no	9.49
IIAPPER	348	8.85	11	794.4660	2		0		no	3.67
IIAPPERK	1702	8.20	3	922.5589	2		0		no	3.88
IKIIAPPER	2257	7.83	2	1035.6449	2		0		no	4.29
IKIIAPPER	11867	---	---	1035.6405	3		0		no	3.12
KDLYANTVLSGGTTMY P GIADR	1824	5.78	1	2358.1409	3		0	[17] Hydroxyl DKNP	no	4.71
KDLYANTVLSGGTTMY P GIADR	6379	5.78	1	2358.1378	2		0	[17] Hydroxyl DKNP	no	7.96
LAPSTM K	3542	0.00	1	762.3959	1		0	[7] Hydroxyl DKNP	no	8.59
L C YVAL D FEQEMATAASSSSLEK	5041	7.29	1	2565.1563	3		0	[2] Carbamidomethyl C [7] Hydroxyl DKNP	no	6.44
LDLAGR	2620	8.03	2	643.3660	2		0		no	3.19
LDLAGR	2533	8.03	2	643.3653	1		0		no	7.89
LDLAGRDLTDYLM K	1225	7.84	1	1638.8282	3		0	[14] Hydroxyl DKNP	no	3.95
LDLAGRDLTDYLM K	8915	---	---	1638.8189	2		0	[14] Hydroxyl DKNP	no	6.99
MQ K EITALAPSTM K	10528	---	---	1579.7929	2		0	[3] Hydroxyl DKNP [14] Hydroxyl DKNP	no	6.23
MQ K EITALAPSTM K	1485	7.63	2	1579.7943	3		0		no	4.16

































Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
								[3] Hydroxyl DKNP [14] Hydroxyl DKNP		
MQK ⁺ EITALA ⁺ PSTMK	3174	6.78	1	1593.7988	3		0	[3] Hydroxyl DKNP [3] Methyl K [10] Hydroxyl DKNP	no	4.16
PEEHPVLLTEAPLNPK	1146	0.00	4	1782.9476	2		0		no	6.93
PEEHPVLLTEAPLNPK	1035	0.00	3	1782.9506	3		0		no	4.57
QEYDESGPSIVHR	1411	7.84	4	1515.7152	3		0		no	4.02
SFTTTAER	2107	0.00	1	911.4350	1		0		no	10.25
SYELPDGQVITIGNER	81	8.82	15	1789.8861	2		0		yes	6.72
SYELPDGQVITIGNER	1803	8.64	1	1789.8841	3		0		no	4.57
SYELPDGQVITIGNER	631	8.82	11	1789.8846	3		0		yes	4.57
SYELPDGQVITIGNER	515	8.64	1	1789.8892	2		0		no	6.58
TALAPSTM ⁺ K	4125	---	---	934.4742	2		0	[9] Hydroxyl DKNP	no	3.81
TALAPSTM ⁺ K	2216	0.00	1	934.4798	1		0	[9] Hydroxyl DKNP	no	10.66
TTGIVM ⁺ DSGDGVTHTVPIYEGYALPHAILR	2362	7.54	2	3198.5904	4		0	[7] Hydroxyl DKNP	no	6.44
TTTAER	2371	0.00	1	677.3341	1		0		no	7.69
VAPEEHPVLLTEAPLNPK	2129	8.81	4	1953.0499	2		0		yes	7.76
VAPEEHPVLLTEAPLNPK	58	8.81	16	1953.0603	3		0		yes	4.92
VA ⁺ PEEH ⁺ PVLLTEAPLNPK	1997	7.00	1	1985.0436	3		0	[3] Hydroxyl DKNP [7] Hydroxyl DKNP	no	5.06
VA ⁺ PEEH ⁺ PVLLTEAPLNPK	1398	7.00	1	1985.0365	2		0	[3] Hydroxyl DKNP [7] Hydroxyl DKNP	no	7.62
VAPEEHPVLLTEAPLNPKANR	3073	7.21	2	2294.2417	4		0		no	4.78

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05




P35579

Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4
51 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance
ADF ⁺ CIHYAGK	7906	5.19	1	1293.6385	2		0	[4] Carbamidomethyl C	no	5.06	167.14
AGVLAHLEERDLK	3032	7.08	2	1578.8263	3		0		yes	3.95	582.22
ALEEA ⁺ MEQKAELER	1760	6.98	2	1661.7914	3		0	[6] Oxidation M	no	4.22	1367.73
ALEEK	5266	0.00	1	588.3137	1		0		no	6.93	130.37
ALELDNLRYR	463	8.06	2	1192.6254	2		0		yes	4.92	2287.45

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	M
ANLQIDQINTDLNLER	6732	7.23	2	1868.9508	3		0		no	4.57	85.27	
ANLQIDQINTDLNLER	4211	7.23	2	1868.9519	2		0		no	6.99	202.42	
ASITALEAK	1302	7.62	2	902.4980	2		0		no	3.88	1022.82	
ASREEILAQAK	4181	7.27	2	1214.6603	2		0		no	5.06	152.42	
ASREEILAQAKENEK	8067	5.86	1	1714.8734	3		0		no	4.43	69.21	
DELADEIANSSGK	3110	5.27	1	1347.6037	3		0		no	3.32	130.89	
DLQGRDEQSEEK	5489	6.58	1	1432.6438	3		0		no	3.53	78.04	
EEVGEEAIVELVENGK	11622	5.46	1	1742.8385	2		0		no	6.65	49.50	
ELEDATETADAM ¹³ NR	2452	7.32	2	1580.6611	2		0	[13] Hydroxyl DKNP	no	5.75	773.03	
ELEDATETADA ¹² ¹³ NR	14300	5.85	1	1596.6622	2		0	[12] Oxidation M [13] Hydroxyl DKNP	no	5.75	52.06	
ELE ⁴ DATETADAMNREVSSLK	6618	5.73	1	2224.0230	3		0	[4] Hydroxyl DKNP	no	5.19	175.07	
E ² MAELEDERK	5883	6.24	1	1393.6024	3		0	[2] Oxidation M	no	3.67	108.61	
EQEVNILK	1165	7.48	2	971.5279	2		0		no	4.09	1171.97	
EQEVNILKK	3127	7.66	2	1099.6218	2		0		no	4.64	325.81	
EQEVNILKK	7345	7.33	1	1099.6211	3		0		no	3.05	26.63	
FDQLLAEEK	1305	7.61	2	1091.5499	2		0		yes	4.57	1321.43	
FVSELWK	5928	5.70	1	907.4750	2		0		no	3.95	104.30	
GALALEEK	2953	7.23	2	829.4534	2		0		no	3.67	621.42	
GALALEEKR	3769	6.43	1	985.5404	2		0		no	4.36	93.29	
GDLPFVVR	5231	6.82	1	998.5534	2		0		no	4.29	72.25	
IAEFTTNLTETEEEEK	4460	7.38	2	1652.7778	2		0		no	6.37	233.80	
IAEFTTNLTETEEEEKSK	1347	7.57	2	1867.9068	3		0		no	4.43	979.17	
IAQLEEEEEEQGNTELINDR	14702	---	---	2471.1615	2		0		no	8.59	10.30	
IAQLEEEEEEQGNTELINDR	6631	6.61	2	2471.1612	3		0		no	5.75	119.25	
IAQLEEQLDNETK	4311	6.85	2	1529.7565	2		0		no	5.96	161.58	
IAQLEEQLDNETKER	1407	7.50	2	1814.9000	3		0		no	4.57	1224.12	
IIGLDQVAG ¹⁰ SETALPGAFK	4075	6.84	2	2033.0437	2		0	[10] Oxidation M	no	7.62	360.90	
IIGLDQVAG ¹⁰ SETALPGAFK	5141	6.84	2	2033.0551	3		0	[10] Oxidation M	no	5.26	285.35	
I ² ⁵ MGIP ² EEEQMGLLR	3101	6.95	2	1646.8000	2		0	[2] Oxidation M [5] Hydroxyl DKNP	no	6.23	732.79	
KANLQIDQINTDLNLER	5212	6.38	2	1997.0548	3		0		no	4.57	171.09	
KEEELQAALAR	6454	6.38	1	1256.6618	2		0		no	4.92	168.39	
KFDQLLAEEK	2449	6.67	2	1219.6372	2		0		no	5.06	327.38	
KVEAQLQELQVK	5652	6.10	2	1411.7987	3		0		no	3.74	96.80	
LEVNLQAM ⁹ K	1558	6.93	2	1060.5514	2		0	[9] Hydroxyl DKNP	no	4.36	1106.39	
LQQELDDLLVLDLHQR	6016	6.42	2	1948.9830	3		0		no	4.92	124.22	
LQVELDNVTGLLSQSDSK	10953	6.50	1	1944.9973	2		0		no	7.34	42.51	
NTDQASMPDNTAAQ ¹⁵ K	4098	4.98	1	1604.6995	2		0	[15] Methyl K	no	5.82	467.45	
QAQQRDELADIANSSGK	3255	6.42	2	2087.9697	3		0		no	4.57	439.38	
QEEEMMAKEEELVK	4992	5.78	1	1721.7840	2		0		no	6.23	240.41	
QLEEAEEEAQR	3690	7.36	2	1330.5986	2		0		no	5.06	362.25	
QLEEAEEEAQRANASR	5068	7.01	2	1829.8517	3		0		no	4.71	389.25	
QLLQANPILEAFGNAK	2308	7.74	2	1725.9382	2		0		no	6.93	596.60	

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	
QTLENERGELANEVK	2207	6.55	1	1728.8470	3		0		no	4.43	775.16	
QTLENERGELANEV K	6834	5.37	1	1742.8722	2		0	[15] Methyl K	no	6.58	256.91	
RGDLPFVVPR	10055	---	---	1154.6544	3		0		no	3.81	18.69	
RGDLPFVVPR	3218	6.18	2	1154.6517	2		0		no	4.78	333.49	
VAAYDKLEK	7053	5.99	1	1035.5604	2		0		no	4.64	36.92	
VEAQLQELQVK	3108	7.12	2	1283.7010	2		0		no	5.12	393.43	
V N K DDIQ K	1921	6.11	1	1006.4966	2		0	[2] Hydroxyl DKNP [4] Hydroxyl DKNP [8] Hydroxyl DKNP	no	4.09	1008.85	
VVFQEFR	1322	7.48	2	923.4874	2		0		no	3.95	916.20	
YEILTPNSIPK	2666	6.80	2	1273.6854	2		0		no	5.06	396.01	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q43707

Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2
36 peptides




























Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	
AGTQIENIDEDFR	961	6.01	2	1506.6955	2		0		no	5.54	1411.67	
AGTQIENIDEDFR	1085	6.71	3	1506.6959	2		0		no	5.47	1548.11	
AGTQIENIDEDFRDGLK	1915	7.86	2	1919.9250	3		0		no	4.43	564.56	
ALDFIASK	2470	7.98	2	863.4727	2		0		no	3.67	380.82	
DA K GISQE M QEFR	5313	6.19	2	1695.7861	3		0	[3] Methyl K [10] Oxidation M	no	3.95	145.34	
DDPVTNLNNAFEVAEK	7967	6.42	1	1774.8352	2		0		no	6.37	86.85	
DFIASK	5454	0.00	1	679.3541	1		0		no	7.76	87.80	
EAQRIAESNH I K	894	5.60	1	1410.7251	2		0	[12] Hydroxyl DKNP	no	5.33	978.57	
EAQRIAESNH I K	1992	---	---	1410.7076	3		0	[12] Hydroxyl DKNP	no	4.02	570.76	
EGLLLW C QR	5931	7.61	2	1173.5980	2		0	[7] Carbamidomethyl C	no	4.64	88.85	
ELPPDQAEY C IAR	4953	6.36	1	1560.7239	2		0	[10] Carbamidomethyl C	no	5.89	933.55	
ETTDTDADQVIASFK	3539	8.29	2	1740.8138	3		0		no	4.29	388.82	
ETTDTDADQVIASFK	918	8.29	7	1740.8040	2		0		no	6.72	1927.38	
FAIQDISVEETSAK	1417	8.02	6	1536.7673	2		0		no	5.89	788.66	
HRPELIEYDKLR	5539	6.41	1	1567.8441	4		0		no	3.46	151.99	

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalise Abundanc
											CTR
IAESNHIK	2520	6.45	2	926.4780	2		0	[8] Hydroxyl DKNP	no	4.02	606.18
ICDQWDALGSLTHSR	8303	6.36	2	1757.8207	3		0	[2] Carbamidomethyl C	no	4.57	108.39
KDDPVTNLNNAFEVAEK	1132	8.03	5	1902.9310	3		0		no	4.64	1379.27
KDDPVTNLNNAFEVAEK	8668	8.03	2	1902.9245	2		0		no	6.99	83.20
KTFTAWCNSHLR	370	4.81	1	1519.7497	2		0	[7] Carbamidomethyl C	no	6.16	2876.63
LEDFRDYR	4357	7.09	2	1112.5211	3		0		no	3.25	97.94
LSNRPAFMPSSEK	1216	6.49	2	1448.7070	3		0	[9] Hydroxyl DKNP	no	4.02	2134.55
MAFYQGPDVPGALDYK	1516	7.55	4	1807.8421	2		0	[3] Hydroxyl DKNP	no	6.72	1117.10
MAFYQGPDVPGALDYK	5436	7.55	1	1807.8416	3		0	[3] Hydroxyl DKNP	no	4.71	149.54
MAFYQGPDAVPGALDYK	6756	6.60	1	1823.8399	2		0	[3] Hydroxyl DKNP [7] Hydroxyl DKNP	no	6.72	133.83
MLDAEDIVNTARPDEK	7399	7.80	1	1831.8569	2		0	[1] Oxidation M	no	7.48	47.77
MLDAEDIVNTARPDEK	816	7.96	3	1831.8660	3		0	[1] Oxidation M	no	4.71	2315.85
NFITAEELR	6655	7.48	1	1091.5626	2		0		no	4.57	191.83
QFASQANVVGPIWQTK	3261	7.93	2	1772.9151	2		0		no	6.99	296.24
QGEAEFNR	4673	7.05	2	949.4351	2		0		no	3.95	161.78
RDHALLEEQSK	5466	6.66	2	1324.6714	3		0		no	3.74	192.31
RDHALLEEQSK	231	4.89	2	1340.6713	2		0	[2] Hydroxyl DKNP	yes	5.26	1.85e+004
RDHALLEEQSK	586	4.00	1	1340.6699	2		0	[2] Hydroxyl DKNP	yes	5.33	6262.96
RDHALLEEQSK	2312	4.96	1	1340.6671	2		0	[11] Hydroxyl DKNP	no	5.26	1191.77
RQFASQANVVGPIWQTK	1292	4.42	1	1945.0107	3		0	[17] Hydroxyl DKNP	no	5.47	710.77
RQFASQANVVGPIWQTK	1260	4.42	1	1945.0086	2		0	[17] Hydroxyl DKNP	no	7.48	611.89
RTIPWLEDR	2840	5.28	1	1184.6134	2		0		no	4.64	1990.97
STLPDADRER	2083	7.60	2	1158.5631	3		0		no	3.39	395.15
STLPDADRER	1827	7.60	2	1158.5629	2		0		no	4.71	562.34
STLPDADREREAILAIHKEAQR	1188	4.94	1	2518.3030	3		0		no	6.51	1214.71
TINEVENQILTR	4721	8.38	1	1428.7559	3		0		no	3.88	144.75
TINEVENQILTR	382	8.50	7	1428.7558	2		0		yes	5.47	5626.98
VGWEQLLTTIAR	2486	7.62	2	1385.7630	2		0		no	5.47	523.35
VLGDKNFITAEELR	1987	7.33	4	1674.8875	3		0		no	4.29	948.60
VQQLVPK	1084	6.41	1	810.4931	2		0		no	3.60	589.05
YLDIPK	3752	6.73	1	747.4164	1		0		no	9.00	84.01
YLDIPK	886	6.73	2	747.4155	2		0		no	3.74	515.16

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P35527

Keratin_ type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3
35 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quant
DIDNTR	826	0.00	4	732.3409	1		0		no
DIENQYETQITQIEHEVSSSGQEVQSSAK	3538	7.20	1	3263.4997	4		0		no
DIENQYETQITQIEHEVSSSGQEVQSSAK	665	7.48	9	3263.5006	3		0		no
DQIVDLTVGNK	502	6.25	2	1314.6675	2		0		no
EIETYHNNLEGGQEDFESSGAGK	247	8.75	16	2509.1238	3		0		no
FEMEQLNR	6330	6.49	1	1065.4998	2		0		no
FSSSSGYGGGSSR	393	8.68	16	1234.5231	2		0		no
GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK	3776	6.57	1	3222.2670	3		0		no
GGSGGSYGGGSGGGYGGGSGSR	2068	7.02	4	1790.7165	2		0		no
GGSGGSYGGGSGGGYGGGSGSR	6570	---	---	1790.7195	3		0		no
GGSGGSYGGGSGGGYGGGSGSR	9107	---	---	1790.7140	3		0		no
GGSGGSYGGGSGGGYGGGSGSR	1550	8.49	7	1790.7159	2		0		no
HGVQELEIELQSLSK	1536	8.05	11	1836.9565	3		0		no
IKFEMEQLNR	2613	7.41	1	1306.6601	2		0		no
IKFEMEQLNR	1124	7.41	6	1306.6703	3		0		no
IKFEMEQLNR	1021	7.78	11	1322.6637	2		0	[5] Oxidation M	no
IKFEMEQLNR	318	7.78	11	1322.6687	3		0	[5] Oxidation M	no
+IKFEMEQLNR	1594	0.00	1	1305.6424	3		0	[N-term] Ammonia-loss [5] Oxidation M	no
+KGPAAIQK	2505	6.48	1	839.4845	2		0	[N-term] Formyl K N-TERM	no
LASYLDKVQALEEANNNDLENK	5364	7.02	1	2376.1729	3		0		no
LASYLDKVQALEEANNNDLENK	2097	7.02	5	2376.1743	3		0		no
LDDFR	1077	0.00	1	664.3184	1		0		no
LDIDNTR	428	0.00	12	845.4244	1		0		no
LDIDNTR	4986	---	---	845.4248	2		0		no
MTLDDFR	8128	---	---	896.4082	1		0		no
MTLDDFR	211	8.47	13	896.4091	2		0		no
MTLDDFR	229	7.82	12	912.4037	2		0	[1] Oxidation M	no
MTLDDFR	1469	6.73	3	912.4023	2		0	[1] Oxidation M	no
NDMRQEYEQLIAK	786	0.00	1	1619.7604	2		0		no
NYSPYYNTIDDLKQIVDLTVGNK	1269	7.48	7	2901.3942	3		0		no
QEYEQLIAK	455	8.19	10	1120.5719	2		0		no
QFSSSYLSR	1273	8.59	5	1073.5278	2		0		no
QGVDAINGLR	167	8.79	16	1156.5867	2		0		no
QVLDNLTMEK	1264	7.28	8	1189.6023	2		0		no
QVLDNLTMEK	557	7.79	4	1205.5979	2		0		no

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation
								[8] Oxidation M	
SGGGGGGGLSGGSIR	228	9.20	16	1231.5931	2		0		yes
SGGGGGGGLSGGSIRSSYSR	8742	5.35	1	1811.8693	3		0		no
STMQELNSR	1565	6.88	4	1080.4885	2		0	[3] Oxidation M	no
TLDDFR	1316	0.00	1	765.3658	1		0		no
TLLDIDNTR	8825	---	---	1059.5552	1		0		yes
TLLDIDNTR	78	8.43	16	1059.5632	2		0		yes
TLLDIDNTRMTLDDFR	2256	6.37	2	1953.9454	3		0	[13] Hydroxyl DKNP	no
TLNDRMQEYEQIAK	5703	7.81	1	1850.9137	2		0		no
TLNDRMQEYEQIAK	1529	4.81	1	1850.9264	2		0		no
TLNDRMQEYEQIAK	552	7.83	12	1850.9205	3		0		no
TLNDRMQEYEQIAK	6898	6.84	1	1866.9021	2		0	[3] Hydroxyl DKNP	yes
TLNDRMQEYEQIAK	351	7.06	6	1866.9174	3		0	[3] Hydroxyl DKNP	yes
TLNDRMQEYEQIAK	3239	6.19	1	1866.9150	3		0	[4] Hydroxyl DKNP	no
VQALEEANNDLENK	2407	5.82	1	1585.7412	2		0		no

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02545

Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1
29 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AAQAR	617	0.00	1	515.2850	1		0		yes	5.89	2193.57	549
AAYEALGDARK	10353	7.22	1	1292.6311	2		0		no	5.33	50.22	
AAYEALGDARK	3850	7.22	2	1292.6350	3		0		no	3.60	320.85	15
AQHEDQVEQYKK	6971	6.18	1	1501.7082	3		0		no	3.81	50.43	1
ATRSGAQASSTPLSPTR	2332	5.46	1	1718.8606	2		0	[12] Hydroxyl DKNP [15] Hydroxyl DKNP	no	6.51	397.75	179
DLEDRLAR	5382	7.01	1	917.4473	2		0		no	3.81	193.47	11
EAALSTALSEKR	4930	7.62	1	1274.6761	2		0		no	5.40	265.48	7
EAALSTALSEKR	4314	7.62	2	1274.6835	3		0		no	3.74	205.41	27
EREMAEMR	1412	6.23	1	1050.4765	2		0		no	4.22	725.92	36
ITESEEVVSR	953	8.03	7	1147.5724	2		0		no	4.43	1870.80	150
+KEGDLIAAQAR	2634	4.62	1	1198.6314	3		0	[N-term] Formyl K N-TERM	no	3.67	676.53	15

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LADALQELR	539	8.07	7	1027.5681	2		0		no	4.29	2130.53	200
LAVYIDR	4793	4.25	1	848.4813	2		0		no	3.95	343.29	10
LAVYIDR	1354	7.95	4	848.4723	2		0		no	3.74	1083.52	76
LEAALGEAK	2430	7.41	2	900.4845	2		0		no	3.81	1101.91	38
LLEGEER	1649	7.65	3	973.4717	2		0		no	4.22	1135.49	72
LLEGEERLR	1689	7.01	2	1242.6578	3		0		no	3.53	462.88	32
LLEGEERLR	4798	7.01	1	1242.6528	2		0		no	5.26	120.48	4
LQEKEDLQELNDR	2063	7.30	5	1628.8041	3		0		no	4.09	622.97	49
LQTMKEELDFQK	1694	6.71	1	1524.7611	3		0	[5] Hydroxyl DKNP	no	3.95	944.67	37
LQTMKEELDFQK	11985	---	---	1524.7252	2		0	[5] Hydroxyl DKNP	no	5.89	18.45	
LRDLEDSLAR	4652	7.76	1	1186.6295	3		0		no	3.53	94.34	2
LRDLEDSLAR	2019	7.76	3	1186.6226	2		0		no	4.99	596.79	37
LSPSPTSQR	1572	8.02	5	971.5031	2		0		no	3.95	693.96	31
MQQQLDEYQELLDIK	5506	7.63	2	1908.9074	2		0	[1] Oxidation M	no	7.20	201.88	3
MQQQLDEYQELLDIK	8595	7.63	2	1908.9198	3		0	[1] Oxidation M	no	4.57	81.54	
NSNLVGAAHEELQQSR	1846	7.40	4	1751.8547	3		0		no	4.29	691.64	58
RTLEGELHDLR	123	5.38	1	1337.7303	3		0		yes	4.09	1.68e+004	4.91e-
SGAQASSTPLSPTR	991	7.94	6	1358.6784	2		0		no	5.12	1455.42	138
SLETENAGLR	687	7.81	6	1088.5449	2		0		yes	4.22	3327.10	228
SNEQDSGMNWQIK	9562	5.95	1	1551.6635	2		0	[4] Hydroxyl DKNP	no	5.75	60.94	2
SVGGSGGGSFGDNLVTR	1966	7.72	6	1565.7414	2		0		no	5.89	428.94	60
SVGGSGGGSFGDNLVTR	2493	4.46	1	1565.7296	2		0		no	5.82	609.69	78
TALINSTGEEVAMR	2204	6.65	2	1506.7291	2		0	[5] Hydroxyl DKNP	no	5.75	644.96	35
VAVEEVDEEGK	1198	5.13	1	1202.5892	2		0		no	4.71	965.40	74
VAVEEVDEEGKFVR	6406	7.85	2	1604.7978	2		0		no	6.44	105.81	5
VYIDR	3961	0.00	1	664.3537	1		0		no	7.96	133.79	7

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P11047

Laminin subunit gamma-1 OS=Homo sapiens OX=9606 GN=LAMC1 PE=1 SV=3
29 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AFDITYVR	5477	6.63	1	983.5064	2		0		no	4.22	141.88	
CELDDGYFGDPLGR	9870	6.63	1	1772.7182	2		0	[1] Carbamidomethyl	no	6.37	52.63	

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
								C [4] Carbamidomethyl C				
YIYNTAGFYCDR	9838	7.10	2	1538.6418	2		0	[1] Carbamidomethyl C [10] Carbamidomethyl C	no	5.89	83.66	
KDGGFGNPLAPNADK	9085	5.94	1	1846.8686	3		0	[1] Carbamidomethyl C	no	4.43	37.99	
CVCKDNVEGFNCER	7247	5.99	1	1785.7484	3		0	[1] Carbamidomethyl C [3] Carbamidomethyl C [12] Carbamidomethyl C	no	4.36	104.38	
DIRNLEDIR	725	5.35	1	1142.5996	2		0		yes	4.64	4790.00	1
DIRNLEDIR	3293	5.35	1	1142.6045	3		0		yes	3.32	468.25	
EAQDVKDQNLMDR	6821	4.99	1	1774.8408	3		0		no	4.78	71.73	
EAQDVKDQNLMDR	2036	6.32	3	1790.8103	3		0	[14] Hydroxyl DKNP	no	4.16	741.16	
EAQQALGSAAADATEAK	1813	7.71	2	1630.7759	2		0		no	6.30	571.59	
ELASR	1130	0.00	1	574.3084	1		0		no	6.58	531.80	
EVVCTNCTPTGTTGK	11017	6.00	1	1522.6750	2		0	[4] Carbamidomethyl C [7] Carbamidomethyl C	no	5.61	37.80	
GKTEQQTADQLLAR	7553	7.31	1	1557.8071	2		0		no	6.16	64.62	
GKTEQQTADQLLAR	2030	7.31	2	1557.8098	3		0		no	3.88	379.76	
LQCSNIDPNAVGNCNR	13792	---	---	2105.8729	2		0	[2] Carbamidomethyl C [4] Carbamidomethyl C [16] Carbamidomethyl C	no	7.41	25.18	
LQCSNIDPNAVGNCNR	7453	6.44	2	2105.8684	3		0	[2] Carbamidomethyl C [4] Carbamidomethyl C [16] Carbamidomethyl C	no	4.64	103.22	
LIEIASR	947	7.28	2	800.4748	2		0		no	3.67	716.20	
LKDIEDLR	201	5.45	2	1050.5483	2		0		yes	4.29	4252.09	1.29
LNEIEGTLNK	1223	6.08	2	1143.6145	2		0	[10] Methyl K	no	4.85	1392.01	
LNEIEGTLNKAK	3572	4.59	1	1344.7088	2		0	[9] Hydroxyl DKNP	no	5.33	398.00	
LNTFGDEVFNDDPK	6007	5.99	1	1494.7005	2		0		no	6.02	88.80	
LSAEDLVLEGAGLR	2673	7.77	3	1441.7749	2		0		no	5.61	722.78	
NATSTKAEAR	1666	5.19	1	1176.5769	3		0		no	3.19	986.65	
NLEDIRK	1882	7.30	2	886.4840	2		0		no	3.67	745.73	
NTIEETGNLAQAR	1116	8.06	4	1544.7407	2		0		no	5.82	1482.28	1
QLQEAQK	376	4.30	1	844.4371	1		0		yes	9.42	2994.36	5
QLQEAQK	374	4.30	1	844.4405	2		0		yes	3.74	3627.86	6
SQECYFDPELYR	6214	7.20	2	1605.6775	2		0		no	6.09	187.58	






















Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
								[4] Carbamidomethyl C				
SWPGCQECPAC ⁺ YR	12856	5.61	1	1669.6463	2		0	[5] Carbamidomethyl C [8] Carbamidomethyl C [11] Carbamidomethyl C	no	6.02	51.26	
TEQQTADQLLAR	4148	7.14	2	1372.6785	2		0		no	5.40	414.56	
TGQCCECPG ⁺ ITGQH ⁺ CE ⁺ R	9147	6.65	1	2016.8155	3		0	[4] Carbamidomethyl C [6] Carbamidomethyl C [15] Carbamidomethyl C	no	4.57	70.89	
TKEVVCTN ⁺ CP ⁺ TGTTGK	10010	---	---	1751.7929	2		0	[6] Carbamidomethyl C [9] Carbamidomethyl C	no	6.23	225.11	
TKEVVCTN ⁺ CP ⁺ TGTTGK	3059	4.35	1	1751.8005	3		0	[6] Carbamidomethyl C [9] Carbamidomethyl C	no	4.36	1072.38	
VSVPLIAQGN ⁺ SY ⁺ SETTVK	6489	6.12	1	1989.0266	2		0		no	7.69	39.21	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05




000468

Agrin OS=Homo sapiens OX=9606 GN=AGRN PE=1 SV=6
23 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
ALGPAGCEADASAPATCAE ⁺ MR	4590	6.23	2	2120.8866	3		0	[7] Carbamidomethyl C [17] Carbamidomethyl C [20] Oxidation M	no	5.61
CDRCEPGFWNFR	11127	5.72	1	1642.6744	3		0	[1] Carbamidomethyl C [4] Carbamidomethyl C	no	4.16
CEPGFWNFR	6542	6.67	2	1211.5224	2		0	[1] Carbamidomethyl C	no	4.71
DLGPGK	22	6.28	1	601.3102	1		0	[1] Hydroxyl DKNP	yes	7.13
DLGPGK	164	6.28	1	601.3107	2		0		yes	2.91













Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
								[1] Hydroxyl DKNP		
EAA ⁺ CLQQTQIEEAR	2022	7.51	2	1645.7699	2		0	[4] Carbamidomethyl C	no	6.30
FGAL ⁺ CEAETGR	1189	7.61	2	1209.5561	2		0	[5] Carbamidomethyl C	yes	4.64
FNAV ⁺ CLSR	2818	6.59	1	965.4766	2		0	[5] Carbamidomethyl C	no	4.02
GAPEGTV ⁺ CGSDGADYPGE ⁺ CQLLR	6144	5.99	1	2408.0365	3		0	[8] Carbamidomethyl C [19] Carbamidomethyl C	no	5.06
G ⁺ M ⁺ L ⁺ CGFGAV ⁺ CEPNAEGPGR	9420	6.62	1	1993.8405	2		0	[2] Oxidation M [4] Carbamidomethyl C [10] Carbamidomethyl C	no	6.99
G ⁺ M ⁺ L ⁺ CGFGAV ⁺ CEPNAEGPGR	11844	6.62	1	1993.8435	3		0	[2] Oxidation M [4] Carbamidomethyl C [10] Carbamidomethyl C	no	4.29
KFDGP ⁺ CDP ⁺ CQALPDPSR	4271	6.30	1	2015.8807	3		0	[6] Carbamidomethyl C [9] Carbamidomethyl C	no	4.29
LLDVNNQR	1573	7.11	2	970.5139	2		0		yes	4.16
QENVFK	2053	6.12	1	763.3862	1		0		no	8.52
QENVFK	5852	6.12	1	763.3863	2		0		no	3.60
QVDVTSFAGHP ⁺ CTRASGHP ⁺ CLNGAS ⁺ CVPR	5323	5.37	1	3137.4264	3		0	[12] Carbamidomethyl C [20] Carbamidomethyl C [26] Carbamidomethyl C	no	6.02
SADGLTAS ⁺ CL ⁺ CPAT ⁺ CR	4728	7.00	2	1738.7427	2		0	[9] Carbamidomethyl C [11] Carbamidomethyl C [15] Carbamidomethyl C	no	6.37
SAGDVDTLAFDGR	2090	7.80	2	1322.6156	2		0		no	5.06
SELFGETAR	2290	7.45	2	1008.4871	2		0		no	4.16
SIESTLDDLFR	5739	7.02	2	1294.6402	2		0		no	5.12
STVPVNTNR	4852	6.66	2	986.5121	2		0		no	3.95
TEATQGLVLWSGK	8250	6.04	1	1388.7145	2		0		no	5.47
TFVGAGLR	6310	6.73	1	819.4545	2		0		no	3.53
VLGAPVPAFEGR	1880	7.28	2	1211.6651	2		0		no	4.64
VLPEGGAQ ⁺ CE ⁺ PLGR	4048	7.07	2	1641.7583	2		0	[9] Carbamidomethyl C [11] Carbamidomethyl C	no	6.09
VT ⁺ CDGAYRPV ⁺ CAQDGR	4970	7.02	2	1823.8043	3		0	[3] Carbamidomethyl C [11]	no	4.22

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
								Carbamidomethyl C		

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P68871

Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2
23 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average N Abundanc
											CTR
DEVGGEALGR	1459	0.00	3	1001.4772	1		0		no	10.60	488.93
EFTPPVQAAYQK	4263	---	---	1377.6980	3		0		no	3.88	218.40
EFTPPVQAAYQK	614	8.55	10	1377.6949	2		0		no	5.26	3573.67
FFESFGDLSTPDVAMGNPK	3876	7.47	2	2073.9328	2		0	[17] Hydroxyl DKNP	no	7.55	495.07
FFESFGDLSTPDVAMGNPK	5776	---	---	2073.9368	3		0	[17] Hydroxyl DKNP	no	5.12	219.17
FFESFGDLSTPDVAMGNPK	3545	---	---	2087.9455	3		0	[11] Hydroxyl DKNP [19] Methyl K	no	5.19	439.39
FFESFGDLSTPDVAMGNPK	3393	7.62	3	2087.9426	2		0	[11] Hydroxyl DKNP [19] Methyl K	no	7.48	457.88
FFESFGDLSTPDVAMGNPK	1365	8.39	3	2089.9277	2		0	[17] Hydroxyl DKNP [18] Hydroxyl DKNP	no	7.48	2350.72
FFESFGDLSTPDVAMGNPK	3948	8.39	3	2089.9267	3		0	[17] Hydroxyl DKNP [18] Hydroxyl DKNP	no	5.19	382.26
FFESFGDLSTPDVAMGNPKVK	1687	7.31	3	2301.0986	3		0	[11] Hydroxyl DKNP	no	4.99	707.49
FFESFGDLSTPDVAMGNPKVK	852	6.92	1	2315.1085	3		0	[17] Hydroxyl DKNP [19] Methyl K	no	4.85	1411.56
GEALGR	565	0.00	1	601.3214	1		0		yes	6.65	6271.54
+KVLGAFSDGLAHLNLIK	784	6.25	1	1856.9748	4		0	[N-term] Formyl K N-TERM [1] Hydroxyl DKNP [8] Hydroxyl DKNP	yes	4.22	1626.07
+KVLGAFSDGLAHLNLIK	848	6.25	1	1856.9735	3		0	[N-term] Formyl K N-TERM [1] Hydroxyl DKNP [8] Hydroxyl DKNP	yes	5.19	1914.44
LHVDPENFR	2359	7.54	3	1125.5689	2		0		no	4.64	1004.25
LLVVPWTQR	224	9.05	10	1273.7223	2		0		no	5.19	1.12e+004

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance CTR
LLVVY ^P WTQR	1727	8.24	4	1289.7100	2		0	[6] Hydroxyl DKNP	no	5.19	959.86
LLVVY ^P WTQR	8274	---	---	1289.7090	3		0	[6] Hydroxyl DKNP	no	3.88	64.03
SAVTALWGK	3979	8.85	1	931.5135	1		0		no	10.80	129.41
SAVTALWGK	494	9.11	7	931.5147	2		0		no	3.88	2951.28
SAVTALWGK ^R VNVDEVGGEALGR	8268	7.55	1	2241.1747	3		0	[9] Methyl K	no	5.96	63.46
TALWGK	1499	0.00	4	674.3754	1		0		no	7.96	408.77
VDEVGGEALGR	3107	0.00	2	1100.5462	1		0		no	11.70	236.00
VGGEALGR	1568	0.00	1	757.4178	1		0		no	9.00	971.79
VHLTPEEK	1190	8.71	6	951.5019	2		0		no	4.22	1433.67
VLGAFSDGLAHLNLIK	2370	7.93	4	1668.8838	3		0		no	4.64	535.43
VNVDEVGGEALGR	4712	9.45	3	1313.6599	3		0		yes	3.67	238.05
VNVDEVGGEALGR	50	9.45	14	1313.6652	2		0		yes	5.19	3.61e+004
V ^N VDEVGGEALGR	6459	7.09	1	1329.6437	2		0	[2] Hydroxyl DKNP	no	5.12	135.10
VNV ^D EVGGEALGR	5164	7.17	1	1329.6472	2		0	[4] Hydroxyl DKNP	no	5.19	256.27
VTALWGK	2236	0.00	2	773.4440	1		0		no	8.93	263.20
VTALWGK	6161	---	---	773.4453	2		0		no	3.46	60.29

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P55268

Laminin subunit beta-2 OS=Homo sapiens OX=9606 GN=LAMB2 PE=1 SV=2
25 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance CTR
AAQLDGLER	768	7.56	5	1042.5354	2		0		yes	4.43	2634.42
AGNSLAASTAETAGSAQGR	4395	7.64	2	1847.8548	2		0		no	7.20	244.77
ALAEGGSILSR	662	7.99	5	1072.5874	2		0		yes	4.43	2406.17
AQEAEQLLR	850	7.66	5	1056.5540	2		0		no	4.36	1519.89
AQGIAQGAIR	998	7.22	5	983.5491	2		0		no	3.95	1709.16
ARSWAEDE ^K	701	4.46	1	1104.5198	2		0	[9] Methyl K	no	4.43	2222.64
ARSWAEDE ^K	3099	---	---	1104.5154	1		0	[9] Methyl K	no	12.26	178.77
EDFNSKHMAN ^N QR	10477	3.85	1	1491.6433	2		0	[10] Hydroxyl DKNP	no	5.40	132.33
GAVADTRDTEQTLYQVQER	2202	6.44	2	2179.0413	3		0		no	5.40	544.30
GLN ^C EQ ^C QDFYR	7961	6.47	1	1588.6385	2		0	[4] Carbamidomethyl C [7]	no	5.82	70.72

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalise Abundanc
											CTR
								Carbamidomethyl C			
GPLGDQYQTVK	1650	7.09	2	1204.6013	2		0		no	4.85	946.82
GSYPATGDLLVGR	6979	6.16	2	1464.7035	2		0	[3] Carbamidomethyl C	no	5.61	133.37
HRTEALMDAQK	2827	5.59	2	1298.6543	3		0		no	3.60	527.60
HSNFLGAYDSIR	3474	4.07	1	1394.6562	2		0	[3] Hydroxyl DKNP	no	5.40	433.59
IQNVVTSFAPQRR	2606	5.00	1	1514.8425	2		0		no	6.23	206.21
LGIVQGIVGAR	1942	7.46	2	1081.6618	2		0		no	4.50	556.89
LQEGQTLEFLVASVPK	11186	---	---	1757.9607	3		0		no	4.71	28.34
LQEGQTLEFLVASVPK	8419	6.02	1	1757.9472	2		0		no	6.86	81.60
LQELEGTYEENER	3070	7.38	2	1608.7258	2		0		no	6.02	320.31
LQELEGTYEENERALESK	5983	6.51	1	2137.0197	3		0		no	4.92	149.21
LVTPGETPSWTGSGFVR	1893	4.24	1	1789.8968	2		0		yes	6.72	791.67
NTSAASTAQLVEATEELRR	11877	5.44	1	2046.0421	3		0		no	4.57	62.22
RAEQLLQDAR	2406	6.69	2	1198.6411	2		0		no	5.12	376.58
RAEQLLQDAR	2076	4.64	1	1198.6481	2		0		no	4.85	875.83
SLADVDAILAR	1111	7.60	4	1142.6293	2		0		no	4.71	946.00
VLDPAIPIPDYSSR	7887	6.40	1	1638.8509	2		0		no	6.23	94.50
VVQDLAAR	3056	4.66	2	870.4904	2		0		no	3.95	347.01
VVQDLAAR	1450	7.18	2	870.4883	2		0		no	3.81	1147.27
YSEIEPSTEGEVIYR	3144	6.88	2	1770.8257	2		0		no	6.72	361.27

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P48681

Nestin OS=Homo sapiens OX=9606 GN=NES PE=1 SV=2
24 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances
											CTR
											MCD
ALEEQNELLSAELGGLR	13351	---	---	1840.9461	3		0		no	4.78	22.98
ALEEQNELLSAELGGLR	7274	6.59	2	1840.9430	2		0		no	6.93	101.65
AQDAPLSLLQTQGGR	6367	6.08	2	1553.7921	2		0		no	5.96	181.66
AQDAPLSLLQTQGGRK	4454	6.46	2	1681.9120	3		0		no	4.29	152.47
AQSADTSWR	3308	5.68	1	1020.4596	2		0		yes	4.09	1786.14
DNLAEELEGVAGR	4737	6.60	2	1371.6628	2		0		no	5.19	214.98
EGRLELQQLQAER	1756	6.98	2	1568.8278	3		0		no	3.88	529.57
EGRLELQQLQAER	13147	---	---	1568.8038	2		0		no	6.02	18.71

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EIQDSQVPLEKETLK	4473	5.69	1	1755.9056	3		0		no	4.22	114.76	104.65
GLVEGASVK	3668	6.25	2	858.4707	2		0		no	3.74	307.01	184.99
GPPAPAPEVEELAR	2665	6.81	2	1431.7266	2		0		no	5.61	403.76	111.41
LELQFPR	2133	7.01	2	901.5011	2		0		no	3.95	399.01	172.16
LELQQLQAER	3784	7.19	2	1226.6484	2		0		no	4.92	294.53	113.45
LLEENQESLR	1787	7.08	2	1358.6651	2		0		no	5.19	720.03	755.22
RLEAYLAR	3569	5.75	1	990.5449	2		0		no	4.43	166.03	63.12
SLDQEIARPLENENQEFLK	8931	6.28	2	2272.1185	3		0		no	4.85	48.17	10.84
SLEDENKEAFR	5088	6.04	2	1336.6274	3		0		no	3.67	240.69	304.61
SLEEDLETLK	4200	6.24	2	1175.5899	2		0		no	4.78	275.47	152.09
SLEEQDQETLR	3045	6.73	2	1346.6294	2		0		no	5.12	374.81	207.84
SLETEILESLEK	2762	6.58	2	1260.6829	2		0		no	5.40	212.30	120.53
SLKEESVEAVK	5683	5.18	1	1217.6445	2		0		no	4.99	88.12	21.28
SPEEVDKESQR	2034	5.21	1	1302.5957	2		0		yes	4.85	804.41	710.13
SPEEVDKESQR	4505	4.58	1	1318.5979	2		0	[6] Hydroxyl DKNP	no	5.12	360.02	91.06
TSLSFQDPK	1470	6.23	2	1021.5106	2		0		yes	4.22	1272.40	483.67
VAIPASVLPGPEEPGGQR	7035	6.31	1	1772.9160	2		0		no	6.51	64.72	40.17
VKALEEQNELLSAELGGLR	8374	5.61	2	2068.0932	3		0		no	4.71	74.10	15.38

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P13647

Keratin_ type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3
22 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalise Abundanc
											CTR
AENEFVMLK	4085	0.00	1	1223.6123	2		0	[9] Hydroxyl DKNP	no	4.85	680.64
AQYEEIANR	383	7.95	14	1092.5220	2		0		yes	4.36	1.09e+004
GRLDSELR	833	7.35	7	944.5026	2		0		no	4.16	4014.17
KDVDAAYMKNK	2541	5.42	2	1153.5530	2		0		no	4.50	1050.29
LSELRNQDLVEDFK	6254	6.25	1	1996.9492	3		0	[2] Hydroxyl DKNP [7] Hydroxyl DKNP [16] Methyl K	no	4.64	577.75
LSELRNQDLVEDFK	1931	6.25	1	1996.9439	2		0	[2] Hydroxyl DKNP [7] Hydroxyl DKNP [16] Methyl K	no	7.20	2331.59
LLREYQELMNTK	6291	6.25	1	1536.7902	3		0		no	4.02	1870.51
QLDSIVGER	797	7.71	9	1015.5318	2		0		no	4.22	2204.01



















Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalise Abundanc
											CTR
QLDSIVGERGR	859	5.81	1	1228.6527	2		0		no	5.06	4146.08
SFSTASAITPSVSR	1833	7.19	6	1409.7090	2		0		no	5.33	807.32
TEAESWYQTK	1734	7.87	4	1241.5758	2		0		no	4.85	2011.05
TEAESWYQTKYEELQQTAGR	5098	7.00	2	2417.1047	3		0		no	5.12	608.64
TSFTSVSR	2579	7.16	2	883.4408	2		0		no	3.74	791.71
TTAENEFVMLK	2247	5.77	2	1297.6048	2		0	[11] Hydroxyl DKNP	no	5.12	606.49
TTAENEFVMLKK	6585	---	---	1409.7155	2		0		no	5.75	285.84
TTAENEFVMLKK	1234	7.95	2	1409.7227	3		0		no	3.60	2960.57
TTAENEFVMLKK	1797	6.91	1	1425.7204	3		0	[9] Oxidation M	no	3.60	5240.18
TTAENEFVMLK	3118	7.16	2	1425.7147	2		0	[11] Hydroxyl DKNP	yes	5.54	477.80
TTAENEFVMLK	530	7.16	6	1425.7179	3		0	[11] Hydroxyl DKNP	yes	3.60	3217.70
VDALMDEINFMK	1962	3.73	1	1424.6886	2		0		no	5.54	467.64
VDALMDEINFMK	7319	6.38	1	1440.6623	2		0	[9] Hydroxyl DKNP	no	5.40	1347.38
VSLAGACGVGGYGSR	1176	7.84	6	1409.6733	2		0	[7] Carbamidomethyl C	no	5.40	2536.54
WTLLEQEGTK	987	5.47	1	1202.6297	2		0		no	4.78	1149.12
YEEIANR	4597	0.00	2	893.4215	1		0		no	9.90	432.58
YEELQQTAGR	812	7.90	14	1193.5690	2		0		yes	4.57	5725.32




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07355

Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2
17 peptides












Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
AEDGSVIDYELIDQDAR	8813	7.88	1	1907.8729	3		0		no	4.71	75.64	1
AEDGSVIDYELIDQDAR	6309	7.88	2	1907.8773	2		0		no	6.99	166.58	2
ASMKGLGTDEDSLIEICSR	1196	5.39	1	2226.0422	3		0	[3] Oxidation M [11] Hydroxyl DKNP [18] Carbamidomethyl C	yes	5.33	514.68	420
ASMKGLGTDEDSLIEICSR	1200	---	---	2226.0393	4		0	[3] Oxidation M [11] Hydroxyl DKNP [18] Carbamidomethyl C	yes	4.50	579.03	385
AYTNFDAER	3664	4.69	1	1085.4825	3		0		no	3.19	755.98	1
AYTNFDAER	2713	4.69	1	1085.4819	2		0		no	4.57	1307.65	10












Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
AYTNFDAER	3379	7.49	2	1085.4906	2		0		no	4.43	815.43	37
AYTNFDAERDALNIETAIK	2066	7.10	2	2154.0530	3		0		no	4.92	511.81	11
DALNIETAIK	4057	7.57	2	1086.5748	2		0		no	4.36	395.41	13
DIISDTSGDFR	2811	6.18	2	1224.5671	2		0		no	4.71	687.45	45
DIISDTSGDFRK	1771	5.65	1	1352.6393	2		0		no	5.26	939.73	76
DLYDAGVK	12839	---	---	879.4344	1		0		no	9.63	12.29	
DLYDAGVK	2987	7.72	2	879.4348	2		0		no	3.81	360.97	15
GVDEVTIVNILTNR	1814	8.18	2	1541.8384	2		0		no	6.09	608.42	15
GVDEVTIVNILTNR	9293	8.18	1	1541.8492	3		0		no	4.09	54.46	
RAEDGSVIDYELIDQDAR	1779	8.55	4	2064.0096	3		0		no	5.12	919.04	171
SYSPYDMLESIR	5575	6.69	1	1475.6595	2		0	[6] Hydroxyl DKNP	no	5.75	124.81	
TDLEKDIISDTSGDFR	10530	8.33	2	1810.8450	2		0		no	6.72	32.10	
TDLEKDIISDTSGDFR	2758	8.33	2	1810.8588	3		0		no	4.22	429.62	7
TKGVDEVTIVNILTNR	6069	6.96	2	1770.9818	3		0		no	4.50	164.15	
TNQELQEINR	640	8.61	8	1243.6155	2		0		yes	4.71	3035.01	139
TNQELQEINRVYK	1494	4.18	1	1633.8314	3		0		yes	4.29	268.48	268
WISIMTER	1708	8.01	2	1050.5296	2		0	[5] Oxidation M	no	4.29	1474.51	83
YDAGVK	4129	0.00	1	651.3247	1		0		no	7.55	109.37	




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P11142

Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1
20 peptides















Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ARFEELNADLFR	9560	6.80	1	1479.7394	2		0		no	5.96	50.38	5.94
ARFEELNADLFR	4761	6.80	2	1479.7468	3		0		no	3.95	174.79	45.64
DAGTIAGLNVLR	1005	7.70	5	1198.6656	2		0		no	4.92	1268.30	656.45
EIAEAYLGK	2184	5.48	1	992.5158	2		0		no	4.09	767.00	757.32
ENKITITNDK	1665	4.66	1	1190.6188	2		0	[2] Hydroxyl DKNP	yes	4.85	1617.62	939.61
FEELNADLFR	6075	6.58	1	1252.6225	2		0		no	4.99	125.74	91.65
FELTGIPPAPR	2150	4.99	1	1196.6751	3		0		no	3.67	555.72	251.19
FELTGIPPAPR	4206	4.99	1	1196.6653	2		0		no	4.78	310.93	107.15
GTLDPVEK	3491	7.00	4	857.4404	2		0		no	3.67	487.45	450.29
HWPFMVVNDAGRPK	6925	5.39	1	1652.7915	2		0		no	6.23	98.48	18.80
IINEPTAAAIAYGLDK	8471	6.55	1	1658.8664	2		0		no	6.37	98.95	10.94

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IINEPTAAAIAYGLDKK	2741	7.41	4	1786.9813	3		0		no	4.92	683.19	197.26
IINEPTAAAIAYGLD K K	3807	6.33	3	1800.9844	3		0	[16] Methyl K	no	4.92	345.30	56.63
IN D E D K QK	4545	6.47	1	1018.4845	2		0	[3] Hydroxyl DKNP [6] Methyl K	no	4.02	418.44	119.05
NQVAM N PTNTVFDAK	2848	6.95	2	1664.7806	2		0	[6] Hydroxyl DKNP	no	6.37	377.50	147.67
NQVAMNPTNTVFDAKR	6555	5.22	1	1804.8862	3		0		no	4.64	194.27	35.20
NQVAM N PTNTVFDAKR	3936	6.13	1	1820.8825	3		0	[6] Hydroxyl DKNP	no	4.50	315.20	102.49
STAGDTHLGGEDFDNR	4868	6.10	1	1690.7237	3		0		no	3.95	229.80	112.91
TPSYVAFTDTER	736	7.68	8	1486.6944	2		0		yes	5.75	2324.71	1855.08
TVTNAVVTVPAYFNSQR	10534	7.07	1	1980.9817	2		0		no	7.41	89.27	0.00
VEIIANDQGNR	1620	7.72	5	1227.6196	2		0		yes	4.71	1194.60	905.12
VSS K NSLESYAFNMK	1590	5.40	1	1719.8145	3		0	[4] Hydroxyl DKNP	no	3.88	788.36	396.57

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02533

Keratin_ type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4
16 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Abunda
											CTR
ALEENADLEVK	2852	6.77	3	1300.6466	2		0		no	5.40	1019.
APSTYGGGLSVSSSR	1279	8.43	8	1424.6868	2		0		no	5.40	1974.
ASLENSLEETKGR	853	7.59	6	1432.7156	3		0		no	3.81	2406.
DAEEWFFTK	1560	7.82	6	1171.5188	2		0		no	4.57	1754.
DAEEWFFTKTEELNR	3757	6.66	2	1913.8748	3		0		no	4.50	858.
EVATNSELVQSGK	741	8.33	12	1360.6841	2		0		yes	5.54	4068.
GS C GIGGGIGGGSSR	2851	7.75	3	1277.5905	2		0	[3] Carbamidomethyl C	no	4.92	853.
ILNEMRDQYE K	14252	---	---	1453.6883	2		0	[11] Hydroxyl DKNP	no	5.61	49.
ILNEMRDQYE K	4027	6.43	1	1453.6890	3		0	[11] Hydroxyl DKNP	no	3.67	3377.
ILNEMRDQYE K	1816	5.61	1	1453.6886	3		0	[11] Hydroxyl DKNP	no	3.67	1403.
ISSVLAGGS C R	1098	8.01	5	1105.5555	2		0	[10] Carbamidomethyl C	no	4.29	1433.
LLEGEDAHLSSSQFSSGSQSSR	1287	8.04	8	2308.0541	3		0		no	4.99	2377.
M SVEADINGLRR	2126	5.74	1	1375.6902	3		0	[1] Oxidation M	no	3.74	1593.
RLLEGE D AHLSSSQFSSGSQSSR	2975	4.89	1	2480.1258	4		0	[7] Hydroxyl DKNP	no	4.92	916.

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Abundance
											CTR
RLLEGE D AHLSSSQFSSGSQSSR	5166	4.89	1	2480.1334	5		0	[7] Hydroxyl DKNP	no	4.09	473.
SEISELRR	4991	---	---	988.5306	3		0		yes	3.05	297.
SEISELRR	707	8.08	7	988.5284	2		0		yes	4.16	4405.
TEELNREVATNSELVQSGK	1503	7.58	3	2103.0405	3		0		no	5.26	1345.
TKYETELNLR	1162	7.39	6	1265.6601	2		0		no	5.19	2407.
TKYETELNLR	1397	7.39	5	1265.6622	3		0		no	3.67	1854.
VLDELTAR	14914	---	---	1028.5847	1		0		yes	11.84	40.
VLDELTAR	182	8.50	16	1028.5897	2		0		yes	4.29	1.03e+0

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P18206

Vinculin OS=Homo sapiens OX=9606 GN=VCL PE=1 SV=4
19 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance
											CTR
AGEVINQ PMM MAAR	7471	6.43	2	1565.6946	2		0	[8] Hydroxyl DKNP [9] Oxidation M [10] Oxidation M	no	5.89	139.87
ALASIDSK	4768	6.55	1	803.4356	2		0		no	3.46	106.29
ALASQLQDSLK	2937	6.46	2	1172.6324	2		0		no	5.06	308.59
AQVVSQGLDVLTA	2938	7.19	2	1456.7809	2		0		no	5.89	480.30
AVAGNISDPGLQK	2028	6.48	2	1268.6671	2		0		no	5.12	416.14
DPSASPGDAGEQAIR	11446	6.06	1	1469.6683	2		0		no	5.40	35.14
ELTPQVVSAR	1366	6.92	2	1169.6358	2		0		yes	4.64	787.86
EVAQK CTD K	2917	5.43	1	1091.5322	2		0	[6] Carbamidomethyl C [9] Methyl K	no	4.43	816.80
EVENSEDPKFR	8319	5.94	1	1348.6226	3		0		no	3.81	92.61
GWLRDPSASPGDAGEQAIR	4017	6.79	2	1981.9555	3		0		no	4.16	322.62
LLAVAAATPPDAPNREEVDFER	2275	6.81	2	2380.2032	3		0		no	5.12	754.78
M TGLVDEAIDTK	3898	6.89	2	1307.6299	2		0	[1] Oxidation M	no	5.06	433.03
QILDEAGK	4187	4.83	1	872.4493	2		0		no	3.81	351.58
SLGEISALTSK	284	5.65	1	1104.5943	2		0		yes	4.50	3460.52
SLLDASEEAIKK	3883	6.04	1	1302.7006	3		0		no	3.60	169.08
SLLDASEEAIKK	5416	6.04	1	1302.6881	2		0		no	5.47	154.49
STVEGIQASVK	3153	6.99	2	1117.5864	2		0		no	4.50	428.40
TDAGFTLR	3458	6.74	2	879.4477	2		0		no	3.74	235.53
TNLLQ V ER	3522	5.80	1	1131.5590	2		0		no	4.57	292.19

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance
											CTR
VMLVNSMNTV ⁺ K	246	5.22	1	1248.6599	2		0	[7] Carbamidomethyl C [11] Methyl K	yes	5.12	3348.13




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P12883

Myosin-7 OS=Homo sapiens OX=9606 GN=MYH7 PE=1 SV=5
18 peptides























Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance
											CTR
DTQIQLDDAVR	4668	6.64	1	1272.6294	2		0		no	5.26	104.5
IEDEQALGSQLQK	5833	6.33	2	1457.7377	2		0		no	5.61	60.9
IEDEQALGSQLQKK	6942	5.44	1	1585.8278	3		0		no	4.36	2.9
IEEEEELEAER	4616	7.04	2	1487.7001	2		0		no	5.75	52.9
ILNPAAIPEGQFIDSR	2181	7.47	2	1739.9151	2		0		no	6.79	0.3
ILNPAAIPEGQFIDSR	5788	7.47	1	1739.9155	3		0		no	4.22	1.1
ILYGDFR	3854	6.75	2	882.4614	2		0		no	4.09	17.6
INATLETK	4303	6.63	2	888.4858	2		0		no	3.81	68.5
IQAQSR	367	3.91	1	701.3718	1		0		no	7.89	1670.9
⁺ KGSSFQTVSALHR	103	4.19	1	1444.7357	2		0	[N-term] Formyl K N-TERM	yes	5.68	3.04e+00
⁺ KGSSFQTVSALHR	11272	---	---	1444.7285	3		0	[N-term] Formyl K N-TERM	yes	3.95	42.7
⁺ KGSSFQTVSALHR	306	5.07	1	1444.7336	2		0	[N-term] Formyl K N-TERM	yes	5.68	1.28e+00
⁺ KMDADLSQLQTEVEEAVQE ⁺ CR	2880	---	---	2492.1271	5		0	[1] Methyl K [20] Carbamidomethyl C	yes	4.22	493.8
⁺ KMDADLSQLQTEVEEAVQE ⁺ CR	1144	5.14	1	2492.1245	4		0	[1] Methyl K [20] Carbamidomethyl C	yes	4.85	2676.5
LAEQLIETSER	3372	7.13	2	1416.7074	2		0		no	5.40	40.0
LQEAAEAVEAVNAK	6090	6.48	1	1499.7418	2		0		no	5.82	4.1
LQQFFNHMHFVLEQEEYKK	2636	4.87	1	2494.2579	3		0		no	6.16	121.6
NKDPLNETVVGLYQK	1743	4.10	1	1716.8979	2		0		no	6.37	515.7
QLDEKEALISQLTR	4423	6.11	2	1642.8784	3		0		no	4.29	14.6
SLSTELFK	3694	6.27	2	923.4967	2		0		no	4.02	11.8
SVNDLTSQR	3673	7.01	2	1018.5000	2		0		no	4.16	247.5
VVDSLQTSLDAETR	5227	7.33	2	1532.7660	2		0		no	5.96	22.8




Tags	
	Anova p-value ≤ 0.05

	
	power>0.8
	q<0.05

P14543





















Nidogen-1 OS=Homo sapiens OX=9606 GN=NID1 PE=1 SV=3
21 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AE ¹ LNPSQPSR	5385	6.93	2	1257.5786	2		0	[3] Carbamidomethyl C	no	4.85	244.64	105
AE ¹ LNPSQPSRR	5172	5.83	1	1413.6853	3		0	[3] Carbamidomethyl C	no	3.74	166.74	7
ALEGLQYPFAVTSYGK	8722	6.14	2	1742.8744	2		0		no	6.44	55.44	54
ASLHGGEPTTIIR	3222	5.60	1	1350.7107	3		0		no	3.95	254.13	393
¹ VPGEVEK	4805	5.76	1	916.4395	2		0	[1] Carbamidomethyl C	no	4.16	240.26	51
EDLSPSITQR	3486	6.71	2	1144.5657	2		0		no	4.57	1009.04	412
EYTVTEPER	4573	4.97	1	1122.5300	2		0		no	4.43	218.89	46
EYTVTEPERDGASPSR	2413	6.92	2	1792.8211	3		0		no	4.36	728.25	888
GNLYWTDWNRDNPK	6000	5.53	1	1777.8143	3		0		no	4.16	139.90	26
GNLYWTDW ¹ NRDNPK	131	5.03	1	1793.8105	2		0	[9] Hydroxyl DKNP	yes	6.37	4196.91	5.44e+
GNLYWTDW ¹ NRDNPK	946	---	---	1793.8080	3		0	[9] Hydroxyl DKNP	yes	4.43	363.03	5315
LASSSR	5523	4.81	1	619.3191	1		0		no	7.06	68.65	9
NIFWTDNSLDRIEVAK	4095	5.90	1	1919.9692	3		0		no	4.78	241.01	68
QAEVTFVGHPGNLVIK	4498	5.47	2	1707.9206	3		0		no	4.57	182.13	91
¹ Q ¹ VAEGSPQR	5430	6.38	1	1130.5153	2		0	[2] Carbamidomethyl C	no	4.36	62.32	31
QDLGSPEGIAVDHLGR	1998	6.51	2	1662.8289	3		0		no	4.57	450.03	485
RVLFTDLVNPR	6145	5.46	1	1457.7942	3		0		no	4.02	85.96	67
TDSVR	2824	0.00	1	576.2860	1		0		no	6.65	213.52	155
TQFT ¹ EC ¹ SIGFR	6647	6.56	2	1504.6528	2		0	[5] Carbamidomethyl C [7] Carbamidomethyl C	no	5.61	171.37	69
VLFTDLVNPR	446	6.79	2	1301.6978	2		0		yes	5.40	2270.48	4472
VTDSVR	9501	---	---	675.3538	2		0		no	3.32	23.46	6
VTDSVR	2081	0.00	1	675.3544	1		0		no	7.89	280.04	235
YALSNSIGPVR	1475	7.22	2	1175.6257	2		0		yes	4.64	1050.40	869




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08572

Collagen alpha-2(IV) chain OS=Homo sapiens OX=9606 GN=COL4A2 PE=1 SV=4
18 peptides

















Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Aver Norr Abur CTR
AHNQDLGLAGS C LAR	2794	6.51	2	1581.7729	3		0	[12] Carbamidomethyl C	no	4.22	386
AHNQDLGLAGS C LAR	13789	6.51	1	1581.7617	2		0	[12] Carbamidomethyl C	no	6.16	16
ATPFIE C NGGR	2971	6.67	2	1220.5668	2		0	[7] Carbamidomethyl C	no	4.71	433
EGF P G P PGFIGPR	1020	5.50	1	1358.6618	2		0	[4] Hydroxyl DKNP [6] Hydroxyl DKNP	no	5.06	1667
EGF P G P PGFIGPR	2700	6.14	1	1374.6572	2		0	[4] Hydroxyl DKNP [6] Hydroxyl DKNP [7] Hydroxyl DKNP	no	5.12	464
FDVP C GGR	2209	5.76	1	906.4166	2		0	[5] Carbamidomethyl C	no	3.88	786
FSTMPFLY CN PGDV C YYASR	11499	---	---	2463.0511	2		0	[9] Carbamidomethyl C [10] Hydroxyl DKNP [15] Carbamidomethyl C	no	8.80	39
FSTMPFLY CN PGDV C YYASR	5419	5.56	1	2463.0334	3		0	[9] Carbamidomethyl C [10] Hydroxyl DKNP [15] Carbamidomethyl C	no	5.06	180
GDPG D TGAPGPVGMK	830	4.43	1	1370.5968	2		0	[5] Hydroxyl DKNP	yes	5.19	3134
GEQGFMG N TGPTGAVGDRGPK	4540	5.52	1	2047.9327	3		0	[8] Hydroxyl DKNP	no	4.43	251
GLDGYQPGDGPR	1174	6.84	2	1230.5682	2		0		yes	4.71	2767
GLPGEVLGAQPGPR	4485	5.62	2	1346.7095	2		0		no	5.12	209
GLPGEVLGAQ P GPR	3879	6.16	2	1362.7194	2		0	[11] Hydroxyl DKNP	no	5.19	254
GL P GEVLGAQ P GPR	767	6.50	2	1378.7189	2		0	[3] Hydroxyl DKNP [11] Hydroxyl DKNP	no	5.19	1344
GPRGEQGFMGNTGPTGAVGDR	341	4.59	1	2059.9466	2		0		yes	7.41	3766
GVSGFPGA D GIPGHPGQGGPR	12138	4.89	1	1931.9517	2		0	[9] Hydroxyl DKNP	no	7.48	52
GVSGFPGA D Gi P GH P GQGGPR	1379	6.25	1	1963.9110	3		0	[9] Hydroxyl DKNP [12] Hydroxyl DKNP [15] Hydroxyl DKNP	no	4.16	1203
IAVQPGTVGPQGR	566	7.15	2	1278.7038	2		0		no	4.92	1480
SVSIGYLLVK	3315	6.62	2	1077.6437	2		0		no	4.57	277
SYWLSTTAPL L MM P VAEDEIKPYISR	11163	5.26	1	3026.4439	3		0		no	6.09	58




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances
								[11] Hydroxyl DKNP [14] Hydroxyl DKNP			

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02538



















Keratin_type II cytoskeletal 6A OS=Homo sapiens OX=9606 GN=KRT6A PE=1 SV=3
12 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ADTLTDEINFLR	571	8.23	16	1406.7042	2		0		no	5.54	3915.82	37
AIGGGLSSVGGGSSTIK	1319	7.31	9	1446.7603	2		0		no	5.61	1012.24	14
GEMALKDAK	2409	6.30	1	993.4826	2		0	[7] Hydroxyl DKNP [9] Hydroxyl DKNP	no	4.22	1747.15	6
ISIGGGSCAISGGYGSR	3837	6.89	2	1597.7466	2		0	[8] Carbamidomethyl C	no	5.96	448.33	5
ISIGGGSCAISGGYGSR	6135	5.94	1	1597.7682	3		0	[8] Carbamidomethyl C	no	4.02	122.38	
LEGLEDALQK	1321	5.91	1	1114.5882	2		0		no	4.50	2984.82	4
NTKQIEAIEINR	1530	6.19	1	1330.6882	3		0	[1] Hydroxyl DKNP	no	3.74	580.86	5
RTAAENEFVTLK	377	6.04	1	1393.7116	3		0	[6] Hydroxyl DKNP	yes	3.81	6210.25	46
RTAAENEFVTLK	2142	6.04	1	1393.7051	2		0	[6] Hydroxyl DKNP	yes	5.54	957.68	4
SGFSSVSISR	1416	7.44	5	1011.4975	2		0		no	4.09	1166.08	11
TAAENEFVTLK	2516	5.43	1	1221.6108	2		0		no	4.85	741.90	4
TAAENEFVTLKK	540	8.05	11	1349.7200	3		0		yes	3.46	2992.63	40
TAAENEFVTLKK	2995	8.05	3	1349.7163	2		0		yes	5.47	362.89	4
VELQAKADTLTDEINFLR	219	4.82	2	2075.0856	3		0		yes	5.68	6061.02	2.27e
VELQAKADTLTDEINFLR	461	4.82	2	2075.0856	4		0		yes	4.78	2509.05	93
YEELQVTAGR	798	7.57	10	1164.5854	2		0		no	4.78	3599.80	26




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P00738

Haptoglobin OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1
16 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	M
AVGDKLPECEAVCGKPK	2978	6.86	2	1856.9182	4		0	[9] Carbamidomethyl C [13] Carbamidomethyl C	no	3.88	322.61	1
DIAPTLTLVVGK	7169	6.28	2	1289.7133	2		0		no	5.19	179.33	
GSFPWQAK	6943	6.71	1	919.4584	2		0		no	3.74	32.91	
HYEGSTVPEK	5502	7.08	1	1145.5334	2		0		no	4.57	75.72	
+KQLVEIEK	2596	6.98	2	1013.5726	2		0	[N-term] Formyl K N-TERM	no	4.50	327.92	1
LNNEK	8622	---	---	616.3169	2		0		yes	3.12	30.60	
LNNEK	1079	0.00	1	616.3193	1		0		yes	7.13	459.15	4
LRTEGDGVYTLNNEK	1643	6.66	2	1707.8351	3		0		no	4.16	429.80	
LRTEGDGVYTLNNEK	14550	---	---	1707.8278	2		0		no	6.44	15.91	
NPANPVQR	4925	6.44	1	894.4583	2		0		no	3.88	130.26	
QLVEIEK	2384	6.57	2	857.4852	2		0		no	4.09	194.60	
SPVGVOPIILNEHTFCAGMSK	4016	6.33	2	2187.0455	3		0	[7] Hydroxyl DKNP [15] Carbamidomethyl C	no	5.12	193.35	
TEGDGVYTLNDK	4934	7.05	1	1310.6034	2		0		no	5.12	193.59	
TEGDGVYTLNDKK	5519	7.10	2	1438.6969	3		0		no	3.95	133.79	
TEGDGVYTLNNEK	1945	7.89	2	1438.6591	2		0		yes	5.54	546.59	
VMPICLPSK	3551	6.70	1	1059.5433	2		0	[2] Oxidation M [5] Carbamidomethyl C	no	4.50	351.66	
VMPICLPSKDYAEVGR	864	7.54	2	1849.9072	3		0	[2] Oxidation M [5] Carbamidomethyl C	yes	4.85	1555.00	1
YVMPVPVADQDQCIR	4109	7.20	2	1722.8001	2		0	[3] Oxidation M [12] Carbamidomethyl C	no	6.44	286.22	

Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q96JY6

PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 PE=1 SV=1
13 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalise Abundance
											CTR
AGDSAVLVLPSPGPR	2130	7.60	2	1531.8273	2		0		no	5.96	1122.72
AGSPFSPPPSSSLTGEAAISR	6994	7.15	1	2102.0193	2		0		no	7.62	102.20
AGSPFSPPPSSSLTGEAAISR	7132	7.15	1	2102.0150	3		0		no	5.12	104.57
STSIANQAVR	4550	7.30	2	1205.5784	2		0	[1] Carbamidomethyl C	no	4.71	147.41
DFHTPIMVTKVAER	7460	6.05	1	1642.8470	3		0		no	4.02	100.58
GGTPAFLPSSLSPQSSLPASR	4044	7.85	2	2056.0517	3		0		no	4.64	172.46
GGTPAFLPSSLSPQSSLPASR	4492	7.85	2	2056.0491	2		0		no	7.69	220.50
GHFVVGELYEK	6091	5.05	1	1654.7158	3		0	[7] Hydroxyl DKNP [11] Carbamidomethyl C	no	3.95	327.35
LLQEALAEER	715	8.71	7	1299.6651	2		0		yes	5.19	1930.85
LQLDR	4255	7.16	1	643.3649	2		0		no	3.19	118.48
LQLDR	6591	---	---	643.3575	1		0		no	7.76	37.15
LSYSGRPGSR	6319	---	---	1078.5519	1		0		no	11.91	42.63
SFQSLASPGLPAADR	5085	7.19	2	1675.7953	2		0	[7] Carbamidomethyl C	no	6.37	81.09
SSYSPTSLSR	1371	8.00	6	1267.6132	2		0		no	4.99	985.96
TYTESQSLR	1455	8.16	6	1170.5497	2		0		yes	4.64	1763.74
YSAPATLSSR	1526	7.92	5	1051.5287	2		0		yes	4.22	1008.94

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P33778

Histone H2B type 1-B OS=Homo sapiens OX=9606 GN=H2BC3 PE=1 SV=2
13 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
MGMNSFVNDIFER	3284	8.00	1	1774.8015	2		0	[2] Oxidation M [5] Oxidation M	no	6.72	279.35	18.4
MGMNSFVNDIFER	3122	6.26	1	1774.7991	2		0	[2] Oxidation M [6] Hydroxyl DKNP	no	6.65	1122.48	615.2
EIQTAVR	432	8.42	12	815.4507	2		0		yes	3.53	5046.49	5616.3
EIQTAVR	1757	8.42	1	815.4506	1		0		yes	8.93	402.54	254.6
EIQTAVR	1348	0.00	3	797.4385	2		0	[C-term] Dehydrated	no	3.46	1001.98	874.8
ESYSIYVYK	3767	6.78	2	1150.5530	2		0		no	4.78	348.35	203.7
IAGEASRLAHYNK	4	5.65	3	1428.7500	2		0		yes	5.61	1.06e+005	3.20e+00
IAGEASRLAHYNK	6049	5.52	1	1458.7519	2		0		no	5.54	295.42	37.0




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
								[12] Hydroxyl DKNP [13] Methyl K				
LLPGELAK	3725	8.59	2	952.5944	1		0		no	11.70	130.90	42.0
LLPGELAK	90	8.59	15	952.6019	2		0		yes	4.22	1.80e+004	2.09e+00
LLPGELAK	4563	6.67	1	966.6097	2		0	[9] Methyl K	no	4.22	92.24	189.3
QTAVR	682	0.00	3	573.3244	1		0		no	6.58	1730.83	1566.9
QTAVR	4246	---	---	573.3238	2		0		no	3.12	117.90	42.1
QVHPDTGISSK	1574	8.00	4	1167.5880	3		0		no	3.60	448.00	245.9
QVHPDTGISSK	4126	8.00	1	1167.5883	2		0		no	4.71	166.97	85.0
QVHPDTGISSK	6443	4.74	1	1167.5851	3		0		no	3.60	25.51	332.7
QVHPDTGISSK	15224	5.73	1	1183.5843	2		0	[5] Hydroxyl DKNP	no	4.78	213.16	52.0
STITSR	971	7.48	1	663.3556	1		0		no	7.69	530.57	283.9
STITSR	8653	---	---	663.3559	2		0		no	3.12	22.79	0.9

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P68363
















Tubulin alpha-1B chain OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1
12 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVFVDLEPTVIDEVR	495	8.69	9	1700.8969	2		0		yes	6.58	3158.47	
AVFVDLEPTVIDEVR	2754	8.69	3	1700.8988	3		0		yes	4.50	415.18	
DVNAAIATIK	661	8.64	4	1014.5670	2		0		yes	4.29	2176.40	
IHFPLATYAPVISA EK	4830	7.07	2	1755.9542	3		0		no	4.78	437.22	
LSVDY GK	3421	6.59	1	780.3994	2		0		no	3.53	196.23	
LSVDY GKK	3520	7.51	2	908.4912	2		0		no	3.95	299.18	
NLDIERPTYTNLNR	7702	6.07	1	1717.8667	3		0		no	4.22	73.84	
QLFHPEQLITGK	7925	6.01	1	1409.7622	3		0		no	4.09	60.10	
QLFHPEQLITGKEDAANNYAR	3860	6.79	2	2414.1878	4		0		no	4.85	382.31	
SIQFVDWCP TGF K	10980	7.60	2	1583.7464	2		0	[8] Carbamidomethyl C	no	5.89	60.06	
TGTYRQLFHPEQLITGK	602	5.04	2	1988.0685	3		0		yes	4.57	1381.79	
TGTYRQLFHPEQLITGK	3104	5.04	2	1988.0634	3		0		no	5.47	95.93	
TIGGGDDSFNTFFSETGAGK	4168	7.59	2	2006.8807	2		0		no	7.06	356.61	
VGINYQPPTVVP GGDLAK	2144	7.76	5	1823.9720	2		0		no	6.79	848.75	
VGINYQPPTVVP GGDLAK	3920	7.76	2	1823.9703	3		0		no	4.71	210.02	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P26038


Moesin OS=Homo sapiens OX=9606 GN=MSN PE=1 SV=3
16 peptides


















Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALELEQER	750	6.70	2	986.5033	2		0		yes	4.22	4381.75	2595.60
ALTSELNARDES K	3650	5.87	1	1517.7682	3		0	[14] Methyl K	no	4.09	491.12	0.28
APDFVFYAPR	1948	7.32	3	1181.5876	2		0		no	4.85	636.30	255.70
AQ M VQEDLEK	4547	6.04	2	1205.5612	2		0	[3] Oxidation M	no	5.06	334.24	49.30
AQ M VQEDLEKTR	6842	5.82	1	1462.7080	3		0	[3] Oxidation M	no	3.88	95.86	15.14
AQQELEEQTR	9545	6.36	1	1230.5830	2		0		no	4.78	69.84	1.30
AQQELEEQTRR	2159	6.45	2	1386.6825	3		0		no	3.60	438.36	105.10
EDAVLEYLK	117	5.33	1	1078.5546	1		0		yes	11.98	3907.25	1.85e+004
ESEAVEWQQK	3972	6.05	2	1232.5744	2		0		no	4.71	442.51	226.60
IGFPWSEIR	3680	6.95	2	1103.5776	2		0		no	4.57	289.92	65.60
ISQLE M AR	1559	6.47	2	962.4801	2		0	[6] Oxidation M	yes	4.02	2682.65	683.70
KTQEQLALE M AELTAR	5129	5.78	1	1846.9354	3		0	[10] Oxidation M	no	4.43	148.45	21.60
QLFDQVVK	3002	5.67	2	975.5385	2		0		no	4.22	416.61	142.40
QRIDEFESM	5582	5.91	2	1153.5188	2		0		no	4.43	246.87	65.60
QRIDEFES M	2468	6.52	3	1169.5060	2		0	[9] Oxidation M	no	4.57	648.94	233.10
RKPDTIEVQQ M K	4229	5.97	2	1487.7746	3		0	[12] Hydroxyl DKNP	no	3.81	324.39	14.10




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01024

Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
17 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normal Abundance
											CTR
AAVYHHFISDGVR	4260	4.67	1	1470.7334	2		0		no	5.68	333.20




















Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normal Abundance CTR
AGDFLEANYMNLQR	3925	6.02	1	1656.7567	2		0	[11] Hydroxyl DKNP	no	6.23	345.08
AGDFLEANYMNLQR	9587	---	---	1656.7577	3		0	[11] Hydroxyl DKNP	no	3.95	56.95
CAEENCIFIQK	9258	5.69	1	1297.5510	2		0	[1] Carbamidomethyl C [6] Carbamidomethyl C	no	4.99	96.04
DICEEQVNSLPGSITK	8576	5.99	2	1788.8475	2		0	[3] Carbamidomethyl C	no	6.65	131.35
DQLTCNKFDLK	10282	5.41	1	1380.6686	2		0	[5] Carbamidomethyl C	no	5.26	131.12
DSCVGSLVVK	4723	5.80	1	1062.5279	2		0	[3] Carbamidomethyl C	no	4.43	179.32
FYYIYNEK	1642	5.28	1	1138.5363	2		0		yes	4.71	1311.43
ILLQGTQVPAQMTEDAVDAER	6337	5.76	2	2172.0636	2		0	[14] Hydroxyl DKNP	no	7.76	170.90
IPIEDGSGEVVLSR	2924	6.33	2	1469.7647	2		0		no	5.61	786.95
IPIEDGSGEVVLSRK	2328	5.64	1	1597.8573	3		0		no	4.02	580.70
ISLPESLK	3509	5.76	2	885.5156	2		0		no	3.88	202.25
NEQVEIR	2722	6.37	2	886.4547	2		0		no	3.95	713.22
NTMILEICTR	878	5.69	2	1265.6147	2		0	[1] Hydroxyl DKNP [8] Carbamidomethyl C	yes	4.99	3678.50
QGALELIK	546	5.46	2	870.5176	2		0		yes	3.88	1683.30
SGSDEVQVGQQR	2873	7.08	2	1288.6011	2		0		no	4.85	406.06
TFISPIK	6108	6.05	1	804.4709	2		0		no	3.67	96.61
VPVAVQGEDTVQSLTQGDGVAK	8916	5.59	2	2197.1057	3		0		no	5.26	131.15



Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P53420

Collagen alpha-4(IV) chain OS=Homo sapiens OX=9606 GN=COL4A4 PE=1 SV=3
18 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normal Abundance CTR
AAPFLEQGR	525	7.01	2	1147.5475	2		0	[7] Carbamidomethyl C	yes	4.50	3698.1
ADLQFSSAPADTLK	4767	6.03	2	1559.7805	2		0		no	6.16	180.4
ADLQFSSAPADTLK	3973	5.32	1	1575.7699	2		0	[9] Hydroxyl DKNP	no	6.16	106.7
ADLQFSSAPADTLKESQAQR	10659	4.96	1	2275.0846	3		0		no	5.06	42.7

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalized Abundance CTR
								[9] Hydroxyl DKNP			
AGPVGPPGLGF ^P GPPGER	3511	4.78	1	1673.8326	3		0	[12] Hydroxyl DKNP	no	4.22	337.0
GD ^P GF ^P GGR	2380	6.10	1	890.3914	2		0	[3] Hydroxyl DKNP [6] Hydroxyl DKNP	no	3.53	541.7
GD ^P GF ^P GGR	10698	---	---	890.3843	1		0	[3] Hydroxyl DKNP [6] Hydroxyl DKNP	no	9.00	24.3
GD ^P GSPGISPPGPR	3452	5.43	2	1321.6230	2		0	[2] Hydroxyl DKNP [3] Hydroxyl DKNP	no	4.85	355.3
GD ^P GSPGIS ^P PGPR	1141	5.92	1	1337.6192	2		0	[3] Hydroxyl DKNP [6] Hydroxyl DKNP [10] Hydroxyl DKNP	no	4.99	1195.9
GEPGPPADVDD ^C PR	10330	3.83	1	1480.6151	3		0	[12] Carbamidomethyl C	no	3.95	27.4
GL ^P GF ^P GF ^P GER	1042	5.79	2	1277.6053	2		0	[3] Hydroxyl DKNP [6] Hydroxyl DKNP [9] Hydroxyl DKNP	yes	4.64	4090.0
GPEGAM ^M GL ^P GM ^R	1629	6.31	2	1219.5329	2		0	[6] Oxidation M [9] Hydroxyl DKNP [11] Oxidation M	no	4.57	1427.5
GPTGL ^P GPR	5781	5.45	1	866.4505	2		0	[6] Hydroxyl DKNP	no	3.60	369.5
GPTGLPGPRGEPGPPADVDD ^C PR	366	4.33	1	2313.0780	4		0	[21] Carbamidomethyl C	yes	4.64	2726.2
GPTGLPGPRGEPGPPADVDD ^C PR	4879	---	---	2313.0680	3		0	[21] Carbamidomethyl C	yes	5.26	61.6
GPTGLPGPRGEPGPPADVDD ^C PR	1432	---	---	2313.0702	5		0	[21] Carbamidomethyl C	yes	3.95	592.7
GQKGDTIS ^C NVTY ^P GR	10602	4.84	1	1767.8206	2		0	[9] Carbamidomethyl C [14] Hydroxyl DKNP	no	6.51	71.8
GVDGV ^P GS ^P GP ^P GR	3194	5.72	1	1295.6079	2		0	[6] Hydroxyl DKNP [9] Hydroxyl DKNP [11] Hydroxyl DKNP	no	4.85	493.7
IPGL ^P GAP ^P GM ^R	1270	5.75	2	1112.5707	2		0	[5] Hydroxyl DKNP [8] Hydroxyl DKNP [10] Oxidation M	no	4.29	2317.9
LWTGYSLLYLEGQEK	9963	5.34	1	1798.9081	2		0		no	6.93	56.2
^P GF ^P GGR	9648	---	---	718.3395	1		0	[1] Hydroxyl DKNP [4] Hydroxyl DKNP	no	7.89	33.5
^P GF ^P GGR	2748	0.00	1	718.3398	2		0	[1] Hydroxyl DKNP [4] Hydroxyl DKNP	no	3.25	318.1

Tags	
	Anova p-value ≤ 0.05
	power>0.8

P69905

Hemoglobin subunit alpha OS=Homo sapiens OX=9606 GN=HBA1 PE=1 SV=2
17 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Av At C
DPVNFK	2635	---	---	718.3646	2		0		no	3.25	
DPVNFK	223	0.00	1	718.3662	1		0		no	8.10	
LRVDPVNFK	5596	---	---	1086.6152	3		0		no	3.32	
LRVDPVNFK	1155	7.48	5	1086.6118	2		0		no	4.78	
MFLSFPTTK	115	8.41	10	1086.5495	2		0	[1] Oxidation M	yes	4.43	2.
MFLSFPTTK	5036	8.41	1	1086.5412	1		0	[1] Oxidation M	no	12.12	
MFLSFPTTK	2336	7.12	4	1100.5582	2		0	[1] Oxidation M [9] Methyl K	no	4.43	
PVNFK	149	0.00	1	603.3376	1		0		yes	6.65	2.
PVNFK	119	0.00	4	603.3396	1		0		no	7.13	
PVNFK	472	0.00	1	603.3400	2		0		no	2.98	
SFPTTK	2197	0.00	1	679.3553	1		0		no	7.62	
TNVKAAWGK	2681	6.25	3	973.5259	2		0		no	4.16	
TYFPHFDLSHGSAQVK	1844	6.02	3	1832.8869	4		0		no	4.02	
TYFPHFDLSHGSAQVK	3075	6.02	2	1832.8859	3		0		no	4.85	
TYFPHFDLSHGSAQVKGHGK	533	4.19	1	2212.0790	3		0		no	4.85	1.
VADALTNAVAHVDMPNALSALSDLHAHK	6206	5.48	1	3011.4797	5		0	[14] Hydroxyl DKNP	no	4.64	
VDPVNFK	778	8.01	4	817.4335	1		0		no	9.35	
VDPVNFK	168	8.01	12	817.4383	2		0		no	3.46	
VGAHAGEYG	2392	0.00	2	841.3708	1		0		no	9.14	
VGAHAGEYG	5145	---	---	841.3721	2		0		no	3.46	
VGAHAGEYGA	3080	0.00	1	912.4068	1		0		no	9.83	
VGAHAGEYGA	2704	0.00	1	912.4150	2		0		no	3.74	
VGAHAGEYGAE	1719	0.00	1	1041.4567	2		0		no	4.02	
VGAHAGEYGAEA	2559	0.00	1	1112.5053	2		0		no	4.29	
VGAHAGEYGAEALER	775	8.18	6	1528.7255	2		0		yes	5.82	
VGAHAGEYGAEALER	127	8.18	12	1528.7329	3		0		yes	3.95	1.
VGAHAGEYGAEALER	1956	0.00	1	1510.7147	3		0	[C-term] Dehydrated	no	4.16	

Tags

Anova p-value ≤ 0.05

power>0.8

q<0.05

P11021

Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2
15 peptides







Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DAGTIAGL ^N VMR	2343	6.38	2	1232.6153	2		0	[9] Hydroxyl DKNP	no	4.92	919.87	385.56
EFFNGKEPSR	2177	4.67	1	1209.5801	2		0		no	4.78	719.21	1411.35
ELEEIVQPIISK	6033	6.37	1	1396.7579	2		0		no	5.54	88.59	87.49
FEELNMDLFRSTMKPQVK	967	5.00	1	2212.0776	3		0		yes	4.78	6807.30	1722.06
IINEPTAAAIAYGLDKR	1739	7.07	3	1814.9894	3		0		no	4.99	630.42	316.18
ITITNDQNR	2325	6.52	2	1073.5386	2		0		no	4.36	1881.74	329.41
ITPSYVAFTPEGER	1037	6.47	5	1565.7896	2		0		no	5.96	1277.04	1224.00
LSSED ^K ETMEK	4236	4.05	1	1309.6181	2		0	[6] Methyl K	no	4.99	323.88	21.43
NQLTSNPENTVFDK	5432	6.64	2	1676.7992	2		0		no	6.44	167.18	62.52
NQLTSNPENTVFDKAKR	3154	6.56	2	1832.8971	3		0		no	4.78	377.28	254.19
SQIFSTASDNQPTVTIK	6568	6.55	2	1835.9072	2		0		no	6.93	161.23	65.47
STMKPQVKVLESD ^L ^K	1505	4.47	2	1830.9937	4		0	[16] Methyl K	yes	3.81	1083.44	363.25
STMKPQVKVLESD ^L ^K	1909	4.47	2	1830.9765	3		0	[16] Methyl K	yes	4.71	1437.23	650.53
TWNDSVQQDIK	3873	4.05	1	1429.6584	2		0		no	5.47	497.64	205.09
VTAEDKGTGN ^K	386	5.84	1	1132.5708	2		0	[11] Methyl K	yes	4.43	3405.05	8894.29
VYGERPLTK	5394	5.16	1	1190.6184	3		0		no	3.53	209.71	80.89




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02787

Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3
12 peptides











Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ASYLD ^C IR	1762	6.39	4	996.4769	2		0	[6] Carbamidomethyl C	no	4.22	1065.70	233.5
DGAGDVAQVK	6980	4.39	1	977.4800	2		0		no	4.02	114.58	55.4
DLLFKDSAAGFLK	8220	4.88	1	1489.7874	2		0		no	5.75	91.67	25.9
DLLFRDDTV ^C LAK	3543	4.90	1	1564.7886	3		0	[10] Carbamidomethyl C	no	4.09	349.94	23.6
DLLFRDDTV ^C LAK	8088	4.90	1	1564.7821	2		0	[10] Carbamidomethyl C	no	6.37	118.38	2.6
DSGFQMNQLR	1107	5.22	1	1194.5225	3		0		yes	3.39	538.13	1881.0
DSGFQMNQLR	1542	5.22	1	1194.5346	2		0		yes	4.92	945.00	1837.2
DSGFQ ^M NQLR	2419	5.84	3	1210.5438	2		0	[6] Oxidation M	no	4.64	1010.90	195.1

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EGT C PEAPTDE C KPVK	3980	5.79	4	1816.7948	3		0	[4] Carbamidomethyl C [12] Carbamidomethyl C	no	4.22	303.44	3.5
IE C VSAETTED C IAK	5527	6.41	4	1724.7591	2		0	[3] Carbamidomethyl C [12] Carbamidomethyl C	no	6.44	215.44	7.8
M YLGYEYVTAIR	2221	6.44	4	1493.7191	2		0	[1] Oxidation M	no	5.82	751.02	103.0
SASDLTWDLNK	3654	6.08	4	1248.6027	2		0		yes	4.92	561.44	644.1
SVIPSDGPSVA C VK	1927	6.53	4	1414.7074	2		0	[12] Carbamidomethyl C	no	5.33	752.10	300.0
YLGEYVK	1744	6.58	4	999.4936	2		0		no	4.36	886.72	158.5

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02462

Collagen alpha-1(IV) chain OS=Homo sapiens OX=9606 GN=COL4A1 PE=1 SV=4
13 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AHGQDLGTAGS C LRK	2556	4.29	1	1569.7866	3		0	[12] Carbamidomethyl C	no	4.09	468.90	
GDHGFPGSSGPR	2997	4.01	1	1169.5138	2		0		no	4.43	370.53	
G D PGT P GVPGK	5645	5.62	1	1012.4824	2		0	[2] Hydroxyl DKNP [6] Hydroxyl DKNP	no	3.88	87.12	
GEAGP P GPPGIVIGTGPLGEK	3598	4.71	1	1915.0031	3		0	[6] Hydroxyl DKNP	no	5.75	155.09	
GEAGP P GPPGIVIGTGPLGEK	3409	4.71	1	1914.9944	2		0	[6] Hydroxyl DKNP	no	7.20	135.53	
GE K GFPGF P GLDMGPK	2561	4.98	1	1759.8520	2		0	[3] Methyl K [9] Hydroxyl DKNP	no	6.72	327.92	
GF P GTSLPGPSGR	3563	5.42	2	1244.6154	2		0	[3] Hydroxyl DKNP	no	4.78	466.73	
GF P GTSL P GPSGR	636	6.33	2	1260.6110	2		0	[3] Hydroxyl DKNP [8] Hydroxyl DKNP	yes	4.78	2933.53	
G P PGGVGF P GSR	845	6.09	2	1115.5389	2		0	[2] Hydroxyl DKNP [9] Hydroxyl DKNP	yes	4.16	1595.06	
GQIGPIGEK	1097	4.20	1	897.5037	2		0		yes	3.88	2667.26	
GVPGIPGPQGSPGLPGDK	7093	4.15	1	1628.8516	2		0		no	6.37	139.96	
GY P GT P GPR	7921	---	---	932.4331	1		0		no	10.32	30.28	



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance
											CTR
								[3] Hydroxyl DKNP [6] Hydroxyl DKNP			
GY ⁺ GT ⁺ PGPR	1466	5.72	2	932.4354	2		0	[3] Hydroxyl DKNP [6] Hydroxyl DKNP	no	3.67	654.22
HSQTIDDPQ ⁺ CP ⁺ SGTK	13760	---	---	1669.7431	2		0	[10] Carbamidomethyl C	no	6.23	10.68
HSQTIDDPQ ⁺ CP ⁺ SGTK	1794	6.03	2	1669.7356	3		0	[10] Carbamidomethyl C	no	3.88	697.56
SAPFIE ⁺ CHGR	3609	6.21	1	1172.5432	2		0	[7] Carbamidomethyl C	no	4.57	335.85
SAPFIE ⁺ CHGR	1875	5.81	1	1172.5423	2		0	[7] Carbamidomethyl C	no	4.57	795.34
SAPFIE ⁺ CHGR	9300	6.21	1	1172.5363	3		0	[7] Carbamidomethyl C	no	3.25	36.59
SAPFIE ⁺ CHGR	5905	---	---	1172.5382	3		0	[7] Carbamidomethyl C	no	3.25	78.07




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P15311

Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=4
13 peptides














Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AERELSEQIQR	256	5.15	1	1357.6971	2		0		yes	5.47	1.41e+004	6201.62
AERELSEQIQR	450	5.06	2	1357.6962	3		0		no	3.74	5991.53	2829.87
AERELSEQIQR ⁺	184	0.00	1	1339.6877	3		0	[C-term] Dehydrated	yes	3.60	1.92e+004	1.12e+004
A ⁺ K ⁺ EELER	3460	5.20	1	889.4489	2		0	[2] Hydroxyl DKNP	no	3.74	270.57	279.51
ALQLEEER	1710	5.10	1	986.4980	2		0		no	4.09	1200.42	568.33
EAQDDL VK	4613	5.69	1	916.4473	2		0		no	3.95	414.59	187.76
ELSEQIQR	1832	6.94	4	1001.5136	2		0		no	4.09	810.34	406.96
ETVEREKEQMMR	3661	5.28	1	1564.7185	3		0		no	4.02	164.24	109.26
ETVEREKEQMMR	5950	5.28	1	1564.7219	4		0		no	3.60	55.51	8.85
IALL ⁺ EEAR	2922	6.73	4	913.5207	2		0		no	4.09	416.67	211.81
LQDYEEK	4483	5.29	1	923.4228	2		0		no	3.95	271.24	85.09
QLEEER	5759	0.00	1	802.3823	1		0		no	8.66	85.69	10.50
QRIDEFEAL	1388	6.96	4	1119.5546	2		0		no	4.43	462.63	665.32
SGYLSSER	6458	6.44	1	897.4220	2		0		no	3.81	217.47	129.48




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VSAQEV RK	421	5.33	1	915.5145	2		0		yes	3.95	1.07e+004	3817.46
VSAQEV RK	14373	---	---	915.5168	3		0		yes	2.98	30.83	0.00

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P62805

Histone H4 OS=Homo sapiens OX=9606 GN=H4C1 PE=1 SV=2
9 peptides














Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DAVTYTEHAK	1959	8.09	5	1133.5365	2		0		no	4.71	561.72	462.64
DAVTYTEHAK	9410	---	---	1133.5328	3		0		no	3.32	34.52	2.97
DNIQGITKPAIR	818	8.28	6	1324.7453	3		0		no	3.95	1530.88	1162.93
DNIQGITKPAIR	1949	8.28	4	1324.7449	2		0		no	5.47	550.44	310.00
ISGLIYEETR	541	8.87	12	1179.6119	2		0		yes	4.71	3617.04	3275.47
ISGLIYEETRGVLK	4667	7.62	2	1576.8809	3		0		no	4.09	226.77	164.45
QGITKPAIR	3436	0.00	1	982.5929	2		0		no	4.22	209.28	137.51
TLYGFGG	73	8.12	12	713.3402	1		0		yes	8.24	1.75e+004	1.64e+004
TVTAM ^{MD} VVYALK	1726	6.98	2	1325.6890	2		0	[5] Oxidation M	no	5.61	606.56	234.94
TVTAM ^{MD} VVYALK	2364	7.60	1	1325.6889	2		0	[5] Oxidation M	no	5.61	585.30	241.03
TVTAM ^{MD} VVYALKR	1293	7.69	2	1481.7920	3		0	[5] Oxidation M	no	3.74	1200.82	544.17
TVTAM ^{MD} VVYALKR	1325	6.96	4	1481.7931	3		0	[5] Oxidation M	no	3.74	1163.44	441.20
VFLENVIR	726	8.71	6	988.5717	2		0		yes	4.36	1179.46	1649.02




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01860

Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2
11 peptides










Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALPAPIEK	1677	7.30	4	837.4897	2		0		no	4.02	383.65	168.9
APIEK	4070	0.00	1	556.3195	1		0		no	6.58	104.61	60.2
DTL M ISR	538	7.55	4	850.4242	2		0	[4] Oxidation M	yes	3.67	4950.25	2246.4
DTL M ISR	4486	7.55	2	850.4229	1		0	[4] Oxidation M	no	9.42	162.44	1.3
EPQVYTLPPSREEMTK	7536	5.39	1	1903.9163	3		0		no	4.29	144.22	22.3
EPQVYTLPP S REEMTK	1749	6.71	2	1919.9293	3		0	[9] Hydroxyl DKNP	yes	4.64	3363.18	377.0
GPSVFPLAP C SR	790	7.75	4	1286.6443	2		0	[10] Carbamidomethyl C	no	4.92	1732.07	206.4
NQVSLT C LVK	1671	8.30	4	1160.6208	2		0	[7] Carbamidomethyl C	no	4.92	1224.40	527.3
PAPIEK	573	0.00	2	653.3754	1		0		no	7.48	1001.12	170.3
PAPIEK	959	0.00	2	653.3751	2		0		no	3.25	670.02	136.5
S CDTPPP C PR	3620	6.62	2	1185.4927	2		0	[2] Carbamidomethyl C [8] Carbamidomethyl C	no	4.50	602.14	11.6
STSGGTAALG C LVK	2289	7.51	4	1320.6467	2		0	[11] Carbamidomethyl C	no	5.19	665.50	156.3
WYVDGVEVHNAK	2879	5.34	1	1415.6685	2		0		yes	5.40	324.31	1125.0

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P68431












Histone H3.1 OS=Homo sapiens OX=9606 GN=H3C1 PE=1 SV=2
6 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DIQLAR	1024	8.54	5	714.4024	1		0		no	8.38	1034.15	1004.35
DIQLAR	1392	8.54	3	714.4024	2		0		no	3.39	607.57	756.33
EIAQDFKTDLR	999	7.49	5	1334.6822	3		0		no	4.02	1204.71	1331.05
EIAQDFKTDLR	2657	7.49	2	1334.6807	2		0		no	5.47	201.14	160.73
EIAQDF K TDLR	727	7.22	1	1348.6991	3		0	[7] Methyl K	yes	3.88	1474.60	1584.27
EIAQDF K TDLR	1834	7.22	1	1348.6964	2		0	[7] Methyl K	yes	5.61	466.81	399.27
EIAQDFKTDLR +	1946	0.00	2	1316.6717	3		0	[C-term] Dehydrated	no	3.88	396.59	398.37
STELLIR	253	8.29	11	830.4883	2		0		yes	3.67	5092.18	5648.60
STELLIR	1569	8.29	2	830.4868	1		0		no	9.63	466.08	327.96
VT M PKDIQLAR	2692	6.45	2	1399.7829	3		0	[4] Oxidation M	yes	4.09	592.99	2476.29

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q15599









Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens OX=9606 GN=SLC9A3R2 PE=1
SV=2
9 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EIFS NF	3213	5.18	1	755.3490	1		0		yes	8.31	182.12	244.05
HA EVVASIK	3917	6.51	2	952.5325	2		0		no	4.57	221.71	47.85
LIEVNGQNVEGLR	6550	6.32	1	1439.7498	2		0		no	5.54	129.30	13.91
LLVVD PETDEHFK	6581	5.31	2	1540.7758	3		0		no	3.95	74.24	13.27
LLVVD PETDEHFKR	4021	6.38	2	1696.8770	3		0		no	4.22	156.84	92.00
LLVVD PETDEHFKR	4733	6.38	2	1696.8754	4		0		no	3.39	129.48	55.16
LLVVD QETDEELR	7257	6.43	2	1557.7726	2		0		no	6.16	115.16	7.29
LLVVD QETDEELRR	3614	6.11	2	1713.8872	3		0		no	4.36	272.56	108.24
RVEPGSPA EAAALR	2689	6.76	2	1422.7497	3		0		yes	4.09	348.68	177.25
RVEPGSPA EAAALR	5253	6.76	1	1422.7466	2		0		yes	5.61	78.54	12.70
SVDPGSPA AR	1320	6.71	2	955.4717	2		0		yes	3.67	568.80	385.89

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

POCG47

Polyubiquitin-B OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EGIPPDQQR	6271	6.56	1	1038.5168	2		0		no	4.22	403.86	84.80
IQDKEGIPPDQQR	2023	6.62	2	1522.7709	3		0		yes	3.81	5860.93	3091.17
LIFAGK	2930	8.16	2	647.4003	1		0		no	7.89	289.59	120.70
LIFAGK	4431	---	---	647.3997	2		0		no	3.19	158.02	42.29
LIFAGK QLEDGR	155	5.74	1	1359.7523	2		0	[6] Methyl K	yes	5.47	4897.06	2.59e+004
QLEDGRTLSDYNIQK	3047	6.25	2	1778.8765	3		0		no	4.22	564.59	238.47
TITLEVEPSDTIENVK	310	9.05	15	1786.9173	2		0		yes	7.06	6360.76	4301.95
TITLEVEPSDTIENVK	3313	9.05	4	1786.9248	3		0		yes	4.64	549.26	250.67

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
TITLEVEPSDTIENVKAK	3132	7.48	4	1986.0488	3		0		no	5.12	645.59	230.7
TLSDYNIQK	605	8.52	11	1080.5455	2		0		no	4.36	3117.50	1984.0

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07911

Uromodulin OS=Homo sapiens OX=9606 GN=UMOD PE=1 SV=1
10 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DGP ⁺ CTVLTR	2061	6.70	3	1074.5317	2		0	[4] Carbamidomethyl C	no	4.29	1111.11	449.61
FSVQ ⁺ MFR	2084	6.03	2	929.4502	2		0	[5] Oxidation M	no	4.02	701.51	126.37
FSVQ ⁺ MFR	2361	6.49	2	929.4448	2		0	[5] Oxidation M	no	3.95	631.61	80.54
INFA ⁺ CSYPLDMK	6701	5.56	2	1473.6643	2		0	[5] Carbamidomethyl C [8] Hydroxyl DKNP	no	5.68	171.04	0.38
MAET ⁺ VPVLR	2542	7.48	1	1174.5861	2		0	[5] Carbamidomethyl C	no	4.57	772.38	65.59
⁺ MAET ⁺ VPVLR	943	7.14	4	1190.5797	2		0	[1] Oxidation M [5] Carbamidomethyl C	yes	4.50	1990.45	208.02
STEYGE ⁺ YACDTDLR	3919	6.99	4	1735.6975	2		0	[10] Carbamidomethyl C	no	6.51	518.80	26.21
TALQ ⁺ P ⁺ MVSALNIR	1429	6.32	4	1428.7665	2		0	[5] Hydroxyl DKNP	yes	5.61	1769.71	448.23
TLDEYWR	1431	7.05	4	981.4572	2		0		no	4.09	1292.07	218.76
VGGTG ⁺ MFTVR	1194	6.58	4	1039.5125	2		0	[6] Oxidation M	yes	4.16	2197.83	158.97
YFIIQDR	2231	6.88	4	953.4973	2		0		no	4.16	744.78	159.42

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07437

Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2
10 peptides





Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AILVDLEPGT ¹ MDSVR	508	7.04	1	1630.8221	2		0	[11] Oxidation M	yes	6.23	3431.46	2167.37
AILVDLEPGT ¹ MDSVR	5117	---	---	1630.8123	3		0	[11] Oxidation M	yes	4.36	91.06	30.72
AILVDLE ¹ PGTMD ¹ SVR	4838	6.47	2	1646.8140	2		0	[8] Hydroxyl DKNP [12] Hydroxyl DKNP	no	6.16	163.89	100.49
ALTVPELTQQVFDAK	3043	5.91	2	1658.8829	2		0		no	6.51	544.81	223.95
ALTVPELTQQVFDAK	6716	5.91	2	1658.8869	3		0		no	4.36	160.33	42.05
FPGQLNADLR	2369	5.97	2	1129.5922	2		0		yes	4.57	1692.98	809.07
FPGQLNADLRK	5686	4.80	1	1257.6794	3		0		no	3.32	181.96	10.04
GHYTEGAELVDSVLDVVR	7293	5.17	1	1958.0014	2		0		no	7.34	206.51	30.85
IM ¹ N ¹ TFSVVPSPK	1933	6.23	2	1334.6860	2		0	[3] Hydroxyl DKNP	no	5.26	924.07	287.89
IREEYPDR	5420	7.16	2	1076.5238	2		0		no	4.36	163.39	5.24
ISEQFTAMFR	2229	5.25	1	1228.5948	2		0		no	4.78	975.98	371.73
ISVYYNEATGGK	1090	6.40	1	1300.6294	2		0		yes	5.06	1294.77	932.61




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q02413

Desmoglein-1 OS=Homo sapiens OX=9606 GN=DSG1 PE=1 SV=2
10 peptides












Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
ALNSMGQDLERPLELR	4797	5.35	2	1840.9389	3		0		no	4.71
IHSD ¹ CAANQQVTYR	3517	6.44	2	1661.7602	3		0	[5] Carbamidomethyl C	yes	4.16
IIRQEPSDSPMFI ¹ NR	4406	5.52	1	1930.9900	3		0	[15] Hydroxyl DKNP	yes	4.29
ISGVGIDQPPYGIFVINQK	3150	6.72	2	2044.0933	3		0		yes	5.19
ISGVGIDQPPYGIFVINQK	4279	6.72	2	2044.0934	2		0		yes	7.62
M ¹ D ¹ WSFFRVVAMLFIFLVVVEVNSEFR	4167	5.53	1	3195.6160	4		0	[2] Hydroxyl DKNP	no	5.75
SAAGFEPVPE ¹ CSDGAIHSWAVEGPQPEPR	4419	5.10	2	3076.3781	3		0	[11] Carbamidomethyl C	no	5.96
TMNNFL ¹ DREQYGQYALAVR	5587	5.33	1	2304.0956	3		0		no	5.12




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
								[7] Hydroxyl DKNP		
VGDFVATDLDTGRPSTTVR	4676	5.16	1	2006.0043	3		0		no	4.64
YQGTILSIDDNLQR	4321	6.81	2	1634.8224	2		0		no	6.37
YYMGNNP ⁺ ADLLAVDSR	4158	5.57	1	1749.8351	2		0	[7] Hydroxyl DKNP	no	6.58

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P67936

Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=3
9 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AEERAEVSELK	6086	5.45	1	1259.6360	3		0		no	3.46	194.18	16
AEFAERTVAK	543	5.47	1	1120.5878	2		0		yes	4.57	6412.91	2262
AEGDVAALNR	3445	6.23	2	1014.5134	2		0		yes	4.16	629.24	323
IQALQQQADEAEDR	12608	6.71	1	1613.7511	2		0		no	6.02	34.36	5
IQALQQQADEAEDRAQGLQR	9387	5.63	1	2267.1228	3		0		no	5.26	98.75	39
IQLVEEELDR	2815	6.93	2	1242.6433	2		0		no	4.92	336.15	230
IQLVEEELDRAQER	464	6.85	2	1726.8872	3		0		yes	4.36	3625.18	4007
IQLVEEELDRAQER	5389	6.85	2	1726.8811	2		0		yes	7.06	141.27	79
LATALQK	3802	6.18	1	743.4521	2		0		no	3.25	169.57	78
LATALQKLEEAEK	2999	6.27	1	1442.7967	3		0		no	3.95	345.65	224
LATALQKLEEAEK	6878	---	---	1442.7816	2		0		no	6.16	51.85	6

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P06396

Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
10 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	MC
AGALNSNDAFVLK	1380	7.14	2	1318.6852	2		0		yes	5.33	944.42	3
A M AELAA	4143	5.76	2	691.3205	1		0	[2] Oxidation M	no	7.55	201.99	
AQPVQVAEGSEPDGFWEALGGK	7448	4.97	1	2271.0675	3		0		no	5.54	92.97	
AQPVQVAEGSEPDGFWEALGGK	12383	---	---	2271.0697	2		0		no	8.10	12.48	
AVEVLPK	1940	5.70	1	754.4553	2		0		no	3.67	214.59	
AVEVLPK	4348	---	---	754.4593	1		0		no	9.00	49.85	
QTQVSVLPEGGETPLFK	4551	6.72	2	1828.9498	2		0		no	6.72	206.47	
TASDFITK	1022	6.50	2	881.4359	2		0		yes	3.74	3487.07	5
TGAQELLR	1396	7.01	2	886.4863	2		0		yes	3.81	949.99	4
TPSAAYLWVG TGASEAEK	12711	5.29	1	1836.8888	2		0		no	6.93	35.49	
YIETDPANR	2914	6.79	2	1077.5103	2		0		no	4.36	616.50	2
YIETDPANRDR	2920	5.93	2	1348.6367	3		0		no	3.74	587.24	1
YIETDPANRDR	14454	---	---	1348.6328	2		0		no	5.19	26.42	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08779

Keratin_ type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4
10 peptides













Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
APSTYGGGLSVSSR	3182	6.61	4	1337.6540	2		0		no	5.19	826.35	58
DAETWFLSK	2046	7.01	4	1095.5241	2		0		no	4.43	779.87	86
D AETWFLSKTEEL N K	3098	5.55	1	1841.8581	3		0	[1] Hydroxyl DKNP [14] Hydroxyl DKNP	no	4.22	289.60	17
DQYEQMAEK	1341	5.94	1	1140.4837	2		0		yes	4.57	2085.03	89
EVFTSSSSSSSR	5291	6.45	3	1259.5612	2		0		no	4.92	323.63	45
IL N EMRDQYEQMAE K	8245	5.81	1	1928.8546	3		0	[3] Hydroxyl DKNP [15] Hydroxyl DKNP	no	4.57	48.68	30
KNHEEMLALR	1865	4.53	1	1368.6923	2		0		yes	5.33	87.13	223
LLEGEDAHLSSQASGQSYSSR	4777	5.73	1	2349.0721	3		0		no	5.06	257.15	51
TEELNKEVASNSLVQSSR	1902	6.86	4	2119.0337	3		0		yes	4.57	897.69	150
TKYEHELALR	2433	6.44	3	1258.6647	3		0		no	3.88	845.38	70




Tags	
	Anova p-value ≤ 0.05
	power>0.8

	
	q<0.05

Q01955

Collagen alpha-3(IV) chain OS=Homo sapiens OX=9606 GN=COL4A3 PE=1 SV=3
12 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	A
AHGQDLGTLGS C LQR	14129	5.94	1	1611.7759	2		0	[12] Carbamidomethyl C	no	6.16	19.79	
ALEPYISR	384	7.16	2	947.5056	2		0		no	4.02	3612.80	3
FTT M PFLF C NVNDV C NFASR	5045	5.52	1	2455.0675	3		0	[4] Oxidation M [9] Carbamidomethyl C [15] Carbamidomethyl C	no	5.33	191.37	
GA P GF P GL P GR	1435	6.15	2	1072.5350	2		0	[3] Hydroxyl DKNP [6] Hydroxyl DKNP [9] Hydroxyl DKNP	no	4.29	1927.41	1
GDLGSTGN P GE P GLR	424	6.95	2	1457.6751	2		0	[9] Hydroxyl DKNP [12] Hydroxyl DKNP	yes	5.33	4711.84	3
GDSGS P ATWTTR	7426	5.27	1	1250.5549	2		0	[6] Hydroxyl DKNP	no	4.78	159.80	
GEPL K	198	5.35	1	613.3448	1		0	[6] Methyl K	yes	7.34	3733.37	3
GFAGN P GEK	4713	4.82	1	891.4114	2		0	[6] Hydroxyl DKNP	no	3.88	205.50	
GF P GR	3902	0.00	1	548.2718	1		0	[3] Hydroxyl DKNP	no	6.44	130.93	
GTLGF P GR	3258	5.47	1	819.4228	2		0	[6] Hydroxyl DKNP	no	3.60	301.75	
LGAP G T P GL P GPGR	321	6.39	2	1236.6469	2		0	[4] Hydroxyl DKNP [7] Hydroxyl DKNP [10] Hydroxyl DKNP	yes	4.78	4248.88	3
PYISR	975	0.00	1	634.3447	1		0		no	7.76	608.93	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P32119

Peroxisredoxin-2 OS=Homo sapiens OX=9606 GN=PRDX2 PE=1 SV=5
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GLFIIDGK	3026	7.23	1	861.4950	2		0		no	3.74	322.17	56.39
GLFIIDGK	10485	---	---	861.4941	1		0		no	9.97	22.82	0.00
KEGGLGPLNIPLLDVTR	6137	7.16	2	1862.0612	3		0		no	4.29	154.59	10.99
LSEDYGVLK	2174	6.81	4	1022.5232	2		0		yes	4.22	568.46	272.90
LSEDYGVLKTDDEGIAYR	4444	6.76	4	1927.9502	3		0		no	4.50	479.04	111.79
QITVNDLPVGR	286	8.24	12	1210.6674	2		0		yes	4.78	6840.89	3658.28
RLSEDYGVLK	6288	6.00	1	1192.6375	2		0	[10] Methyl K	no	4.99	92.93	3.70
SVDEALR	1881	7.59	4	788.4035	2		0		yes	3.53	799.23	286.76
TDEGIAYR	3822	7.68	3	923.4328	2		0		no	3.81	543.48	80.04

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

PODMV8

Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DAGVIAGLNVLR	2200	7.60	2	1196.6865	2		0		no	4.99	344.97	101.34
FGDPVVQSDMK	1028	5.10	1	1221.5477	2		0		yes	4.57	1299.45	957.59
IINEPTAAAIAYGLDR	2011	8.02	5	1686.8923	2		0		yes	6.44	706.67	339.91
IINEPTAAAIAYGLDR	4315	8.02	2	1686.8923	3		0		yes	4.64	215.97	79.23
NQVALNPQNTVFDAK	3872	7.68	2	1657.8335	2		0		no	6.37	228.87	84.17
NQVALNPQNTVFDAKR	5541	6.76	2	1813.9372	3		0		no	4.50	148.09	52.97
STLEPVEK	1869	7.39	4	901.4840	2		0		yes	3.88	1654.06	774.65
YKAEDEVQR	6500	5.73	1	1150.5589	2		0	[2] Methyl K	no	4.71	123.83	26.26

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01876

Immunoglobulin heavy constant alpha 1 OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=2
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
QEPSQGTTFVAVTSILR	2788	7.96	4	1834.9403	2		0		yes	6.86	852.96	80.45
QEPSQGTTFVAVTSILR	4854	7.96	3	1834.9423	3		0		yes	4.92	327.67	245.02
SAVQGPPER	1390	8.15	4	939.4772	2		0		yes	3.81	1277.55	229.55
TFTCTAAYPESK	1627	7.70	4	1374.6136	2		0	[4] Carbamidomethyl C	no	5.33	998.76	254.69
TPLTATLSK	427	8.29	4	930.5397	2		0		yes	3.95	3184.12	941.82
VAAEDWK	2360	7.59	3	817.3975	2		0		no	3.39	993.39	46.40
WLQGSQELPR	1699	7.36	4	1212.6234	2		0		no	4.78	1145.51	249.32

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02679

Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=3
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AIQLTYNPDESSKPNMIDAATLK	4589	6.46	1	2535.2389	3		0	[14] Hydroxyl DKNP	no	5.54	207.46	
DNCCILDER	1240	7.76	2	1193.4848	2		0	[3] Carbamidomethyl C [4] Carbamidomethyl C	yes	4.57	872.62	
EGFGHLSPTGTTEFWLGNEK	9565	5.57	1	2206.0265	3		0		no	4.71	53.88	
LDGSVDFK	4177	6.43	1	879.4332	2		0		no	3.60	209.22	
TSTADYAMFK	1674	7.05	2	1149.5068	2		0	[10] Hydroxyl DKNP	yes	4.57	1027.66	
VELEDWNGR	2931	6.85	2	1116.5320	2		0		no	4.43	421.13	
VGPEADKYR	4244	7.04	2	1033.5162	2		0		no	4.36	182.04	
VGPEADKYR	6645	---	---	1033.5174	3		0		no	3.19	39.89	
YLQEIYNSNNQK	2195	7.62	2	1512.7203	2		0		yes	5.75	712.56	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04406

Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance
											CTR
GALQNIIPASTGAAK	977	8.06	6	1410.7712	2		0		yes	5.47	2796.54
IISNASCTTNCLAPLAK	5318	6.25	2	1832.9050	2		0	[7] Carbamidomethyl C [11] Carbamidomethyl C	no	6.93	265.04
LISWYDNEFGYSNR	3077	7.76	5	1762.7919	2		0		no	6.58	684.81
LWRDGR	269	4.75	1	801.4228	1		0		yes	8.86	4802.35
VIISAPSADAPMFVMGVNHEK	3602	6.02	1	2244.0839	3		0	[11] Hydroxyl DKNP [18] Hydroxyl DKNP	no	5.54	536.39
VVDLMAMMASKE	1016	5.97	1	1361.6314	3		0	[5] Oxidation M [8] Oxidation M	yes	3.81	2424.13
VVDLMAMMASKE	8095	5.97	1	1361.6279	2		0	[5] Oxidation M [8] Oxidation M	yes	5.33	141.62
VVKQASEGPLK	927	4.92	1	1170.6575	3		0	[3] Hydroxyl DKNP	no	3.67	1349.71
VVKQASEGPLK	2458	4.92	1	1170.6582	2		0	[3] Hydroxyl DKNP	no	4.71	446.16

Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P00761

Trypsin OS=Sus scrofa OX=9823 PE=1 SV=1
14 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Norm Abundances
											CTR
ATLNSR	354	0.00	9	660.3556	1		0		no	7.55	2328.52
ATVSLPR	13	0.00	6	742.4350	1		0		no	8.93	2.32e+004
ATVSLPR	381	0.00	6	742.4289	2		0		no	3.39	2335.91
ATVSLPR	301	0.00	1	724.4237	1		0		no	8.52	1899.00
ATVSLPR	643	---	---	724.4224	2		0		no	3.88	757.06
LGEHNDVLEGNEQFINAAK	391	7.84	16	2210.0963	3		0		no	4.92	8450.27
LGEHNDVLEGNEQFINAAK	720	7.09	16	2224.1107	3		0	[20] Methyl K	no	4.92	2912.68
LSSPATLNSR	21	8.35	15	1044.5696	2		0		yes	4.16	7.18e+004
LSSPATLNSR	1315	8.35	3	1044.5559	1		0		yes	11.70	643.97
LSSPATLNSR+	491	0.00	3	1026.5453	2		0	[C-term] Dehydrated	no	4.16	2695.91
LSSPATLNSR	1770	5.87	1	1076.5419	2		0	[4] Hydroxyl DKNP [8]	no	4.36	217.66

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Norm Abundances	
											CTR	MCD
								Hydroxyl DKNP				
PATLNSR	190	0.00	1	757.4086	1		0		no	8.66	5015.07	
PATLNSR	599	0.00	1	757.4077	2		0		no	3.46	1677.33	
SSPATLNSR	349	0.00	11	931.4708	1		0		no	10.11	3679.84	
TLNSR	507	0.00	6	589.3191	1		0		no	6.99	1431.37	
TVSLPR	5	0.00	8	671.3995	1		0		yes	8.10	4.27e+004	8.7
TVSLPR	129	0.00	8	671.3980	2		0		yes	3.46	5074.01	1.2
VATVSLPR	141	8.07	15	841.5021	1		0		yes	10.11	3842.21	
VATVSLPR	14	8.07	12	841.5132	2		0		yes	3.67	6.78e+004	1.5
VATVSLPR ⁺	23	0.00	1	823.4945	2		0	[C-term] Dehydrated	no	3.74	2.35e+004	5.6
VSLPR	30	0.00	11	570.3501	1		0		no	7.20	1.31e+004	3.0
VSLPR	3424	---	---	570.3483	2		0		no	3.12	90.68	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07195

L-lactate dehydrogenase B chain OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=2
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FRYLMAEK	2004	4.76	1	1056.5485	2		0		yes	4.29	1746.24	1397.48
GLTSVINQK	2240	6.89	2	958.5295	2		0		yes	4.09	1228.14	1798.55
IVADKDYSVTANSK	2259	6.71	3	1509.7615	3		0		yes	4.02	1248.22	242.89
IVVVTAGVR	2726	6.74	2	912.5686	2		0		no	3.88	521.07	96.65
LIAPVAEEEEATVPNNK	2002	7.69	3	1693.8862	2		0		no	6.51	903.67	214.51
LNLVQR	2438	7.23	3	741.4489	2		0		no	3.32	322.81	80.36
SADTLWDIQK	3330	5.86	2	1175.5965	2		0		no	4.57	598.02	214.16
VIGSG ⁺ CNLD SAR	2316	7.38	3	1247.5914	2		0	[6] Carbamidomethyl C	no	5.06	608.41	238.84

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08238

Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ADLINNLGTIAK	3454	6.84	4	1241.6948	2		0		no	4.99	329.45	67.19
EQVANSAFVER	2307	6.97	4	1248.6080	2		0		no	4.92	669.55	339.69
GVVDSIDLPLNISR	1458	7.92	4	1512.7747	2		0		yes	5.75	1212.48	616.52
IDIIPNPQER	2454	6.68	4	1193.6437	2		0		yes	4.71	1305.10	909.82
NPDDITQEEYGEFYK	7047	6.37	2	1846.7906	2		0		no	6.86	117.77	38.03
TLTLVDYTGIGMTK	5210	6.08	1	1364.7080	2		0	[11] Oxidation M	no	5.33	116.00	34.08
YHTSQSGDEMTSLSEYVSR	11979	5.36	1	2191.9532	3		0	[8] Hydroxyl DKNP	no	4.78	56.96	18.13
YIDQEELNK	2149	6.56	3	1150.5518	2		0		yes	4.50	700.27	446.39




Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P00558









Phosphoglycerate kinase 1 OS=Homo sapiens OX=9606 GN=PGK1 PE=1 SV=3
10 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AEPKIEAFR	4756	5.63	1	1130.5874	2		0		yes	4.64		
ALESPERPFLAILGGAK	4878	6.08	1	1767.9870	3		0		no	4.16		
ALMDEVYK	3092	5.48	2	919.4691	2		0	[3] Oxidation M	yes	4.02		
ITLPVDFVTADKFDENAK	4552	6.44	1	2022.0328	3		0		no	5.12		
ITLPVDFVTADKFDENAK	5769	5.94	1	2022.0285	3		0		no	5.12		
LGDIVYVNDVAFGTAHR	3976	6.13	2	1633.7859	3		0		no	4.16		
LGDIVYVNDVAFGTAHR	8400	5.15	1	1649.7733	2		0	[3] Hydroxyl DKNP	no	6.37		
LTLDKLDVK	8919	---	---	1043.6223	3		0		no	3.19		
TGQATVASGIPAGWMGLDCEGPSSK	16	5.62	2	2476.1495	4		0	[19] Carbamidomethyl C	yes	4.92	6.18	
TGQATVASGIPAGWMGLDCEGPSSK	194	---	---	2476.1356	3		0	[19] Carbamidomethyl C	yes	5.54	4.18	
VLNMEIGTSLFDEEGAK	6411	5.69	1	1981.9188	2		0	[3] Hydroxyl DKNP	no	7.27		
YAEAVTR	2643	6.26	1	808.4048	2		0		no	3.53		
YAEAVTR	11644	---	---	808.4039	1		0		no	9.49		

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02675




Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DNDGWLTSDPR	3633	5.93	1	1274.5767	2		0		yes	5.06	387.17	
DNDGWLTSDPRK	4556	4.73	1	1402.6506	2		0		no	5.26	213.60	
ECEEIIR	1673	7.44	2	947.4410	2		0	[2] Carbamidomethyl C	yes	4.22	438.58	
EEAPSLRPAPPPISGGGYR	4317	6.16	1	1949.9906	3		0		no	4.43	141.51	
QDGSVDFGR	1426	7.72	2	979.4382	2		0		yes	4.02	1735.88	2
QGFNVATNTDGK	4570	6.71	2	1307.6115	2		0		no	5.12	207.36	
TPCTVSCTNIPVVSQK	2956	7.23	2	1617.7835	2		0	[3] Carbamidomethyl C [7] Carbamidomethyl C	no	5.96	342.39	
TPCTVSCTNIPVVSQKECEEIIR	3461	6.44	1	2547.2020	3		0	[3] Carbamidomethyl C [7] Carbamidomethyl C [17] Carbamidomethyl C	no	5.75	250.06	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P50895

Basal cell adhesion molecule OS=Homo sapiens OX=9606 GN=BCAM PE=1 SV=2
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AGAAGTAEATAR	3331	6.86	1	1045.5153	2		0		no	4.36	138.93	61.81
DGISCEASNPNGNR	4156	5.32	1	1640.7353	3		0	[5] Carbamidomethyl C	yes	4.02	466.29	5.70
DGISCEASNPNGNR	4367	5.32	1	1640.7366	4		0	[5] Carbamidomethyl C	yes	3.39	262.77	0.74

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GDGSPSPEYTLFR	4571	5.75	2	1424.6570	2		0		no	5.33	252.68	138.09
LSVPFLVEVMR	5236	5.21	1	1254.6915	2		0	[5] Hydroxyl DKNP	no	4.92	369.25	96.99
SPPYQLDSQGR	3836	6.61	2	1246.5915	2		0		yes	4.78	312.44	144.45
TAEIEPKADGSWR	5843	4.43	1	1458.6913	2		0		no	5.61	210.12	92.17
VAYLDPLELSEGK	2251	7.33	2	1432.7445	2		0		yes	5.96	460.51	264.60
VEDYDAADDVQLSK	9534	5.49	1	1566.7092	2		0		no	6.02	34.33	3.92

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04083

Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DITSDTSGDFR	3618	7.05	2	1212.5390	2		0		yes	4.57	329.56	173.6
DLAKDITSDTSGDFR	6509	6.77	2	1639.7692	3		0		no	4.09	121.77	22.6
DLAKDITSDTSGDFR	9449	6.77	2	1639.7741	2		0		no	6.23	60.22	2.0
GDRSEDFGVNEDLADSDAR	5804	6.46	2	2066.8806	3		0		no	4.43	165.18	102.2
GLGTDEDTLIEILASR	8289	6.60	1	1701.8706	2		0		no	6.44	65.88	11.7
GLGTDEDTLIEILASR	13691	---	---	1701.8712	3		0		no	4.29	15.29	0.0
GVDEATIIDILTKR	5511	5.83	1	1542.8627	3		0		no	4.16	80.85	3.4
QQIKAAAYLQETGKPLDETLK	2622	5.68	2	2273.2231	3		0		yes	5.61	777.71	1144.3
TPAQFDADELRL	2876	6.98	2	1261.5967	2		0		yes	4.99	669.12	385.8

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P12036

Neurofilament heavy polypeptide OS=Homo sapiens OX=9606 GN=NEFH PE=1 SV=4
10 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AKSPTK	303	5.51	1	630.3709	1		0		no	7.48	6124.43	1990.56
AKSPTK	4283	---	---	630.3700	2		0		no	2.91	234.67	29.66
EEKPKQEVKVK	93	4.12	1	1357.7065	3		0	[9] Hydroxyl DKNP	yes	3.74	4.46e+004	3.13e+004
EPSKPK	749	4.15	1	684.3830	2		0		no	3.46	895.62	2253.06
KPEAVEKPK	262	4.77	2	1052.6233	2		0	[1] Methyl K [7] Methyl K	yes	4.50	2698.16	8516.42
+KPEAVEKPKESK	298	5.58	1	1428.7394	3		0	[N-term] Formyl K N-TERM [1] Hydroxyl DKNP [9] Hydroxyl DKNP	yes	4.09	3319.06	1.08e+004
LGAAR	394	5.29	2	486.2920	1		0		no	6.02	2545.26	3295.39
SAQEEITEYR	7805	5.70	1	1224.5521	2		0		no	4.85	51.68	3.11
SPPAEAAASPEKEAK	10266	5.31	1	1553.7546	2		0	[12] Methyl K	no	6.02	43.34	1.84
SSSTQKQSKPPEK	8707	5.16	1	1548.7170	2		0	[5] Hydroxyl DKNP	no	5.82	67.77	4.68
VEVKEDAKPK	928	4.55	1	1141.6194	2		0		no	4.71	3499.85	590.70
VEVKEDAKPK	5179	---	---	1141.6188	3		0		no	3.32	356.51	0.68

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P61981

14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LAEQAERYDDMAAAMK	3949	4.37	1	1825.8508	3		0	[16] Methyl K	no	4.43	417.79	89.15
NLLSVAYK	1212	7.36	4	906.5175	2		0		yes	3.88	926.48	472.71
NVTELNEPLSNEER	5797	7.49	4	1642.7735	2		0		no	6.09	233.97	53.49
RATVVESSEK	1695	4.32	1	1104.5655	2		0		yes	4.16	4006.31	1105.21
SSWRVISSIEQK	5693	5.48	1	1418.7572	3		0		no	4.02	177.79	38.92
VISSIEQK	997	7.36	4	902.5048	2		0		yes	3.81	1511.27	722.01
YLAEVATGEKR	6224	6.76	1	1235.6478	3		0		no	3.60	113.32	18.64
YLAEVATGEKR	7134	6.76	1	1235.6267	2		0		no	4.78	136.28	11.08

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q5TZA2

Rootletin OS=Homo sapiens OX=9606 GN=CROCC PE=1 SV=1
10 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALAQLEAEKR	4323	4.47	1	1127.6330	2		0		no	4.64	288.79	372
DEGLLLAESEK	2910	4.57	1	1232.6166	2		0	[1] Hydroxyl DKNP [11] Methyl K	no	4.92	807.06	388
DELRTQTSALNR	9102	4.43	1	1418.7019	2		0	[11] Hydroxyl DKNP	no	5.40	44.18	3
DLAQQQMQSDLDK	255	5.18	1	1518.6976	2		0		yes	5.68	7456.84	3937
DLAQQQMQSDLDK	1577	4.19	1	1534.6900	2		0	[1] Hydroxyl DKNP	yes	5.82	1827.52	615
EELSEEIAALQGER	10416	4.18	1	1643.7720	2		0		no	6.23	99.51	0
QLEQLEGK	9480	4.60	1	943.4936	2		0		no	3.95	149.96	40
QMKMLDSENTR	3544	4.54	1	1383.6081	2		0	[2] Oxidation M [3] Hydroxyl DKNP	no	5.33	228.47	135
REEESFNAYFSNEHSR	1929	4.55	1	2000.8674	3		0		yes	4.36	681.92	841
REEESFNAYFSNEHSR	3720	4.55	1	2000.8717	2		0		yes	6.93	274.99	262
SVDGRLSGVQAELALQEESVR	4150	4.53	1	2242.1252	3		0		no	5.06	331.66	166




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q06830

Peroxiredoxin-1 OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1
6 peptides









Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ATAVM ⁺ PDGQFK	4705	6.55	3	1179.5581	2		0	[5] Oxidation M	no	4.64	346.98	35.76
GLFIIDDK	2644	7.30	4	919.5011	2		0		no	3.95	414.10	132.37
GLFIIDDKGILR	6194	6.79	3	1358.7879	3		0		no	4.02	330.76	20.22
GLFIIDDKGILR	8805	6.76	1	1358.7890	2		0		no	5.68	201.80	20.06
LVQAFQFTDK	2377	7.07	4	1195.6202	2		0		yes	4.85	668.76	343.30
SVDETLR	1545	7.65	2	818.4113	2		0		yes	3.67	1658.26	638.13
SVDETLR	13390	---	---	818.3997	1		0		yes	9.14	28.42	0.00
TIAQDYGVLK	1384	7.48	4	1106.5940	2		0		yes	4.57	1157.33	589.54




Tags	
	Anova p-value ≤ 0.05

	
	power>0.8
	q<0.05

Q05682










Caldesmon OS=Homo sapiens OX=9606 GN=CALD1 PE=1 SV=3
8 peptides


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ASVDTKEAGAPQVEAGK	11103	5.45	1	1785.8726	3		0		no	4.02	42.74	10.77
EAEGAPQVEAGK	6858	6.04	2	1184.5655	2		0		no	4.71	96.23	8.36
LQEALER	1120	6.90	2	857.4604	2		0		yes	3.67	1145.68	950.53
NDDDEEEAARER	7694	5.30	1	1447.5803	3		0		no	3.88	57.01	39.96
QKEFDPTITDASLSLPSR	5915	6.20	2	2004.0081	3		0		no	4.50	125.87	27.73
QQEAALEELKK	3589	6.32	2	1527.8031	3		0		yes	3.95	194.13	298.22
RLQEALER	8987	5.70	1	1013.5570	2		0		no	4.50	136.27	47.31
VLEEEER	3724	7.16	2	1030.4929	2		0		yes	4.22	241.37	73.46




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q03252

Lamin-B2 OS=Homo sapiens OX=9606 GN=LMNB2 PE=1 SV=4
9 peptides








Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AAATMATPLPGR	761	5.32	1	1155.6134	2		0		yes	4.64	1440.76	970.71
AGGPATPLSPTR	5125	5.79	2	1123.5881	2		0		no	4.36	226.16	85.63
ALELENDRLLLK	6192	4.96	1	1425.8178	2		0		no	5.89	81.88	3.40
ATSSSSGSLSATGR	7930	6.25	1	1267.5914	2		0		no	4.85	67.03	4.16
QQLQEELDFR	2365	4.17	1	1423.6611	3		0	[1] Carbamidomethyl C	yes	4.29	454.40	250.97
EGELTVAQGR	5130	6.28	1	1058.5284	2		0		no	4.16	258.24	105.67
ELEEAMAGER	2775	4.05	1	1133.5239	2		0		yes	4.43	746.99	635.14
ELEEAMAGERDK	8910	4.47	1	1376.6386	2		0		no	5.33	97.29	13.92
GLESDVAELR	4114	6.33	2	1087.5599	2		0		no	4.43	449.65	165.66




Tags	
	Anova p-value ≤ 0.05

	
	power>0.8
	q<0.05

P02671










Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA PE=1 SV=2
8 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALTDMPQMR	3497	5.17	1	1093.4943	2		0	[5] Oxidation M [6] Hydroxyl DKNP	yes	4.36	452.60	496.64
GDFSSANNRDNTYNR	9843	5.52	1	1729.7351	3		0		no	3.95	64.79	10.81
GLIDEVNQDFTNR	5971	6.05	2	1519.7253	2		0		no	5.89	129.92	24.36
GSESGIFTNTK	1331	7.00	2	1139.5449	2		0		yes	4.57	1005.31	1093.89
MELERPGGNEITR	1786	5.89	2	1516.7313	3		0	[1] Oxidation M	yes	4.16	1111.87	1061.12
QFTSSTSYNR	9653	5.30	1	1189.5366	2		0		no	4.71	102.75	20.17
QFTSSTSYNRGDSTFESK	4811	6.38	2	2040.9033	3		0		no	4.78	77.82	130.34
QLEQVIK	2607	5.99	2	927.5359	2		0		no	4.16	191.80	83.23




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04004

Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1
8 peptides










Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DVWGIEGPIDAAFR	5421	6.67	2	1645.8072	2		0		no	6.23	320.04	1
DWHGVPGQVDAAMAGR	3923	5.11	1	1681.7622	3		0	[13] Oxidation M	no	4.16	281.66	
FEDGVLDPDYPR	2451	6.34	3	1421.6537	2		0		yes	5.47	1196.43	2
FEDGVLDPDYPR	5255	5.59	1	1421.6324	2		0		no	5.54	593.53	3
GQYCYELDEK	2044	6.04	4	1303.5381	2		0	[4] Carbamidomethyl C	no	5.12	826.77	3
QPQFISR	2137	5.58	4	874.4623	2		0		no	3.81	1040.51	3
RVDTVD	2819	0.00	3	685.3403	1		0		no	7.48	451.97	2
RVDTVD	10276	---	---	685.3405	2		0		no	3.05	43.12	
RVDTVDPPYPR	2215	5.96	4	1313.6673	2		0		yes	5.19	1415.72	6




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
RVDTVDPPYPR	3398	5.96	4	1313.6706	3		0		yes	4.02	445.77	
VDTVDPPYPR	139	5.35	3	1157.5706	2		0		yes	4.64	8445.72	2.21

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08758





Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=2
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GLGTDEESILTLTISR	6384	6.94	1	1703.8923	2		0		no	6.58	69.13	12.
GLGTDEESILTLTISR	11578	---	---	1703.8985	3		0		no	4.43	20.33	1.
GTVTDFPGFDER	2122	7.44	4	1339.6069	2		0		yes	5.06	633.20	377.
GTVTDFPGFDERADAETLR	3630	5.78	2	2095.9790	3		0		no	4.64	526.26	282.
QEISAAFK	327	5.38	2	892.4683	2		0		yes	4.09	2253.81	6711.
QEISAAFK	14554	---	---	892.4670	1		0		yes	10.32	8.68	57.
SEIDLFNIR	3557	7.13	2	1105.5797	2		0		no	4.71	297.68	58.
SEIDLFNIRK	6947	6.39	1	1233.6673	3		0		no	3.46	86.26	14.
VLTEIIASR	712	7.20	4	1000.5874	2		0		yes	4.22	1834.02	1202.

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P14618

Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
APIIAVTR	2865	6.52	2	839.5210	2		0		no	3.81	364.4	
GDLGIEIPAEK	1421	7.13	4	1140.5988	2		0		yes	4.57	1654.1	
ITLDNAYMEK	328	3.73	1	1196.5793	2		0		yes	4.57	3826.0	
SVETLK	921	5.52	1	675.3786	1		0		no	7.89	798.7	

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances
											CTR
TATESFASDPILYRPVAVALDTK	8069	6.46	2	2464.2747	3		0		no	5.26	133.7
TATESFASDPILYRPVAVALDTKGPEIR	7034	5.40	1	3016.5976	4		0		no	5.89	169.3
VFLAQKMMIGR	1178	5.63	1	1308.6922	2		0	[7] Oxidation M	yes	5.26	1554.9
VNFAMNVGKAR	7660	5.72	1	1219.6514	2		0	[9] Methyl K	no	4.85	158.1

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P09467

Fructose-1_6-bisphosphatase 1 OS=Homo sapiens OX=9606 GN=FBP1 PE=1 SV=5
9 peptides









Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances
											CTR
AGIAHLYGIAGSTNVTGDQVK	4981	4.78	2	2071.0676	3		0		no	4.50	311.56
APVILGSPDDVLEFLK	6986	5.42	1	1711.9264	2		0		no	7.06	62.51
DFDPAVTEYIQR	2685	6.30	2	1452.6877	2		0		no	5.61	407.48
EAVLDVIPTDIHQQR	4602	6.28	2	1604.8505	3		0		no	4.36	199.37
FVMEEGR	110	6.12	1	866.3985	2		0		yes	3.74	1.10e+004
FVMEEGR	3851	5.59	1	882.3919	2		0	[3] Oxidation M	no	3.67	413.54
+KLDVLSNDLVMNMLK	1486	5.11	1	1759.9203	3		0	[N-term] Formyl K N-TERM	yes	5.06	709.67
STDEPSEKDALQPGR	3857	6.20	2	1628.7619	3		0		no	4.16	550.58
VMEEGR	96	0.00	1	719.3257	1		0		yes	7.76	6972.39




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q07157

Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=3
9 peptides











Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances
											CTR
AEQLASVQYTLPK	6552	4.83	1	1446.7580	2		0		no	5.89	83.43




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DGNIQEGDVVLK	3892	5.11	1	1285.6547	2		0		yes	5.06	978.21	330.74
EEPDIYQIAK	6211	4.87	1	1204.6002	2		0		no	4.71	290.66	79.14
EISQDSLAAAR	3364	5.56	1	1088.5510	2		0		yes	4.36	881.07	209.76
FEPPAPLSYDSRPR	2973	5.60	1	1662.8026	3		0		yes	4.57	251.04	116.92
IPEPQKPKLPPEDIVR	8508	4.62	1	1983.0986	4		0		no	4.29	74.83	5.82
LASHIFVK	4434	4.53	1	913.5211	1		0		no	9.97	62.49	1.04
QYFEQYSR	8186	5.16	1	1119.5099	2		0		no	4.57	128.15	77.13
YESSSYTDQFSR	8343	5.09	1	1468.6211	2		0		no	5.40	70.58	19.02

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

O14745

Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens OX=9606 GN=SLC9A3R1 PE=1 SV=4
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EALAEAALESPPALVR	2123	6.83	4	1791.9774	3		0		no	4.92	901.40	436.38
KGPSGYGFNLHSDK	2169	5.48	3	1505.7102	2		0		no	5.54	839.58	427.41
KNELFSNL	1977	5.71	1	963.5011	2		0		no	3.95	724.90	525.61
LLVDPETDEQLQK	2500	7.41	4	1625.8491	2		0		no	6.23	717.56	368.67
LVEPGSPA EK	1304	7.31	4	1025.5387	2		0		yes	4.09	1097.73	393.56
QHGDVVS AIRAGG  ETK	438	4.89	1	1754.8483	3		0	[14] Hydroxyl DKNP	yes	4.36	4205.19	3655.05
QHGDVVS AIRAGG  ETK	5993	---	---	1754.8395	2		0	[14] Hydroxyl DKNP	yes	6.86	130.49	53.38
SVDPDSPA EASGLR	1230	7.56	6	1399.6568	2		0		yes	5.19	1175.92	655.72

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P25705

ATP synthase subunit alpha_ mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVDSLVPVIGR	1413	7.09	4	1025.5879	2		0		yes	4.22	767.34	560.64
ILGADTSVDLEETGR	4819	6.64	4	1574.7707	2		0		no	5.89	371.32	244.97
QMSLLLR	3378	5.43	1	875.4873	2		0	[2] Oxidation M	no	4.16	249.24	107.16
TGAIVDVPVGEELLGR	1735	7.04	6	1623.8847	2		0		yes	6.30	1337.53	933.62
TGTAEVMSILEER	5361	5.52	1	1438.6599	2		0	[6] Oxidation M	no	5.54	210.65	113.63
VVDALGNAIDGK	2587	6.62	4	1170.6139	2		0		yes	4.78	559.12	337.82
VVDALGNAIDGKPIGSK	3675	6.08	4	1709.9290	3		0		no	4.36	545.61	288.53

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04792

Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AQLGGPEAAK	2734	6.25	2	940.4847	2		0		no	3.95	723.42	567.51
AQLGGPEAAKSDETAAK	2502	6.79	5	1642.8162	3		0		no	4.36	1244.79	564.61
LATQSNEITIPVTFESR	1800	7.78	6	1904.9792	2		0		yes	7.06	1087.12	694.65
LFDQAFGLPR	2746	7.20	4	1162.6075	2		0		no	4.64	406.82	253.04
QLSSGVSEIR	677	7.63	6	1074.5568	2		0		yes	4.43	2606.09	1483.54
VSLDVNHFADELTVK	1592	7.18	5	1782.9146	3		0		yes	4.22	1623.92	744.54

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q5T749

Keratinocyte proline-rich protein OS=Homo sapiens OX=9606 GN=KPRP PE=1 SV=1
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Av No Ab
CPVEIPPIR	2296	6.89	2	1079.5789	2		0		yes	4.64	36

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances
											CT
FEP ¹ CSSYLPLRPSEGFNPY ¹ TPRR	4307	4.89	1	3113.4357	4		0	[1] Carbamidomethyl C	no	5.75	81
IEISSP ¹ CCPR	1050	7.02	2	1217.5588	2		0	[4] Carbamidomethyl C [21] Carbamidomethyl C	yes	4.71	27
RLDQ ¹ CESPLQR	1244	5.53	1	1497.7357	3		0	[5] Carbamidomethyl C	no	3.67	18
RLDQ ¹ CESPLQR	6910	---	---	1497.7330	2		0	[5] Carbamidomethyl C	no	5.61	2
SEPIYNSR	5551	6.45	2	964.4648	2		0		no	4.02	6
SPSP ¹ CWGP ¹ NPVPYPGDLG ¹ CHES ¹ PHR	655	5.16	1	2918.2421	4		0	[5] Carbamidomethyl C [9] Hydroxyl DKNP [19] Carbamidomethyl C [24] Hydroxyl DKNP	yes	5.33	15
SPSP ¹ CWGP ¹ NPVPYPGDLG ¹ CHES ¹ PHR	3758	---	---	2918.2487	3		0	[5] Carbamidomethyl C [9] Hydroxyl DKNP [19] Carbamidomethyl C [24] Hydroxyl DKNP	yes	5.96	1
TSFSP ¹ CV ¹ PQ ¹ CQTQGSYGSFTEQHR	4034	6.78	2	2788.1870	3		0	[6] Carbamidomethyl C [10] Carbamidomethyl C	no	5.61	10

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q8N3V7

Synaptopodin OS=Homo sapiens OX=9606 GN=SYNPO PE=1 SV=2
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances
											CTR
AASPAKPSLDLVPNLPK	3657	5.06	1	1803.9882	3		0		no	4.92	164.91
¹ CTLLIDK	5631	3.48	1	948.4811	1		0	[1] Carbamidomethyl C	no	10.46	46.32
SPPSYSLVLPSSDPK	4093	5.77	2	1622.7767	2		0		yes	6.37	184.78
TARPFGIQAPGGTSQ ¹ MER	3710	5.04	2	1918.9311	3		0	[16] Oxidation M	no	4.16	266.12

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
TGILEESMAR	1991	5.88	2	1121.5409	2		0	[8] Oxidation M	yes	4.43	1024.95	54
VASEEEVPLVVYLK	7963	5.13	2	1702.8928	2		0		no	6.72	61.67	19
VTPNPDLDDLVTQADEK	5654	5.63	1	1866.9460	2		0		no	7.13	106.98	12
VTPNPDLDDLVTQADEK	10317	5.55	1	1866.9537	2		0		no	7.27	59.26	5
YVIESSHTPELAR	2641	5.06	1	1587.8004	3		0		yes	4.02	299.81	14

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P19012

Keratin_ type I cytoskeletal 15 OS=Homo sapiens OX=9606 GN=KRT15 PE=1 SV=3
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift tim (ms)
CEMEANQNEYK	2206	---	---	1442.5842	3		0	[1] Carbamidomethyl C [11] Methyl K	yes	3.7
CEMEANQNEYK	5576	5.79	1	1442.5890	2		0	[1] Carbamidomethyl C [11] Methyl K	yes	5.3
GGSLLAGGGGFGGGSLSGGGSRISASSAR	5390	5.23	1	2580.2329	3		0		no	5.1
LKYENELALR	9294	5.78	1	1247.6844	3		0		no	3.7
QGV EADINGLR	3677	5.33	1	1170.6026	2		0		yes	4.7
RDVEAWFFSK	4099	5.43	1	1299.6248	2		0	[10] Hydroxyl DKNP	no	5.6
TIEELRDK	5932	6.21	1	1002.5253	2		0		no	4.2
VILEIDNAR	3327	6.56	2	1041.5803	2		0		yes	4.5

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P35749

Myosin-11 OS=Homo sapiens OX=9606 GN=MYH11 PE=1 SV=3
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
ALEEALAKEELER	13277	4.23	1	1628.8416	2		0		no	6.44	26.95	
DADFNQTKASE	4624	4.69	1	1153.4900	2		0		yes	4.57	1153.90	4
ENADLAGELR	5835	4.81	1	1086.5467	2		0		no	4.36	470.16	11
IAQLEEQVEQEAR	1180	5.53	1	1541.7683	3		0		yes	3.81	1384.14	20
LQAQM ^K DFQRELE ^D AR	5667	4.98	1	2006.9756	3		0	[6] Methyl K [14] Hydroxyl DKNP	no	4.36	135.93	2
QQKAEN ^L ELK	3929	5.31	1	1102.5534	2		0	[6] Hydroxyl DKNP	no	4.57	326.93	12
TEFSIIHYAGKVDY ^N ASAWLTK	4494	4.98	1	2529.2386	3		0	[15] Hydroxyl DKNP	no	5.12	144.51	6
VIQYLAVVASSHK	831	5.45	1	1413.7897	3		0		yes	3.95	2067.36	151




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02042

Hemoglobin subunit delta OS=Homo sapiens OX=9606 GN=HBD PE=1 SV=2
5 peptides









Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
FFESFGDLSS ^P DAVMGNPK	3782	6.49	2	2059.9128	2		0	[11] Hydroxyl DKNP	no	7.62	338.85	
FFESFGDLSS ^P DAVMGNPK	7910	---	---	2059.9136	3		0	[11] Hydroxyl DKNP	no	5.12	148.97	
FFESFGDLSSPDVMGN ^P K	183	6.13	1	2073.9363	2		0	[18] Hydroxyl DKNP [19] Methyl K	yes	7.62	1.40e+004	
FFESFGDLSSPDVMGN ^P K	434	---	---	2073.9373	3		0	[18] Hydroxyl DKNP [19] Methyl K	yes	5.19	5288.67	
TAVNALWGK	3245	7.50	1	958.5111	2		0		no	3.88	365.28	
VNVDAVGGEALGR	695	7.76	7	1255.6506	2		0		yes	4.92	2011.86	
V ^N VDAVGGEALGRLLVVY ^P PWTQR	277	5.58	1	2543.3871	5		0	[2] Hydroxyl DKNP [19] Hydroxyl DKNP	yes	4.16	4515.26	
V ^N VDAVGGEALGRLLVVY ^P PWTQR	283	5.58	1	2543.3778	4		0	[2] Hydroxyl DKNP [19] Hydroxyl DKNP	yes	4.57	3162.64	
V ^N VDAVGGEALGRLLVVY ^P PWTQR	2352	---	---	2543.3711	6		0	[2] Hydroxyl DKNP [19] Hydroxyl DKNP	yes	3.74	131.84	
V ^N VDAVGGEALGRLLVVY ^P PWTQR	7124	---	---	2543.3685	3		0	[2] Hydroxyl DKNP [19] Hydroxyl DKNP	yes	5.75	8.31	

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08473

Neprilysin OS=Homo sapiens OX=9606 GN=MME PE=1 SV=2
7 peptides







Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALYGTSETATWR	1004	3.77	1	1455.6834	3		0		yes	3.95	782.26	2734.
ALYGTSETATWR	5997	6.59	2	1455.6972	2		0		no	5.61	267.06	46.
AYQNYIKK	1539	4.24	1	1042.5411	2		0	[8] Hydroxyl DKNP	yes	4.43	524.11	1262.
+KNGEEK	5062	---	---	731.3422	2		0	[N-term] Formyl K N-TERM	no	3.19	65.43	207.
LGLPSRDYYECTGIYK	7562	6.17	1	1933.9243	3		0	[11] Carbamidomethyl C	no	4.36	107.50	2.
LIQNMDATTEPCTDFFK	7461	5.60	1	2045.9112	2		0	[4] Hydroxyl DKNP [12] Carbamidomethyl C	no	7.83	152.05	7.
LIQNMDATTEPCTDFFK	8355	---	---	2045.9243	3		0	[4] Hydroxyl DKNP [12] Carbamidomethyl C	no	4.78	102.17	31.
LYVEAAFAGESK	6312	4.93	1	1283.6183	2		0		no	4.85	145.84	123.
TEDIVAVQK	1943	7.33	3	1001.5308	2		0		yes	4.09	1845.14	859.

Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9NZN3

EH domain-containing protein 3 OS=Homo sapiens OX=9606 GN=EHD3 PE=1 SV=2
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ADQIETQQLMR	8046	5.25	1	1347.6418	2		0	[10] Oxidation M	no	5.33	109.39	4
ELVNNLAIEYGR	8934	5.16	1	1389.7155	2		0		no	5.61	43.88	0
IVNTPEVIR	9758	5.27	1	1039.5832	2		0		no	4.16	25.06	13
LEGHELPNELPAHLLPPSK	243	3.75	1	2090.0874	4		0		yes	4.71	4931.11	1.89e+(
LEGHELPNELPAHLLPPSK	297	3.75	1	2090.0832	3		0		yes	5.68	4095.68	1.60e+(
LFEAEEQDLFR	7618	5.38	1	1395.6688	2		0		no	5.61	96.85	29

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
M QDQLQAQDFSK	5845	5.70	1	1453.6555	2		0	[1] Oxidation M	yes	5.54	213.07	35
MQ D QLQAQDFSK	6688	4.33	1	1453.6385	2		0	[3] Hydroxyl DKNP	yes	5.40	150.38	29

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P60660

Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=2
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALGQNPTNAEVLK	305	8.31	4	1353.7252	2		0		yes	5.47	2869.51	3518.18
EAFLFDR	379	6.02	2	1024.5000	2		0		yes	4.29	1270.61	3806.29
EAFLFDR	895	8.09	3	1024.4996	2		0		yes	4.22	1172.08	2643.46
EAFLFDRTGDG K	4275	4.00	1	1496.7462	2		0	[13] Methyl K	no	5.89	376.05	25.27
HVLVTLGEK	1210	5.31	1	994.5798	2		0		no	4.36	717.67	1685.33
HVLVTLGEK	3932	6.67	1	994.5708	2		0		no	4.36	439.55	449.88
ILYS C GDVMR	2990	5.75	1	1340.6000	2		0	[6] Carbamidomethyl C	no	5.33	431.03	161.94
VLGNPKSDEMNV K	3129	5.60	1	1443.7201	3		0	[13] Methyl K	no	3.88	977.86	169.21

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q93088

Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens OX=9606 GN=BHMT PE=1 SV=2
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Norm Abundances	
											CTR	M
AGPWTPEAAVEHPEAVR	3220	6.58	3	1815.8924	3		0		no	4.71	747.07	
AIAEELAPER	425	7.77	4	1097.5733	2		0		yes	4.43	3713.82	
EAYNLGVR	1219	6.92	2	920.4698	2		0		yes	3.88	1843.53	
GNVYLEK	4775	6.27	1	821.4275	2		0		no	3.60	228.55	

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Norm Abundances	
											CTR	M
ISGQEVNEAACDIAR	6970	6.65	2	1631.7520	2		0	[11] Carbamidomethyl C	no	6.02	155.48	
WDIQKYAR	86	4.10	1	1078.5604	2		0		yes	4.43	1.05e+004	3.

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q03154

Aminoacylase-1 OS=Homo sapiens OX=9606 GN=ACY1 PE=1 SV=1
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVGVPALGFSPMNR	2025	4.96	1	1414.7428	2		0		no	5.61	1374.54	125.40
AVGVPALGFSPMNR	2072	6.39	2	1430.7313	2		0	[11] Hydroxyl DKNP	yes	5.47	1631.07	267.31
DIYTR	2623	0.00	1	666.3335	1		0		no	7.55	379.81	67.49
EGSVTSVNLTK	1318	7.07	2	1133.5791	2		0		yes	4.57	1269.32	301.63
GPEEHPSVTLFR	6088	5.52	2	1496.7265	3		0		no	4.22	163.50	66.81
GVDIYTR	3180	6.97	2	822.4260	2		0		no	3.60	403.39	144.39
LLPALASVPALPSDS	1009	7.06	2	1449.8075	2		0		yes	5.75	1953.97	682.16

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P62937

Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=2
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EGM̄NIVEAM̄ER	4234	5.34	1	1309.5644	2		0	[3] Oxidation M [9] Oxidation M	yes	5.06	865.75	76.36
KITIADCGQLE	2844	5.72	1	1246.6189	2		0	[7] Carbamidomethyl C	no	4.92	443.99	224.75
SIYGEKFEDENFILK	1613	4.79	1	1830.9024	3		0		yes	4.36	1007.92	414.46
SIYGEKFEDENFILK	10891	4.79	1	1830.8942	2		0		yes	7.20	35.11	0.00

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VSFELFADK	7459	5.33	1	1054.5366	2		0		no	4.29	75.88	62.44
VSFELFADKVPK	1222	5.44	1	1378.7493	3		0		yes	3.88	1109.56	276.95
VSFELFADKVPK	2932	5.44	1	1378.7479	2		0		yes	5.75	275.96	22.09

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P05556

Integrin beta-1 OS=Homo sapiens OX=9606 GN=ITGB1 PE=1 SV=2
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DDLEALK	4432	5.35	1	962.4485	2		0	[1] Carbamidomethyl C	no	4.43	149.44	46.16
DNTNEIYSGK	7713	6.35	1	1139.5127	2		0		no	4.36	186.41	10.70
IGFGSFVEK	2420	6.92	2	982.5137	2		0		yes	4.02	436.90	217.90
LSEGVTSISK	908	5.18	1	1633.7814	2		0	[13] Carbamidomethyl C	yes	6.16	2735.71	2195.55
SGEPQTFTLK	1605	6.97	2	1106.5584	2		0		yes	4.29	1242.46	550.87
TVMPYISTTPAK	4740	6.03	1	1323.6643	2		0	[3] Oxidation M	no	5.19	412.11	166.24

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P30086

Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PEBP1 PE=1 SV=3
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	M
DEPILSNR	417	5.56	1	1102.5174	2		0	[1] Carbamidomethyl C	yes	4.36	2611.69	67
GNDISSGTVLSDYVGSGPPK	3730	7.31	3	1948.9310	2		0		no	7.20	226.64	8
LYEQLSGK	1108	7.92	4	936.4900	2		0		yes	3.95	1916.64	6

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	MCD
LYTLVLTDPDAPSR	3482	7.83	4	1559.8123	2		0		no	6.16	589.72	1
VLTPTQVK	990	7.79	4	884.5332	2		0		yes	3.81	1326.27	4
VLTPTQVK ⁺	3117	0.00	2	866.5196	2		0	[C-term] Dehydrated	no	3.81	305.80	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P10909

Clusterin OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1
7 peptides





Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ASSIIDELFQDR	5861	5.92	2	1392.6887	2		0		no	5.26	168.57	30.14
EILSVD ⁺ CTNNPSQAK	4377	6.13	3	1761.8160	2		0	[7] Carbamidomethyl C	no	6.51	218.19	46.88
F ⁺ METVAEK	3578	5.65	3	969.4529	2		0	[2] Oxidation M	yes	4.22	679.66	94.00
FYARV ⁺ CR	1862	5.48	1	970.4821	2		0	[6] Carbamidomethyl C	yes	4.09	701.62	267.17
LFSDSPITVTPVEVSR	5034	3.97	1	1873.0029	2		0		no	7.27	115.87	24.02
NPKFMETVAEK ⁺	1783	3.93	1	1308.6284	2		0	[11] Hydroxyl DKNP	yes	4.92	789.64	1384.80
TLLS ⁺ NLEEAKK	5014	5.26	1	1260.6752	2		0	[5] Hydroxyl DKNP	no	5.06	154.47	47.27




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P59665

Neutrophil defensin 1 OS=Homo sapiens OX=9606 GN=DEFA1 PE=1 SV=1
4 peptides











Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IPA ⁺ CIAGER	459	7.86	6	985.5045	2		0	[4] Carbamidomethyl C	yes	4.09	3507.85	945.36




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IPAC ¹ IAGERR	2817	6.45	2	1141.6037	3		0	[4] Carbamidomethyl C	yes	3.32	312.67	14.07
IPAC ¹ IAGERR	6333	6.45	2	1141.5966	2		0	[4] Carbamidomethyl C	yes	4.78	104.17	0.75
LWAF ¹ CC	3259	6.62	2	855.3401	1		0	[5] Carbamidomethyl C [6] Carbamidomethyl C	no	9.14	337.42	21.47
YGT ¹ IYQGR	1045	8.54	5	1116.5072	2		0	[4] Carbamidomethyl C	yes	4.29	1729.78	462.13

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q6S8J3

POTE ankyrin domain family member E OS=Homo sapiens OX=9606 GN=POTEE PE=2 SV=3
9 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Norm Abundances	
											CTR	M
AGDDAPR	1046	0.00	2	700.3145	1		0		no	8.10	542.72	
ALLYGADIESK	442	4.37	1	1291.6772	2		0		yes	5.12	8016.47	
EIAALAPSMK	2646	5.85	1	1160.5957	2		0		no	4.71	592.35	
EKDVLHENSTLR	1925	6.15	1	1439.7235	2		0		no	5.47	1877.54	
GDDAPR	839	0.00	2	629.2773	1		0		no	7.34	602.37	
ISSENSNPEQELKLTSEESQR	635	4.39	1	2533.1452	4		0		yes	4.85	2060.51	1.
ISSENSNPEQELKLTSEESQR	847	4.44	1	2533.1635	4		0		no	4.85	1283.13	
LKGSENGQ ¹ FEK	333	5.26	1	1201.5974	2		0	[9] Hydroxyl DKNP	yes	4.78	1.03e+004	
MVVEVDSMPAASSVK	2131	5.13	1	1548.7604	2		0		no	6.02	291.62	
T ¹ ENQQFPDNESEYYHR	2981	4.65	1	2134.8684	3		0	[2] Hydroxyl DKNP	no	4.57	765.00	
T ¹ ENQQFPDNESEYYHR	9422	---	---	2134.8678	4		0	[2] Hydroxyl DKNP	no	3.95	179.78	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q14847

LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1 PE=1 SV=2
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GFSVVADTPELQR	3671	6.67	2	1417.7185	2		0		yes	5.54	269.33	133.05
QQSELQSQVR	7760	6.91	1	1201.5985	2		0		no	4.78	84.59	10.32
QSFTM̄VADTPENLR	8908	5.72	1	1623.7591	2		0	[5] Oxidation M	no	6.02	147.32	31.95
TGDTGMLP̄ANYVEAI	5704	4.62	1	1566.7226	2		0	[8] Hydroxyl DKNP	no	5.89	220.67	126.06
TQDQISNIK	2298	5.81	1	1045.5394	2		0		yes	4.36	522.00	96.78
TQDQISNIKȲHEEFEK	1142	5.81	1	2021.9629	3		0	[9] Methyl K	yes	4.36	1773.92	1604.56

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

B9A064

Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2
5 peptides







Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normal Abundance	
											CTR	
SSLRSLWGR	2031	4.44	1	1060.5743	2		0		yes	4.50	474.20	
SYSQ̄VTHEGSTVEK	2331	7.59	3	1710.7552	3		0	[4] Carbamidomethyl C	yes	4.57	1124.51	
SYSQ̄VTHEGSTVEKTVAPTECS̄	2475	4.63	1	2556.1036	4		0	[4] Carbamidomethyl C [22] Carbamidomethyl C	yes	4.99	1822.50	
SYSQ̄VTHEGSTVEKTVAPTECS̄	4096	4.63	1	2556.1206	5		0	[4] Carbamidomethyl C [22] Carbamidomethyl C	yes	4.29	985.22	
TVAPTECS̄	1409	7.30	3	863.3686	1		0	[7] Carbamidomethyl C	no	9.00	689.22	
TVAPTECS̄	6912	---	---	863.3740	2		0	[7] Carbamidomethyl C	no	3.53	72.76	
YAASSYLSLTPEQWK	6852	6.78	2	1742.8404	2		0		no	6.58	123.71	




Tags	
	Anova p-value ≤ 0.05
	power>0.8

 q<0.05

P02649








Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1
6 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AATVGS ⁺ LAGQPLQER	3240	6.24	3	1496.7885	2		0		no	5.75	262.57	230
AYKSELEEQLTPVAEETR	9344	5.35	1	2092.0210	3		0		no	4.71	136.94	4
LAVYQAGAR	2959	6.62	2	947.5163	2		0		no	3.88	512.98	99
LGAD ⁺ MEDV ⁺ CGR	3726	5.82	1	1237.5093	2		0	[4] Hydroxyl DKNP [9] Carbamidomethyl C	yes	4.71	669.26	43
LGPLVEQGR	2162	6.55	3	967.5411	2		0		yes	3.88	428.45	273
SWFE ⁺ PLVEDMQR	2833	4.77	1	1551.6899	2		0	[5] Hydroxyl DKNP	yes	5.75	1880.21	1143

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P12109






Collagen alpha-1(VI) chain OS=Homo sapiens OX=9606 GN=COL6A1 PE=1 SV=3
6 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EP ⁺ GGLEDAVNEAK	11709	4.65	1	1487.6452	2		0	[3] Carbamidomethyl C	no	5.82	22.82	
GIDGVDGVKGEMGYPLPG ⁺ CK	2764	5.32	1	2118.9977	2		0	[20] Carbamidomethyl C [21] Methyl K	yes	7.55	399.31	
IALVITDGR	1521	7.29	2	956.5561	2		0		yes	4.02	611.59	
KGLEQLLVGGSHL ⁺ K	6760	5.63	1	1491.8729	2		0	[14] Methyl K	no	5.75	121.44	
KGLEQLLVGGSHL ⁺ K	10264	---	---	1491.8802	3		0	[14] Methyl K	no	3.95	33.58	
VAVVQYSGTGQQRPER	3608	6.81	2	1773.9082	3		0		yes	4.22	353.62	
VFSVAITPDHLEPR	6092	5.45	1	1579.8341	3		0		no	4.29	55.48	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P60174






Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=4
5 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IYGGSVTGATCK	4051	6.91	4	1325.6558	2		0	[12] Carbamidomethyl C	yes	4.99	302.63	150.56
SNVSDAVAQSTR	1819	7.70	4	1233.5955	2		0		yes	4.78	1471.60	509.00
TATPQQAQEVHEK	3792	6.43	2	1465.7125	3		0		no	3.81	209.08	14.12
VVFEQTK	2610	6.94	4	849.4578	2		0		yes	3.67	723.25	129.91
VVLAYEPVWAGTGK	5362	6.55	4	1601.8741	2		0		no	6.30	221.88	19.86

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

POCOL4

Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=2
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance
											CTR
EMSGSPASGIPVK	2425	5.04	1	1274.6270	2		0	[2] Oxidation M	yes	4.99	619.84
GSFEFPVGDAVSK	3529	6.04	2	1338.6449	2		0		yes	5.19	340.47
QGSFQGGFR	4339	6.32	2	982.4671	2		0		yes	3.81	229.41
VGDTLNLNLR	4352	6.05	2	1113.6112	2		0		no	4.57	226.21
VTASDPLDTLGSEGALSPGGVASLLR	5244	5.62	1	2482.2737	3		0		no	6.65	95.64
YVLPNFEVK	7571	5.36	1	1107.5912	2		0		no	4.50	99.62

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P37802

Transgelin-2 OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=3
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GASQAGMTGYGMPR	6921	5.04	1	1414.5973	2		0	[12] Oxidation M [13] Hydroxyl DKNP	no	5.26	110.71	22.48
GPAYGLSR	8589	6.16	1	819.4207	2		0		no	3.67	92.96	49.01
NFSDNQLQEGK	2306	6.77	2	1278.5836	2		0		yes	4.92	464.01	422.36
NVIGLQMG TNR	1531	6.61	2	1217.6120	2		0	[7] Oxidation M	yes	4.78	1598.93	925.83
QMEQISQFLQAAER	926	4.59	1	1693.8029	3		0	[2] Oxidation M	yes	4.22	1947.55	1739.16
QMEQISQFLQAAER	7112	---	---	1693.7958	2		0	[2] Oxidation M	yes	6.30	54.05	2.32
TLMNLGGLAVAR	3681	5.19	1	1230.6650	2		0	[4] Hydroxyl DKNP	no	4.99	480.99	207.69

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P19440






Glutathione hydrolase 1 proenzyme OS=Homo sapiens OX=9606 GN=GGT1 PE=1 SV=2
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	M
FVDVTEVVR	3157	5.32	2	1062.5666	2		0		no	4.36	446.93	1
GGLSVAVPGEIR	5007	5.87	2	1153.6411	2		0		no	4.64	228.73	
GLAAALENKR	919	4.23	1	899.5066	1		0	[9] Methyl K	yes	9.83	1432.94	
GLAAALENKR	2507	4.23	1	899.5124	2		0	[9] Methyl K	yes	3.74	557.77	1
LFQPSIQLAR	6699	6.07	2	1171.6677	2		0		no	4.71	162.53	
QPLSSMCPTIMVGQDGGQVR	1170	4.12	1	2118.9981	3		0	[7] Carbamidomethyl C [15] Hydroxyl DKNP	yes	5.40	2208.31	43
QPLSSMCPTIMVGQDGGQVR	2082	4.12	1	2118.9999	4		0	[7] Carbamidomethyl C [15] Hydroxyl DKNP	yes	4.43	1060.51	18




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P63104

14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1
4 peptides







Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FLIPNASQAESK	1994	6.50	3	1303.6716	2		0		yes	5.26	1013.52	263.86
FLIP ^N ASQAESK	6228	6.03	1	1319.6685	2		0	[5] Hydroxyl DKNP	no	5.19	272.64	141.59
SVTEQGAELSNEER	3202	7.87	4	1547.7047	2		0		yes	5.61	685.26	180.58
YLAEVAAGDDKK	3966	6.54	2	1278.6397	3		0		yes	3.74	360.74	162.46
YLAEVAAGDDKK	7731	6.54	1	1278.6398	2		0		no	5.47	119.29	8.23

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q16555

Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=DPYSL2 PE=1 SV=1
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GSPLVVISQ GK	4833	5.84	2	1083.6172	2		0		yes	4.57	227.32	45.06
M ^D ENQFVAVTSTNAAK	13614	5.40	1	1740.7974	2		0	[2] Hydroxyl DKNP	no	6.51	46.19	0.00
MVI ^P GGIDVHTR	7193	4.75	1	1309.6767	3		0	[4] Hydroxyl DKNP	no	3.81	63.91	19.13
QIGENLIVPGGVK	2850	5.92	2	1322.7447	2		0		yes	5.26	232.58	100.79
SSAEVIAQAR	3061	5.70	2	1030.5421	2		0		yes	4.09	548.70	195.81
VFNLVPR	5096	5.44	1	907.4902	2		0		no	3.88	101.11	9.46

Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P06576

ATP synthase subunit beta_ mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=3
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AHGGYSVFAGVGER	891	4.88	1	1405.6830	2		0		yes	6.23	724.89	2781.43
AIAELGIYPAVDPLDSTSR	2993	6.48	4	1987.0191	2		0		no	7.41	507.67	394.93
AIAELGIYPAVDPLDSTSR	4418	---	---	1987.0132	3		0		no	4.64	180.49	100.14
IPVGPE ⁺ PETLGR	1464	4.33	1	1069.5632	2		0	[2] Hydroxyl DKNP [5] Hydroxyl DKNP	yes	4.29	1222.29	748.12
TIAM ⁺ MDGTEGLVR	1317	5.63	1	1277.6279	2		0	[4] Oxidation M	yes	4.92	1375.63	700.68
VLDSGAPIKIPVGPETLGR	2677	6.14	4	1918.0761	3		0		no	4.50	1765.60	316.49
VVDLLAPYAK	2735	5.46	4	1087.6197	2		0		no	4.64	405.80	239.76

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P81605







Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DAVEDLESVGK	2779	5.55	1	1160.5618	2		0		yes	4.64	417.36	780.72
GAVHDV ⁺ K	213	6.14	1	754.3984	1		0	[7] Hydroxyl DKNP [7] Methyl K	yes	8.38	1.08e+004	1970.90
GAVHDV ⁺ K	718	6.14	1	754.3982	2		0	[7] Hydroxyl DKNP [7] Methyl K	yes	3.39	3077.53	609.41
LGKDAVEDLESVGK	634	7.23	8	1458.7565	3		0		yes	3.74	2518.69	4282.77
LGKDAVEDLESVGK	2893	7.23	4	1458.7480	2		0		yes	5.61	451.91	703.32

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

O14950







Myosin regulatory light chain 12B OS=Homo sapiens OX=9606 GN=MYL12B PE=1 SV=2
5 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ATSNVFAMFDQSQIQEFK	7922	5.48	1	2105.9728	3		0	[4] Hydroxyl DKNP	no	4.92	56.81	2.65
ATSNVFAMFDQSQIQEFK	14085	---	---	2105.9556	2		0	[4] Hydroxyl DKNP	no	7.62	23.33	1.05
ELLTTMGDR	4081	6.07	1	1050.5050	2		0	[8] Hydroxyl DKNP	yes	4.29	391.78	157.76
ELLTTMGDRFTDEEVDELRY	5987	6.13	1	2447.1226	3		0	[16] Hydroxyl DKNP	no	5.19	189.24	36.55
GNFNIEFTR	2230	7.95	3	1259.5950	2		0		yes	4.99	728.51	480.03
LNGTDPEDVIR	4420	6.65	2	1227.6093	2		0		yes	4.78	575.35	237.60

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P14625


Endoplasmic OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GLFDEYGSK	2614	4.29	1	1014.4835	2		0		yes	4.02	730.46	435.17
GLFDEYGSK	4306	4.29	1	1014.4720	3		0		no	3.05	94.33	16.00
GVVDSDDLPLNYSR	4529	6.47	2	1484.7415	2		0		no	5.61	257.20	121.30
SGTSEFLNK	4091	5.77	1	981.4777	2		0		no	3.95	286.09	133.17
SGYLLPDTKAYGDR	2387	4.36	1	1570.7592	2		0	[7] Hydroxyl DKNP	yes	5.89	564.79	895.92
SILFVPTSAPR	2640	6.49	2	1186.6655	2		0		yes	4.85	353.39	153.25

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

O75083

WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=WDR1 PE=1 SV=4
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AHDGGIYAIWSPDSTHLLSASGDK	12126	4.00	1	2584.1889	3		0		no	6.44	36.13	2

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	CTR
DYSGQGVVK	6992	5.35	1	951.4703	2		0		yes	3.95	218.98	5
IAVVGEGR	5653	5.80	1	799.4520	2		0		no	3.53	151.62	2
LYSILGTTLKDEGK	4526	5.06	1	1536.8331	3		0		yes	4.22	290.49	6
VFASLPQVER	4726	5.60	1	1144.6241	2		0		yes	4.57	249.34	4
YAPSGFYIASGDVSGK	9580	5.57	1	1617.7648	2		0		no	6.02	92.60	1

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P68133

Actin_ alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
GYSFVTTAER	1655	7.77	2	1129.5450	2		0		no	4.9
GYSFVTTAER	6128	6.74	1	1129.5532	2		0		no	4.9
TTGIVLDSGDGVTHNVPIYEGYALPHAIR	562	5.42	2	3195.6273	5		0		yes	4.9
TTGIVLDSGDGVTHNVPIYEGYALPHAIR	698	5.42	2	3195.6238	4		0		yes	5.9
VAPEEHPTLLTEAPLNPK	799	7.33	3	1955.0359	3		0		yes	4.9
YSVWIGGSILASLSTFQQMWITKQEYDEAGPSIVHR	1697	5.19	1	4097.0650	5		0		yes	6.9
YSVWIGGSILASLSTFQQMWITKQEYDEAGPSIVHR	5757	---	---	4097.0634	4		0		yes	7.9




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01871

Immunoglobulin heavy constant mu OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=4
5 peptides






Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	CTR	MCD
DGFFGNPR	6560	5.86	1	908.4306	2		0		no	3.81	102.03	2.28	
LI ¹³ QATGFSPR	5009	6.10	2	1248.6212	2		0	[3] Carbamidomethyl C	yes	4.99	309.43	91.46	




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
QIQVSWLR	5616	6.39	1	1028.5721	2		0		no	4.29	86.68	9.26
QVGSGVTDDQVQAEAK	3833	6.90	2	1616.7992	2		0		yes	6.09	282.17	27.95
YVTSAPMPEPQAPGR	4383	5.46	2	1615.7621	2		0	[8] Hydroxyl DKNP	yes	5.96	402.98	3.73

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P10412






Histone H1.4 OS=Homo sapiens OX=9606 GN=H1-4 PE=1 SV=2
4 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AKKPAAAAAGAK	10	5.38	1	1012.6054	2		0	[2] Hydroxyl DKNP [11] Methyl K	yes	4.29	1.00e+005	2.79e+005
ALAAAGYDVEK	4120	5.52	1	1106.5495	2		0		no	4.78	198.58	108.35
ASGPPVSELITK	844	6.79	3	1197.6582	2		0		yes	4.57	1657.39	1727.63
KASGPPVSELITK	1684	6.50	2	1325.7523	3		0		yes	3.46	433.23	300.24
KASGPPVSELITK	3201	6.50	2	1325.7471	2		0		yes	5.12	220.80	196.18

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08729

Keratin_type II cytoskeletal 7 OS=Homo sapiens OX=9606 GN=KRT7 PE=1 SV=5
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance:	
											CTR	M
AEAEAWYQT	4686	5.55	1	1211.5564	2		0	[10] Hydroxyl DKNP	no	4.92	143.95	
AKLEAAIAEAER	1345	4.84	1	1399.7470	3		0		yes	4.02	852.69	21
AKLEAAIAEAER	2577	---	---	1399.7481	2		0		yes	5.96	349.93	11
LSSARPGGLGSSSLYGLGASRPR	3179	4.95	1	2245.1806	3		0		no	5.06	651.53	10
SLDLGIIAEV	3211	4.55	1	1285.7215	3		0	[12] Methyl K	no	3.53	355.03	
SLDLGIIAEV	813	5.65	1	1301.7080	2		0		yes	5.26	3412.10	24

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
								[12] Hydroxyl DKNP [12] Methyl K			CTR	M
YEDEI ^N HR	1763	4.81	1	1090.4827	2		0	[6] Hydroxyl DKNP	yes	4.22	2091.32	5

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q6UXI9

Nephronectin OS=Homo sapiens OX=9606 GN=NPNT PE=2 SV=3
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
CKHGE ^C IGPN ^K	2761	4.39	1	1312.6082	2		0	[1] Carbamidomethyl C [6] Carbamidomethyl C [11] Methyl K	yes	5.06	724.88	525.97
Q ^C PSPLQLAPDGR	8902	6.10	1	1654.7483	2		0	[1] Carbamidomethyl C [3] Carbamidomethyl C	no	5.96	51.56	4.10
ID ^C WGWAR	8587	6.14	1	1222.5138	2		0	[3] Carbamidomethyl C [4] Carbamidomethyl C	no	4.71	98.02	13.98
QIVSSIGL ^C R	3177	6.65	2	1131.6022	2		0	[9] Carbamidomethyl C	yes	4.57	467.73	161.53
T ^C VDVDE ^C ATGR	4742	6.89	2	1381.5654	2		0	[2] Carbamidomethyl C [8] Carbamidomethyl C	yes	5.26	273.36	25.80

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P09210

Glutathione S-transferase A2 OS=Homo sapiens OX=9606 GN=GSTA2 PE=1 SV=4
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FLQPGSPR	2245	6.98	2	900.4762	2		0		yes	3.88	828.01	125.40
ISNLPTVK	3803	6.30	1	870.5169	2		0		no	3.74	218.17	26.33
LALIQEK	2151	7.19	2	813.4925	2		0		yes	3.67	546.61	88.33
SHGQDYLVGNK	735	4.74	1	1230.6015	2		0	[11] Methyl K	yes	4.57	3932.67	2668.95
YFPAFEK	4949	4.95	1	900.4556	2		0		no	3.95	358.26	95.80

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P39060

Collagen alpha-1(XVIII) chain OS=Homo sapiens OX=9606 GN=COL18A1 PE=1 SV=5
5 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ELLREETGAALKPR	3165	5.85	2	1581.8602	3		0		no	4.36	210.12	149.81
GADFQCFQQR	2191	7.30	2	1326.5835	2		0	[6] Carbamidomethyl C	yes	4.99	804.45	299.50
GPPGPQGPPGPSFR	10071	4.08	1	1597.8218	2		0		no	6.44	40.99	9.00
LTESYCTWR	3581	6.17	2	1343.6068	2		0	[6] Carbamidomethyl C	yes	5.12	644.66	221.10
TEAPSATGQASSLLGGR	1944	6.37	2	1601.7952	2		0		yes	6.09	524.67	516.20




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P06733

Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2
5 peptides









Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GNPTVEVDLFTSK	2417	6.66	4	1405.7075	2		0		no	5.33	773.68	361.55
IDKLMIEDGTENK	4527	4.83	1	1651.7826	3		0	[2] Hydroxyl DKNP	no	4.16	146.01	36.69
IEEELGSK	1110	6.80	4	903.4557	2		0		yes	3.81	1796.66	767.57




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SGKYDLDFK	2608	4.84	1	1087.5239	2		0	[7] Hydroxyl DKNP	yes	4.29	1294.23	410.62
YISPDQLADLYK	1291	6.42	4	1424.7169	2		0		yes	5.68	1267.36	634.72

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q86Y46



Keratin_type II cytoskeletal 73 OS=Homo sapiens OX=9606 GN=KRT73 PE=1 SV=1
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AQYEEIARK	1203	4.65	1	1106.5669	2		0		yes	4.64	1062.52	
EGEECR	1585	0.00	2	778.2922	1		0	[5] Carbamidomethyl C	no	8.10	1999.06	
GLSGGFSSR	4069	4.59	1	866.4131	1		0		no	9.63	175.62	
HGDDLKHTK	132	5.89	1	1049.5333	2		0		yes	4.22	1.22e+004	3.4
LDELEGALQQAEEELAR	5882	4.65	1	1911.9870	2		0		no	7.41	72.04	
LDELEGALQQAEEELAR	10819	---	---	1911.9609	3		0		no	4.85	75.88	
LEGEECR	4055	0.00	2	891.3742	1		0	[6] Carbamidomethyl C	no	9.42	516.40	
LGSASEFR	316	4.67	2	865.4183	1		0		yes	9.70	1.02e+004	4
VLNNKFASFIDK	2421	4.88	1	1410.7400	2		0	[3] Hydroxyl DKNP	no	5.61	406.52	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01009

Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVLTIDEK	3082	5.67	2	887.4941	2		0		no	3.81	257.46	100.36
FLENEDRR	3599	4.71	2	1077.5215	3		0		no	3.12	241.23	57.90

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FLENEDRR	4226	4.71	2	1077.5212	2		0		no	4.50	251.27	79.91
QINDYVEK	4047	4.53	1	1007.5030	2		0		yes	4.36	432.10	153.83
SPLFMGK	3228	3.97	1	794.4006	2		0	[7] Hydroxyl DKNP	yes	3.53	384.73	96.73
SVLGQLGITK	4772	5.59	1	1014.5979	2		0		yes	4.22	258.33	138.15

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P00915

Carbonic anhydrase 1 OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=2
5 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GGPFSDSYR	2069	6.30	2	984.4351	2		0		yes	4.02	589.03	195.07
SVLKGGPFSDSYR	188	4.98	1	1411.7127	2		0		yes	5.89	5300.44	1.82e+004
VGEANPKLQK	5957	5.07	1	1098.6030	2		0	[10] Hydroxyl DKNP	no	4.64	106.13	17.49
YSAELHVAHWNSAK	2740	5.61	1	1611.7895	3		0		yes	4.29	641.59	217.70
YSSLAEAASK	3760	7.11	2	1025.5049	2		0		no	4.16	358.52	74.76

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P22626






Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1 PE=1
SV=2
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GGGGNFGPGGSNFR	1853	7.24	3	1376.6266	2		0		yes	5.12	607.02	499.81
GGNFGGDSR	1306	7.23	3	1012.4422	2		0		yes	4.09	749.41	788.10
IDTIEITDR	5465	7.00	1	1187.6356	2		0		no	4.78	149.54	80.76
TLETVPLER	2534	7.14	2	1056.5712	2		0		yes	4.29	770.84	470.33

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01857





Immunoglobulin heavy constant gamma 1 OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MC
FNWYVDGVEVHNAK	5154	6.55	4	1676.7968	3		0		no	4.29	240.23	38
GPSVFPLAPSSK	868	8.20	4	1185.6380	2		0		yes	4.57	1371.46	57
TPEVT C VVVDVSHEDPEVK	3814	7.39	3	2138.0169	3		0	[6] Carbamidomethyl C	yes	5.40	443.21	40
TTPPVLDSDGSFFLYSK	3515	6.46	1	1872.9172	2		0		yes	6.93	363.95	10
TTPPVLDSDGSFFLYSK	4658	6.35	1	1872.8979	2		0		no	6.93	108.83	1

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01834






Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundance	
											CTR	MC
TVAAPSVFIFPPSDEQLK	2694	7.57	4	1945.0106	2		0		yes	7.41	1624.32	1
TVAAPSVFIFPPSDEQLK	3121	7.57	2	1945.0114	3		0		yes	5.12	951.74	1
VDNALQSGNSQESVTEQDSK	6830	6.12	1	2134.9529	3		0		yes	4.71	182.89	1
VYAC C EVTHQGLSPVTK	1766	7.16	4	1874.9195	3		0	[4] Carbamidomethyl C	yes	4.36	958.04	3

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P30101





Protein disulfide-isomerase A3 OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=4
5 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ELSDFISYLQR	8609	6.20	1	1369.6867	2		0		no	5.47	86.26	22.47
FV ^M QEEFSR	3571	5.11	2	1187.5425	2		0	[3] Oxidation M	yes	4.85	305.26	124.35
IFRDGEEAGAYDGPR	4910	5.76	2	1651.7570	3		0		yes	4.29	242.51	132.23
LAPEYEEAATR	2382	6.21	2	1190.5889	2		0		yes	4.64	1102.92	637.23
M ^D ATANDVPSPYEVR	10592	5.06	1	1679.7525	2		0	[2] Hydroxyl DKNP	no	6.09	72.79	19.33

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P59998

Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens OX=9606 GN=ARPC4 PE=1 SV=3
4 peptides






Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AENFFILR	3628	7.73	2	1008.5386	2		0		yes	4.29	206.28	50.39
ELLQPTVISR	4400	6.92	2	1267.7432	2		0		yes	5.06	185.09	46.80
IVAEFFLK	1337	7.41	3	947.5299	2		0		yes	4.16	559.70	361.01
VLIEGSINSVR	5709	6.25	2	1185.6652	2		0		no	5.06	98.84	40.80




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P06702

Protein S100-A9 OS=Homo sapiens OX=9606 GN=S100A9 PE=1 SV=1
3 peptides







Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LGHPDTLNQGEFK	2225	6.60	2	1454.7117	3		0		yes	3.67	984.30	250.02




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
												
LGHPDTLNQGEFK	10480	---	---	1454.7043	2		0		yes	5.61	84.03	10.22
LTWASHEK	2346	6.92	2	970.4885	2		0		yes	4.22	1822.03	378.16
NIETIINTFHQYSVK	2526	7.27	2	1805.9307	3		0		yes	4.71	1950.39	20.93
NIETIINTFHQYSVK	7685	7.27	1	1805.9291	2		0		yes	7.41	324.38	0.02

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q99798





Aconitate hydratase_ mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=2
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GEFDPGQDTYQHPPK	5052	4.16	1	1714.7595	2		0		yes	6.37	203.03	114.51
NAVQTQEGPVPDTAR	6095	5.54	1	1600.7775	2		0		yes	5.96	224.51	176.08
NTIVTSYNRNFTGR	5911	4.12	1	1641.8130	2		0		no	6.30	95.76	8.92
SQFTITPGSEQIR	5650	4.64	1	1462.7401	2		0		no	5.68	239.38	38.57
TGREDIANLADEFK	2201	4.77	1	1577.7636	2		0		yes	5.96	356.46	185.00
WVIGDENYGEQSSR	4225	4.54	1	1666.7627	2		0		no	6.16	330.29	1.50

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P35580

Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AKLQELEGAVK	2474	3.85	1	1184.6746	3		0		yes	3.67	710.57	439.04
ALEQQVEEMR	5891	5.07	1	1231.5965	2		0		no	5.06	235.38	25.48
ELDDATEANEGLSR	4192	5.10	1	1518.6571	2		0		no	6.02	132.12	52.93
ELDDATEANEGLSR	8269	5.35	1	1518.6766	2		0		no	5.61	80.08	28.21

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LQNELDNVSTLLEEAEK	2584	4.53	1	1943.9505	3		0		yes	4.85	1045.58	405.73
QEVMSIDLEER	2845	4.52	1	1347.6142	2		0		no	5.06	223.90	19.45
QLRADMEDLMSSK	3312	4.39	1	1536.7275	3		0	[13] Methyl K	yes	3.88	787.50	148.68

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P05062

Fructose-bisphosphate aldolase B OS=Homo sapiens OX=9606 GN=ALDOB PE=1 SV=2
4 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ETTIQGLDGLSER	1175	7.84	2	1417.7042	2		0		yes	5.47	1839.3	
GILAADESVMGMR	1581	7.37	1	1505.7126	2		0	[14] Hydroxyl DKNP	yes	5.61	1243.7	
LDQGGAPLAGTNK	2742	6.80	2	1240.6384	2		0		yes	4.92	657.0	
LDQGGAPLAGTNKETTIQGLDGLSER	6217	5.62	2	2640.3316	3		0		no	5.68	248.6	




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

O00592

Podocalyxin OS=Homo sapiens OX=9606 GN=PODXL PE=1 SV=2
4 peptides






Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ATFNPAQDK	5175	6.50	1	990.4818	2		0		yes	4.09	236.29	9.01
EDLETQTQSEK	3338	7.36	2	1466.6119	2		0	[1] Carbamidomethyl C	yes	5.54	496.58	18.32
LASVPGSQTVVVK	468	7.01	2	1283.7473	2		0		yes	5.12	2284.88	1053.11
LISLIR	4282	6.69	1	873.5079	2		0	[6] Carbamidomethyl C	no	3.81	111.59	8.87




Tags	

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01833






Polymeric immunoglobulin receptor OS=Homo sapiens OX=9606 GN=PIGR PE=1 SV=4
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GLGINSR	4857	6.31	1	875.4297	2		0	[1] Carbamidomethyl C	yes	3.81	294.40	1.1
EEFVATTESTTETKEPK	804	4.12	1	1939.9237	2		0	[14] Methyl K	yes	7.13	5146.50	2128.1
EEFVATTESTTETKEPK	2560	4.12	1	1939.9250	3		0	[14] Methyl K	yes	4.36	1185.64	286.9
GGITLISSEGYVSSK	7667	5.40	1	1656.8154	2		0	[3] Carbamidomethyl C	no	6.44	208.96	5.1
QSSGENDVVVNTLGK	4496	5.98	1	1705.7925	2		0	[7] Carbamidomethyl C	yes	6.37	230.77	1.1

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P68104











Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IGGIGTVPVGR	857	7.58	4	1024.6027	2		0		yes	4.16	2142.11	937.03
QLIVGVNK	100	4.93	1	869.5337	2		0		yes	4.29	6511.42	1.59e+004
QTVAVGVK	1032	6.93	4	913.5541	2		0		yes	4.16	838.83	645.85
QTVAVGVK ⁺	4690	0.00	1	895.5402	2		0	[C-term] Dehydrated	no	3.88	145.42	102.39
TIEKFEK	4794	6.44	1	893.4831	2		0		no	3.95	291.07	69.96




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q04695

Keratin_ type I cytoskeletal 17 OS=Homo sapiens OX=9606 GN=KRT17 PE=1 SV=2
10 peptides






Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AADDFR	65	0.00	12	693.3101	1		0		yes	7.76	3.20e+004	1.43e+004
AADDFR	1810	0.00	1	693.3086	2		0		yes	3.25	743.62	165.
ADDFR	61	0.00	12	622.2733	1		0		yes	7.13	3.13e+004	1.55e+004
ADDFR	4635	---	---	622.2714	2		0		yes	3.12	268.31	45.
ASLEGNLAETENR	8450	4.97	1	1418.6629	2		0	[12] Hydroxyl DKNP	no	5.47	257.51	12.
ASYLDK	2075	0.00	1	695.3494	1		0		no	8.03	554.32	430.
ASYLDKVR	1879	0.00	1	950.5044	2		0		no	4.16	1329.56	280.
ATMQNLNDRLASYLEDK	3347	5.08	1	1851.9062	3		0		no	4.29	219.85	686.
ATMQNLNDRLASYLEDK	1261	6.03	1	1867.9018	3		0	[5] Hydroxyl DKNP	yes	4.36	1476.48	4482.
DELTAR	1427	0.00	1	816.4406	1		0		no	9.14	862.65	565.
LSVEADINGLR	1280	4.63	2	1185.6487	2		0		no	4.92	748.55	2186.
TIEELQNK	6142	5.07	1	989.4985	2		0	[8] Hydroxyl DKNP	no	4.16	196.50	41.

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P00918

Carbonic anhydrase 2 OS=Homo sapiens OX=9606 GN=CA2 PE=1 SV=2
5 peptides








Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVLKGGPLDGTYSR	1061	4.46	1	1361.7283	2		0	[4] Hydroxyl DKNP	yes	5.54	637.95	1857.86
DFPIAK	352	4.53	1	689.3736	1		0		yes	7.41	1.89e+004	5.88e+004
GGPLDGTYSR	3224	6.34	4	934.4531	2		0		no	3.88	610.14	203.35
KYAAELHLVHWNTK	4159	3.97	1	1722.9163	3		0	[14] Methyl K	no	4.71	384.55	61.71
SADFTNFDPR	2054	6.29	4	1168.5254	2		0		yes	4.71	1012.98	289.09




Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P05787






Keratin_type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=7
5 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AFSSR	176	4.96	1	566.2831	1		0		yes	6.58	1.29e+004	2977.25
AFSSR	2153	---	---	566.2821	2		0		yes	2.91	711.38	89.66
ASLEAAIADAEQR	1575	4.73	1	1343.6695	2		0		no	5.12	789.19	961.03
HGDDLRR	931	4.90	1	867.4337	2		0		yes	3.95	2610.13	6745.19
IETRDGK	462	4.68	1	817.4333	1		0		yes	8.66	1283.47	4582.52
IETRDGK	2823	---	---	817.4313	2		0		yes	3.53	95.04	331.41
LQAEIEGLKGQR	2763	5.67	1	1340.7364	3		0		no	3.88	215.84	574.22

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P55290







Cadherin-13 OS=Homo sapiens OX=9606 GN=CDH13 PE=1 SV=1
5 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DLHPNTDPFK	6350	4.84	1	1182.5638	2		0		yes	4.57	376.40	160.51
INENTGSVSVTR	5874	5.56	1	1275.6370	2		0		no	4.92	110.64	27.49
SIVVSPILIPENQR	13274	5.18	1	1563.9011	2		0		no	6.02	9.33	1.44
VNSDGGGLVALRNITAVGK	4471	4.45	1	1782.9669	3		0		yes	4.57	269.06	48.93
VVDSDRPER	4685	4.66	1	1071.5277	2		0		yes	4.36	283.27	14.43

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

PODP25







Calmodulin-3 OS=Homo sapiens OX=9606 GN=CALM3 PE=1 SV=1
5 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EAFSLFDKGDGTITTK	2518	6.77	3	1843.8836	3		0		yes	4.36	867.70	431.59
ELGTVMR	1495	6.18	3	820.4100	2		0	[6] Oxidation M	yes	3.53	1058.76	439.72
GTVMR	3484	0.00	1	578.2855	1		0	[4] Oxidation M	no	6.37	255.64	60.06
MKDTDSEEEIREAFR	5116	5.45	2	1870.8332	3		0	[2] Hydroxyl DKNP	yes	4.64	326.33	180.67
MKDTDSEEEIREAFR	7220	---	---	1870.8471	4		0	[2] Hydroxyl DKNP	yes	3.81	174.53	52.42
VFDKDGNGYISAAELR	4438	5.72	3	1753.8610	3		0		no	4.36	387.53	159.49

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q7Z406


Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=2
4 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALSLTR	1935	4.88	1	659.3948	1		0		yes	7.69	288.56	26.19
HEVPPHYAVTEGAYR	1256	4.52	1	1823.8884	4		0		yes	3.53	709.61	379.51
HEVPPHYAVTEGAYR	1733	4.52	1	1823.8852	3		0		yes	4.16	648.22	298.75
LKGLEAEVLR	5919	4.81	1	1126.6577	2		0		no	4.99	72.35	8.86
LKGLEAEVLR	13440	---	---	1126.6666	3		0		no	3.53	11.38	0.00
LLGLGVTDFSR	3829	5.35	1	1176.6455	2		0		yes	4.85	249.51	90.92

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P09382

Galectin-1 OS=Homo sapiens OX=9606 GN=LGALS1 PE=1 SV=2
4 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LPDGYEFK	2554	5.94	2	967.4668	2		0		yes	3.95	574.63	295.97
LPDGYEFKFPNR	3350	5.92	2	1481.7441	3		0		yes	3.95	343.82	128.80

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LPDGYEFKFPNR	4293	5.45	1	1527.7463	3		0	[8] Methyl K [10] Hydroxyl DKNP [11] Hydroxyl DKNP	yes	3.95	274.03	123.21
SFVLNLGK	3884	6.36	1	876.5051	2		0		no	3.81	109.63	8.41

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P00338

L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=2
4 peptides


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DKEQWKEVHK	294	5.48	1	1339.6869	2		0	[2] Methyl K	yes	5.47	1.60e+004	4331.94
LVITAGAR	4368	6.78	1	912.5665	2		0		no	3.88	266.62	124.28
VIGSGCNLDSARFR	4124	4.39	1	1550.7575	2		0	[6] Carbamidomethyl C	yes	5.96	531.95	61.56
VTLTSEEEAR	1714	7.01	4	1133.5576	2		0		yes	4.85	835.18	395.49




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01591

Immunoglobulin J chain OS=Homo sapiens OX=9606 GN=JCHAIN PE=1 SV=4
3 peptides





Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
CYTAVVPLVYGGETK	5595	7.96	2	1655.8209	2		0	[1] Carbamidomethyl C	yes	6.30	550.53	254.87
MVETALTPDACYPD	3762	6.87	2	1597.6587	2		0	[1] Oxidation M [11] Carbamidomethyl C	yes	5.89	522.49	1.09




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SSEDPNEDIVER	1073	8.48	3	1388.6079	2		0		yes	5.19	2279.57	96.41

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04075




Fructose-bisphosphate aldolase A OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=2
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ADDGRFPQVIK	2012	4.78	1	1341.7018	3		0		yes	3.81	549.62	331.98
DGADFAKWR	2222	4.21	1	1064.5208	2		0		yes	4.22	743.88	593.86
GILAADESTGSIK	2121	7.19	2	1331.6848	2		0		no	5.26	531.80	293.89
LQSIGTENTEENRR	2647	6.46	2	1645.8031	3		0		yes	4.09	553.69	382.77

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P05783





Keratin_ type I cytoskeletal 18 OS=Homo sapiens OX=9606 GN=KRT18 PE=1 SV=2
4 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)
AQYDELARK	1480	5.44	1	1092.5514	2		0		no	4.64
GPQVRDWSHYFK	960	5.59	1	1518.7658	2		0		yes	6.58
IVLQIDNAR	1247	6.67	4	1040.5937	2		0		yes	4.50
STSFRRGGMGSGGLATGIAGGLAGMGGIQNEK	1423	4.70	1	2868.3949	3		0	[8] Oxidation M [31] Methyl K	yes	5.75




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q01995

Transgelin OS=Homo sapiens OX=9606 GN=TAGLN PE=1 SV=4
4 peptides






Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EFTESQLQEGK	5165	6.48	2	1294.6048	2		0		yes	5.06	177.83	105.92
QMEQVAQFLK	4921	5.30	1	1236.6187	2		0	[2] Oxidation M	no	5.47	175.53	47.10
VPENPPSMVF K	2676	5.28	1	1291.6348	2		0	[4] Hydroxyl DKNP [6] Hydroxyl DKNP [11] Hydroxyl DKNP	yes	4.92	538.09	166.46
VPENPPSMVF K	4266	5.27	1	1289.6316	2		0	[6] Hydroxyl DKNP [11] Hydroxyl DKNP [11] Methyl K	yes	4.99	321.25	125.51

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P06703

Protein S100-A6 OS=Homo sapiens OX=9606 GN=S100A6 PE=1 SV=1
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ELKELIQK	5796	6.45	2	999.5833	2		0		yes	4.16	96.73	13.84
ELTIGSK	3023	7.08	1	746.4146	2		0		yes	3.25	195.30	28.57
ELTIGSK	9692	---	---	746.4086	1		0		yes	8.31	41.22	0.00
LQDAEIAR	336	8.49	8	914.4840	2		0		yes	3.95	6323.38	3029.62
LQDAEIAR	8199	---	---	914.4807	1		0		yes	10.53	30.30	0.00

Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P29400

Collagen alpha-5(IV) chain OS=Homo sapiens OX=9606 GN=COL4A5 PE=1 SV=2
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GDAGP ¹⁷ GIPGQPGLK	172	4.35	1	1375.7039	3		0	[6] Hydroxyl DKNP	yes	3.39	1.30e+004	7
GDPGLPGQPGR	4917	3.87	1	1150.5545	2		0		yes	4.57	142.58	
GDPGLPGV ³⁷ GFPGMK	3719	4.32	1	1440.7145	3		0	[9] Hydroxyl DKNP	no	3.95	278.44	
GFP ⁴¹ PGPPGRTGLDGLPGP ⁴⁸	4180	4.44	1	1984.0302	3		0	[21] Methyl K	yes	4.92	506.85	
GL ⁴⁴ PGIPGAPGAPGFPGSK	4446	4.76	1	1591.8310	2		0	[3] Hydroxyl DKNP	no	6.86	315.86	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q15365




Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IANPVEGSSGR	3616	6.10	3	1085.5452	2		0		yes	4.22	496.02	210.2
INISEGN ⁶⁹ PER	6967	5.17	1	1287.5917	2		0	[8] Carbamidomethyl C	yes	4.85	121.86	20.3
LVVPATQ ⁹² GLIGKGG ⁹⁸ K	9224	4.31	1	1843.9936	3		0	[8] Carbamidomethyl C [17] Carbamidomethyl C	no	4.57	31.76	0.0
QGANINEIR	3472	6.05	2	1013.5243	2		0		yes	4.16	747.67	417.9

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

O00159





Unconventional myosin-Ic OS=Homo sapiens OX=9606 GN=MYO1C PE=1 SV=4
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DGTIDFTPGSELLITK	10401	5.17	2	1705.8783	2		0		no	6.65	69.59	6.80
LLQSNPVLEAFGNAK	6754	5.74	2	1599.8469	2		0		yes	6.09	73.19	5.15
SLASKDVESPSWR	8241	4.80	1	1476.7117	2		0	[5] Hydroxyl DKNP	yes	5.75	133.31	68.51
TLFATEDALEVR	1639	5.85	1	1363.7129	2		0		yes	5.40	337.18	1423.75

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q12931





Heat shock protein 75 kDa_ mitochondrial OS=Homo sapiens OX=9606 GN=TRAP1 PE=1 SV=3
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AFLDALQNQAEASSK	5868	5.43	2	1591.7849	3		0		yes	4.02	93.79	41.39
LNELLVK	52	6.11	2	827.5127	1		0		yes	9.83	9900.80	3.08e+004
LNELLVK	1039	5.41	1	827.5106	2		0		yes	3.74	818.22	2224.70
NPAWSLQAGR	2050	4.58	1	1098.5628	2		0		yes	4.43	433.28	331.66




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P23526

Adenosylhomocysteinase OS=Homo sapiens OX=9606 GN=AHCY PE=1 SV=4
4 peptides





Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALDIAENEMPGLMR	7208	4.71	1	1590.7273	2		0	[7] Hydroxyl DKNP [13] Oxidation M	no	5.96	148.22	19.00
IILLAEGR	3090	5.33	1	883.5478	2		0		yes	4.02	330.10	54.49
VAVVAGYGDVGK	1988	5.32	1	1133.6061	2		0		yes	4.57	331.65	836.67
VPAINVNDSVTK	1912	5.79	2	1255.6732	2		0		yes	4.99	598.22	1081.27




Tags	
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	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

076013






Keratin_type I cuticular Ha6 OS=Homo sapiens OX=9606 GN=KRT36 PE=1 SV=1
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EQYEALVENNR	8029	5.26	1	1394.6258	2		0	[1] Carbamidomethyl C	no	5.47	60.28	8.0
LEGEIATYRHLLEGEDCK	2013	4.93	1	2132.0206	3		0	[17] Carbamidomethyl C	yes	4.50	1024.35	620.0
SENARLVLQIDNAK	3600	5.27	1	1569.8438	3		0		yes	4.16	165.47	25.0
TIEDFQQK	1451	4.99	1	1021.5067	2		0	[8] Methyl K	yes	4.29	1432.55	910.0

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q3LXA3




Triokinase/FMN cyclase OS=Homo sapiens OX=9606 GN=TKFC PE=1 SV=2
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalise Abundanc	
											CTR	MCD
AILEVLQS	3739	5.05	2	871.5012	1		0		no	10.11	200.32	
LEQPDPGAVAAAAILR	4372	5.90	2	1590.8719	2		0		yes	6.23	295.34	
SRVAPAEPEAPDSTAAGGSASK	8520	3.86	1	2215.0440	3		0	[5] Hydroxyl DKNP [23] Hydroxyl DKNP	no	4.50	243.28	
VAPAEPEAPDSTAAGGSASKR	5122	5.54	2	2096.0098	3		0		yes	5.54	289.69	
YGKAPGDR	347	0.00	1	931.4569	2		0	[6] Hydroxyl DKNP [C-term] Dehydrated	yes	3.88	2274.27	7




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P26006

Integrin alpha-3 OS=Homo sapiens OX=9606 GN=ITGA3 PE=1 SV=5
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AAFVSEQQK	2494	6.38	2	1134.5629	2		0		yes	4.64	660.33	189.80
SETVLTATGR	4349	6.74	2	1193.5684	2		0	[7] Carbamidomethyl C	yes	4.64	282.45	86.38
YLLLAGAPR	2669	7.00	2	972.5725	2		0		yes	4.29	339.22	122.47

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02743

Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IVLGQEQDSYGGK	5109	6.29	1	1392.6869	2		0		yes	5.33	220.40	84.64
IVLGQEQDSYGGKFDR	2042	6.52	3	1810.8844	3		0		yes	4.57	847.95	451.67
VGEYSLYIGR	2603	7.06	3	1155.5960	2		0		yes	4.78	650.78	230.83




Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P23396







40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AELNEFLTR	5615	7.01	2	1091.5636	2		0		yes	4.43	276.37	90.29
DEILPTTPISEQK	8457	5.90	1	1469.7512	2		0		yes	5.61	106.37	15.07
ELAEDGYSGVEVR	4640	6.80	3	1422.6606	2		0		yes	5.40	301.77	148.40

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9NP85







Podocin OS=Homo sapiens OX=9606 GN=NPHS2 PE=1 SV=1
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
 AAEILSGTPAAVQLR	5877	6.42	2	1642.8583	2		0	[1] Oxidation M	yes	6.16	158.50	31.30
 AAEILSGTPAAVQLR	13194	---	---	1642.8750	3		0	[1] Oxidation M	yes	4.78	10.63	0.00
SLTEILLER	5314	6.96	1	1072.6093	2		0		yes	4.50	103.83	7.24
TQGSLPFPSPSKPVEPLNPK	4908	6.10	1	2119.0987	3		0		yes	5.26	141.38	5.92

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P68371




Tubulin beta-4B chain OS=Homo sapiens OX=9606 GN=TUBB4B PE=1 SV=1
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVLVDLEPGTM  SVR	623	7.11	2	1616.8060	2		0	[12] Hydroxyl DKNP	yes	6.16	2750.84	958.24
AVLVDLE  PGTM  SVR	4344	6.11	2	1632.7918	2		0	[8] Hydroxyl DKNP [12] Hydroxyl DKNP	yes	6.16	263.04	97.04
INVYYNEATGGK	1368	6.10	2	1327.6417	2		0		yes	5.19	1082.81	610.42

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q96KP4






Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EGGSIPVTLTFQEATGK	5566	6.36	3	1733.8843	2		0		yes	6.44	231.08	85.18
QLGGSVELVDIGK	4025	6.03	3	1313.7082	2		0		yes	5.19	431.30	113.78
TVFGVEPDLTR	1601	6.87	3	1232.6305	2		0		yes	4.78	1128.10	784.38

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9HC38




Glyoxalase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GLOD4 PE=1 SV=1
4 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ELPDLEDLMKR	177	4.31	1	1357.7014	3		0		yes	3.74	2.58e+004	1.21e+004
ELPDLEDLMKR	734	---	---	1357.6946	2		0		yes	5.54	5284.67	1451.03
FYRDVLGMK	2723	4.94	1	1127.5672	2		0		yes	4.57	1003.69	724.79
ILTPLVSLDTPGK	6948	5.37	1	1352.7814	2		0		yes	5.40	172.86	5.51
ITEDSFSPYDGK	7521	4.44	1	1485.6920	2		0		no	5.61	76.22	20.50




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P17661

Desmin OS=Homo sapiens OX=9606 GN=DES PE=1 SV=3
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Norn Abundances	
											CTR	M
IESLNEEIAFLK	9288	5.58	1	1404.7471	2		0		no	5.61	39.71	
LQEEIQLK	2437	4.94	1	999.5759	2		0		yes	4.36	283.31	
TIETRDGEVVSEATQQQHEVL	2190	3.72	1	2368.1537	3		0		yes	6.30	108.57	
VSDLTQAANK	84	4.50	1	1045.5510	2		0		yes	4.22	2.01e+004	4.




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Norm Abundances	
											CTR	M

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q08554




Desmocollin-1 OS=Homo sapiens OX=9606 GN=DSC1 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VQDQDLNP ⁺ PHSK	3716	5.44	2	1477.7159	3		0		yes	3.88	832.50	105.09
VTATDLDEPDTLHTR	1015	6.73	2	1682.8118	3		0		yes	4.29	2616.36	800.19
VTIFTVPEN ⁺ CR	2007	6.53	2	1334.6651	2		0	[10] Carbamidomethyl C	yes	5.12	1504.41	352.47

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P12110





Collagen alpha-2(VI) chain OS=Homo sapiens OX=9606 GN=COL6A2 PE=1 SV=4
4 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EEGIRLFAVAPNQNLK	6202	3.92	1	1797.9524	2		0		no	6.65	59.16	59.55
GDPGRPGFSYPGPR	1964	4.25	1	1458.6828	2		0		yes	5.26	1200.20	418.34
GPQGALGE ⁺ PGK	1438	5.95	1	1025.5133	2		0	[9] Hydroxyl DKNP	yes	4.09	719.73	243.45
IDSLSSFKEAVK	4232	4.37	1	1322.7040	3		0		yes	3.67	234.37	127.73

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P00966




Argininosuccinate synthase OS=Homo sapiens OX=9606 GN=ASS1 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IDIVENR	1071	6.99	3	857.4590	2		0		yes	3.67	1502.42	485.07
TQDPAKAPNTPDILEIEFK	9177	4.45	1	2126.0816	3		0		no	4.71	138.47	23.95
VFIEDVSR	3496	4.71	1	963.4985	2		0		yes	4.02	413.22	160.77
VFIEDVSR	3953	6.80	2	963.5014	2		0		yes	4.22	370.45	84.86

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P30041



Peroxioredoxin-6 OS=Homo sapiens OX=9606 GN=PRDX6 PE=1 SV=3
3 peptides


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FHDFLG ⁵ SWGILFSH ¹⁶ PR	8211	5.22	1	2061.9675	3		0	[7] Hydroxyl DKNP [16] Hydroxyl DKNP	yes	4.36	55.66	21.27
LPFPIIDDR	4135	6.67	2	1084.5949	2		0		yes	4.50	172.88	15.95
NFDEILR	3143	6.34	2	905.4645	2		0		yes	3.95	219.57	186.17




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P09493

Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AEQAEADKK	1818	5.05	1	988.4921	2		0		yes	4.16	563.56	278.16
ATDAEADVASLNR	4587	7.24	2	1331.6287	2		0		yes	5.06	324.23	147.82




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SKQLEDELVSLQK	5414	5.91	1	1515.8218	3		0		yes	4.02	89.41	3.29

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07900




Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DQVANSFVER	3433	7.18	4	1234.6004	2		0		yes	4.78	530.47	356.22
HIYYITGETK DQVANSFVER	6097	4.46	1	2454.2126	3		0	[10] Methyl K	yes	5.19	225.40	38.76
NPDDITNEEYGEFYK	6684	6.31	4	1832.7722	2		0		yes	6.65	231.80	40.32

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q13885




Tubulin beta-2A chain OS=Homo sapiens OX=9606 GN=TUBB2A PE=1 SV=1
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALTVPELTQQMFDSK	3821	6.12	2	1706.8498	2		0		yes	6.65	502.18	129.57
ALTVPELTQQMFDSK	7229	6.12	2	1706.8506	3		0		yes	4.29	151.07	23.34
ALTVPELTQQMFDSK	9402	5.15	1	1722.8400	2		0	[5] Hydroxyl DKNP	yes	6.72	84.05	3.80

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P05023




Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 PE=1 SV=1
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AAVPDAVGKCR	6789	5.54	1	1142.5859	2		0	[10] Carbamidomethyl C	yes	4.71	180.53	29.13
LNIPVSQVNPR	3588	5.54	1	1235.6774	2		0		yes	5.06	278.72	71.85
SPDFTNENPLETR	4595	6.28	1	1518.6973	2		0		yes	5.82	292.23	100.66

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01040




Cystatin-A OS=Homo sapiens OX=9606 GN=CSTA PE=1 SV=1
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IPGGLSEAKPATPEIQEIVDK	2908	5.35	2	2191.1632	3		0		yes	4.85	1282.56	391.07
TNETYGLKLEAVQYK	3274	6.75	1	1642.8218	3		0		yes	4.22	716.63	350.27
TQVVAGTNYIYK	2948	5.07	1	1355.6986	2		0		yes	5.40	534.01	304.80

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P14550




Aldo-keto reductase family 1 member A1 OS=Homo sapiens OX=9606 GN=AKR1A1 PE=1 SV=3
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GLEVTAYSPLGSSDR	3546	6.33	3	1550.7608	2		0		yes	5.82	568.25	592.39
SPAQILLR	2557	6.14	3	896.5433	2		0		yes	3.88	494.91	130.83
VFDFTFSPPEMK	2276	4.53	1	1491.6441	2		0	[3] Hydroxyl DKNP	yes	5.61	444.89	1572.15

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07737




Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DSLLQ ⁵ GEFSMDLR	6993	5.75	2	1640.7381	2		0	[6] Hydroxyl DKNP	yes	6.09	177.96	37.91
SSFYV ¹ NGLTLGGQK	5079	5.23	1	1485.7373	2		0	[6] Hydroxyl DKNP	yes	5.96	164.72	72.74
TFVNITPAEVGVLVGK	9104	5.76	1	1642.9265	2		0		yes	6.44	51.31	1.06

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P17066




Heat shock 70 kDa protein 6 OS=Homo sapiens OX=9606 GN=HSPA6 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DLSGNK	1811	5.11	1	632.3127	1		0		yes	7.27	637.33	206.93
LSKEEVER	6301	6.40	1	988.5107	2		0		yes	4.16	150.77	17.25
LV ¹ NHFMEEFR	2182	5.03	1	1336.6249	2		0	[3] Hydroxyl DKNP	yes	5.40	583.38	463.32

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9BR76




Coronin-1B OS=Homo sapiens OX=9606 GN=CORO1B PE=1 SV=1
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AIFLADGK	3635	5.32	1	833.4620	2		0		yes	3.67	210.40	251.43
DADPILISLR	6666	6.04	1	1111.6212	2		0		yes	4.50	93.62	82.33
LEEVMQELR	2986	4.66	1	1145.5957	2		0		yes	4.50	530.72	296.45

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01011




Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ADLSGITGAR	1096	6.65	2	959.5031	2		0		yes	4.02	905.82	1180.57
LINDYV ^K NGTR	325	4.51	1	1307.6836	2		0	[7] Hydroxyl DKNP	yes	5.19	1866.20	6590.89
LINDYV ^K NGTR	1873	4.75	2	1305.7038	2		0	[7] Methyl K	yes	5.26	769.86	378.08

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q08380




Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ELSEALGQIFDSQR	7808	5.32	1	1591.7841	2		0		yes	6.16	202.50	29.24
SDLAVPSELALLK	6001	6.13	1	1354.7671	2		0		yes	5.54	276.96	52.41
SQLVYQSR	1937	4.28	1	979.4954	2		0		yes	4.29	783.40	375.70

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q5D862




Filaggrin-2 OS=Homo sapiens OX=9606 GN=FLG2 PE=1 SV=1
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ENQPPQNCGGQWR	2783	4.30	1	1545.6449	3		0	[2] Hydroxyl DKNP [8] Carbamidomethyl C	yes	3.74	1862.27	418.32
FSNSSSSNEFSK	2378	6.32	1	1319.5655	2		0		yes	5.33	1522.81	469.41
VLSKEYCK	1290	4.78	1	1025.5252	2		0	[7] Carbamidomethyl C	yes	4.16	1843.34	571.09

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9NSB2

Keratin_type II cuticular Hb4 OS=Homo sapiens OX=9606 GN=KRT84 PE=2 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DLNLDGIIAEVK	85	4.95	1	1328.7222	2		0	[12] Hydroxyl DKNP [12] Methyl K	yes	5.54	3.84e+004	1.82e
LEGVGPVNISVSSSR	3649	5.24	1	1659.8197	3		0	[2] Carbamidomethyl C	yes	3.95	186.91	1
SRADAEAWYQTK	8140	5.10	1	1440.6435	2		0	[12] Hydroxyl DKNP	yes	5.89	108.55	




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9BSE5

Agmatinase_mitochondrial OS=Homo sapiens OX=9606 GN=AGMAT PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GSSTLDPYR	2934	5.57	1	1095.5174	2		0		yes	4.36	368.09	270.20
GSSTLDPYRYNR	676	4.96	1	1560.7167	2		0	[7] Hydroxyl DKNP [8] Hydroxyl DKNP	yes	5.75	4029.97	2118.25
GSSTLDPYRYNR	1963	4.63	1	1560.7125	2		0	[7] Hydroxyl DKNP [12] Hydroxyl DKNP	yes	5.68	860.75	350.16

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P52566







Rho GDP-dissociation inhibitor 2 OS=Homo sapiens OX=9606 GN=ARHGDIB PE=1 SV=3
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
APNVVTR	4220	5.26	1	854.4903	2		0		yes	3.67	162.83	40.05
GTYHNKSFFTDDDK	2912	4.12	1	1673.7171	2		0		yes	6.02	1075.58	551.66
TLLGDGPVTPDK	3916	5.74	1	1310.6940	2		0		yes	5.19	328.64	128.71

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

O43809




Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens OX=9606 GN=NUDT21
PE=1 SV=1
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DSSVAARFQR	24	3.88	2	1135.5788	2		0		yes	4.64	5.89e+004	1.73e+005
DSSVAARFQR	289	3.88	1	1135.5728	3		0		yes	3.19	4837.33	1.51e+004
EPLYEK	180	5.75	3	777.3917	1		0		yes	8.73	2590.87	1.21e+004
EPLYEK	395	7.28	2	777.3914	1		0		yes	8.66	1126.58	4035.32
EPLYEK	3606	---	---	777.3898	2		0		yes	3.60	78.72	407.74
EPLYEK	4848	---	---	777.3912	2		0		yes	3.60	48.37	206.79

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04040





Catalase OS=Homo sapiens OX=9606 GN=CAT PE=1 SV=3
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FNTANDDNVTQVR	2472	5.99	1	1492.6853	2		0		yes	5.61	775.58	251.35
FSTVAGESGSADTVR	3119	4.43	1	1482.6745	2		0		yes	5.54	404.78	130.59
FSTVAGESGSADTVRDPR	1706	4.54	1	1850.8733	3		0		yes	4.71	1055.02	646.27

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01859




Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GLPAPIEK	2637	6.75	2	823.4789	2		0		yes	3.88	220.81	23.31
L̄MISR	2292	0.00	1	634.3476	1		0	[2] Oxidation M	yes	7.55	461.50	15.17
L̄MISR	6438	---	---	634.3469	2		0	[2] Oxidation M	yes	3.32	87.57	1.05
STSESTAALḠCLVK	1095	8.19	4	1422.7012	2		0	[11] Carbamidomethyl C	yes	5.47	1759.58	404.42

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q13642




Four and a half LIM domains protein 1 OS=Homo sapiens OX=9606 GN=FHL1 PE=1 SV=4
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AIVAGDQNVEYK	5287	5.06	1	1305.6480	2		0		yes	5.40	108.32	38.24
DNPGTTTASTA K NAP	7621	4.68	1	1458.6944	2		0	[12] Methyl K	yes	5.61	112.24	44.24
QVIGTGSFFPK	11316	5.02	1	1179.6180	2		0		yes	4.85	46.36	13.12

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P50395




Rab GDP dissociation inhibitor beta OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=2
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DLGTESQIFISR	6065	5.99	1	1364.6854	2		0		yes	5.33	78.21	119.70
VTEGSFVYK	5190	4.33	1	1028.5176	3		0		yes	3.05	79.55	1.49
VTEGSFVYK	2410	4.33	1	1028.5183	2		0		yes	4.43	1133.69	161.82

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P06727




Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=4
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
I D QTVEELR	1493	3.91	1	1117.5575	2		0	[2] Hydroxyl DKNP	yes	4.43	505.68	1.14
LAPLAEDVR	4944	5.89	1	982.5400	2		0		yes	4.22	243.20	
Q K LGPAGDVEGHLSFLEK	134	4.76	1	2077.0632	3		0	[2] Hydroxyl DKNP	yes	4.64	2.36e+004	1.14

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q14240




Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=2
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DVIMREFR	2563	4.12	1	1064.5364	2		0		yes	4.36	809.94	549.96
ERDVIMR	4922	4.63	1	917.4584	2		0		yes	3.88	274.46	75.84
VLITDLLAR	3816	5.66	2	1113.6753	2		0		yes	4.64	238.32	89.62

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P55060

Exportin-2 OS=Homo sapiens OX=9606 GN=CSE1L PE=1 SV=3
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
NLFEDQNTLTSC IK EK	3592	4.57	1	1810.8489	3		0	[13] Carbamidomethyl C	yes	4.50	548.38	348.45
QLSDAIIIGREDFPQ K	2301	4.84	1	1930.0391	3		0	[17] Methyl K	yes	5.06	612.30	358.57
QLSDAIIIGREDFPQ K	1903	4.84	1	1930.0322	2		0	[17] Methyl K	yes	7.41	660.02	400.75

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P22061

Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=4
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifica
MGYAEAPYDAIHVGAAAPVVPQALIDQLKPGGRLILPVGAGG ^N QMLEY ^{DK}	275	3.98	1	5573.8191	6		0	[45] Hyd DKNP Hyd DKNP Met
MGYAEAPYDAIHVGAAAPVVPQALIDQLKPGGRLILPVGAGG ^N QMLEY ^{DK}	579	3.98	1	5573.8354	5		0	[45] Hyd DKNP Hyd DKNP Met
VQLVVG DGR	3190	6.16	2	941.5315	2		0	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P20700

Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
^C QSLTEDLEFR	6354	4.45	1	1396.6498	2		0	[1] Carbamidomethyl C	yes	5.33	125.76	74.19
IESLSSQLSNLQK	1149	4.78	1	1445.7712	2		0		yes	5.82	1027.53	841.72
LALDMEISAYRK	5265	4.52	1	1408.7280	2		0		yes	5.82	615.24	1870.10




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04899

Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAI2 PE=1
SV=3
2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IAQSDYIPTQQDVLR	5384	6.55	2	1745.8886	2		0		yes	6.58	114.25	20.38
LLLLGAGESGK	2194	6.90	2	1056.6167	2		0		yes	4.50	479.30	244.17




Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P52943



Cysteine-rich protein 2 OS=Homo sapiens OX=9606 GN=CRIP2 PE=1 SV=1
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ASSVTFTGEPNTCP ^R	6880	6.75	2	1723.7824	2		0	[14] Carbamidomethyl C	yes	6.30	103.42	47
GVNTGAVGSYIYDRDPEGK	4088	6.48	2	1996.9485	3		0		yes	4.29	231.50	143

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04439


HLA class I histocompatibility antigen_ A alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FSDAASQR	3737	6.98	2	995.4315	2		0		yes	4.02	171.04	36.60
FIAVGYVDDTQFVR	3738	6.23	1	1628.8087	2		0		yes	6.23	428.44	190.26

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q7Z794

Keratin_ type II cytoskeletal 1b OS=Homo sapiens OX=9606 GN=KRT77 PE=1 SV=3
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GEQALQDAWQK	7026	5.01	1	1272.6103	2		0		yes	5.12		

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Ave Abundance
QIEQMQLISDAEERGEQALQDAWQK	225	4.04	1	3030.4615	4		0		yes	5.89	2
QIEQMQLISDAEERGEQALQDAWQK	2612	4.04	1	3030.4595	3		0		yes	8.03	
VYSTSSSAGSGGGSPAVGSV ^[21] YARGR	59	---	---	2476.1534	5		0	Carbamidomethyl C	yes	4.22	2.9

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9BW30

Tubulin polymerization-promoting protein family member 3 OS=Homo sapiens OX=9606 GN=TPPP3
PE=1 SV=1
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
QDILDDSGYVSAYK	7113	6.29	2	1572.7262	2		0		yes	6.16	122.87	21.39
SVTGTDVDIVFSK	4074	6.62	2	1366.6924	2		0		yes	5.26	269.89	138.52



Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P61626

Lysozyme C OS=Homo sapiens OX=9606 GN=LYZ PE=1 SV=1
2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Ave Abundance
STDYGIFQINSR	1346	7.47	6	1399.6669	2		0		yes	5.40	1
TPGAVN ^[6] ACHLS ^[8] C ^[12] SALLQ ^[18] DIADAVAC ^[26] AK	3481	5.08	1	2958.3312	3		0	[6] Hydroxyl DKNP [8] Carbamidomethyl C [12] Carbamidomethyl C [18] Hydroxyl DKNP [26] Carbamidomethyl C	yes	5.75	




Tags	
	Anova p-value ≤ 0.05

	power>0.8
	q<0.05

P21291



Cysteine and glycine-rich protein 1 OS=Homo sapiens OX=9606 GN=CSRP1 PE=1 SV=3
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GYGYGQGAGTLSTDK	9577	5.92	1	1473.6607	2		0		yes	5.54	73.64	4.79
GYGYGQGAGTLSTDKGESLGIK	8130	6.49	1	2158.0458	3		0		yes	4.99	74.57	2.97

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P61224



Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LVVLGSGGVGK	2509	6.72	2	984.5900	2		0		yes	4.16	4108.20	1.36e+004
YDPTIEDSYRK	7751	5.67	1	1385.6487	3		0		yes	3.74	85.39	18.68




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P05109

Protein S100-A8 OS=Homo sapiens OX=9606 GN=S100A8 PE=1 SV=1
2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALNSIIDVYHK	5671	4.96	1	1271.6987	2		0		yes	5.26	131.49	12.54
LLETCPQYIR	1660	7.11	4	1420.6991	2		0		yes	5.54	1767.71	538.53




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
								[6] Carbamidomethyl C				

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P31946



14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=3
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVTEQGHELSNEER	7851	5.01	1	1597.7340	3		0		yes	3.88	94.88	10.66
YLSEVASGDNK	4154	6.90	2	1181.5560	2		0		yes	4.64	254.37	47.82

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02760



Protein AMBP OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ETLLQDFR	1310	7.17	4	1020.5250	2		0		yes	4.29	1244.50	475.14
TVAA [~] NLPIVR	2297	4.51	1	1212.6636	2		0	[5] Carbamidomethyl C	yes	4.92	469.89	302.91

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P13646




Keratin_type I cytoskeletal 13 OS=Homo sapiens OX=9606 GN=KRT13 PE=1 SV=4
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ILTATIENNR	4379	6.37	2	1143.6118	2		0		yes	4.71	311.35	178.21
VLDELTLSK	55	5.31	1	1030.5984	2		0	[9] Methyl K	yes	4.29	6.34e+004	3.94e+004

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9UN36



Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 PE=1 SV=2
2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
RPAILTYHDVGLNYK	9257	4.83	1	1758.9356	2		0		yes	6.99	50.81	0.23
RPAILTYHDVGLNYK	14383	---	---	1758.9577	3		0		yes	4.57	11.24	0.00
TASLTSAAASVDGNR	4479	6.82	2	1348.6538	2		0		yes	5.19	143.83	3.35

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P05089

Arginase-1 OS=Homo sapiens OX=9606 GN=ARG1 PE=1 SV=2
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
TIGIIGAPFSK	3232	6.42	2	1102.6365	2		0		yes	4.64	629.59	80.74
YFSMTEVDNR	4043	5.21	1	1146.5096	2		0		yes	4.50	993.66	79.89




Tags	
	Anova p-value ≤ 0.05
	power>0.8

 q<0.05

P00403



Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1
2 peptides




Sequence	Peptide ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LLDVDNR	1311	5.22	1	843.4538	2		0		yes	3.60	1659.71	1214.59
LLDVDNR	13258	---	---	843.4557	1		0		yes	9.21	43.56	0.00
VVLPIEAPIR	3793	6.22	1	1105.6858	2		0		yes	4.50	187.20	93.23

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q562R1


Beta-actin-like protein 2 OS=Homo sapiens OX=9606 GN=ACTBL2 PE=1 SV=2
2 peptides


Sequence	Peptide ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EIITLAPSTMK	1161	5.57	1	1202.6468	2		0		yes	4.78	2943.34	1601.46
KDLVANTVLSGGSTMYPGIADR	984	5.86	1	2358.1543	3		0	[1] Methyl K [15] Oxidation M	yes	5.19	1601.46	601.46




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P06753

Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=2
2 peptides



Sequence	Peptide ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AADAAEAVASLNRR	2339	6.17	2	1471.7379	3		0		yes	4.16	460.30	276.43
KAADAAEAVASLNRR	5366	5.11	1	1457.7353	2		0	[1] Methyl K	yes	5.75	246.97	100.85




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
												

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P42765



3-ketoacyl-CoA thiolase_ mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1 SV=2
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ETPALTINR	2929	6.18	1	1013.5474	2		0		yes	4.22	337.17	358.53
SLDLDISK	2854	5.01	1	889.4814	2		0		yes	3.95	384.47	544.46

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9NZT1



Calmodulin-like protein 5 OS=Homo sapiens OX=9606 GN=CALML5 PE=1 SV=2
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ARAGLE D LQVAFR	3319	4.73	1	1460.7717	2		0	[7] Hydroxyl DKNP	yes	5.89	768.30	250.05
NLSEAQLR	903	6.39	5	929.4886	2		0		yes	3.95	3736.67	2656.23




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P52758

2-iminobutanoate/2-iminopropanoate deaminase OS=Homo sapiens OX=9606 GN=RIDA PE=1 SV=1
2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AAGCDFTNVV ^K	114	4.94	1	1194.5751	2		0	[4] Carbamidomethyl C [11] Methyl K	yes	4.85	9478.10	2.82e+004
AAQQAALPK	1439	6.14	1	1030.5686	2		0		yes	4.43	1463.77	638.61

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q13228

Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=2
2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IYVVDVGSEPR	2422	5.97	1	1232.6344	2		0		yes	5.06	947.88	277.49
NTGTEAPDYLATVDVDPK	6117	5.11	1	1904.9026	2		0		yes	7.06	184.46	20.55

Tags


	Anova p-value ≤ 0.05
	power>0.8
	q<0.05



P61978

Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DYD ^K MSPR	5544	5.32	1	1013.3758	2		0	[4] Hydroxyl DKNP	yes	4.22	109.34	13.02
TDYNASVSPDSSGPER	6124	5.68	1	1779.7916	2		0		yes	6.44	142.57	115.40




Tags




	Anova p-value ≤ 0.05
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	power>0.8
	q<0.05

P13797



Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4
3 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FSADIK	3188	0.00	1	679.3546	1		0		yes	7.62	170.61	47.78
INNFSADIK	606	5.03	1	1020.5291	2		0		yes	4.09	1455.32	737.94
VYALPEDLVEVKPK	2514	5.83	1	1598.8912	3		0		yes	4.22	496.38	199.42

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P54652


Heat shock-related 70 kDa protein 2 OS=Homo sapiens OX=9606 GN=HSPA2 PE=1 SV=1
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DAGTITGLNVLR	5630	6.37	1	1228.6698	2		0		yes	4.99	139.68	46.80
VAAKNALESYTYNIK	6499	4.44	1	1683.8898	2		0		yes	6.58	203.49	96.69




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P37837

Transaldolase OS=Homo sapiens OX=9606 GN=TALDO1 PE=1 SV=2
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ILDWHVANTDKK	2267	5.18	1	1438.7524	2		0		yes	5.75	310.18	189.12
LLGELLQDNAK	3659	5.58	1	1212.6612	2		0		yes	5.06	312.42	271.20




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P09496




Clathrin light chain A OS=Homo sapiens OX=9606 GN=CLTA PE=1 SV=1
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EEQMERLEALDANSR	1232	4.85	1	1789.8372	2		0		yes	6.44	3531.74	578.75
LEALDANSR	5091	5.89	1	987.4985	2		0		yes	4.16	523.80	150.31

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q7Z4W1



L-xylulose reductase OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=2
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
MELFLAGR	1443	4.14	1	935.5085	2		0		yes	3.88	917.39	457.10
TQADLDSLVR	3036	6.58	1	1116.5744	2		0		yes	4.43	655.72	316.92




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P30038

Delta-1-pyrroline-5-carboxylate dehydrogenase_ mitochondrial OS=Homo sapiens OX=9606
GN=ALDH4A1 PE=1 SV=3
2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SADVESVVGTLR	4790	5.33	1	1318.6648	2		0		yes	5.12	240.94	111.42
STGSIVGQQPFGGAR	5228	5.37	1	1460.7298	2		0		yes	5.40	145.85	87.48

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9UBI6

Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens OX=9606
GN=GNG12 PE=1 SV=3
2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SDPLLIGIPTSENPFKDK	1805	5.15	1	1984.0447	3		0	[16] Methyl K	yes	4.99	760.27	220.09
TASTNNIAQAR	7756	5.54	1	1145.5731	2		0		yes	4.50	93.77	4.60

Tags


	Anova p-value ≤ 0.05
	power>0.8
	q<0.05



P10809

60 kDa heat shock protein_ mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=2
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DGKTLNDELEIIEGMK	1540	4.28	1	1819.8911	2		0	[1] Hydroxyl DKNP	yes	6.86	690.39	922.04
VTDALNATR	1789	6.41	1	959.4989	2		0		yes	4.02	861.22	921.08



Tags




	Anova p-value ≤ 0.05
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	power>0.8
	q<0.05

P14923


Junction plakoglobin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3
2 peptides




Sequence	Peptide ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AGDKDDITEPAV C ALR	3437	5.78	1	1729.8285	3		0	[13] Carbamidomethyl C	yes	4.22	815.69	80.32
LLNDEDPVVVTK	2183	4.90	1	1340.6938	2		0		yes	5.26	1412.34	600.28

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P38646

Stress-70 protein_ mitochondrial OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=2
2 peptides



Sequence	Peptide ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DQLPADE C N K LK	777	4.17	1	1443.7042	3		0	[8] Carbamidomethyl C [10] Methyl K	yes	4.16	1495.86	6075.22
TTPSVVAFTADGER	4089	6.33	1	1449.7052	2		0		yes	5.47	474.94	391.64




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P12277

Creatine kinase B-type OS=Homo sapiens OX=9606 GN=CKB PE=1 SV=1
2 peptides



Sequence	Peptide ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VISMQKGGNMK	4384	3.87	1	1207.5947	2		0	[11] Hydroxyl DKNP	yes	4.85	206.49	83.83
VLTPELYAELR	3106	6.52	2	1302.7140	2		0		yes	5.26	242.83	74.95

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P23246



Splicing factor_ proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SPFQ PE=1 SV=2
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FGQGGAGPVGGQGPR	4577	5.64	1	1340.6527	2		0		yes	4.92	124.61	64.30
SEEKISDSEGFK	7051	4.64	1	1354.6269	3		0		yes	3.88	69.04	10.14

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P61313



60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=2
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
QSDVMRFLLR	2105	4.39	1	1263.6673	2		0		yes	5.40	342.71	278.98
SLQSVAEER	3416	5.83	2	1017.5075	2		0		yes	4.22	587.98	227.09

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P62424



60S ribosomal protein L7a OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=2
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
NFGIGQDIQPK	3498	5.75	1	1215.6265	2		0		yes	4.92	485.66	287.14
VVNPLFEK	2244	4.36	1	944.5420	2		0		yes	4.02	366.88	200.45

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q15366



Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1
2 peptides


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IANPVEGSTDR	6147	5.45	2	1157.5656	2		0		yes	4.50	243.23	74.64
LVVPASQ ⁺ GSLIGK	951	4.53	1	1427.7788	2		0	[8] Carbamidomethyl C	yes	5.68	2524.25	1198.98

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P50995

Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 PE=1 SV=1
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DAQELYAAGENR	5846	4.43	1	1335.6001	2		0		yes	5.12	130.37	26.21
SETDLLDIR	4808	5.41	1	1060.5362	2		0		yes	4.29	202.26	148.52



Tags	
	Anova p-value ≤ 0.05
	power>0.8




	
	q<0.05

Q14195

Dihydropyrimidinase-related protein 3 OS=Homo sapiens OX=9606 GN=DPYSL3 PE=1 SV=1

2 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
D KGVNSFMVY MAYK	2119	4.81	1	1683.7632	3		0	[1] Hydroxyl DKNP [5] Hydroxyl DKNP	yes	4.22	335.25	87.37
QIGDNLIVPGGVK	4110	4.79	1	1308.7241	2		0		yes	5.47	139.33	153.42




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07196

Neurofilament light polypeptide OS=Homo sapiens OX=9606 GN=NEFL PE=1 SV=3

2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LAAKNMQNAEEW FK	5968	4.49	1	1692.8318	2		0	[14] Methyl K	yes	6.23	246.22	27.37
VHELEQQ NK	4820	4.98	1	1153.5695	2		0	[8] Hydroxyl DKNP [9] Methyl K	yes	4.71	273.86	240.18



Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05




O95571

Persulfide dioxygenase ETHE1_ mitochondrial OS=Homo sapiens OX=9606 GN=ETHE1 PE=1 SV=2

2 peptides





Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EAVLIDPVLETAPR	10312	5.32	1	1521.8327	2		0		yes	6.09	38.67	41.07
FALETR	5770	4.12	1	735.3933	1		0		yes	8.31	70.12	14.18

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P09211





Glutathione S-transferase P OS=Homo sapiens OX=9606 GN=GSTP1 PE=1 SV=2
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
 KYISLIYTNYEAG 	3781	4.26	1	1835.9170	3		0	[1] Carbamidomethyl C [15] Methyl K	yes	4.29	259.60	72.82
FQDGDLTLYQSNILR	10567	5.07	1	1882.9321	2		0		yes	6.99	82.81	1.15

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q96AC1





Fermitin family homolog 2 OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
G  EVTDPVNISGQK	9155	4.89	1	1502.6968	2		0	[2] Carbamidomethyl C	yes	5.54	46.81	3.81
SKEESSGTPAHQM  NLR	8695	3.94	1	1786.8179	3		0	[14] Hydroxyl DKNP	yes	4.22	63.98	90.50




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P16104

Histone H2AX OS=Homo sapiens OX=9606 GN=H2AX PE=1 SV=2
3 peptides



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AGLQFPVGR	212	8.52	15	943.5278	2		0		yes	3.88	7249.13	8346.32
AGLQFPVGR	14032	---	---	943.5205	1		0		yes	10.53	11.80	0.00
FPVGR	1444	0.00	2	574.3234	1		0		yes	6.79	361.48	226.30
QFPVGR	2317	0.00	2	702.3814	1		0		yes	7.83	237.92	128.69

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q99456

Keratin_ type I cytoskeletal 12 OS=Homo sapiens OX=9606 GN=KRT12 PE=1 SV=1
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GTGTADASQSDYSK	313	4.02	1	1386.5922	2		0		yes	5.06	3919.36	1.32e+004
LELEIETYRR	346	4.31	1	1320.7095	3		0		yes	4.02	3626.79	9824.41

Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05




Q2TBA0

Kelch-like protein 40 OS=Homo sapiens OX=9606 GN=KLHL40 PE=1 SV=2
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalise Abundanc
											CTR
EEAVFEAVMRWAGSGDAEAQAER	197	3.88	1	2508.1245	4		0		yes	4.85	3209.97
EEAVFEAVMRWAGSGDAEAQAER	441	3.88	1	2508.1272	5		0		yes	4.16	1478.06
EEAVFEAVMRWAGSGDAEAQAER	3084	---	---	2508.1280	3		0		yes	5.40	65.31


Tags




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	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08590

Myosin light chain 3 OS=Homo sapiens OX=9606 GN=MYL3 PE=1 SV=3
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ALGQNPTQAEVLR	1571	7.69	2	1395.7445	2		0		yes	5.47	57.29	793.71

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P16520

Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Homo sapiens OX=9606
GN=GNB3 PE=1 SV=1
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LLVSASQDGK	2294	7.30	3	1016.5453	2		0		yes	4.22	539.22	202.21




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

A0A0A0MRZ8

Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LLIYDASNR	2476	7.25	4	1063.5660	2		0		yes	4.57	732.02	148.69




Tags	

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

A0A0B4J1V1



Immunoglobulin heavy variable 3-21 OS=Homo sapiens OX=9606 GN=IGHV3-21 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AEDTAVYYC ⁺ AR	4850	7.23	4	1317.5728	2		0	[9] Carbamidomethyl C	yes	5.12	440.61	101.13

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P48741


Putative heat shock 70 kDa protein 7 OS=Homo sapiens OX=9606 GN=HSPA7 PE=5 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalis Abundances	
											CTR	MCD
VLPIINEATAAAIAYGLDR	70	3.60	1	1970.0675	4		0		yes	4.50	2.54e+004	8.96e-
VLPIINEATAAAIAYGLDR	332	3.60	1	1970.0594	3		0		yes	5.47	4993.30	1.90e-
VLPIINEATAAAIAYGLDR	13293	3.60	1	1970.0561	4		0		yes	2.15	0.00	

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P52565


Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDI1 PE=1 SV=3
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AEEYEFLTPVEEAPK	3250	7.17	2	1750.8237	2		0		yes	6.65	419.52	100.95

Tags	
	Anova p-value ≤ 0.05
	power >0.8
	q <0.05

Q14103


Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IFVGGLSPDTPEEK	1936	7.15	2	1487.7468	2		0		yes	5.89	548.38	403.01

Tags	
	Anova p-value ≤ 0.05
	power >0.8
	q <0.05

P16444


Dipeptidase 1 OS=Homo sapiens OX=9606 GN=DPEP1 PE=1 SV=3
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVGFGGDFDGVPR	3289	6.75	2	1292.6153	2		0		yes	5.12	580.79	107.70

Tags	
	Anova p-value ≤ 0.05
	power >0.8
	q <0.05

P51153


Ras-related protein Rab-13 OS=Homo sapiens OX=9606 GN=RAB13 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LLLIGDSGVGK	3540	6.75	2	1070.6301	2		0		yes	4.50	240.51	211.04

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P27348


14-3-3 protein theta OS=Homo sapiens OX=9606 GN=YWHAQ PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVTEQGAELSNEER	9689	6.61	1	1531.7039	2		0		yes	5.54	74.47	2.54

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9BVC6

Transmembrane protein 109 OS=Homo sapiens OX=9606 GN=TMEM109 PE=1 SV=1
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EAPVDVLTQIGR	2753	6.58	2	1296.6985	2		0		yes	5.06	373.49	277.22




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01619

Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LLIYGASSR	3130	6.58	1	978.5398	2		0		yes	4.22	339.97	104.31




Tags	
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	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9BVQ7

Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens OX=9606 GN=SPATA5L1 PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GVLLAGPPGVGK	2198	6.56	2	1063.6356	2		0		yes	4.36	390.97	406.69

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9NVA2


Septin-11 OS=Homo sapiens OX=9606 GN=SEPTIN11 PE=1 SV=3
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SYELQESNVR	3426	6.54	1	1223.5785	2		0		yes	4.78	527.35	162.71

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q15517

Corneodesmosin OS=Homo sapiens OX=9606 GN=CDSN PE=1 SV=3
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IILQPCTGSK	1721	6.54	1	1014.5344	2		0	[6] Carbamidomethyl C	yes	4.16	1686.79	852.69

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01889

HLA class I histocompatibility antigen_ B alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=3
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FDSAASPR	4077	6.51	2	964.4290	2		0		yes	3.95	340.29	54.62

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P31944


Caspase-14 OS=Homo sapiens OX=9606 GN=CASP14 PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
TNPEIQSTLR	1715	6.45	1	1157.5940	2		0		yes	4.64	2145.05	947.15

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q86UL8


Membrane-associated guanylate kinase_ WW and PDZ domain-containing protein 2 OS=Homo sapiens OX=9606 GN=MAGI2 PE=1 SV=3
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
APGLAAADAADAAR	3912	6.37	1	1239.6156	2		0		yes	4.92	239.55	51.53

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q02252


Methylmalonate-semialdehyde dehydrogenase [acylating]_ mitochondrial OS=Homo sapiens OX=9606
 GN=ALDH6A1 PE=1 SV=2
 1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AGEYIFER	3215	6.32	1	983.4738	2		0		yes	4.09	376.98	326.25

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P52209

6-phosphogluconate dehydrogenase_ decarboxylating OS=Homo sapiens OX=9606 GN=PGD PE=1 SV=3
 1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GILFVGSGVSGGEEGAR	6249	6.22	2	1590.7911	2		0		yes	5.96	148.66	32.80

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P47755


F-actin-capping protein subunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 PE=1 SV=3
 1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LLLNNNDNLLR	1930	6.18	3	1196.6812	2		0		yes	4.85	481.62	470.55

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P01877


Immunoglobulin heavy constant alpha 2 OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=4
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DASGATFTWTPSSGK	8051	6.13	1	1511.6833	2		0		yes	5.54	168.91	47.53

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02748


Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=2
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AIEDYINEFSVR	4374	6.11	2	1454.7031	2		0		yes	5.61	264.15	97.46




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P18124

60S ribosomal protein L7 OS=Homo sapiens OX=9606 GN=RPL7 PE=1 SV=1
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IALTDNALIAR	2857	6.10	1	1169.6724	2		0		yes	4.78	275.13	133.66




Tags	
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	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q969L2


Protein MAL2 OS=Homo sapiens OX=9606 GN=MAL2 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VTLPAGPDILR	2264	6.07	2	1150.6699	2		0		yes	4.64	336.00	120.76

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9BVM4

Gamma-glutamylaminocyclotransferase OS=Homo sapiens OX=9606 GN=GGACT PE=1 SV=2
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LVEGEVYAVDER	4644	6.06	2	1377.6713	2		0		yes	5.33	212.03	51.87



Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q00796

Sorbitol dehydrogenase OS=Homo sapiens OX=9606 GN=SORD PE=1 SV=4
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VAIEPGAPR	3937	6.05	1	908.4999	2		0		yes	3.81	295.24	118.10




Tags	
	Anova p-value ≤ 0.05

	power>0.8
	q<0.05

P14649


Myosin light chain 6B OS=Homo sapiens OX=9606 GN=MYL6B PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
+KDVPV K	295	6.03	1	726.4265	1		0	[N-term] Formyl K N-TERM [6] Methyl K	yes	8.38	3277.60	3337.28

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P13489


Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VNPALAEINLR	3439	6.00	1	1208.6807	2		0		yes	4.92	207.60	57.58

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9H299


SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens OX=9606 GN=SH3BGL3 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VYSTVTGSR	5300	5.98	1	1055.5172	2		0		yes	4.29	306.53	82.07

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P62942


Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens OX=9606 GN=FKBP1A PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GVQVETISPGDGR	7021	5.94	1	1313.6502	2		0		yes	5.06	246.87	141.58

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P35237

Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=3
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
IAELLSPGSVDPLTR	6119	5.94	1	1566.8531	2		0		yes	6.16	136.06	6.18




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P61158

Actin-related protein 3 OS=Homo sapiens OX=9606 GN=ACTR3 PE=1 SV=3
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LSEELSGGR	4853	5.92	1	946.4716	2		0		yes	3.88	399.99	57.49




Tags	
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	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P50453


Serpin B9 OS=Homo sapiens OX=9606 GN=SERPINB9 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AQLLELPYAR	7585	5.83	1	1172.6406	2		0		yes	4.78	105.38	7.25

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q92597

Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
TASGSSVTSLDGTR	5173	5.82	2	1337.6359	2		0		yes	5.12	329.30	434.82



Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q96A08

Histone H2B type 1-A OS=Homo sapiens OX=9606 GN=H2BC1 PE=1 SV=3
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
KESYSIYIK	2705	5.82	1	1292.6500	2		0		yes	5.06	878.89	436.93




Tags	
	Anova p-value ≤ 0.05

	power>0.8
	q<0.05

P45880


Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606 GN=VDAC2 PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
YQLDPTASISAK	4144	5.79	1	1292.6531	2		0		yes	5.12	373.54	124.84

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07858


Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=3
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LPASFDAR	747	5.72	1	875.4459	2		0		yes	3.81	2962.50	1506.91



Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02766

Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AADDTWEPFASGK	7483	5.72	1	1393.6127	2		0		yes	5.19	169.47	65.60




Tags	
	Anova p-value ≤ 0.05

	power>0.8
	q<0.05

P59910


DnaJ homolog subfamily B member 13 OS=Homo sapiens OX=9606 GN=DNAJB13 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SNPSSAEIFR	226	5.66	1	1235.5805	2		0		yes	5.33	4241.96	1.25e+004

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P61604


10 kDa heat shock protein_ mitochondrial OS=Homo sapiens OX=9606 GN=HSPE1 PE=1 SV=2
1 peptide



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VLLPEYGGTK	2478	5.62	1	1075.5829	2		0		yes	4.43	464.51	504.67

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P12035

Keratin_ type II cytoskeletal 3 OS=Homo sapiens OX=9606 GN=KRT3 PE=1 SV=3
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
KDQDSAYMNK	3977	5.62	1	1169.5292	2		0		yes	4.50	598.93	114.72




Tags	
	Anova p-value ≤ 0.05
	power>0.8

	q<0.05
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P61106


Ras-related protein Rab-14 OS=Homo sapiens OX=9606 GN=RAB14 PE=1 SV=4
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LTSEPQQR	7687	5.57	1	1054.5357	2		0		yes	4.09	44.13	1.11

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P51148


Ras-related protein Rab-5C OS=Homo sapiens OX=9606 GN=RAB5C PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GVDLQENNPASR	6999	5.55	1	1298.6181	2		0		yes	5.12	128.50	46.32

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

A0A075B6P5

Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=1
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
FSGSGSGTDFTLK	3825	5.55	2	1302.6142	2		0		yes	5.06	554.05	140.14

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05



P22528

Cornifin-B OS=Homo sapiens OX=9606 GN=SPRR1B PE=1 SV=2
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VPEPQPK	3407	5.53	1	953.4619	2		0	[5] Carbamidomethyl C	yes	4.09	759.85	129.43

Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9BQI9

Nuclear receptor-interacting protein 2 OS=Homo sapiens OX=9606 GN=NRIP2 PE=1 SV=3
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VAVDGTQYNR	7376	5.49	1	1222.5866	2		0		yes	4.71	71.53	21.17

Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q14894

Ketimine reductase mu-crystallin OS=Homo sapiens OX=9606 GN=CRYM PE=1 SV=1
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LVTFYEDR	5970	5.47	1	1041.5209	2		0		yes	4.36	338.30	96.42


Tags




	Anova p-value ≤ 0.05
	power>0.8

	q<0.05
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P07339

Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VSTLPAITLK	4113	5.47	1	1041.6416	2		0		yes	4.36	400.26	268.46

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P28072


Proteasome subunit beta type-6 OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=4
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
QVLLGDQIPK	686	5.44	2	1109.6436	2		0		yes	4.64	1207.01	3410.32

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P62750

60S ribosomal protein L23a OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LAPDYDALDVANK	3265	5.40	1	1403.6949	2		0		yes	5.47	306.58	266.00

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05



P62258

14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VAGMVELTVEER	4963	5.39	2	1462.6977	2		0	[5] Hydroxyl DKNP	yes	5.75	821.16	174.45

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q2M2I5

Keratin_ type I cytoskeletal 24 OS=Homo sapiens OX=9606 GN=KRT24 PE=1 SV=1
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VVSSQVSSISEVK	11	5.38	1	1347.7387	2		0		yes	5.33	4.94e+004	1.62e+005

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P14136

Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
HLQEYQDLLNVK	6477	5.37	1	1498.7703	2		0		yes	6.09	94.19	3.52
HLQEYQDLLNVK	13651	---	---	1498.7810	3		0		yes	3.95	19.09	0.08




Tags	
	Anova p-value ≤ 0.05
	power>0.8

	q<0.05
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O75971


snRNA-activating protein complex subunit 5 OS=Homo sapiens OX=9606 GN=SNAPC5 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VEELALQSMISSRR	12	5.36	2	1617.8578	3		0		yes	4.29	1.17e+005	3.82e+005

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P19013


Keratin_ type II cytoskeletal 4 OS=Homo sapiens OX=9606 GN=KRT4 PE=1 SV=5
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VELEAALQQAK	457	5.34	1	1198.6560	2		0		yes	4.85	3045.39	1730.95

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P47914



60S ribosomal protein L29 OS=Homo sapiens OX=9606 GN=RPL29 PE=1 SV=2
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AQAAAPASVPAQAPK	4474	5.28	1	1376.7358	2		0		yes	5.61	128.70	91.38




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04259

Keratin_type II cytoskeletal 6B OS=Homo sapiens OX=9606 GN=KRT6B PE=1 SV=5
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ATGGGLSSVGGGSSTIK	2491	5.28	1	1434.7526	3		0		yes	3.88	1282.66	184.63
ATGGGLSSVGGGSSTIK	7506	---	---	1434.7365	2		0		yes	5.82	309.48	10.29

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P07305

Histone H1.0 OS=Homo sapiens OX=9606 GN=H1-0 PE=1 SV=3
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GVGASGSFR	2828	5.27	1	836.4027	2		0		yes	3.53	1008.62	431.01

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P29401

Transketolase OS=Homo sapiens OX=9606 GN=TKT PE=1 SV=3
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SVPTSTVFYPSDGVATEK	6156	5.24	1	1883.9069	2		0		yes	7.06	153.05	24.82




Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P02792


Ferritin light chain OS=Homo sapiens OX=9606 GN=FTL PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LGGPEAGLGEYLFER	4295	5.17	1	1606.7946	2		0		yes	6.30	483.73	331.07

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9H0W9




Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
DPGFDLR	2295	5.04	1	818.3932	2		0		yes	3.74	650.47	105.86



Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P69892

Hemoglobin subunit gamma-2 OS=Homo sapiens OX=9606 GN=HBG2 PE=1 SV=2
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EFTPEVQASWQK	2037	5.04	1	1464.6841	2		0	[4] Hydroxyl DKNP	yes	5.19	1541.83	396.62
VYPWTQR	7115	0.00	1	1047.5449	1		0		yes	11.50	38.92	0.55
VYPWTQR	6371	0.00	1	948.4794	1		0		yes	10.46	76.00	13.52


Tags	
	Anova p-value ≤ 0.05




	power>0.8
	q<0.05

P02008

Hemoglobin subunit zeta OS=Homo sapiens OX=9606 GN=HBZ PE=1 SV=2

1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LSELHAYILRVDPVNFK	17	5.00	1	2061.0841	3		0	[12] Hydroxyl DKNP [13] Hydroxyl DKNP [15] Hydroxyl DKNP	yes	4.64	8.60e+004	3.48e+0




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9H082

Ras-related protein Rab-33B OS=Homo sapiens OX=9606 GN=RAB33B PE=1 SV=1

1 peptide



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AVEIDGERIK	4804	4.91	1	1144.5988	2		0	[10] Hydroxyl DKNP	yes	4.64	237.13	84.30




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P08311

Cathepsin G OS=Homo sapiens OX=9606 GN=CTSG PE=1 SV=2



1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GTDTLREVQLR	5048	---	---	1286.7108	3		0		yes	3.60	90.31	42.47
GTDTLREVQLR	5123	4.90	1	1286.6747	2		0		yes	5.26	209.48	89.95

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P04350

Tubulin beta-4A chain OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
GHYTEGAELV D AVLDVVRK	9153	4.83	1	2086.0631	3		0	[11] Hydroxyl DKNP	yes	5.47	55.02	2.76
GHYTEGAELV D AVLDVVRK	12139	---	---	2086.0705	4		0	[11] Hydroxyl DKNP	yes	4.22	26.16	1.91

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q58FF8


Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens OX=9606 GN=HSP90AB2P PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
PEEVHLGEK	2000	4.77	1	1036.5299	2		0		yes	4.02	777.19	287.58

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

A0A075B6H7


Probable non-functional immunoglobulin kappa variable 3-7 OS=Homo sapiens OX=9606 GN=IGKV3-7
PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EIVMTQSPPTLSLSPGER	7507	4.63	1	1956.9737	3		0	[4] Oxidation M	yes	4.92	83.75	19.28

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P21695


Glycerol-3-phosphate dehydrogenase [NAD(+)]_ cytoplasmic OS=Homo sapiens OX=9606 GN=GPD1
PE=1 SV=4
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
VTWVWFEEIGGKK	3394	4.62	1	1653.7961	2		0	[3] Oxidation M	yes	6.30	607.86	223.35

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9NZ72


Stathmin-3 OS=Homo sapiens OX=9606 GN=STMN3 PE=1 SV=3
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
MASTISAYKEK	2776	4.38	1	1257.6236	2		0	[9] Hydroxyl DKNP [9] Methyl K	yes	4.99	902.44	353.58

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P78417



Glutathione S-transferase omega-1 OS=Homo sapiens OX=9606 GN=GSTO1 PE=1 SV=2
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LLPDDPYEK	3764	4.29	1	1088.5500	2		0		yes	4.29	308.37	93.24

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q3MJ62


Zinc finger and SCAN domain-containing protein 23 OS=Homo sapiens OX=9606 GN=ZSCAN23 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
AFSQNAGLFHHLR	702	4.17	1	1512.7590	2		0	[5] Hydroxyl DKNP	yes	6.09	1091.53	7469.26
AFSQNAGLFHHLR	1297	---	---	1512.7592	4		0	[5] Hydroxyl DKNP	yes	3.39	371.41	2899.54

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9BUT1

3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens OX=9606 GN=BDH2 PE=1 SV=2
1 peptide

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
SGNIINMSSVASSVKGVVNR	554	4.13	1	2034.0569	3		0	[6] Hydroxyl DKNP	yes	5.82	1883.68	1.38e+1




Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P12882

Myosin-1 OS=Homo sapiens OX=9606 GN=MYH1 PE=1 SV=3
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LI N DLTAQRR	1461	3.84	1	1285.7169	2		0	[3] Hydroxyl DKNP	yes	5.19	821.52	1029.17

Tags




	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q9H2M3

S-methylmethionine--homocysteine S-methyltransferase BHMT2 OS=Homo sapiens OX=9606
GN=BHMT2 PE=1 SV=1
1 peptide




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LVKAGASIVGVN C R	217	3.53	1	1442.7874	2		0	[13] Carbamidomethyl C	yes	5.61	3090.94	1.48e+00




Tags

	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q8N257




Histone H2B type 3-B OS=Homo sapiens OX=9606 GN=H2BU1 PE=1 SV=3
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
LLPGELAK	1334	0.00	3	839.5112	1		0		yes	10.18	508.42	343.18
LLPGELAK	9603	---	---	839.5090	2		0		yes	3.74	45.61	24.47
LPGELAK	1597	---	---	726.4259	2		0		yes	3.46	378.97	287.67

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

Q5TEC6




Histone HIST2H3PS2 OS=Homo sapiens OX=9606 GN=H3-2 PE=1 SV=1
2 peptides




Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
ELLIR	443	0.00	2	642.4071	1		0		yes	7.76	1591.29	1470.87
ELLIR	8771	---	---	642.4043	2		0		yes	3.39	41.24	24.23
STELLIR ⁺	1101	0.00	2	812.4725	2		0	[C-term] Dehydrated	yes	3.88	762.87	857.01

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05

P48668

Keratin_ type II cytoskeletal 6C OS=Homo sapiens OX=9606 GN=KRT6C PE=1 SV=3
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Drift time (ms)	Average Normalised Abundances	
											CTR	MCD
EEIAQR	3226	0.00	1	744.3763	1		0		yes	7.96	611.95	113.06
YEEIAQR	10175	---	---	907.4382	2		0		yes	3.81	187.58	24.90
YEEIAQR	1034	0.00	2	907.4389	1		0		yes	10.11	2229.37	482.45

Tags	
	Anova p-value ≤ 0.05
	power>0.8
	q<0.05