

TABLE S1 - RICHTER ET AL.

GENE	UNIPROT	PROT ID	PROT NAME	Protein descriptions			Protein identification data						empAI abundance data	
				C1_PROTSCORE	C1_NRpeps	C1_NRions	ICTL1_PROTSCORE	ICTL1_NRpeps	ICTL1_NRions	C1_EMPAI	ICTL1_EMPAI			
ATAD3B	Q5T9A4	NP_114127.3	AAA-ATPase TOB3	53	1	1	133	4	4	0.033	0.139			
ACAD9	Q9H845	NP_054768.2	acyl-Coenzyme A dehydrogenase family, member 9	8	1	1	315	7	7	0.036	0.281			
ACADVL	P49748	NP_000009.1	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	102	5	5	237	7	7	0.153	0.220			
ACOT9		NP_001028755.2	acyl-Coenzyme A thioesterase 2, mitochondrial isoform b	0	0		337	10	12	0.000	0.624			
AP2M1	Q96CW1	NP_004059.2	adaptor-related protein complex 2, mu 1 subunit isoform a	0	0		31	1	1	0.000	0.045			
AFG3L2	Q9Y4W6	NP_006787.1	AFG3 ATPase family gene 3-like 2	28	1	1	112	2	2	0.026	0.053			
AARS2	A2RRN5	NP_065796.1	alanyl-tRNA synthetase like	0	0		221	6	6	0.000	0.142			
ALDH1L2	Q3SY69	NP_001029345.1	aldehyde dehydrogenase 1 family, member L2	0	0		707	17	19	0.000	0.415			
ALDH1B1	Q8WX76	NP_000683.3	aldehyde dehydrogenase 1B1 precursor	8	1	1	136	4	4	0.044	0.190			
AASS	Q9UDR5	NP_005754.2	aminoadipate-semialdehyde synthase	0	0		137	4	4	0.000	0.100			
RARS2	Q96FUS	NP_064716.1	arginyl-tRNA synthetase-like	0	0		28	1	1	0.000	0.031			
ATPSF1	P24539	NP_001679.2	ATP synthase, H+ transporting, mitochondrial FO complex, subunit B1 precursor	20	1	1	61	2	2	0.080	0.166			
ATPSH	O75947	NP_006347.1	ATP synthase, H+ transporting, mitochondrial FO complex, subunit d isoform a	6	1	1	58	3	3	0.136	0.468			
ATPSL	O75964	NP_006467.4	ATP synthase, H+ transporting, mitochondrial FO complex, subunit G	0	0		100	4	4	0.000	0.931			
ATPSA1	P25705	NP_001001937.1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit precursor	486	15	18	978	21	30	0.995	2.162			
ATPSB	P06576	NP_001677.2	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit precursor	304	14	18	752	18	25	0.874	1.392			
ATPSC1	P36542	NP_001001973.1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isoform L (liver) precursor	45	1	1	205	4	5	0.083	0.487			
ATAD3A	Q8N275	NP_060658.2	ATPase family, AAA domain containing 3A	115	3	3	273	8	8	0.104	0.301			
ABCB7	O75027-2	NP_004290.2	ATP-binding cassette, sub-family B, member 7	0	0		24	1	1	0.000	0.032			
PGAM5	Q96HS1-2	NP_612642.1	Bcl-XL-binding protein v68	41	1	1	278	9	11	0.066	1.021			
CPT2	P23786	NP_000089.1	carnitine palmitoyltransferase II	0	0		43	1	1	0.000	0.031			
CECR5	Q9BXW7-2	NP_060299.4	cat eye syndrome chromosome region, candidate 5 isoform 1	0	0		181	5	7	0.000	0.546			
NDUFA13		NP_057049.3	cell death-regulatory protein GRIM19	0	0		137	5	5	0.000	0.417			
CABC1	Q8NI60	NP_064632.2	chaperone, ABC1 activity of bc1 complex like precursor	0	0		93	2	2	0.000	0.086			
HSPD1	P10809	NP_955472.1	chaperonin	709	24	34	1513	34	58	2.275	6.565			
C3orf60	Q9BU61	NP_951032.1	chromosome 3 open reading frame 60 isoform a	0	0		205	5	5	0.000	1.154			
GTPBP10	A4D1E9	NP_149098.2	claudin 12 isoform 2	0	0		399	10	11	0.000	0.598			
CLPX	O76031	NP_006651.2	ClpX caseinolytic protease X homolog	0	0		60	2	2	0.000	0.059			
MMAB	Q96EY8	NP_443077.1	cob(I)alamin adenosyltransferase precursor	0	0		152	3	3	0.000	0.318			
CCDC109A	Q8NE86	NP_612366.1	coiled-coil domain containing 109A	0	0		61	3	3	0.000	0.218			
CHCHD1	Q96BP2	NP_976043.1	coiled-coil-helix-coiled-coil-helix domain containing 1	8	1	1	140	3	4	0.259	1.512			
C1QBP	Q07021	NP_001203.1	complement component 1, q subcomponent binding protein precursor	33	2	2	378	8	11	0.194	1.649			
COX2	P00403	NP_536846.1	cytochrome c oxidase subunit II	40	3	3	170	4	8	0.501	1.955			
COX4I1	P13073	NP_001852.1	cytochrome c oxidase subunit IV isoform 1 precursor	0	0		176	7	8	0.000	1.310			
DDX28	Q9NUL7	NP_060850.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	8	1	1	723	16	20	0.038	1.127			
DHX30	Q7L2E3	NP_619520.1	DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 1	248	8	9	1349	37	51	0.145	1.154			
DHX30	Q7L2E3-2	NP_619519.1	DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 3	0	0		365	8	11	0.000	0.714			
DAP3	P51398	NP_387506.1	death-associated protein 3	190	7	7	568	12	20	0.389	1.560			
DBT	Q5VVL8	NP_001909.2	dihydroipoamide branched chain transacylase precursor	8	1	1	191	5	9	0.042	0.448			
DLD	B2R5X0	NP_000099.2	dihydroipoamide dehydrogenase precursor	68	2	2	316	8	11	0.096	0.660			
POLDIP2	Q9Y2S7	NP_056399.1	DNA polymerase delta interacting protein 2	0	0		127	3	3	0.000	0.170			
TOP1	P11387	NP_003277.1	DNA topoisomerase I	0	0		9	1	1	0.000	0.034			
DNAJ3	Q96EY1	NP_005138.2	DnaJ (Hsp40) homolog, subfamily A, member 3	0	0		113	4	5	0.000	0.248			
DCI	P42126	NP_001910.2	dodecenoyl-Coenzyme A delta isomerase precursor	0	0		72	1	1	0.000	0.086			
ETFA	P13804	NP_000117.1	electron transfer flavoprotein, alpha polypeptide	0	0		54	3	3	0.000	0.194			
ERAL1	O75616	NP_005693.1	Era G-protein-like 1	0	0		189	4	4	0.000	0.194			
FASTKD1	Q8TEA9	NP_078898.2	FAST kinase domains 1	0	0		105	3	3	0.000	0.074			
FASTKD2	Q9NYY8	NP_055744.2	FAST kinase domains 2	0	0		584	12	14	0.000	0.409			
FLAD1	Q8NFF5	NP_079483.3	flavin adenine dinucleotide synthetase isoform 1	0	0		25	1	1	0.000	0.034			
GLUD1	P00367	NP_005262.1	glutamate dehydrogenase 1	50	4	4	302	8	8	0.143	0.306			
GLDC	Q2M2F8	NP_000161.2	glycine dehydrogenase (decarboxylating)	0	0		104	4	4	0.000	0.090			
GRSF1	Q12849-2	NP_002083.2	G-rich RNA sequence binding factor 1	0	0		333	10	14	0.000	0.817			
GADD45GIP1	Q8TAE8	NP_443082.2	growth arrest and DNA-damage-inducible, gamma interacting protein 1	12	2	2	340	8	16	0.194	3.125			
GRPEL1	Q9HAV7	NP_079472.1	GrpE-like 1, mitochondrial	97	3	3	212	6	9	0.318	1.291			
MTG1	Q9BT17	NP_612393.2	GTP-binding protein	0	0		159	6	7	0.000	0.431			
HSPA1A	P08107	NP_005336.2	heat shock 70kDa protein 1A	0	0		62	2	2	0.000	0.067			
HSPA9	P38646	NP_004125.3	heat shock 70kDa protein 9B precursor	626	16	24	1450	31	59	0.962	4.242			
HNRPDL	O14979	NP_112740.1	heterogeneous nuclear ribonucleoprotein D-like	0	0		18	1	1	0.000	0.061			
HK1	P19367	NP_000179.1	hexokinase 1 isoform HK1	0	0		35	2	2	0.000	0.048			
HARS2	P49590	NP_036340.1	histidyl-tRNA synthetase-like	0	0		123	4	4	0.000	0.169			
HSD17B10	Q99714	NP_004484.1	hydroxysteroid (17-beta) dehydrogenase 10 isoform 1	216	7	7	630	11	21	0.711	4.012			
C7orf30	Q96EH3	NP_612455.1	hypothetical protein LOC115416	0	0		185	4	5	0.000	0.450			
C18orf55	Q9P010	NP_054896.1	hypothetical protein LOC29090	0	0		11	1	1	0.000	0.086			
C6orf203	Q9POP8	NP_057571.1	hypothetical protein LOC51250	0	0		170	4	5	0.000	0.616			

C17orf42	Q6PJ19	NP_078959.2	hypothetical protein LOC79736	0	0		116	3	4	0.000	0.407
C18orf22	Q9H776	NP_079081.1	hypothetical protein LOC79863	0	0		58	4	4	0.000	0.274
C4orf14	Q8NC60	NP_115689.1	hypothetical protein LOC84273	2	1	1	451	12	13	0.027	0.422
KIAA0391	Q8N5L5	NP_055487.2	hypothetical protein LOC9692	0	0		52	1	1	0.000	0.036
ICT1	Q14197	NP_001536.1	immature colon carcinoma transcript 1	71	2	2	709	16	33	0.222	26.213
IMMT		NP_006830.1	inner membrane protein, mitochondrial	53	1	1	146	5	5	0.026	0.138
IGF2BP2	Q9Y6M1	NP_001007226.1	insulin-like growth factor 2 mRNA binding protein 2 isoform b	0	0		29	1	1	0.000	0.044
LETM1	O95202	NP_036450.1	leucine zipper-EF-hand containing transmembrane protein 1	6	1	1	86	2	2	0.027	0.056
LRPPRC	P42704	NP_573566.2	leucine-rich PPR motif-containing protein	2934	75	134	4009	80	148	4.398	5.438
KARS	Q15046	NP_005539.1	lysyl-tRNA synthetase	14	1	1	107	4	4	0.037	0.157
ME2	P23368	NP_002387.1	malic enzyme 2, NAD(+)-dependent, mitochondrial	0	0		64	3	3	0.000	0.109
NGRN		NP_001028260.2	mesenchymal stem cell protein DSC92 isoform 2	0	0		189	5	6	0.000	0.484
MCC2	Q9HCCO	NP_071415.1	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	36	1	1	215	6	7	0.040	0.314
MUT	P22033	NP_000246.1	methylmalonyl Coenzyme A mutase precursor	9	1	1	119	4	4	0.029	0.122
METT11D1	Q9H7H0	NP_073571.1	methyltransferase 11 domain containing 1 isoform 2	0	0		322	6	8	0.000	0.456
ALDH2	P05091	NP_000681.2	mitochondrial aldehyde dehydrogenase 2 precursor	0	0		395	11	13	0.000	0.759
POLRMT	O00411	NP_005026.3	mitochondrial DNA-directed RNA polymerase precursor	44	1	1	1022	25	33	0.016	0.701
LONP1	P36776	NP_004784.2	mitochondrial lon peptidase 1	94	3	3	482	12	14	0.077	0.414
MCAT	Q8IVS2	NP_775738.3	mitochondrial malonyltransferase isoform a precursor	0	0		196	4	4	0.000	0.239
PMPCB	O75439	NP_004270.2	mitochondrial processing peptidase beta subunit precursor	0	0		187	4	5	0.000	0.238
MRPL1	Q9BYD6	NP_064621.2	mitochondrial ribosomal protein L1	35	2	2	731	16	23	0.166	4.843
MRPL10	Q7Z7H8	NP_660298.2	mitochondrial ribosomal protein L10 isoform a	0	0		317	7	15	0.000	2.433
MRPL11	Q9Y3B7	NP_057134.1	mitochondrial ribosomal protein L11 isoform a	23	2	2	598	16	23	0.245	11.452
MRPL12	P52815	NP_002940.2	mitochondrial ribosomal protein L12	78	3	5	326	7	16	0.730	4.780
MRPL13	Q9BYD1	NP_054797.2	mitochondrial ribosomal protein L13	54	4	4	384	9	15	0.425	2.775
MRPL14	Q6P1L8	NP_115487.2	mitochondrial ribosomal protein L14	85	3	3	253	4	9	0.438	1.976
MRPL15	Q9P015	NP_054894.1	mitochondrial ribosomal protein L15	169	5	5	889	19	39	0.403	13.030
MRPL16	Q9NX20	NP_060310.1	mitochondrial ribosomal protein L16	0	0		274	10	14	0.000	3.642
MRPL17	Q9NRX2	NP_071344.1	mitochondrial ribosomal protein L17	33	2	2	381	10	18	0.274	7.859
MRPL18	Q9H0U6	NP_054880.2	mitochondrial ribosomal protein L18	24	1	1	271	7	11	0.110	2.162
MRPL19	P49406	NP_055578.2	mitochondrial ribosomal protein L19	0	0		569	15	26	0.000	4.043
MRPL2	Q5T653	NP_057034.2	mitochondrial ribosomal protein L2	0	0		444	11	18	0.000	3.924
MRPL21	A6NKU0	NP_852615.1	mitochondrial ribosomal protein L21 isoform d	12	1	1	497	11	19	0.093	4.380
MRPL22	Q9NWU5	NP_054899.2	mitochondrial ribosomal protein L22 isoform a	60	3	3	414	11	18	0.334	4.623
MRPL23		NP_066957.2	mitochondrial ribosomal protein L23	100	3	3	251	6	11	0.468	3.084
MRPL24	Q96A35	NP_663781.1	mitochondrial ribosomal protein L24	0	0		401	10	23	0.000	5.629
MRPL27	Q9P0M9	NP_057588.1	mitochondrial ribosomal protein L27 isoform a	23	1	1	137	3	4	0.166	0.848
MRPL28	Q13084	NP_006419.2	mitochondrial ribosomal protein L28	0	0		659	17	27	0.000	9.926
MRPL3	P09001	NP_009139.1	mitochondrial ribosomal protein L3	34	1	1	375	9	15	0.058	1.322
MRPL32	Q9BYC8	NP_114109.1	mitochondrial ribosomal protein L32	34	1	1	160	3	5	0.136	0.896
MRPL37	Q9BZE1	NP_057575.2	mitochondrial ribosomal protein L37	57	3	3	785	16	27	0.142	2.305
MRPL38	B2R894	NP_115867.1	mitochondrial ribosomal protein L38	52	2	3	500	15	20	0.241	3.217
MRPL39	Q9NYK5-2	NP_542984.2	mitochondrial ribosomal protein L39 isoform b	38	4	4	653	17	27	0.252	3.556
MRPL4	Q9BYD3	NP_057040.2	mitochondrial ribosomal protein L4 isoform a	57	4	4	558	11	25	0.311	4.436
MRPL40	Q9NQ50	NP_003767.2	mitochondrial ribosomal protein L40	16	1	1	215	5	11	0.110	2.162
MRPL41	Q8IXM3	NP_115866.1	mitochondrial ribosomal protein L41	47	4	4	157	4	9	0.931	3.394
MRPL43	Q8N983-4	NP_115488.2	mitochondrial ribosomal protein L43 isoform a	142	4	4	401	8	17	0.551	5.449
MRPL43	Q8N983	NP_789762.1	mitochondrial ribosomal protein L43 isoform b	142	4	4	373	8	16	0.551	4.780
MRPL44	Q9H9J2	NP_075066.1	mitochondrial ribosomal protein L44	78	3	3	626	15	24	0.212	3.642
MRPL45		NP_115727.3	mitochondrial ribosomal protein L45	11	1	1	480	16	22	0.064	2.932
MRPL46	Q9H2W6	NP_071446.2	mitochondrial ribosomal protein L46	0	0		378	10	15	0.000	1.683
MRPL47	Q9HD33	NP_065142.2	mitochondrial ribosomal protein L47 isoform a	49	2	2	509	13	21	0.233	8.006
MRPL48	Q96GC5	NP_057139.1	mitochondrial ribosomal protein L48	45	2	3	266	4	10	0.468	2.594
MRPL49	Q13405	NP_004918.1	mitochondrial ribosomal protein L49	61	2	2	409	7	14	0.233	3.329
MRPL50	Q8N5N7	NP_061924.1	mitochondrial ribosomal protein L50	14	1	1	247	8	11	0.110	2.162
MRPL51	Q4U2R6	NP_057581.2	mitochondrial ribosomal protein L51	0	0		166	6	10	0.000	5.813
MRPL54	Q6P161	NP_758455.1	mitochondrial ribosomal protein L54	0	0		117	3	6	0.000	1.894
MRPL55	Q7Z7F7	NP_852130.1	mitochondrial ribosomal protein L55 isoform a	0	0		224	5	12	0.000	7.377
MRPL9	Q9BYD2	NP_113608.1	mitochondrial ribosomal protein L9	43	3	3	512	11	18	0.269	3.175
MRPS10	P82664	NP_060611.2	mitochondrial ribosomal protein S10	36	2	3	304	8	11	0.280	1.471
MRPS11	P82912	NP_073750.2	mitochondrial ribosomal protein S11 isoform a	0	0		172	4	4	0.000	0.624
MRPS14	O60783	NP_071383.1	mitochondrial ribosomal protein S14	78	3	4	129	3	6	1.154	2.162
MRPS15	P82914	NP_112570.2	mitochondrial ribosomal protein S15	27	2	3	130	4	4	0.334	0.468
MRPS16	Q9Y3D3	NP_057149.1	mitochondrial ribosomal protein S16	37	2	2	161	6	9	0.311	2.384
MRPS17	Q9Y2R5	NP_057053.1	mitochondrial ribosomal protein S17	31	2	2	232	5	7	0.585	4.012
MRPS18A	Q9NV52	NP_060605.1	mitochondrial ribosomal protein S18A	18	1	1	220	6	10	0.110	1.848
MRPS18B	Q9Y676	NP_054765.1	mitochondrial ribosomal protein S18B	0	0		261	8	8	0.000	1.031

MRPS2	Q9Y399	NP_057118.1	mitochondrial ribosomal protein S2	0	0		408	11	15	0.000	1.943
MRPS21	P82921	NP_061870.1	mitochondrial ribosomal protein S21	0	0		218	4	10	0.000	16.783
MRPS22	P82650	NP_064576.1	mitochondrial ribosomal protein S22	250	10	13	795	18	35	0.917	4.766
MRPS23	Q9Y3D9	NP_057154.2	mitochondrial ribosomal protein S23	122	4	4	350	8	9	0.445	1.291
MRPS24	Q96EL2	NP_114403.1	mitochondrial ribosomal protein S24	10	1	1	137	3	4	0.105	0.492
MRPS25	P82663	NP_071942.1	mitochondrial ribosomal protein S25	60	5	6	321	9	14	0.995	4.012
MRPS26	Q9BYN8	NP_110438.1	mitochondrial ribosomal protein S26	84	4	6	425	8	16	1.254	7.733
MRPS27	Q92552	NP_055899.1	mitochondrial ribosomal protein S27	126	7	7	795	17	23	0.363	1.769
MRPS28	Q9Y2Q9	NP_054737.1	mitochondrial ribosomal protein S28	109	3	4	392	6	10	0.492	1.721
MRPS30	Q9NP92	NP_057724.2	mitochondrial ribosomal protein S30	5	1	1	537	11	21	0.051	1.861
MRPS31		NP_005821.1	mitochondrial ribosomal protein S31	99	4	5	841	17	27	0.334	3.732
MRPS34	P82930	NP_076425.1	mitochondrial ribosomal protein S34	14	1	1	388	12	15	0.101	3.217
MRPS35	P82673	NP_068593.2	mitochondrial ribosomal protein S35	115	7	8	449	10	21	0.693	2.981
MRPS5	P82675	NP_114108.1	mitochondrial ribosomal protein S5	0	0		436	12	19	0.000	1.537
MRPS6	P82932	NP_115865.1	mitochondrial ribosomal protein S6	41	3	4	236	9	11	0.931	5.105
MRPS7	Q9Y2R9	NP_057055.1	mitochondrial ribosomal protein S7	71	4	5	383	10	20	0.532	4.505
MRPS9	P82933	NP_872578.1	mitochondrial ribosomal protein S9	37	2	3	850	20	38	0.158	5.434
MRRF	Q96E11	NP_620132.1	mitochondrial ribosome recycling factor isoform 1	0	0		274	4	6	0.000	0.638
MRM1	Q6IN84	NP_079140.2	mitochondrial rRNA methyltransferase 1 homolog	8	1	1	83	2	2	0.070	0.145
MTERF	Q99551	NP_008911.1	mitochondrial transcription termination factor precursor	0	0		140	4	4	0.000	0.198
MTIF2		NP_002444.2	mitochondrial translational initiation factor 2 precursor	0	0		52	2	2	0.000	0.080
HADHA	P40939	NP_000173.2	mitochondrial trifunctional protein, alpha subunit precursor	126	6	6	610	17	21	0.164	0.701
MOV10	Q9HCE1	NP_066014.1	Mov10, Moloney leukemia virus 10, homolog	0	0		54	3	3	0.000	0.061
MTERFD1	Q96E29	NP_057026.3	MTERF domain containing 1	0	0		370	10	13	0.000	1.006
MTERFD2		NP_872307.2	MTERF domain containing 2	0	0		333	9	9	0.000	0.619
AGK	Q53H12	NP_060708.1	multiple substrate lipid kinase	29	1	1	117	3	3	0.050	0.158
NDUFA9	Q16795	NP_004993.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	0	0		110	3	3	0.000	0.134
NDUFS1	P28331	NP_004997.4	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa precursor	0	0		534	10	13	0.000	0.422
NDUFS2	Q75306	NP_004541.1	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	0	0		104	4	4	0.000	0.190
NDUFS3	Q75489	NP_004542.1	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	44	3	3	231	7	7	0.259	0.711
NDUFS8	O00217	NP_002487.1	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	13	1	1	67	2	2	0.096	0.202
NDUHV1	P49821	NP_009034.2	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	0	0		205	5	5	0.000	0.265
NIPSNAP1		NP_003625.1	nipsnap homolog 1	31	1	1	61	2	3	0.075	0.241
NSUN4	Q96CB9	NP_950245.2	NOL1/NOP2/Sun domain family 4 protein	0	0		185	5	6	0.000	0.540
NME4	O00746	NP_005000.1	nucleoside-diphosphate kinase 4	0	0		173	7	10	0.000	1.994
OAT	P04181	NP_000265.1	ornithine aminotransferase precursor	204	6	6	408	10	12	0.326	0.758
OXA1L		NP_005006.1	oxidase (cytochrome c) assembly 1-like	0	0		52	2	2	0.000	0.133
PAPD1	Q9HA74	NP_060579.2	PAP associated domain containing 1	0	0		192	8	8	0.000	0.306
PTCD1	Q75127	NP_056360.2	pentatricopeptide repeat domain 1	0	0		606	14	16	0.000	0.668
PTCD3	Q96EY7	NP_060422.4	Pentatricopeptide repeat domain 3	134	6	7	1049	23	46	0.251	3.354
PMPCA	Q10713	NP_055975.1	peptidase (mitochondrial processing) alpha	3	1	1	170	6	7	0.038	0.302
PRDX5	P30044	NP_036226.1	peroxiredoxin 5 precursor, isoform a	11	1	1	152	4	5	0.093	0.557
ECH1	Q13011	NP_001389.2	peroxisomal enoyl-coenzyme A hydratase-like protein	0	0		156	3	4	0.000	0.266
FARS2	Q95363	NP_006558.1	phenylalanine-tRNA synthetase 2	0	0		80	2	2	0.000	0.094
PNPT1	Q8TCS8	NP_149100.1	polyribonucleotide nucleotidyltransferase 1	92	3	3	301	6	8	0.083	0.236
LOC642393	Q9BYC9	XP_001125910.1	PREDICTED: similar to mitochondrial ribosomal protein L20	0	0		301	8	9	0.000	3.394
PGAM5		XP_001126125.1	PREDICTED: similar to phosphoglycerate mutase family member 5	41	1	1	209	7	9	0.043	0.458
LOC648605		XP_944686.1	PREDICTED: similar to Trimethyllysine dioxygenase, mitochondrial precursor	0	0		117	4	4	0.000	0.233
LOC729317	A6NLE7	XP_001133585.1	PREDICTED: similar to voltage-dependent anion channel 2	20	2	2	197	5	5	0.150	0.417
AIFM1	Q95831	NP_004199.1	programmed cell death 8 isoform 1	0	0		29	1	1	0.000	0.032
PHB	P35232	NP_002625.1	prohibitin	0	0		313	9	10	0.000	0.896
PHB2	Q99623	NP_009204.1	prohibitin 2	166	5	6	284	9	13	0.369	0.974
PARS2	Q7L3T8	NP_689481.2	prolyl-tRNA synthetase (mitochondrial)(putative)	0	0		22	1	1	0.000	0.043
PCCB	P05166	NP_000523.2	propionyl Coenzyme A carboxylase, beta polypeptide	0	0		153	5	5	0.000	0.204
PUS1	Q9Y606	NP_079491.2	pseudouridylylase synthase 1 isoform 1	0	0		86	3	3	0.000	0.122
PUSL1	Q8NOZ8	NP_699170.1	pseudouridylylase synthase-like 1	0	0		135	5	5	0.000	0.403
PYCR2	Q96C36	NP_037460.2	pyrroline-5-carboxylate reductase family, member 2	0	0		222	6	8	0.000	0.887
ALDH18A1	P54886	NP_002851.2	pyrroline-5-carboxylate synthetase isoform 1	47	2	2	397	11	14	0.047	0.380
PKD3	Q15120	NP_005382.1	pyruvate dehydrogenase kinase, isoenzyme 3	0	0		72	2	2	0.000	0.091
RG9MTD1	Q9NRG5	NP_060289.2	RNA (guanine-9-) methyltransferase domain containing 1	15	1	1	318	8	9	0.045	0.490
RNMTL1	Q9HC36	NP_060616.1	RNA methyltransferase like 1	0	0		409	12	19	0.000	2.621
RPUSD3	Q6P087	NP_775930.1	RNA pseudouridylylase synthase domain containing 3	0	0		138	5	5	0.000	0.334
RPUSD4	Q96K56	NP_116184.1	RNA pseudouridylylase synthase domain containing 4	0	0		117	3	3	0.000	0.174
SHMT2	P34897	NP_005403.2	serine hydroxymethyltransferase 2 (mitochondrial)	30	1	1	327	7	8	0.038	0.346
SARS2	Q9NP81	NP_060297.1	seryl-tRNA synthetase 2	0	0		416	11	12	0.000	0.540
SFXN1	Q9H9B4	NP_073591.2	sideroflexin 1	18	1	1	247	5	6	0.061	0.425
SSBP1	Q04837	NP_003134.1	single-stranded DNA binding protein 1	52	4	4	493	10	21	0.668	13.678

SLC25A18	Q9H1K4	NP_113669.1	solute carrier	0	0		16	1	1	0.000	0.064
SLC25A12	O75746	NP_003696.2	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	0	0		101	3	3	0.000	0.093
SLC25A4	P12235	NP_001142.2	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	0	0		203	6	6	0.000	0.468
SLC25A1	P53007	NP_005975.1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	0	0		144	5	6	0.000	0.540
SLC25A10	Q9UBX3	NP_036272.2	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	0	0		29	2	2	0.000	0.160
SLC25A11	Q02978	NP_003553.2	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	0	0		141	4	4	0.000	0.301
SLC25A3	Q00325-2	NP_002626.1	solute carrier family 25 member 3 isoform b precursor	25	1	1	185	5	5	0.066	0.377
SLC25A13	Q9UJ50	NP_055066.1	solute carrier family 25, member 13 (citrin)	0	0		166	6	7	0.000	0.240
SLC25A5	P05141	NP_001143.1	solute carrier family 25, member 5	30	1	1	249	9	9	0.066	0.778
SLC25A6		NP_001627.1	solute carrier family 25, member A6	0	0		327	9	9	0.000	0.751
ERLIN2	O94905	NP_009106.1	SPFH domain family, member 2 isoform 1	0	0		93	2	2	0.000	0.133
C14orf156	Q9GZT3	NP_112487.1	SRA stem-loop-interacting RNA-binding protein	61	2	2	221	4	10	0.425	4.878
STOML2	Q9UJZ1	NP_038470.1	stomatin (EPB72)-like 2	26	2	2	250	5	6	0.129	0.438
SDHA		NP_004159.1	succinate dehydrogenase complex, subunit A, flavoprotein precursor	33	1	1	175	4	5	0.034	0.182
SUCLA2	Q9P2R7	NP_003841.1	succinate-CoA ligase, ADP-forming, beta subunit	0	0		16	1	1	0.000	0.050
SDPV3L1	Q8IYB8	NP_003162.2	suppressor of var1, 3-like 1	0	0		119	4	5	0.000	0.153
PRDX4	Q13162	NP_006397.1	thioredoxin peroxidase	0	0		58	2	2	0.000	0.136
THNSL1		NP_079114.2	threonine synthase-like 1	3	1	1	551	9	14	0.028	0.475
TARS2	Q9BW92	NP_079426.2	threonyl-tRNA synthetase-like 1	0	0		348	8	9	0.000	0.247
TFAM	Q00059	NP_003192.1	transcription factor A, mitochondrial	74	3	3	187	6	6	0.304	0.701
TFB1M	Q9Y384	NP_057104.1	transcription factor B1, mitochondrial	0	0		290	9	13	0.000	1.075
TRUB2	O95900	NP_056494.1	TruB pseudouridine (psi) synthase homolog 2	0	0		371	9	9	0.000	0.751
TUFM		NP_003312.3	Tu translation elongation factor, mitochondrial	327	11	14	683	17	24	0.727	1.551
C10orf2	Q96RR1	NP_068602.2	twinkle	0	0		76	3	3	0.000	0.091
YARS2	Q9Y2Z4	NP_001035526.1	tyrosyl-tRNA synthetase 2 (mitochondrial)	0	0		460	11	12	0.000	0.684
UQCRC1	P31930	NP_003356.2	ubiquinol-cytochrome c reductase core protein I	0	0		188	5	7	0.000	0.380
UQCRC2	P22695	NP_003357.2	ubiquinol-cytochrome c reductase core protein II	20	1	1	363	8	11	0.055	0.802
ISCA1	Q9BUE6	NP_112202.2	ubiquinol-cytochrome c reductase core protein II	0	0		166	3	4	0.000	0.778
UQCRCF51	A8K519	NP_005994.1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	0	0		188	4	5	0.000	0.509
VARS2	Q5ST30	NP_065175.3	valyl-tRNA synthetase 2-like	0	0		111	4	4	0.000	0.085
VDAC1	P21796	NP_003365.1	voltage-dependent anion channel 1	83	3	3	375	10	10	0.218	0.931
VDAC3	Q9Y277	NP_005653.3	voltage-dependent anion channel 3	0	0		136	3	3	0.000	0.241
WBSCR16	Q96151	NP_110425.1	Williams-Beuren syndrome chromosome region 16	0	0		152	6	7	0.000	0.431
YME1L1	Q96TA2	NP_647473.1	YME1-like 1 isoform 1	0	0		54	2	2	0.000	0.049

Column: Description:

GENE Gene name

UNIPROT Uniprot identifier (if available)

PROT ID refseq protein identifier

PROT NA Refseq protein name / description

C1_PROT: Cumulative peptide identification score for the negative control sample

C1_NRpej Total number of unique peptide sequences identified for each protein in the negative control sample

C1_NRIor Total number of unique precursor matches for each protein in the negative control sample

ICTL1_PR Cumulative peptide identification score for the ICT1 IP sample

ICTL1_NR Total number of unique peptide sequences identified for each protein in the ICT1 IP sample

ICTL1_NRI Total number of unique precursor matches for each protein in the ICT1 IP sample

C1_EMPA Estimate of protein abundance for negative control sample*

ICTL1_EM Estimate of protein abundance for ICT1 IP sample*

* about emPAI: in 2005 Ishihama et al (Molecular & Cellular Proteomics 4:1265-1272, 2005) showed that emPAI can be used to obtain an estimate of protein abundance. It was already known that respective protein abundance roughly corresponded to the number of matched spectra. However, since tryptic cleavage of proteins yields different number of detectable peptides for each protein (depending on protein sequence length and physicochemical properties of the generated peptides) it was necessary to calculate a Protein Abundance Index (PAI) that takes these factors into account. Protein abundance expressed as PAI (or emPAI) can thus be used to compare protein abundance between samples and different proteins thanks to this correction.

PAI is calculate as: Nobserved / Ntheoretical

Where Nobserved is the number of unique precursor identification from all peptides of an identified protein and Ntheoretical is the total number of theoretically detectable peptides for that protein

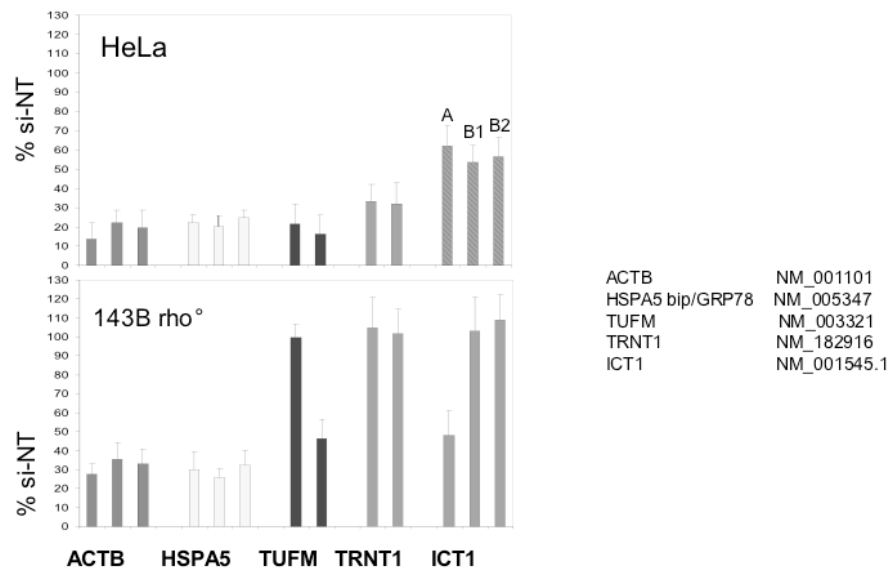
Ishihama et al further improved this PAI method by exponential modification (exponentially modified protein abundance index: emPAI) that showed better linear relationship between PAI and protein abundance. Since the initial emPAI publication this method has been accepted as a label-free quantitation method and is up till now (15 Jan 2010) referenced by 222 manuscripts

Table S2 – Richter et al.

Mitoribosomal proteins identified as co-purifying components of the ICT1 immunoprecipitation	
Large Subunit (39S)	Small Subunit (28S)
MRPL1, MRPL2, MRPL3, MRPL4, MRPL9, MRPL10, MRPL11, MRPL12, MRPL13, MRPL14, MRPL15, MRPL16, MRPL17, MRPL18, MRPL19, MRPL21, MRPL22, MRPL23, MRPL24, MRPL27, MRPL28, MRPL32, MRPL37, MRPL38, MRPL39, MRPL40, MRPL41, MRPL43-a, MRPL43-b, MRPL44, MRPL45, MRPL46, MRPL47, MRPL48, MRPL49, MRPL50, MRPL51, MRPL54, MRPL55	MRPS2, MRPS5, MRPS6, MRPS7, MRPS9, MRPS10, MRPS11, MRPS18A MRPS18B, MRPS21, MRPS22, MRPS23, MRPS24, MRPS25, MRPS26, MRPS27, MRPS28, MRPS29/DAP3, MRPS30, MRPS31, MRPS34, MRPS35, METT11D1
39 MRPL of 50	23 MRPS of 31

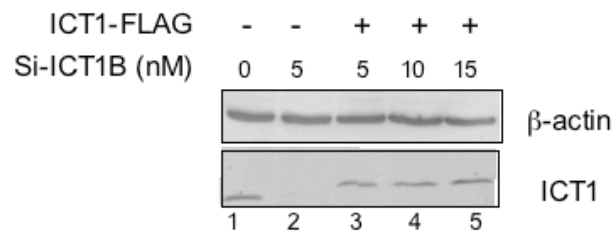
Proteomic analysis employing LCMSMS identified the tabulated mitoribosomal proteins as co-precipitants with ICT1. Analysis was performed as described in the Supplemental Experimental Procedures.

Supplemental data – Richter et al.



Supp Fig 1 si-ICT1B does not affect the growth of rho0 cells.

Equal numbers (~5000) of HeLa or 143B.206 rho0 cells were grown in DMEM supplemented with 50 $\mu\text{g}\cdot\text{ml}^{-1}$ uridine in independent wells of a 96 well plate and exposed to 3 different siRNAs designed against the indicated transcripts or to the non-targeting control. After 3 days, medium was aspirated and 200 μl per well of 0.5 mg/ml MTT in DMEM medium was added. Plates were incubated for 3 h at 37 °C, MTT solution removed and 200 μl DMSO added to dissolve formazan crystals and incubation at 37 °C for 5 min. Absorbance was measured at 550 nm in a microplate reader (Bio-Tek). In two cases, (TUFM and TRNT1) no affect on growth of either cell line was noted for one siRNA and consequently data is not shown. All siRNAs were assayed from quadruplicate wells in one plate except for si-ICTB, where quadruplicates were performed in two independent plates (B1 and B2). Results are shown normalised to the growth of cells treated with the non-targeting siRNA from which the mean absorbance was taken. Transcripts were designed against the REFSEQ accession numbers given.



Supp Fig 2 Standard curve of si-ICT1B.

To determine the concentration of si-ICT1B that caused depletion of endogenous ICT1 and which resulted in similar steady state levels of inducibly expressed ICT1 to natural endogenous levels, lysates were produced from HEK293T cells uninduced (lane 1, 2) or after 3 days expression of ICT1-Flag (lanes 3-6, 1 $\mu\text{g}\cdot\text{ml}^{-1}$ tet as inducer) in the presence of no (lane 1) or varying concs of si-ICT1B (5 - 30 nM, lanes 2-6). Anti-ICT1 and anti- β -actin antibodies are used.