

Supporting Information

ID	PEPTIDE SEQUENCE	m/z	EXPER MASS	THEOR MASS	ERROR ppm	ABUNDANCE
7328890	TPSAAYLVVGTGASEAEK	613.3037	1836.889	1836.889	0	2967460
6771226	IINEPTAAAIAYGLDKK	895.0002	1786.983	1786.983	0.16	1290252
7125138	WKNFSPVDAAFR	512.2648	1533.773	1533.773	-0.18	1075847
9279579	LAILGIHNEVSK	647.3804	1292.746	1292.745	0.87	663308
132248808	AIQLTQSPSSLSASVGER	915.9826	1829.951	1829.948	1.41	636506
7332470	QPSSAFAAFVK	576.806	1151.597	1151.598	-0.05	580306
7425994	YVLPNFEVK	554.805	1107.595	1107.596	-0.9	497637
6654398	KYFIDFVAR	579.8187	1157.623	1157.623	-0.32	493181
112405027	AIRMTQSPFSLASVGD	970.4901	1937.963	1937.963	-0.05	464425
8685934	NRPSSGSLIQVVTTEGR	901.4833	1799.949	1799.949	0.18	456381
6756383	GMADQDGLKPTIDKPSSEDSPP LEMLGPR	999.1578	2993.449	2993.447	0.44	444614
6866205	AGLLRPDYALLGHR	517.9634	1550.868	1550.868	0.22	406712
6709031	VTTSQDMLSIMEK	741.8632	1481.712	1481.711	0.95	391829
64113971	GSEAFATDFQDSAAAKK	872.9147	1742.812	1742.811	0.54	391579
72689136	VAVPPLTEEDVLFNVNSDTR	739.3803	2214.116	2214.117	-0.28	347766
13026727	YNPVVIDFEMQPIHEVLR	739.3803	2214.116	2214.114	0.85	347766
10260529	ESVTDHVNLIITPLEK	565.6378	1693.892	1693.889	1.78	327885
13240301	MEEVEAMLLPETLKR	602.3118	1803.914	1803.911	1.4	318595
7328780	IHLISTQSAIPYALR	561.6578	1681.952	1681.952	0.03	314714
10240623	KSPQELLCGASLISDR	591.977	1772.909	1772.909	0.12	304564
11378836	KDSHSLTTNIMEILR	591.977	1772.909	1772.909	0.12	304564
6654264	STVGNSSNNYLHLSVLR	592.3138	1772.917	1772.917	-0.03	295500
6702483	LNMGITDLQGLR	665.8609	1329.707	1329.707	-0.15	286931
195682756	MTMDKTGLLLSD	719.3696	1436.725	1436.725	-0.5	284752
13117803	ASQHGSDDVIETDFGLR	611.3052	1829.891	1829.891	0.05	282158
10734426	GVTFLLR	403.2502	804.4859	804.4857	0.21	260910
64393591	AASGTQNNVLRGEPFIR	915.9868	1828.956	1828.954	0.98	245924
6709133	QTQVSVLPEGGETPLFK	915.9868	1828.956	1828.957	-0.49	245924
169532409	GLRQEMSKDLEEVKAK	620.9993	1859.976	1859.977	-0.65	203800
64208568	QVLLVGAPTYDDVSK	802.9305	1603.847	1603.846	0.59	200545
6654267	VHQYFNVELIQGAVK	614.6685	1840.984	1840.984	0.01	199262
10132157	LLCQCLGFGSGHFR	551.266	1650.776	1650.776	0.16	190981
72168592	GRYYCFQGNQFLR	551.2646	1650.772	1650.773	-0.21	186531
15463308	TSCLLFMGR	542.7673	1083.52	1083.521	-0.34	179125
1758	LGEHNIDVLEGNEQFINAAK	738.0406	2210.097	2210.097	0.2	178747
8623821	REPIPSLEAIYLLSPTEK	1029.071	2055.125	2055.125	0	177218
10119531	TFSGEADCGLRPLFEK	628.6368	1882.889	1882.888	0.18	163835
6885157	RFNALQYLR	590.8327	1179.651	1179.651	-0.35	160291
10151351	EVQLVAHSPWLK	469.5979	1405.772	1405.772	0.06	154179
152226471	SVNDIVVLGPEQFYATR	954.4966	1906.979	1906.979	-0.1	143327
15462989	LGQSLDCNAEVYVVPWEKK	746.0429	2234.104	2234.104	-0.07	141752
10248350	KLQSLDCNAEVYVVPWEK	746.0429	2234.104	2234.104	-0.07	141752
7800323	IVEIGDENATLDGTDVLFTR	746.0429	2234.104	2234.107	-1.18	141752
65398961	VLFYVDSEKLLQNDFNVSVEEK	845.0952	2530.259	2530.259	-0.16	140362
6702580	DIPTNSPELEETLTHITK	714.0324	2138.073	2138.074	-0.79	134637
6683458	MVSGFIPLKPTVK	472.9477	1415.821	1415.821	0.16	134154

114008962	ASEANLQAAQDFVR	760.8792	1518.741	1518.743	-0.98	133033
10773467	VLNYVDWIKK	639.366	1276.717	1276.718	-0.39	131775
9410111	TPWSLAR PQGSCSLEGVEIK	739.378	2214.109	2214.11	-0.4	131529
21517113	VKLEQQVDDLEGSLEQEKK	739.0525	2214.136	2214.138	-0.97	126577
6634793	SLAELGGHLDQQVEEFR	643.6562	1926.944	1926.944	0.33	124152
8588496	VLDELTLAR	515.3008	1028.587	1028.587	0.53	120052
15463148	CFKEHSSLAFWK	513.9186	1538.734	1538.734	-0.03	117464
170270850	SSALDKLKEFGNTLEDK	632.3307	1893.97	1893.968	1.07	111931
10160290	EFTEAFLGCPAIHPR	582.6221	1743.842	1743.84	0.75	110487
72078096	DLGLAADLPGGAEGAAAQP QAVLR	754.7352	2260.181	2260.181	-0.06	109543
4208278	EDLIAYLKK	546.8185	1091.622	1091.623	-0.19	109008
6705793	NTLIYLDK	546.8185	1091.622	1091.623	-0.19	109008
12244801	ALWEKPFISSR	667.3668	1332.719	1332.719	0.03	99550
10312183	YGGPNHHLPLPDNWK	582.2893	1743.846	1743.848	-1.18	97414
10441457	PDTFEGHFDGVPVISK	582.2893	1743.846	1743.847	-0.41	97414
6634484	DTVIKPLLVEPEGLEK	891.0104	1779.003	1779.003	0.24	96658
9660686	AVAIDLPLGLGHSK	639.3636	1276.713	1276.714	-0.92	93693
72055615	DIIAEENIVSR	629.8353	1257.656	1257.656	-0.33	89574
6654384	IHWESASLLR	606.3305	1210.647	1210.646	0.58	88691
15463457	KIYPTVNCQPLGMISLM	661.3378	1979.989	1979.988	0.32	86214
72034727	LGADAVGMSTVPEVIVAR	901.481	1799.945	1799.945	-0.18	82631
35082238	QKTGLDSPTGIDFSDITA NSFTVH	851.416	2550.223	2550.224	-0.11	79247
10144509	WILTAAHTLYPK	472.2687	1412.781	1412.782	-0.11	76106
6959179	FQDGDLTLYQSNTILR	942.9811	1882.945	1882.942	1.28	73804
6748545	LSNNALSGLPQGVFGK	801.4359	1600.857	1600.857	0.05	72356
72667317	EAEFGQGTGPIWLNEVK	625.9819	1873.921	1873.921	0.09	71149
6955550	GADFLVTEVENGGSLGSKK	636.9957	1906.962	1906.964	-0.59	68527
6674655	HLSLLTTLNLR	418.91	1253.708	1253.709	-0.65	64741
10729654	SKLPGIVAEGRDDLY VSDAFHK	605.3175	2416.238	2416.239	-0.19	64202
74177566	QLANGVDRYISKYEL DKAFSDR	863.7756	2587.302	2587.303	-0.32	60368
13059938	KYNPIPSVQLMGNGFH FLAGEPR	863.7756	2587.302	2587.3	0.64	60368
6654443	TKNDFTWFK	396.2009	1185.581	1185.582	-0.85	54991
10807919	LDDYVNTQGASLFSVTKK	663.0119	1985.011	1985.011	0.26	54525
8088237	AAPSVTLFPPSSEELQANK	663.0119	1985.011	1985.011	0.26	54525
72034760	VLAPQISFAPEIASEEER	663.0119	1985.011	1985.011	0.26	54525
197641614	SLEKEVVCEEPLSPATVPGMH TEDNPGK	1004.48	3008.412	3008.411	0.32	54352
9393613	VLLDGVQNPRAE DLVGK	608.3387	1821.994	1821.995	-0.31	53052
7184618	YGYTHLSTGDLLR	748.3808	1494.747	1494.747	0.25	52289
49127698	FLILPMER	509.7918	1017.569	1017.568	1.01	50879
51567926	KTSLEDFYLDEERTVR	668.0044	1999.989	1999.985	1.81	50874
10408034	KWWTQAQAHDLVK	862.9692	1722.921	1722.921	0.24	49981
70148524	HTGKPLEVFPFGK	486.2706	1455.79	1455.787	1.74	49864
76455137	GVGWSHPLPQCEIVK EPTMYGEILSPNYPQAY	825.4272	1648.84	1648.84	0.26	49074
10274919	PSEVEK	881.7502	2641.226	2641.226	0.13	48991
10506629	GVPIPNKVIFIR	451.6182	1351.833	1351.834	-0.76	48643
6723022	SPEQQETVLDGNLIIR	906.9816	1810.946	1810.942	1.82	46845
7098221	DLIIAYYDVDYEK	540.5998	1618.778	1618.777	0.63	45302

10388522	CFEGFGIDGPAIAK	741.3582	1480.702	1480.702	-0.06	44470
10186032	PLSIEPIGVR	540.8243	1079.634	1079.634	0.24	43883
14679936	LQGGKDFNMPLTISR	838.9432	1675.872	1675.872	0.18	42554
131960069	IKMKPVPDLVPGNFK	561.6601	1681.958	1681.959	-0.27	42093
10641663	SMNIDGMTYPGIK	770.3807	1538.747	1538.747	-0.27	41006
10092907	ALPQPQNVTSLLGCTH	868.4427	1734.871	1734.872	-0.76	40997
59632480	LEYLLLSR	503.8009	1005.587	1005.586	1.46	38031
91533920	TFGSGEADCGLRPLFEKK	978.488	1953.959	1953.962	-1.66	36235
116884174	MPNALSALSDLHAHK	540.9432	1619.808	1619.809	-0.73	35656
100044619	YYTYLIMNKGR	711.8659	1420.715	1420.717	-1.93	35441
72305331	VVSTNYNQHAMVFFK	595.631	1783.871	1783.872	-0.22	34827
33874899	GFKLPDTPQGLLGEAR	566.9766	1697.908	1697.91	-1.11	34693
6747999	MVFQALAQYQK	663.8471	1325.68	1325.68	-0.32	32199
31044770	TMLESAGGLIQTAR	483.2569	1446.749	1446.75	-0.75	31235
112410993	DAPVIHQEMIGGLR	512.6041	1534.791	1534.793	-1.25	29643
7070784	SQQQADGSFQDLSPIHR	671.9981	2011.97	2011.971	-0.68	29493
10094122	VELLHNPAFCSLATTK	601.3159	1799.923	1799.924	-0.51	28689
70164282	EGAIHREELVYELNPLDHRG	587.8001	2346.168	2346.172	-1.34	27122
12644757	DKENALMPNWLHLPVGYHGR	587.8001	2346.168	2346.169	-0.27	27122
8861298	LPGIVAEGRDDLYVSDAFHK ATFMVGSYGPRPEEYEFPTV	735.045	2201.11	2201.112	-0.53	25285
9510901	EEAPK	982.4752	2943.401	2943.4	0.33	21097
6781985	TEVSSNHVLIYLDK	809.4288	1616.843	1616.841	1.29	21024
71982138	ALNAPPGTSLISFSDK	809.4288	1616.843	1616.841	1.29	21024
11351333	IRYYTYLIMNK	493.2674	1476.78	1476.78	0.31	18125
6922723	STQDTVIALDALSA	523.2666	1566.778	1566.778	0.23	15208

Table 1. Results of matching the IMS-TOFMS features detected in fraction 14 (experiment 4) against the database of human blood plasma. Matching was performed at a mass measurement accuracy of 5 ppm and a normalized retention time tolerance of 4%. From left to right, the columns represent peptide ID, peptide sequences, experimental m/z corresponding to the monoisotopic peak, experimental monoisotopic mass, theoretical monoisotopic mass, mass measurement error in ppm , and monoisotopic peak abundance. IMS-TOFMS signals from fraction 14 were encoded with a 5-bit PRS, corresponding to 16 2-ms-long accumulation events in the IFT throughout a single IMS separation. A total number of matched peptides from fraction 14 was found to be 118.