

Supplemental materials:

Table II: MALDI-TOF data of the associated proteins with MT-3.

Protein ID	MW	Score	PPM/MISS	Peptide sequence	Sequence
HSP 84	85134	68			
			200/0	K.HNDDEQYAWESSAGGSFTVR.T	154 - 173
			137/0	K.EDQTEYLEER.R	192 - 201
			161/0	K.TKPIWTR.N	294 - 300
			190/0	R.NPDDITNEEYGEFYK.S	301 - 315
			124/0	K.SLTNDWEEHLAVK.H	316 - 328
			86/0	K.HFSVEGQLEFR.A	329 - 339
			216/0	R.ALLFVPR.R	340 - 346
			134/0	R.APFDLFENR.K	348 - 356
			185/0	R.VFIMDNCEELIPEYLNfir.G	369 - 387
			104/0	K.DQVANSafver.L	501 - 511
180/0	R.LVTSPCCIVTSTYGWTANMER.I	593 - 613			
Exocyst complex component 8 (Exo84)	81668	65			
			-101/1	SDSGASRLR	2 - 10
			-143/1	RQLESGGFEAR	11 - 21
			-45/1	EGSGTGEEGKQR	140 - 151
			-189	GAVQAGFLPGPAGVPR	124 - 139
			-248/1	YNALYPLDRLAVVNVK	218 - 233
			-89/1	DMFKLLMFESR	240 - 251
			-213/1	NRAAAVHTAIR	425 - 435
			-56/0	ESLSTAAECVK	504 - 514

			-72/1	NSEEMWRR	561 - 568
			-30/0	NSEEMWR	561 - 567
			92/0	CEQDPEK	655 - 661
			-50/1	CEQDPEKK	655 - 662
DRP-2	62239	99			
			-126/0	R.MVIPGGIDVHTR.F	64 - 75
			-100/0	K.GIQEEMEALVK.D	147 - 157
			-78/0	R.DIGAIAQVHAENGDIIEEQQR.I	190 - 211
			-58/0	K.DNFTLIPEGTNGTEER.M	346 - 361
			30/0	R.MSVIWDK.A	362 - 368
			-32/0	K.VFNLYPR.K	391 - 397
			-96/0	K.IVLEDGTLHVTEGSGR.Y	452 - 467
			-95/0	R.KPFPDFVYK.R	472 - 480
			29/0	K.QQAPPVR.N	526 - 532
			-68/0	R.NLHQSGFSLGAQIDDNIPR.R	533 - 552
			43/0	R.IVAPPGGR.A	558 - 565
ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	56265	61			
			-41/0	R.LVLEVAQHLGESTVR.T	95 - 109
			-33/0	K.IPVGPETLGR.I	134 - 143
			-64/0	R.IMNVIGEPIDER.G	144 - 155
			-51/0	K.AHGGYSVFAGVGER.T	226 - 239
			-38/0	K.VALVYQMNEPPGAR.A	265 - 279
			-62/0	R.VALTGLTVAEYFR.D	282 - 294
			-65/0	R.FTQAGSEVSALLGR.I	311 - 324
			29/0	R.IPSAVGYQPTLATDMGTMQER.I	325 - 345
			-27/0	R.AIAELGIYPAVDPLDSTSR.I	388 - 406

			0/0	R.IMDPNIVGNEHYDVAR.G	407 - 422
α - Enolase	47322	77	-196/0	R.GNPTVEVDLYTAK.G	15 - 27
			-146/0	R.AAVPSGASTGIYEALR.D	32 - 49
			-153/0	K.LAMQEFMILPVGASSFR.E	162 - 178
			-125/0	K.DATNVGDEGGFAPNILENK.E	202 - 220
			-154/0	R.YITPDQLADLYK.S	269 - 280
			-171/0	K.LAQSNWGVMSHR.S	358 - 371
			Creatine kinase	42971	85
-162/0	K.DLFDPIIEER.H	87 - 96			
-119/0	K.TDLNPDNLQGGDDLDPNYVLSSR.V	108 - 130			
188/1	K.TDLNPDNLQGGDDLDPNYVLSSRVR.T	108 - 132			
-131/0	R.GFCLPPHCSR.G	139 - 148			
76/0	R.DWPDAR.G	210 - 215			
-155/0	K.TFLVWINEEDHLR.V	224 - 236			
-159/0	R.FCTGLTQIETLFK.S	253 - 265			
-117/0	R.GTGGVDTAAVGGVFDVSNADR.L	321 - 341			
-156/0	R.LGFSEVELVQMVVDGVK.L	342 - 358			
-93/0	K.LLIEMEQR.L	359 - 366			
γ -Actin	41335	84	74/0	K.AGFAGDDAPR.A	12 - 21
			-21/0	R.AVFPSIVGRPR.H	22 - 32
			1/0	K.IWHHTFYNELR.V	78 - 88
			28/0	R.VAPEEHPVLLTEAPLNPK.A	89 - 106
			36/0	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	141 - 170
			12/0	R.GYSFTTTAER.E	190 - 199

			42/0	K.LCYVALDFEQEMATAASSSSLEK.S	209 – 231
			21/0	K.SYELPDGQVITIGNER.F	232 – 247
			36/0	K.DLYANTVLSGGTTMYPGIADR.M	285 – 305
			123/0	K.IIAPPER.K	322 – 328
			-5/1	R.KYSVWIGGSILASLSTFQQMWISK.Q	329 – 352
Aldolase 1	39656	84	-41/0	- .PHPYPALTPEQK.K	1 - 12
			22/0	R.VNPCIGGVILFHETLYQK.A	69 – 86
			-23/0	K.ADDGRFPQVIK.S	87 - 98
			-37/1	K.ADDGRFPQVIKSK.G	87 - 100
			35/0	K.GVVPLAGTNGETTTQGLDGLSER.C	111 - 133
			49/0	K.IGEHTPSALAIMENANVLAR.Y	153 - 172
			36/1	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	173 - 200
			-4/1	R.CQYVTEKVLAAVYK.A	201 - 214
			17/0	K.FSNEEIAMATVTALR.R	243 - 257
			-33/0	R.ALANSLACQ GK.Y	331 - 363
			37/0	K.YTPSGQSGAAASESLFISNHAY	342 - 363
			β-Actin	39446	86
41/0	R.AVFPSIVGR.S	3 - 11			
1/-	K.IWHHTFYNELR.V	59 - 69			
28/0	R.VAPEEHPVLLTEAPLNPK.A	70 - 87			
36/0	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	122 - 151			
12/0	R.GYSFTTTAER.E	171 - 180			
42/0	K.LCYVALDFEQEMATAASSSSLEK.S	190 - 212			
21/0	K.SYELPDGQVITIGNER.F	213 - 228			
36/0	K.DLYANTVLSGGTTMYPGIADR.M	266 - 286			

			123/0	K.IIAPPER.K	303 - 309
			-5/1	R.KYSVWIGGSILASLSTFQQMWISK.Q	310 - 333
Malate dehydrogenase	36045	68	85/0	R.LTLYDIAHTPGVAADLSHIETR.A	53 - 74
			43/0	K.GYLGPEQLPDCLK.G	79 - 91
			15/0	K.GCDVVVIPAGVPR.K	92 - 104
			24/0	K.IFGVTTLDIVR.A	166 - 176
			57/0	K.VDFPQDQLATLTGR.I	216 - 229
			51/0	K.AGAGSATLSMAYAGAR.F	242 - 257
			14-3-3 zeta	27908	76
-99/0	K.SVTEQGAELSNEER.N	28 - 41			
-16/0	R.NLLSVAYK.N	42 - 49			
-120/0	R.FLIPNASQPESK.N	104 - 115			
44/1	K.MKGDYYR.Y	121 - 127			
17/1	K.MKGDYYR.Y Oxidation (M)	121 - 127			
-104/1	R.YLAEVAAGDDKK.V	128 - 139			
-107/2	K.KEMQPTHPIR.L	158 - 167			
-42/0	K.EMQPTHPIR.L	159 - 167			
-55/0	k. KEMQPTHPIR.L Oxidation (M)	159 - 167			