SP	Name	DIGE Analysis					MS Fingerprint			MS/MS	
		Number	T Test	Ratio	Mw	pI	Score	Coverage	Querries	Score	Coverage
	COMPLEX I										
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit	478	0,022	1,41	80724.00	5,51	176	42	41	63	3
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit	471	0,0014	1,47	80724.00	5,51	187	41	39	177	4
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit	472	0,0026	1,73	80724.00	5,51	185	40	36	187	4
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit	466	0,00017	2,13	80724.00	5,51	218	41	19	172	4
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit	462	0,013	1,48	80724.00	5,51	64	24	10	ni	ni
Q9DCT2	NADH-ubiquinone oxidoreductase 30 kDa subunit	1619	0,00077	1,51	30360.00	6,4	94	30		211	14
	COMPLEX III										
Q9CZ13	Ubiquinol-cytochrome-c reductase complex core protein	924	0,0044	1,5	53420.00	5,75	56	26	13	89	5
Q9CZ13	Ubiquinol-cytochrome-c reductase complex core protein	980	0,035	1,25	53420.00	5,75	92	41	18	ni	ni
	ATP SYNTHASE										
P10719	ATP synthase beta chain	822	0,0068	1,32	56318.00	5,18	127	48	26	138	7
P10720	ATP synthase beta chain	825	0,0043	1,41	56318.00	5,18	184	57	28	407	14
	UCP-1										
P04633	Mitochondrial brown fat uncoupling protein 1	1319	0,011	3,65	33080	9,21	118	56	33	265	16
	BETA OXIDATION										
P15650	Acyl-CoA dehydrogenase, long-chain specific	937	0,045	1,33	80724.00	7,63	187	41	26	86	3
P15650	Acyl-CoA dehydrogenase, long-chain specific	1054	0,036	1,35	48242.00	7,63	131	46	27	243	10
P15650	Acyl-CoA dehydrogenase, long-chain specific	1053	0,0074	1,48	48242.00	7,63	120	47	28	159	10
P15650	Acyl-CoA dehydrogenase, long-chain specific	1051	0,0067	1,51	48242.00	7,63	129	46	22	ni	ni
P45953	Acyl-CoA dehydrogenase, very-long-chain specific	629	0,013	1,31	71047.00	9,01	105	38	27	ni	ni
P45953	Acyl-CoA dehydrogenase, very-long-chain specific	538	0,034	1,41	71047.00	9,01	128	42	27	ni	ni
P45953	Acyl-CoA dehydrogenase, very-long-chain specific	611	0,004	1,34	71047.00	9,01	148	54	33	210	6
P45953	Acyl-CoA dehydrogenase, very-long-chain specific	595	0,0027	1,67	71047.00	9,01	342	60	43	ni	ni
P45953	Acyl-CoA dehydrogenase, very-long-chain specific	791	0,0039	1,47	71047.00	9,01	53	25	19	ni	ni
P08503	Acyl-CoA dehydrogenase, medium-chain specific	1037	0,013	1,29	46925.00	8,63	110	45	22	114	5
Q60587	Trifunctional enzyme beta subunit	1590	0,015	-1,96	51667.00	9,5	88	43	20	208	11
P23965	3,2-trans-enoyl-CoA isomerase	1529	0,00085	3	32348.01	9,55	63	37	14	100	8
P14604	Enoyl-CoA hydratase	1580	0,002	-1,46	31516	8,4	83	46	16	195	14
	ETF										
Q99LC5	Electron transfer flavoprotein alpha-subunit	1294	0,017	-1,56	35360.01	7,62	77	48	12	27	4
Q99LC6	Electron transfer flavoprotein alpha-subunit	1308	0,036	-1,54	35360.00	7,62	86	41	13	45	8
Q921G7	Electron transfer flavoprotein alpha-subunit	1306	0,0015	-1,7	35360.00	7,62	118	63	17	361	21

	PYRUVATE CARBOXYLASE										
P52873	Pyruvate carboxylase	191	0,0061	1,51	130349.00	6,25	378	54	59	174	3
P52874	Pyruvate carboxylase	197	0,029	1,48	130344.00	6,25	295	52	60	219	4
P52873	Pyruvate carboxylase	195	0,025	1,5	130349.00	6,25	242	49	53	135	3
	PYRUVATE DEHYDROGENASE										
P49432	Pyruvate dehydrogenase E1 component beta subunit	2400	0,0016	1,42	38848	5,94	100	62	17	222	19
P08460	Dihydrolipoyllysine-residue acetyltransferase	633	0,023	1,36	59126.01	5,7	68	28	15	130	11
P08461	Dihydrolipoyllysine-residue acetyltransferase	644	0,03	1,36	59126.00	5,7	100	29	17	ni	ni
P08461	Dihydrolipoyllysine-residue acetyltransferase	649	0,018	1,34	59126.00	5,7	62	24	15	81	3
P08461	Dihydrolipoyllysine-residue acetyltransferase	640	0,0037	1,37	59126.00	5,7	72	29	17	88	7
	KREBS CYCLE										
Q9ER34	Aconitate hydratase	547	0,0031	1,39	86121.00	7,87	198	34	27	182	4
Q9ER34	Aconitate hydratase	491	0,016	1,41	86121.00	7,87	212	53	36	291	5
Q9ER34	Aconitate hydratase	554	0,00057	1,62	86121.00	7,87	169	43	32	193	4
Q9ER34	Aconitate hydratase	596	0,0061	1,37	86121.00	7,87	110	32	25	241	5
Q9ER34	Aconitate hydratase	593	0,011	1,48	86121.00	7,87	169	32	25	253	5
Q9ER34	Aconitate hydratase	549	0,015	1,29	86121.00	7,87	173	33	27	ni	ni
O08749	Dihydrolipoyl dehydrogenase	802	0,00037	1,78	54212	8	99	39	15	ni	ni
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha	1207	0,029	-1,23	40069.00	6,27	121	44	21	207	8
P04636	Malate dehydrogenase	1256	0,004	1,34	36089.00	8,92	112	55	19	241	14
P14408	Fumarate hydratase	923	0,0067	1,76	54714.00	9,06	53	18	10	91	7
	FATTY ACID IMPORT										
Q704S8	Carnitine O-acetyltransferase	595	0,0027	1,67	71211.00	8,73	139		23	119	4
P18886	Carnitine O-palmitoyltransferase II	608	0,017	1,41	74634.00	6,89	226	47	37	144	4
	OTHERS										
Q6P8J7	Creatine kinase	2408	0,0036	-1,58	47899.00	8,64	110	43	20	71	7
Q9Z0X1	Programmed cell death protein 8	679	0,027	1,4	66952.00	9,23	93	31	18	ni	ni
Q8CAQ8	Mitochondrial inner membrane protein (Mitofilin)	409	0,018	1,34	84247.00	6,18	97	22	19	113	5
Q9D0K2	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1	768	0,00065	-2,87	56352.00	8,73	60	37	21	96	6
Q920F5	Malonyl-CoA decarboxylase	873	0,0042	1,29	55298.00	8,96	100	40	17	ni	ni
Q02253	Methylmalonate-semialdehyde dehydrogenase	750	0,0019	-1,99	58227.00	8,47	157	57	30	119	5
Q02253	Methylmalonate-semialdehyde dehydrogenase	798	0,00028	-1,94	58227.00	8,47	243	56	33	188	7
Q02253	Methylmalonate-semialdehyde dehydrogenase	2406	0,01	-1,36	58227.00	8,47	143	42	24	125	6
P35571	Glycerol-3-phosphate dehydrogenase	504	0,034	1,54	81549	6,2	101	31	20	ni	ni
P35571	Glycerol-3-phosphate dehydrogenase	508	0,04	1,6	81549	6,2	248	44	34	ni	ni
P35571	Glycerol-3-phosphate dehydrogenase	586	0,00037	1,78	81549	6,2	99	39	41	ni	ni