Glycation Isotopic Labelling (GIL) with ^{13}C-reducing Sugars for Quantitative Analysis of Glycated Proteins in Human Plasma*

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Supplementary table 1: Glycated proteins identified in plasma analysis with information about the glycation sites and m/z value of the precursor ion corresponding to the glycated peptides. Quantitative data are based on peak area ratio between $^{12}C_6$- and $^{13}C_6$-glucose labelled peptides with standard deviation estimated by measurement of three analytical replicates. The last two columns indicate the MS-mode that detected each peptide.

Protein	**Peptide**	**gly site**	**charge**	**m/z 12Glu**	**Peak area ratio**	**SD**	**HCD**	**NL**
Serum albumin	I/AFAQYLQQCPFEDHV**K**LVNE/V	K65	3	867.08	0.5569	0.0136		X
	E/VTEFA**K**TCVADESAE/N	K75	2	909.9	1.0333	0.1127		X
	E/NCD**K**SLHTLFGDKLCTVATLRE/T	K88	3	914.45	0.9077	0.0149	X	X
	E/SAENCDKSLHTLFGD**K**LCTVATLRE/T	K97	3	1009.82	0.9810	0.0330	X	X
	E/TYGEMADCCA**K**QEPERNE/C	K117	3	783.98	0.6590	0.0076	X	
	E/RNECFLQH**K**DDNPNLPRLVRPE/V	K130	5	582.69	0.2505	0.0553	X	
	C/TAFHDNEETFL**K**KYLYE/I	K160	4	578.28	0.9956	0.0142	X	X
	E/VDVMCTAFHDNEETFLK**K**YLYE/I	K161	3	972.45	0.9949	0.0101		X
	E/LLFFA**K**RYKAAFTECCQAADKAACLLPKLDE/L	K183	2	934	0.8818	0.0236	X	
	E/CCQAAD**K**AACLLPKLDE/L	K198	3	708.99	0.7086	0.0032	X	
	E/CCQAADKAACLLP**K**LDELRDE/G	K205	3	880.08	0.3667	0.0060	X	
	E/LRDEGKASSA**K**QRLKCASLQKFGE/R	K219	5	574.7	0.8248	0.0110	X	X
	E/RAFKAWAVA**R**LSQRFPKAE/F	R242	3	798.77	0.1415	0.0152	X	X
	E/VS**K**LVTDLTKVHTE/C	K257	3	577.98	1.2937	0.0124	X	X
	E/VSKLVTDLT**K**VHTECCHGDLLE/C	K264	3	906.08	1.3840	0.0126	X	X
	E/CADDRADLA**K**YICE/N	K286	2	931.4	0.6850	0.0282	X	
	E/NQDSISS**K**LKE/C	K298	6	705.85	0.5170	0.0087		X
	E/A**K**DVFLGMFLYE/Y	K347	2	805.89	0.4879	0.0933		X
	E/**K**CCAAADPHECYAKVFDE/F	K383	3	778.32	0.7851	0.2300	X	X
	D/PHECYA**K**VFDE/F	K396	3	778.65	0.6628	0.0057		X
	E/F**K**PLVEEPQNLIKQNCE/L	K402	3	750.04	0.6924	0.0045	X	X
	E/FKPLVEEPQNLI**K**QNCE/L	K413	3	750.04	0.6924	0.0045	X	
	E/LFEQLGEY**K**FQ/N	K426	2	782.38	0.7172	0.0036		X
	Q/NALLVRYTK**K**VPQVSTPTLVE/V	K437	2	1259.71	0.3781	0.0199	X	X
	E/VSRNLG**K**VGSKCCKHPE/A	K456	4	530.26	0.7064	0.0476	X	

	E/VSRNLGKVGS**K**CCKHPE/A	K460	4	530.26	0.6713	0.0275	X	X
	E/VSRNLGKVGSKCC**K**HPE/A	K463	4	530.26	0.6713	0.0275	X	X
	H/PEA**K**RMPCAEDYLSVVLNQLCVLHE/K	K468	3	1050.94	0.5233	0.1586	X	
	E/**K**TPVSDRVTKCCTE/S	K490	3	614.96	0.8258	0.0377		X
	E/KTPVSD**R**VTKCCTE/S	R496	3	614.96	0.7236	0.0064	X	
	E/KTPVSDRVT**K**CCTE/S	K499	3	614.96	0.8734	0.0311	X	
	E/SLVNRRPCFSALEVDETYVP**K**EFNAE/T	K524	3	1078.19	0.5799	0.1059	X	
	E/TFTFHADICTLSE**K**E/R	K543	3	654.3	0.4466	0.0101	X	X
	E/RQIK**K**QTALVE/L	K549	3	492.62	1.4990	0.0226		X
	E/G**K**KLVAASQAALGL/-	K597	2	745.44	0.8320	0.1510		X
Serotransferrin	E/LLCLDNTR**K**PVDE/Y	K252	2	846.43	0.3625	0.0484		X
	E/YKDCHLAQVPSHTVVARSMGG**K**EDLIWE/L	K278	3	1130.21	0.3978	0.0208	X	
	E/FQLFSSPHGKDLLF**K**/D	K315	3	643.01	0.9035	0.0459		X
	E/C**K**PVKWCALSHHE/R	K359	4	454.21	0.6489	0.0294	X	
	E/RLKCDEWSVNSVG**K**IE/C	K384	3	814.03	0.5152	0.0767	X	
	E/FFSEGCAPGS**K**KDSSLCKLC/M	K508	3	814.37	0.8316	0.1272	X	
	E/GCAPGSKKDSSLC**K**LCMGSGLNLCEPNNKE/G	K515	4	869.14	0.4677	0.1429	X	
	E/KGDVAFV**K**HQTVPQNTGGKN/P	K553	4	572.55	0.3167	0.0400	X	
	E/KGDVAFVKHQTVPQNTGG**K**NPDPWAKN/L	K564	4	774.64	0.2980	0.0166	X	
	E/LLCLDGTR**K**PVEE/Y	K588	2	846.43	0.3625	0.0484		X
	E/YVKAVGNLRKCSTSSLLE/A	K676		1094.57	0.5894	0.0650		X
Apolipoprotein A-I	/DEPPQSPWDRV**K**D/L	K12	2	866.4	1.2085	0.0143		X
	E/GSALGKQLNL**K**LLDNWDSVTSTFSKLRE/Q	K45	4	821.44	0.6681	0.0626	X	
	E/QLGPVTQEFWDNLE**K**E/T	K77	2	1048.49	1.0091	0.1084		X
	E/VKAKVQPYLDDFQ**K**KWQEE/M	K106	4	636.08	0.8426	0.0171	X	
	E/MELY**R**QKVEPLRAE/L	R116	4	481.75	0.6045	0.0453	X	
	E/LYRQ**K**VEPLRAELQE/G	K118	2	1018.05	0.5479	0.0683		X
	E/SF**K**VSFLSALEE/Y	K226	2	759.88	0.4792	0.0703		X
Haptoglobin β chain	K/**K**QWINKAVGDKLPECE/A	K72	2	1039.52	0.4452	0.0774		X
	K/KQWIN**K**AVGDKLPE/C	K77	4	447.74	0.3599	0.0226	X	
	E/KQWINKAVGD**K**LPECE/A	K82	3	693.01	0.5140	0.0350	X	
	E/AVCG**K**PKNPANPVQR/I	K151	4	450.24	0.5414	0.0986	X	

	E/RVMPICLPS**K**DYAE/V	K270	2	920.94	0.5499	0.0602		X
	E/GSTVPE**K**KTPKSPVGVQPILNE/H	K321	2	1234.67	0.5113	0.0881		X
α-1-antitrypsin	E/NELTHDIIT**K**FLEN/E	K298	2	868.45	0.7833	0.1376		X
	E/EAPL**K**LSKAVHKAVLTIDEKGTE/A	K352	3	880.49	0.6272	0.1355	X	
	E/EAPLKLS**K**AVHKAVLTIDEKGTE/A	K355	3	880.49	0.3997	0.0495	X	
	E/QNT**K**SPLFMGKVVNPTQK/-	K404	3	727.05	0.4994	0.0506	X	
	N/TKSPLFMG**K**VVNPTQK/-	K411	3	646.35	0.5308	0.0721	X	
Apolipoprotein A-II	E/AKSYFE**K**SKEQLTPLIKKAGTE/L	K44	3	886.81	0.4970	0.0134	X	
	E/AKSYFEKS**K**EQLTPLIKKAGTE/L	K46	3	886.81	0.3843	0.0748	X	
	E/KSKEQLTPLI**K**KAGTE/L	K54	3	645.03	0.5126	0.0315	X	
Haptoglobin-related protein	KQWIN**K**AVGDKLPECE	K77	3	693.01	0.5008	0.0059	X	
	KQWINKAVGD**K**LPECE	K82	3	693.01	0.5008	0.0059	X	
	AVCG**K**PKNPANPVQR	K151	4	450.24	0.5414	0.0986	X	
Ig γ-1 chain C region	E/LLGGPSVFLFPP**K**PKDTLMISRTPE/V	K129	3	968.19	0.5690	0.0102	X	
	E/YKCKVSNKALPAPIEKTIS**K**AKGQPREPQVYTLPPSRDE/L	K221	6	765.25	0.3638	0.0409	X	
β-2-glycoprotein 1	./GRTCPKPDDLPFSTVVPL**K**TFYEPGEE/I	K19	3	704.33	0.3302	0.0683	X	
	E/HSSLAFW**K**TDASDVKPC/-	K317	4	811.15	0.4049	0.0647	X	
Complement factor H	E/VVKCLPVTAPENG**K**IVSSAMEPDRE/Y	K138	4	723.11	0.5098	0.0870	X	
	E/MHCSDDGFWS**K**EKPKCVE/I	K182	4	601.26	0.4092	0.1363	X	
	E/GFGIDGPAIA**K**CLGE/K	K954	2	833.9	1.0963	0.0439		X
	E/GN**K**RITCRNGQWSEPPKCLHPCVISRE/I	K1130	5	689.13	0.5110	0.0738	X	
Complement C3c α' chain fragment	E/SPMYSIITPNIL**R**LE/S	R35	2	955.5	0.1855	0.0148		X
	E/AHDAQGDVPVTVTVHDFPG**K**KLVLSSE/K	K43	5	602.51	0.4982	0.0454	X	
	R/SVQLTEKRMD**K**VGKYPKELRKCCE/D	K660	3	1048.87	0.5759	0.1235	X	
	R/SVQLTEKRMDKVG**K**YPKELRKCCE/D	K663	3	1048.87	0.5454	0.1140	X	
	E/AC**K**KVFLDCCNYITE/L	K721	2	1042.46	0.4732	0.0451		X
Ig γ-4 chain C region	L/FPP**K**PKDTLMISRTPE/V	K126	4	734.89	0.7074	0.0589	X	

Histidine-rich glycoprotein	E/SCPG**K**FKSGFPQVSMFFTHTFPK/-	K489	4	706.84	0.3392	0.0793	X	
Ugl-Y3	E/FKCDPHEATCYDDG**K**TYHVGE/Q	K1922	4	673.78	0.5242	0.0716	X	
α-2-HS-glycoprotein chain B	E/TTCHVLDPTPVA**R**CSVRQLKE/H	R81	3	877.11	0.7703	0.0188	X	
	E/**K**QYGFCKATLSEKLGGAE/V	K207	2	1075.53	0.8623	0.1190		X
	E/FTVSGTDCVAKE/A	K211	2	738.33	0.8080	0.0803		X
	E/KQYGFC**K**ATLSEKLGGAE/V	K213	3	717.02	0.5899	0.0474	X	
Ig γ-2 chain C region	N/FGTQTYTCNVDH**K**PSNTKVDKTVE/R	K88	4	733.85	0.4808	0.0295	X	
	E/RKCCVECPPCPAPPVAGPSVFLFPP**K**PKDTLMISRTPE/V	K125	5	900.45	0.2844	0.0173	X	
Fibrinopeptide B	E/YCRTPCTVSCNIPVVSG**K**ECEE/I	K195	3	936.4	0.3881	0.0301	X	
Spectrin β chain, brain 1	W/KSLLDACESRRV**R**LVD/T	R1893	3	693.7	1.2992	0.0484	X	
Ig α-1 chain C region	E/S**K**TPLTATLSKSGNTFRPE/V	K212	3	733.05	0.3304	0.0207	X	
	E/SKTPLTATLS**K**SGNTFRPE/V	K221	3	733.05	0.3304	0.0207	X	
Fibrinopeptide A	D/LVPGNF**K**SQLQKVPPEWKALTDMPQMRME/L	K338	4	891.45	0.4513	0.0286	X	
α-2-macroglobulin	./SVSG**K**PQYMVLVPSLLHTE/T	K5	3	749.72	0.3098	0.0251	X	
Afadin	E/K**R**MQEF/R	R232	3	499.29	0.2904	0.0779	X	
Crooked neck-like protein 1	K/EE**R**LMLLE/S	R590	3	404.2	0.7511	0.1243	X	
A-kinase anchor protein 9	E/KETIIEELNT**K**IIEE/E	K349	2	980.03	0.4504	0.0297		X
Microtubule-actin cross-linking factor 1	A/PDSQG**K**TDLTEIQCD/M	R2341	3	595.99	1.2817	0.0371		X
	D/I**K**ARAEEREI/K	K3901	2	688.39	0.7046	0.1619		X
Plasmin light chain B	D/GKRAPWCHTTNSQVRWE/Y	K252/R253/R265	3	757.1	0.1447	0.0338		X

Myosin-15	I/DIYLLE**K**S**R**VIFQQAGE/R	K283 o R285	2	1125.05	0.6073	0.0136	X
Hemopexin	E/**K**GYPKLLQDEFPGIPSPLDAAVE/C	K103	2	1324.18	0.6199	0.0675	X
Receptor-interacting serine/threonine-protein kinase 5	E/LYESLMNIANR**K**QEE/M	K412	2	1008.45	0.5191	0.1124	X
Obscurin-like protein 1	D/GGFVL**K**VLYCQAKD/R	K305	2	880.4	0.9896	0.0449	X
Myomegalin	D/LDTVAGLE**K**E/L	K753	2	576.29	0.3370	0.0897	X
UPF0639 protein	E/YLD**K**LMEETEE/L	K169	2	750.41	0.4540	0.0628	X
Ubiquitin carboxyl-terminal hydrolase 15	D/**K**YQEELNFDNPLGMRGEI/A	K292	3	750.04	0.6775	0.0310	X
Rho GTPase-activating protein 10	E/KFRKEQLGAV**K**EEKKK/F	K128	2	1054.47	0.4989	0.0137	X
Remodeling and spacing factor 1	D/**R**WEKYLIKYLCE/C	R76	2	931.89	0.7567	0.0379	X

Supplementary table 2: Glycated proteins identified in plasma analysis with the prediction approach.

Protein	peptide	gly site	charge	m/z 12Glu	Peak area ratio	SD	% increase
Serum albumin	I/AFAQYLQQCPFEDHV**K**LVNE/V	K65	3	867.08	3.4527	0.2841	82.25
	E/VTEFA**K**TCVADESAE/N	K75	2	909.90	4.2010	0.1189	62.54
	E/NCD**K**SLHTLFGDKLCTVATLRE/T	K88	4	685.84	1.7275	0.1213	280.38
	E/SAENCDKSLHTLFGD**K**LCTVATLRE/T	K97	4	757.61	2.1800	0.0604	169.79
	E/TYGEMADCCA**K**QEPERNE/C	K117	3	783.98	1.9826	0.1188	205.68
	E/RNECFLQH**K**DDNPNLPRLVRPE/V	K130	5	582.69	1.8020	0.0553	250.15
	E/CFLQHKDDNPNLP**R**LVRPE/V	R138	3	837.42	1.9867	0.0608	203.21
	C/TAFHDNEETFL**K**KYLYE/I	K160	4	578.27	2.6194	0.1890	124.69
	E/VDVMCTAFHDNEETFLK**K**YLYE/I	K161	3	977.78	2.6362	0.2000	123.51
	E/LLFFAK**R**YKAAFTE/C	R184	2	934.50	2.5395	0.3140	134.13
	E/CCQAAD**K**AACLLPKLDE/L	K198	3	708.99	2.2734	0.0919	157.61
	E/CCQAADKAACLLP**K**LDELRDEGKASSAKQRLKCASLQKFGE/R	K205	6	803.07	1.8450	0.0341	236.94
	E/LRDEG**K**ASSAKQRLKCASLQKFG/E	K214	5	548.89	2.0810	0.1205	186.52
	R/DEGKASSA**K**QRLKCASLQKFGE/R	K219	4	650.83	3.8603	0.2522	70.27
	E/LRDEGKASSAKQ**R**LKCASLQKFGE/R	R221	5	574.70	2.4759	0.0206	135.53
	E/LRDEGKASSAKQRL**K**CASLQKFGE/R	K223	5	574.70	2.4759	0.0206	135.53
	E/LRDEGKASSAKQRLKCASLQ**K**FG/E	K229	5	548.89	2.0810	0.1205	186.52
	E/LRDEGKASSA**K**Q**R**LKCASLQKFGE/R	K219R221	5	607.11	5.9930	0.1294	40.07
	E/LRDEGKASSAKQ**R**L**K**CASLQKFGE/R	R221K223	5	607.11	5.9930	0.1294	40.07
	E/LRDEGKASSAKQ**R**LKCASLQ**K**FGE/R	R221K229	5	607.11	5.9930	0.1294	40.07
	E/RAFKAWAVA**R**LSQRFPKAE/F	R242	4	479.67	1.0863	0.0165	2379.77
	K/AWAVARLSQRFP**K**AE/F	K249	3	631.67	2.4648	0.2580	139.15
	E/VS**K**LVTDLTKVHTE/C	K257	3	577.98	4.8835	0.0635	51.51
	E/VSKLVTDLT**K**VHTECCHGDLLE/C	K264	3	906.11	4.5198	0.0700	56.84
	E/CADDRADLA**K**YICE/N	K286	2	931.40	2.6254	0.0869	123.28
	E/NQDSISS**K**LKE/C	K298	2	705.85	2.3950	0.0849	143.73
	E/NQDSISSKL**K**ECCEKPLLE/K	K300	3	814.06	2.1797	0.3488	182.11
	E/NQDSISSKLKECCE**K**PLLE/K	K305	3	814.06	2.1797	0.3488	182.11
	E/A**K**DVFLGMFLYE/Y	K347	2	805.89	2.7657	0.1946	114.25
	E/**K**CCAAADPHECYAKVFDE/F	K383	3	778.32	3.3029	0.0262	86.85
	D/PHECYA**K**VFDE/F	K396	3	778.32	3.3440	0.0298	85.33
	E/F**K**PLVEEPQNLIKQNCE/L	K402	3	750.04	3.2217	0.0305	90.03

	E/FKPLVEEPQNLI**K**QNCE/L	K413	3	750.04	3.2217	0.0305	90.03
	E/LFEQLGEY**K**FQ/N	K426	2	782.38	2.7954	0.0977	111.62
	Q/NALLV**R**YTKKVPQVSTPTLVE/V	R434	2	1260.21	2.3466	0.1925	150.43
	R/YT**K**KVPQVSTPTLVE/V	K437	2	927.00	3.8202	0.3883	71.82
	Q/NALLVRYTK**K**VPQVSTPTLVE/V	K438	2	1260.21	2.3466	0.1925	150.43
	E/VSRNLG**K**VGSKCCKHPE/A	K456	4	530.26	3.4084	0.3502	84.32
	E/VSRNLGKVGS**K**CCKHPE/A	K460	4	530.26	3.4084	0.3502	84.32
	E/VSRNLGKVGSKCC**K**HPE/A	K463	4	530.26	3.4084	0.3502	84.32
	E/KTPVSDRVT**K**CCTE/S	K499	3	614.96	3.8699	0.0948	69.74
	E/SLVN**RR**PCFSALE/V	R508/R509	2	855.93	1.7271	0.0533	276.02
	E/SLVNRRPCFSALEVDETYVP**K**EFNAE/T	K524	3	1078.19	1.9065	0.2118	229.47
	E/TFTFHADICTLSE**K**E/R	K543	3	654.30	1.6370	0.0656	316.19
	E/RQIK**K**QTALVE/L	K549	3	492.62	6.5192	0.0130	36.24
	E/G**K**KLVAASQAALGL/-	K597	3	744.94	3.6728	0.0155	74.83
Serotransferrin	A/VPD**K**TVRWCAVSE/H	K23	2	854.91	2.0552	0.2725	95.01
	D/AYLAPNNL**K**PVVAE/F	K97	2	830.94	3.8603	0.1986	70.16
	E/FYGSKEDPQTFYYAVAVV**K**KD/S	K121	3	873.43	1.7841	0.0492	255.75
	E/FYGSKEDPQTFYYAVAVVK**K**D/S	K122	3	873.43	1.7841	0.0492	255.75
	P/QTFYYAVAVV**KK**D/S	K121K122	2	873.43	3.0817	0.4106	98.95
	N/IPIGLLYCDLPEP**R**KPLE/K	K162	3	763.19	2.1103	0.0877	180.85
	K/DGAGDVAFV**K**HSTIFE/N	K225	2	927.94	3.0195	0.2601	100.07
	E/Y**K**DCHLAQVPSHTVVARSMGGKEDLIWE/L	K258	5	678.53	1.3617	0.0181	553.80
	E/YKDCHLAQVPSHTVVA**R**SMGGKE/D	R273	3	911.78	1.0741	0.1445	965.90
	E/FQLFSSPHGKDLLF**K**/D	K315	3	643.01	3.0271	0.1654	99.12
	E/WSVNSVG**K**IE/C	K384	2	640.82	2.1554	0.0996	173.94
	E/FFSEGCAPGS**K**KDSSLCKLC/M	K508	3	814.37	3.7103	0.0528	73.81
	E/FFSEGCAPGSK**K**DSSLCKLC/M	K509	4	657.79	1.9429	0.1067	213.93
	E/KGDVAFVKHQTVPQNTGG**K**NPDPWAKNLN/E	K564	5	665.34	1.9385	0.0565	213.60
	N/PDPWA**K**NLNEKDYE/L	K571	3	627.62	2.7389	0.1073	115.31
	E/LLCLDGT**R**KPVEE/Y	R587	2	846.43	2.6776	0.1856	120.24
	E/LLCLDGTR**K**PVEE/Y	K588	2	846.43	2.6776	0.1856	120.24
	E/**K**YLGEEYVKAVGNLRKCSTSSLLE/A	K668	3	967.47	1.9425	0.2318	222.38
	E/YV**K**AVGNLRKCSTSSLLE/A	K676	2	1094.07	1.8228	0.0455	243.56

Titin	R/EVSRKTWT**K**VMD/F	K14587		547.94	3.0812	0.0772	96.18
Haptoglobin β chain	E/HSV**R**YQCKNYYKLRTE/G	R49	4	537.02	4.6194	0.4786	55.93
	E/GDGVYTLND**K**KQWINKAVGDKLPE/C	K76	3	951.16	2.7233	0.2251	117.46
	K/KQWIN**K**AVGDKLPE/C	K77	3	596.65	2.7970	0.0937	111.50
	K/KQWINKAVGD**K**LPECE/A	K82	3	693.01	2.6014	0.0305	124.92
	E/AVCG**K**PKNPANPVQR/I	K151	4	450.24	4.5284	0.2733	56.91
	E/RVMPICLPS**K**DYAE/V	K270	3	614.30	2.1056	0.0824	181.59
	E/**K**KTPKSPVGVQPILNE/H	K321	2	949.04	3.0825	0.1091	96.22
	E/GSTVPEK**K**TPKSPVGVQPILNE/H	K322	2	1234.67	3.0408	0.1829	98.54
Apolipoprotein A-I	./DEPPQSPWDRV**K**D/L	K12	3	563.65	4.2997	0.4251	61.31
	E/FWDNLE**K**ETE/G	K77	2	736.83	2.9621	0.2513	103.03
	E/V**K**AKVQPYLDDFQKKWQEE/M	K94	3	847.77	1.3809	0.0311	527.26
	E/VKA**K**VQPYLDDFQKKWQEE/M	K96	3	847.77	1.3809	0.0311	527.26
	E/MELY**R**QKVEPLRAE/L	R116	3	642.00	3.0683	0.2103	97.34
	E/LYRQ**K**VEPLRAELQE/G	K118	3	678.70	2.6561	0.0556	120.86
	E/YHA**K**ATEHLSTLSEKAKPALE/D	K195	4	622.32	2.4860	0.1557	135.53
Haptoglobin-related protein	K/KQWIN**K**AVGDKLPE/C	K77	3	596.65	2.7970	0.0937	111.50
	K/KQWINKAVGD**K**LPECE/A	K82	3	693.01	2.6014	0.0305	124.92
	E/AVCG**K**PKNPANPVQR/I	K151	4	450.24	4.5284	0.2733	56.91
Plasmin light chain B	E/LCDIPRCTTPPPSSGPTYQCL**K**GTGE/N	K258	3	1018.80	2.6289	0.0613	122.89
Ig γ-4 chain C region	L/FPP**K**PKDTLMISRTPE/V	K126	3	673.69	1.9653	0.2180	213.62
α-1-antitrypsin	E/GLKLVD**K**FLE/D	K153	2	662.37	2.5551	0.2162	130.18
	E/LTHDIIT**K**FLE/N	K298	3	497.93	3.5686	0.1205	77.98
	G/**K**LQHLENELTHDIIT**K**FLE/N	K283K298	2	867.95	3.0064	0.4063	102.18
	E/EAPL**K**LSKAVHKAVLTIDE/K	K352	2	1113.13	2.0188	0.1569	199.69
	E/EAPLKLS**K**AVHKAVLTIDEKGTE/A	K355	4	660.62	2.9440	0.0554	102.94
	E/EAPLKLSKAVH**K**AVLTIDEKGTE/A	K359	4	660.62	2.9440	0.0554	102.94
	N/T**K**SPLFMGKVVNPTQK/-	K404	3	646.35	2.9835	0.3288	102.85
	E/QNTKSPLFMGKVVNPTQ**K**/-	K418	3	727.05	2.2207	0.3217	171.33

Girdin (APE) (HkRP1)	S/EVS**R**Y**K**E/R	R331K333	3	412.19	2.8321	0.1307	109.53
α-2-HS-glycoprotein chain B	E/V**K**VWPQQPSGELFE/I	K49	2	903.45	2.9152	0.3063	106.42
	E/TTCHVLDPTPVA**R**CSV/R	R81	3	658.98	2.4859	0.1301	202.28
	E/FTVSGTDCVA**K**EATE/A	K193	3	888.90	2.0658	0.1211	189.32
	E/AAKCNLLAE**K**QYGFCKATLSE/K	K207	2	855.93	1.7500	0.0651	267.99
	G/FC**K**ATLSEKLGGAE/V	K213	3	558.28	1.7131	0.2072	295.10
	E/KQYGFCKATLSE**K**LGGAE/V	K219	3	717.02	3.8009	0.2399	71.77
Centriolin	H/ERAR**R**LM**K**E/L	R2115/K2118	3	510.26	4.4383	0.3934	58.71
Complement factor H	E/VV**K**CLPVTAPENGKIVSSAMEPDRE/Y	K127	3	961.82	2.9292	0.4225	106.86
	E/MHCSDDGFWS**K**EKPKCVE/I	K200	4	601.26	4.0614	0.1642	65.46
	E/ISC**K**SPDVINGSPISQ**K**IIYKENE/R	K193 o K206	3	961.82	1.8912	0.2486	235.42
	E/TTCYMG**K**WSSPPQCE/G	K501	2	997.90	2.3201	0.2439	154.88
Ig γ-1 chain C region	E/LLGGPSVFLFPP**K**PKDTLMISRTPE/V	K129	3	673.69	1.9907	0.1311	204.46
	P/**K**DTLMISRTPE/V	K131	3	674.02	2.4707	0.1130	136.52
β-2-glycoprotein 1	./GRTCPKPDDLPFSTVVPL**K**TFYEPGEE/I	K19	4	811.14	1.4574	0.1616	486.61
	E/KFKNGMLHGD**K**VSFFCKNKE/K	K276	3	860.09	1.2985	0.0620	688.00
	E/HSSLAFW**K**TDASDVKPC/-	K317	3	704.33	2.7325	0.0760	115.59
Ig γ-2 chain C region	N/FGTQTYTCNVDH**K**PSNTKVDKTVE/R	K88	4	733.85	4.188749987	0.443489	63.57
	E/RKCCVECPPCPAPPVAGPSVFLFPP**K**PKDTLMISRTPE/V	K125	5	900.45	1.1342	0.0396	1570.34
α-2-macroglobulin	./SVSG**K**PQYMVLVPSLLHTETTE/K	K5	3	860.10	4.5263	0.1135	56.76
	E/GL**R**VGFYE/S	R681	2	551.77	1.7237	0.1118	281.03
Nesprin-1	E/SLD**K**LSQ**R**/G	K2583/R2587	2	635.82	5.8942	0.5242	41.17
Centrosome-associated protein	G/ERELLQAA**K**E/N	K1294	3	450.24	2.9619	0.1153	102.17
Coiled-coil domain-containing protein 135	R/EEEERLMEAE**K**AKPD/A	K225	3	655.34	3.1375	0.3244	94.94

Nucleoprotein TPR	R/SQNTKISTQLDFAS**KR**YE/M	K722/R723	4	610.79	1.6746	0.0539	297.69
Ig κ chain C region	E/A**K**VQWKVDNALQSGNSQESVTE/Q	K37	2	1291.62	1.0368	0.0362	22644.48
	Y/E**K**HKVYACEVTHQGLSSPVTKSFNRGEC/-	K80	3	1134.04	2.5931	0.0997	125.88
	E/**K**H**K**VYACEVTHQGLSSPVTKSFNRGEC/-	K80/K82	2	1133.54	2.4075	0.0990	142.55
	E/VTHQGLSSPVT**K**SFNRGEC/-	K99	3	756.03	1.5876	0.0264	340.82
Nebulette	D/AAY**K**GVHPHIVEMDRRPGII/V	K822	5	485.06	1.9903	0.1493	205.26
Ig α-1 chain C region	E/S**K**TPLTATLSKSGNTFRPE/V	K212	3	733.05	2.8178	0.1237	110.36
Histidine-rich glycoprotein	E/SCPG**K**FKSGFPQVSMFFTHTFPK/-	K489	4	706.84	1.1471	0.0695	1558.36
Fibrinopeptide A	E/SSSHHPGIAEFPS**R**GKSSSYS**K**QFTSSTSYNRGDSTFE/S	R573 o K581	5	861.39	2.4299	0.0402	139.94
Fibrinopeptide B	E/R**K**APDAGGCLHADPDLGVLCPTGCQLQE/A	K44	3	539.25	1.9038	0.1289	224.61
	E/YCRTPCTVSCNIPVVSG**K**ECEE/I	K195	3	936.40	3.1492	0.1627	93.42
	E/MEDW**K**GDKVKAHYGGFTVQNE/A	K304	3	868.07	1.7966	0.2224	267.22
Apolipoprotein A-II	E/AKSYFE**K**SKEQLTPLIKKAGTE/L	K44	5	532.49	2.6724	0.0739	119.74
	E/AKSYFEKS**K**EQLTPLIKKAGTE/L	K46	5	532.49	2.6724	0.0739	119.74
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit α	R/EKK**K**ELE**R**EE/L	K447 o R451	3	547.95	3.2961	0.2921	88.02
TBC1 domain family member 1	E/EVQKL**R**P**R**NEQRENE/L	R437 o R439	3	750.37	2.8718	0.0334	106.87
Protein max	F/QSAAD**K**RAHHNALERKRRD/H	K24	5	485.06	1.9495	0.1023	212.19
Vitamin D-binding protein	E/ACCAEGADPDCYDTRTSALSA**K**SCE/S	K78	3	986.72	2.9824	0.0682	100.97
	E/**R**KLCMAALKHQPQEFPTYVEPTNDEICE/A	R103	3	1190.23	2.0961	0.2027	186.32
	R/**K**LCMAALKHQPQEFPTYVEPTNDEICE/A	K104	3	1189.89	2.0961	0.2027	186.32
Complement C3c α' chain	**./S**PMYSIITPNILRLE/S	Nterm	2	955.51	1.2567	0.0463	798.20
	E/AC**K**KVFLDCCNYITE/L	K699	2	1041.96	3.1165	0.2680	95.51

	E/**K**EDGKLNKLC**R**D/E	K1475/R1485	2	879.48	4.1808	0.0686	62.90
Apolipoprotein C-I	P/DVSSALD**K**LKE/F	K10	2	683.86	3.5058	0.0337	79.82
	./TPDVSSALDKL**K**E/F	K12	2	782.90	0.9851	0.0962	-7153.82
Low molecular weight growth-promoting factor	E/AT**K**TVGSDTFYSF**K**YE/I	K46 o K57	2	1003.47	2.6208	0.2090	124.09
	E/IKEGDCPVQSG**K**TWQDCE/Y	K71	3	767.33	2.4972	0.2027	135.11
Fibrinogen γ chain	./YVAT**R**DNCCILDE**R**FG/S	R5 o R14	3	767.33	2.4972	0.2027	135.11
	E/IYNSNNQ**K**IVNLKE/K	K120	2	919.98	4.3279	0.4520	60.47
Vitamin K-dependent protein S	E/GYRYNL**K**SKSCEDIDECSE/N	K196	3	839.36	2.9659	0.2260	102.68
	E/T**K**VYFAGFPRKVE/S	K383	3	568.64	1.2968	0.0574	720.41
Apolipoprotein C-II	./TQQPQQDEMPSPTFLTQV**K**E/S	K19	2	1248.09	2.3605	0.1958	148.20
Apolipoprotein D	E/IE**K**IPTTFE/N	K31	3	620.32	1.2724	0.1010	1273.73
Complement C1s subcomponent light chain	E/VLGPELP**K**CVPVCGVPREPFEE/K	K405	3	891.11	1.5555	0.0316	360.64
Golgin subfamily A member 3	E/QVRLQARKWLEEQLKQY**R**V**K**RQQ/E	R166/K168	2	1125.56	3.6073	0.1217	76.83
DnaJ homolog subfamily C member 13	E/H**R**TELLTEALRFRTD/F	R90	2	1009.98	1.4006	0.0725	517.62
Hemopexin	E/FVW**K**SHKWDRELISE/R	K54	3	708.36	1.5739	0.1749	386.46
Receptor-interacting serine/threonine-protein kinase 5	E/LYESLMNIAN**R**KQEE/M	R412	2	1007.95	2.2719	0.0170	157.44
Apolipoprotein A-IV	E/LTQQLNALFQD**K**LGE/V	K45	2	940.49	3.3190	0.4918	90.58
WW domain-binding protein 11	K/M**K**DPKQIIRDME/K	K48	2	849.43	2.0001	0.2673	210.25
Complement C4 γ chain	E/V**K**KYVLPNFE/V	K215	2	699.88	1.1009	0.0629	2757.35
Obscurin-like protein 1	D/GGFVL**K**VLYCQAKD/R	K305	2	880.40	4.1786	0.0929	62.98

Transmembrane and TPR repeat-containing protein 3	E/L**K**ALPILEELLRYYPD/H	K720	2	1054.98	2.6859	0.0404	118.68
Putative alpha-1-antitrypsin-related protein	E/YITNFPLFIG**K**VVNPTQ**K**/-	K392 o K399	3	721.71	1.7335	0.0128	273.96