

Table S1. SRM transitions applicable to peptide sequences of mtProteins.*

Protein	Accession	Sequence	Source	Q1_mz	Q1_chg	Q3_mz	Q3_chg	Ion	SSRT	N_map
NADH-ubiquinone oxidoreductase chain 1	P03886	GPNVVGYPYGLLQPFADAMK	IonTrap	987.51	2	779.38	1	y7	41.7	1
						1195.65	1	b12		
						1020.52	1	y9		
						1190.62	1	y11		
						547.3	1	y4		
NADH-ubiquinone oxidoreductase chain 2	P03891	WAIIEEFTK	IonTrap	568.8	2	879.48	1	y7	34.3	1
						766.4	1	y6		
						653.31	1	y5		
						371.21	1	b3		
						440.74	2	y7		
NADH-ubiquinone oxidoreductase chain 3	P03897	STPYEC[160]GFDPMSPAR	IonTrap	857.86	2	763.82	2	y13	26.5	1
						658.33	1	y6		
						1057.39	1	b9		
						773.36	1	y7		
						1290.67	2	b24		
NADH-ubiquinone oxidoreductase chain 4	P03905	AHVEAPIAGSMVLA AVLK	QTOF	630.7	3	508.252	1	b5	45.6	1
						437.2149	1	b4		
						718.3888	1	b7		
			IonTrap	563.37	2	308.1723	1	b3	34.2	1
						685.42	1	y6		
						911.59	1	y8		
			IonTrap	919.57	2	798.51	1	y7	55.1	1
						441.31	1	b4		
						756.95	2	y13		
			IonTrap	734.41	2	844.49	1	y7	44.8	1
						1201.7	1	y10		
						806.48	2	y14		
			IonTrap	513.27	2	963.58	1	y8	17	1
						668.89	2	y11		
						620.37	2	y10		
NADH-ubiquinone oxidoreductase chain 5	P03915	FPTLTNINENNPTLLNPIK	IonTrap	1077.08	2	1366.73	1	y12	37.7	1
						895.56	1	y8		
						1123.65	1	y10		
						471.29	1	y4		
						1178.66	1	y11		
			IonTrap	937.01	2	829.94	2	y15	24.6	1
						722.39	2	y13		
						457.25	1	y4		
						272.17	1	y2		
						558.3	1	y5		
			IonTrap	802.92	2	772.43	1	y7	31.8	1
						565.31	1	y4		
						452.23	1	y3		
						1040.54	1	b11		
						877.49	1	y7		
IonTrap	846.74	3	710.39	1	y6	54.8	1			
			1077.55	1	y9					
			1041	2	y17					
			1121.02	2	y18					
			914.44	1	y8					
NADH-ubiquinone oxidoreductase chain 6	P03923	EDPIGAGALYDYGR	IonTrap	748.86	2	1042.5	1	y10	27.8	1
						673.29	1	y5		
						786.38	1	y6		
						644.39	1	y5		
						921.49	1	y7		
						492.21	1	b4		
Cytochrome b	P00156	DVNYGWIIR	IonTrap	568.3	2	401.29	1	y3	31.4	1
						784.42	1	y6		
						534.78	2	y8		
						585.3	2	y9		
						499.27	1	b4		
						401.29	1	y3		
Cytochrome c oxidase subunit 1	P00395	AYFTSATMIIAIPGVK	IonTrap	892.49	2	501.3	1	y5	40.4	1
						614.39	1	y6		
						1170.59	1	b11		
						1283.67	1	b12		
						673.31	1	y6		
			IonTrap	795.91	2	958.48	1	y9	38.2	1
						887.44	1	y8		
						536.25	1	y5		
						1191.87	3	y29		
						867.91	2	y14		
			IonTrap	516.77	2	976.44	2	y16	24.3	1
						701.35	1	b6		
						733.36	1	y6		
						586.29	1	y5		
						447.24	1	b3		
IonTrap	1317.26	2	367.19	2	y6	80.8	1			
			943.59	1	y9					
			1212.77	1	y12					
			1056.68	1	y10					
			1283.81	1	y13					
Cytochrome c oxidase subunit 2	P00403	MMITSQDVLHSAWPTLGLK	QTOF	743.06	3	628.4034	1	y6	45.4	1
						1071.62	1	y10		
						317.2189	1	y3		
			QTOF	553.85	2	1208.679	1	y11	31.6	1
						795.4729	1	y7		

						398.2403	2	y7		
						585.336	1	y5		
						456.2934	1	y4		
		ILYMTDEVNDPSLTIK	IonTrap	926.47	2	887.48	1	y8	36.3	1
						658.41	1	y6		
						1194.54	1	b10		
		LLDVDNR	IonTrap	422.73	2	813.39	2	y14		
						618.28	1	y5	15.9	1
						289.16	1	y2		
						503.26	1	y4		
		IFEMGPVFTL	IonTrap	577.3	2	556.3	1	b5		
						774.39	1	b7	39.7	1
						380.22	1	y3		
						633.36	1	y6		
		TDAIPGR	IonTrap	365.2	2	921.45	1	b8		
						329.19	1	y3	10	1
						513.31	1	y5		
						401.2	1	b4		
		LNQTTFTATRPVYVYGGQC[160]SEIC[160]GANHSFMPIVLELIPLK	IonTrap	1107.31	4	442.28	1	y4		
						1319.63	3	b35	55.1	1
						1357.18	2	y24		
						1290.31	3	y34		
						1241.29	3	y33		
Cytochrome c oxidase subunit 3	P00414	ESTYQGHHTPPVQK	IonTrap	804.89	2	568.35	1	y5	9.2	1
						1041.44	1	b9		
						740.37	2	y13		
						669.39	1	y6		
ATP synthase subunit a	P00846	LITTQQWLIK	QTOF	622.37	2	1017.573	1	y8	32.6	1
						260.1974	1	y2		
						559.3608	1	y4		
						373.2815	1	y3		
ATP synthase protein 8	P03928	IC[160]SLHSLPPQS	IonTrap	619.81	2	811.41	1	b7	21.7	1
						428.21	1	y4		
						567.29	2	b10		
						908.47	1	b8		
		NYNKPWEPK	IonTrap	588.3	2	656.34	1	y5	19.4	1
						932.43	1	b7		
						898.48	1	y7		
						244.17	1	y2		

*The information was drawn from PeptideAtlas (www.peptideatlas.org).

Source: Source from which transitions were obtained;

Q1_mz: Mass to charge ratio of Q1 (precursor) peptide ion;

Q1_chg: Charge on Q1 (precursor) peptide ion;

Q3_mz: Mass to charge ratio of Q3 (fragment) ion;

Q3_chg: Charge on Q3 (fragment) ion;

Ion: Ion-series designation for fragment ion (Q3);

SSRT: Sequence Specific Retention time provides a hydrophobicity measure for each peptide using the algorithm of Krohkin et al. Version 3.0;

N_map: Number of proteins in target proteome to which peptide maps.