

**Table 1.** List of Proteins Examined and Their Turnover Rate Constants

gene	symbol	annotation	class	score <sup>a</sup>	rank <sup>b</sup>	$k_{\text{maintag}} \pm 2 \times \text{SE}^c$ (h <sup>-1</sup> )	spectra <sup>d</sup>
Amino acids, nucleotide and fatty acids metabolism							
SCO4645	AspC	Aspartate aminotransferase	Aspartate metabolism	8.39	41	0.086 ± 0.010	2
SCO1815	FabG	Probable 3-oxacyl-(acyl-carrier-protein) reductase	Fatty acid biosynthesis	10.89	6	0.056 ± 0.008	2
SCO1814	InhA	Putative enoyl-(acyl-carrier-protein) reductase	Fatty acid biosynthesis	6.1	42	0.086 ± 0.028	2
SCO2210	GlnI	Glutamine synthetase	Glutamine metabolism	21.28	66	0.105 ± 0.010	16
SCO3023	SahH	Adenosylhomocysteinase	Methionine metabolism	30.72	5	0.052 ± 0.013	15
SCO0985	MetE	Putative methionine synthase	Methionine metabolism	61.45	100	0.130 ± 0.003	38
SCO4723	Adk	Adenylate kinase	Purine metabolism	6.13	102	0.133 ± 0.009	2
SCO4079	PurL	Phosphoribosyl formylglycinamide synthase II	Purine metabolism	14.46	21	0.077 ± 0.014	9
SCO4087	PurM	Phosphoribosyl formylglycinamide cyclo-ligase	Purine metabolism	2.11	17	0.071 ± 0.015	3
SCO1254	PurB	Putative adenylosuccinoyl lyase	Purine metabolism	9.82	18	0.073 ± 0.009	5
SCO3890	TrxB	Thioredoxin reductase (NADPH)	Pyrimidine metabolism	3.17	3	0.050 ± 0.014	3
SCO5515	SerA	Probable D-3-phosphoglycerate dehydrogenase	Serine metabolism	28.5	13	0.066 ± 0.019	4
SCO4366		Putative phosphoserine aminotransferase	Serine metabolism	10.09	71	0.107 ± 0.032	6
SCO3615	Ask	Putative aspartokinase	Threonine metabolism	18.82	25	0.078 ± 0.007	5
SCO5514		Acetolactate synthase small subunit	Valine, leucine, isoleucine metabolism	18.42	74	0.109 ± 0.011	4
Energy metabolism and related proteins							
SCO5371	AtpA	ATP synthase alpha chain	ATP synthesis	47.25	48	0.090 ± 0.021	29
SCO5369	AtpF	ATP synthase B chain	ATP synthesis	11.4	36	0.084 ± 0.026	4
SCO5373	AtpD	ATP synthase beta chain	ATP synthesis	36.53	83	0.115 ± 0.026	19
SCO5368	AtpE	ATP synthase C chain	ATP synthesis	2	72	0.107 ± 0.017	2
SCO5372	AtpG	ATP synthase gamma chain	ATP synthesis	12.41	11	0.063 ± 0.006	4
SCO2149	QcrA	Rieske iron-sulfur protein	Electron transport	10.8	65	0.103 ± 0.026	6
SCO3096	Eno	Enolase	Glycolysis	25.25	2	0.049 ± 0.007	3
SCO6659		Glucose-6-phosphate isomerase	Glycolysis	7.66	63	0.102 ± 0.007	2
SCO1947	Gap1	Glyceraldehyde-3-phosphate dehydrogenase	Glycolysis	37.94	33	0.083 ± 0.016	30
SCO1946	Pgk	Phosphoglycerate kinase	Glycolysis	22.53	7	0.056 ± 0.015	2
SCO2014	Pyk1	Pyruvate kinase	Glycolysis	3.23	112	0.171 ± 0.023	2
SCO5423	Pyk2	Pyruvate kinase	Glycolysis	13.94	10	0.059 ± 0.009	2
SCO3877		Putative 6-phosphogluconate dehydrogenase	Pentose phosphate pathway	8.28	106	0.150 ± 0.020	2
SCO3123	PrsA2	Ribose-phosphate pyrophosphokinase	Pentose phosphate pathway	9.54	44	0.087 ± 0.027	2
SCO1936	Tal2	Transaldolase	Pentose phosphate pathway	22.2	87	0.117 ± 0.023	4
SCO1935	TktA1	Transketolase	Pentose phosphate pathway	20.34	54	0.096 ± 0.020	3
SCO3127	Ppc	Phosphoenolpyruvate carboxylase	Pyruvate metabolism	30.74	111	0.166 ± 0.035	2
SCO2180	PdhL	Putative dihydrolipoamide dehydrogenase	Pyruvate metabolism	34.16	22	0.077 ± 0.010	2
SCO5999	SacA	Aconitase	TCA cycle	51.69	55	0.096 ± 0.015	25
SCO2736	CitA	Citrate synthase	TCA cycle	28.43	77	0.110 ± 0.015	2
SCO7000	Idh	Isocitrate dehydrogenase	TCA cycle	52.85	75	0.109 ± 0.011	9
SCO5281		Putative 2-oxoglutarate dehydrogenase	TCA cycle	48.3	73	0.107 ± 0.009	6
SCO4856	DhsA	Putative succinate dehydrogenase flavoprotein subunit	TCA cycle	12.4	93	0.120 ± 0.018	2
SCO4855	DhsB	Putative succinate dehydrogenase iron-sulfur subunit	TCA cycle	6.79	90	0.118 ± 0.018	3
SCO4808	SucC	Succinyl-CoA synthetase beta chain	TCA cycle	34.57	88	0.117 ± 0.019	12
Other functional classes							
SCO4295		Cold shock protein	Adaptation	7.56	108	0.151 ± 0.015	2
SCO1866		Putative condensing enzyme	Adaptation	7.05	30	0.082 ± 0.006	4
SCO3122		Putative nucleotidyltransferase	Aminosugars metabolism	4.03	78	0.110 ± 0.019	3
SCO2620		Putative cell division trigger factor	Cell division	53.29	80	0.111 ± 0.013	24
SCO5838		Putative protease	Degradation of proteins	6.02	26	0.079 ± 0.024	4
SCO4277		Putative tellurium resistance protein	Detoxification	25.54	34	0.083 ± 0.022	11
SCO0999	SodF2	Superoxide dismutase	Detoxification	10.01	1	0.030 ± 0.007	5
SCO3375		Putative Lsr2-like protein	Exported/lipoprotein	4.05	98	0.126 ± 0.033	5
SCO0888		Putative secreted protein	Exported/lipoprotein	7.44	115	0.223 ± 0.031	7
SCO3182	GtaB	UTP-glucose-1-phosphate uridylyltransferase	Galactose metabolism	10	107	0.150 ± 0.026	5
SCO4403	PurU	formyltetrahydrofolate deformylase	Glyoxylate and dicarboxylate metabolism	2	35	0.083 ± 0.022	2
SCO3768		Putative translocase protein	Protein export	4	110	0.158 ± 0.022	2
SCO2950	Hup	DNA-binding protein Hu	Regulation	9.85	95	0.123 ± 0.016	26
SCO2158		Putative kinase	Regulation	3.71	113	0.180 ± 0.028	3
SCO5776	GluB	Glutamate binding protein	Transport/binding proteins	20.13	84	0.115 ± 0.023	12
SCO1922		Putative ABC transporter ATP-binding subunit	Transport/binding proteins	9.76	94	0.122 ± 0.040	3
SCO5396		Putative cellulose-binding protein	Transport/binding proteins	13.37	103	0.142 ± 0.043	2

**Table 1** Continued

gene	symbol	annotation	class	score <sup>a</sup>	rank <sup>b</sup>	$k_{\text{mutintag}} \pm 2 \times \text{SE}^c$ (h <sup>-1</sup> )	spectra <sup>d</sup>
SCO1965		Putative export associated protein	Transport/binding proteins	10.32	56	0.096 ± 0.025	3
SCO5584	GlnB	nitrogen regulatory protein P-II	Two Component system	7.74	79	0.110 ± 0.036	4
Proteins with unknown functions							
SCO0247		Hypothetical protein	Unknown	5.62	99	0.126 ± 0.021	4
SCO1480		Hypothetical protein	Unknown	11.33	4	0.050 ± 0.006	3
SCO3659		Hypothetical protein	Unknown	7.2	96	0.124 ± 0.023	3
SCO3767		Hypothetical protein	Unknown	12.65	53	0.094 ± 0.015	5
SCO3884		Hypothetical protein	Unknown	4.03	19	0.076 ± 0.028	2
SCO3899		Hypothetical protein	Unknown	30.66	104	0.143 ± 0.015	16
SCO4252		Hypothetical protein	Unknown	12.03	105	0.143 ± 0.012	13
SCO4253		Hypothetical protein	Unknown	29.56	45	0.089 ± 0.029	7
SCO4614		Hypothetical protein	Unknown	6	109	0.156 ± 0.019	2
SCO5464		Hypothetical protein	Unknown	10.3	89	0.117 ± 0.011	2
SCO6482		Hypothetical protein	Unknown	5.61	91	0.118 ± 0.023	4
SCO6660		Hypothetical protein	Unknown	6.14	51	0.093 ± 0.021	2
Transcription, translation and protein folding machinery							
SCO4761	GroES	10 kD chaperonin	Chaperones	15.7	60	0.099 ± 0.017	23
SCO4762	GroEL1	60 kD chaperonin	Chaperones	75.68	27	0.079 ± 0.013	30
SCO4296	GroEL2	Chaperonin 2	Chaperones	73.98	31	0.082 ± 0.018	25
SCO3671	DnaK	Heat shock protein 70	Chaperones	63.75	58	0.097 ± 0.016	21
SCO5805	NrdJ	Ribonucleotide reductase	DNA replication, repair	17.71	8	0.056 ± 0.019	4
SCO4729	RpoA	DNA-directed RNA polymerase alpha chain	Transcription	27.26	59	0.097 ± 0.022	27
SCO4654	RpoB	DNA-directed RNA polymerase beta chain	Transcription	39.06	97	0.125 ± 0.020	6
SCO4655	RpoC	DNA-directed RNA polymerase beta' chain	Transcription	62.49	52	0.093 ± 0.016	2
SCO5737	GpsI	Guanosine pentaphosphate synthetase	Transcription	21.72	38	0.085 ± 0.013	4
SCO3198	GlpR	Putative deoR-family transcriptional regulator	Transcription	2	50	0.091 ± 0.007	3
SCO4647	NusG	Transcription antitermination protein	Transcription	11.4	14	0.068 ± 0.012	5
SCO1998	RpsA	30S ribosomal protein S1	Translation	40.77	61	0.099 ± 0.016	34
SCO4727	RpsM	30S ribosomal protein S13	Translation	8.9	32	0.082 ± 0.009	5
SCO5736	RpsO	30S ribosomal protein S15	Translation	8.86	12	0.064 ± 0.005	5
SCO5624	RpsB	30S ribosomal protein S2	Translation	38.3	57	0.096 ± 0.021	24
SCO4708		30S ribosomal protein S3	Translation	19.39	15	0.069 ± 0.015	14
SCO1505	RpsD	30S ribosomal protein S4	Translation	13.43	37	0.084 ± 0.024	4
SCO4719	RpsE	30S ribosomal protein S5	Translation	17.98	23	0.077 ± 0.011	6
SCO3906	RpsF	30S ribosomal protein S6	Translation	6.37	76	0.109 ± 0.026	16
SCO4735	RpsL	30S ribosomal protein S9	Translation	12.43	68	0.106 ± 0.018	11
SCO4649	RlpA	50S ribosomal protein L1	Translation	21.45	81	0.112 ± 0.014	11
SCO4652	RplJ	50S ribosomal protein L10	Translation	15.42	46	0.089 ± 0.029	2
SCO4734	RplM	50S ribosomal protein L13	Translation	11.77	28	0.079 ± 0.023	3
SCO4712	RplN	50S ribosomal protein L14	Translation	13.25	24	0.077 ± 0.015	11
SCO4721	RplO	50S ribosomal protein L15	Translation	11.14	9	0.058 ± 0.009	2
SCO4730		50S ribosomal protein L17	Translation	19.81	39	0.085 ± 0.008	7
SCO4718	RplR	50S ribosomal protein L18	Translation	10.22	69	0.106 ± 0.028	6
SCO4704	RplW	50S ribosomal protein L23	Translation	15.23	20	0.076 ± 0.014	8
SCO4710	RpmC	50S ribosomal protein L29	Translation	9.63	62	0.101 ± 0.012	9
SCO4702	RplC	50S ribosomal protein L3	Translation	12.56	85	0.115 ± 0.007	4
SCO4720	RpmD	50S ribosomal protein L30	Translation	5.54	101	0.132 ± 0.010	4
SCO4703	RplD	50S ribosomal protein L4	Translation	19.22	40	0.085 ± 0.009	20
SCO4714	RplE	50S ribosomal protein L5	Translation	14.8	16	0.070 ± 0.021	6
SCO3909	RplL	50S ribosomal protein L9	Translation	20.53	70	0.106 ± 0.020	17
SCO1501	AlaS	Alanine tRNA synthetase	Translation	4.76	64	0.102 ± 0.002	2
SCO3795	AspS	Aspartyl-tRNA synthetase	Translation	13.81	92	0.118 ± 0.012	2
SCO4661	FusA	Elongation factor G	Translation	45.26	47	0.089 ± 0.018	12
SCO1491	Efp	Elongation factor P	Translation	8.78	49	0.090 ± 0.028	7
SCO5625	Tsf	Elongation factor Ts	Translation	26.8	82	0.114 ± 0.021	3
SCO4662	Tuf1	Elongation factor Tu-1	Translation	57.92	67	0.105 ± 0.021	21
SCO5547	GltX	Glutamyl-tRNA synthetase	Translation	6.15	114	0.209 ± 0.033	2
SCO5706		Probable translational initiation factor	Translation	10.17	86	0.116 ± 0.032	3
SCO5580		Putative prokaryotic docking protein	Translation	2.73	29	0.080 ± 0.016	3
SCO1600	InfC	Putative translation initiation factor IF-3	Translation	8.25	43	0.086 ± 0.018	4

<sup>a</sup> Protein identification scores (unused protscore) from ProteinPilot v2.0 software. Higher value indicates higher confidence of identification taking all peptide hits into consideration, irrespective of presence of arginine. <sup>b</sup> Rank of protein in order of  $k_{\text{mutintag}}$  values is shown in Figure 6. Proteins are ranked as 1–115 corresponding to lowest through highest rate constant values. <sup>c</sup> Standard error estimates are obtained from curve fit data. A lower value indicates a better fit to an exponential decay curve. <sup>d</sup> Number of MS/MS spectra with hits to heavy arginine containing peptides that were used for quantification of rate constant.