

ID	Identified Peptide (ID)	Modified lysine residue	Total number of times identified	Average retention time	Best Scoring CID spectrum				Best Scoring HCD spectrum			
					Charge	MH+ (Da)	DeltaM (ppm)	Max Xcorr	Charge	MH+ (Da)	DeltaM (ppm)	Max Xcorr
1	TVRkkEEY	1967+1968	9	25.3 ± 0.7	4	1502.881	-2.4	1.25	4	1502.892	4.7	1.61
2.1	GkksSPLTESGGPL	924+925	10	31.8 ± 0.9	3	1808.04233	-0.87	2.53	3	1808.05112	3.99	4.14
2.2	GkksSPL	924+925	10	27.7 ± 0.7	3	1166.74005	-1.51	1.07	3	1166.7417	-0.1	1.37
3	SLSEENNDskLL	946	8	35.7 ± 0.4	2	1573.81279	-1.37	2.91	2	1573.8145	-0.29	1.3
4	LSEkNkVVVGkGEF	1147+1149+1154	8	33.2 ± 0.5	4	2209.32949	-0.73	3.01	4	2209.33022	-0.4	3.74
5.1	SLSDLQEAkY	812	14	35.9 ± 0.6	2	1378.736	4.9	2.48	2	1378.730	0.4	1.28
5.2	SDLQEAkY	812	5	30.9 ± 0.7	2	1178.61821	4.16	2.09	2	1178.6126	-0.61	0.82
6	TkDNALF	986	8	36.6 ± 0.4	2	1033.575	-0.6	1.59	2	1033.575	-0.8	1.30
7	AVFDEGkSW	206	9	38.7 ± 0.6	2	1263.64372	-0.99	2.56	2	1263.64372	-0.99	1.46
8	RLNEkLGTTAAATEL	862	8	33.3 ± 0.5	3	1741.98465	-2.41	1.76	3	1741.98465	-2.41	2.94
9	MkNLF	1225	8	38.6 ± 0.4	2	877.50469	0.14	1.37	2	877.50377	-0.9	0.88
10	VkPNETkTY	1808+1813	10	27.1 ± 0.7	3	1529.8913	4.22	2.6	3	1529.88105	-2.48	1.91
11	kVQHhMAPTkDEF	1818+1827	11	27.7 ± 0.6	4	2018.07534	-2.46	2.42	4	2018.07802	-1.13	3.51
12	kkTLF	47+48	6	34.1 ± 0.6	3	1086.72498	4.93	0.67	3	1086.71848	-1.05	0.92
13	NIAkPRPPWMGL	63	8	39.7 ± 0.4	3	1604.91501	-1.58	2.43	3	1604.91501	-1.58	2.59
14	AkEktQTL	168+188	6	27.0 ± 1.0	3	1368.83631	-0.64	1.21	3	1368.84272	4.05	1.61
15.1	FTIFDEtkSW	1887	8	46.5 ± 0.3	2	1498.76409	-1.15	2.29	2	1498.76384	-1.32	1.19
15.2	TIFDEtkSW	1887	8	42.4 ± 0.4	2	1351.70354	4.55	2.69	2	1351.69438	-2.23	0.96
16	QVLkENGMASDPL	142	5	36.6 ± 0.7	2	1723.91973	3.95	2.99	2	1723.91106	-1.08	1.2
17.1	EEDQRQGAEPkRkNF	1804	11	26.5 ± 0.7	4	1928.96352	-1.03	1.43	3	1928.97416	4.48	2.46
17.2	SSLISYEEDQRQGAEPkRkNF	1804	8	35.7 ± 0.4	2	1573.81279	-1.37	2.91	2	1573.8145	-0.29	1.3
18	ETVEMLPskAGIW	1992	10	45.6 ± 0.4	2	1685.90911	4.63	2.67	2	1685.90911	4.63	1.41
19.1	FGNVdSSGikHNIFNPPiIARY	2136	5	40.7 ± 0.1	4	2684.433	-2.21	4.07	4	2684.4313	-2.85	3.25
19.2	FGNVdSSGikHNIF	2136	5	37.6 ± 0.1	3	1759.91983	-0.53	3.12	3	1759.91892	-1.05	1.67
20	SDVDLEkDVHSGLIGPL	1845	7	41.5 ± 0.4	3	2019.09427	5.14	3.15	3	2019.09427	5.14	3.25
21.1	GMESkAISDAQITASSY	2183	9	38.0 ± 0.3	2	1983.97539	-1	3.38	2	1983.9865	4.6	1.83
21.2	GMESkAISDAQITASSYF	2183	9	43.9 ± 0.3	3	2131.04166	-1.94	3.35	2	2131.05425	3.97	1.71
22	GQWAPkLARL	2049	10	36.4 ± 0.4	3	1364.82364	-0.47	2.21	3	1364.82364	-0.47	1.87
23	FQNGkVkvF	2279+2281	6	34.5 ± 0.5	3	1516.91379	-1.53	1.69	3	1516.91379	-1.53	1.95
24	SLDGkkW	2110+2111	8	33.3 ± 0.5	3	1283.76825	3.87	1.91	3	1283.76267	-0.48	1.33
25.1	NNGPQRIGRkY	422	8	24.7 ± 0.7	3	1527.86487	4.22	2.07	3	1527.86487	4.22	1.37
25.2	LNNGPQRIGRkY	422	15	25.7 ± 0.7	3	1640.9379	-2.8	2.5	3	1640.93973	-1.68	2.55
26	kESVDQRGNQIMSDkRNVILF	556+570	14	37.2 ± 1.0	5	2927.60389	-0.28	2.88	5	2927.60053	-1.43	4.92
27	STkEPF	2065	8	31.0 ± 0.5	2	933.51201	-0.14	1.69	2	933.51085	-1.39	0.92
28	SRRLPkGVkHL	493+496	13	25.8 ± 2	4	1741.1205	-1.68	1.74	5	1741.12058	-1.63	3.19
29	RPQVNNPkEW	2227	7	30.9 ± 0.6	3	1492.81601	3.97	1.66	3	1492.81601	3.97	2.7

Table S1. Identified peptides that were obtained employing the workflow shown in figure S1 on plasma-derived FVIII. The non-capitalized letter k within a peptide sequence indicates that this residue was modified with a TMT label. The CID and HCD spectra of the peptide Thr1964-Tyr1971 (TVRkkEEY) are shown in figure S2.