

TABLE 1. Quantitative data^a

Function	Name	CAI	mRNA	Adjusted mRNA	Protein (Glu) (10 ³)	Protein (Eth) (10 ³)	E/G ratio
Carbohydrate metabolism	Adh1	0.810	197	197	1,230	972	0.79
	Adh2	0.504	0		0	963	>20
	Cit2	0.185	1	2.8	23	288	12
	Eno1	0.870	No <i>Nla</i>		410	974	2.4
	Eno2	0.892	248	248	650	215	0.33
	Fba1	0.868	179	179	640	608	0.95
	Hxk1,2	0.500	13	10.5	62	46	
	Icl1	0.251	0		0	671	>20
	Pdb1	0.342	5	5	41	33	
	Pdc1	0.903	226	226	280	205	0.73
	Pfk1	0.465	5	5	75	53	0.71
	Pgi1	0.681	14	14	160	120	0.75
	Pyc1	0.260	1	0.7	37	34	
	Tal1	0.579	5	5	110	35	
	Tdh2	0.904	63	63	430	876	NR
	Tdh3	0.924	460	460	1,670	1,927	NR
	Tpi1	0.817	No <i>Nla</i>		No Met	No Met	
Protein synthesis	Efb1	0.762	33	16.5	358	362	
	Eft1,2	0.801	26	26	99	54	0.55
	Prt1	0.303	4	0.7	12	6	
	Rpa0	0.793	246	246	277	100	0.36
	Tif1,2	0.752	29	29	233	106	0.46
	Yef3	0.777	36	36	14	ND	
Heat shock	Hsc82	0.581	2	2.9	112	75	0.67
	Hsp60	0.381	9	2.3	35	82	2.3
	Hsp82	0.517	2	1.3	52	135	2.6
	Hsp104	0.304	7	7	70	161	2.3
	Kar2	0.439	5	10.1	43	102	2.4
	Ssa1	0.709	2	4.3	303	421	1.4
	Ssa2	0.802	10	5	213	324	1.5
	Ssb1,2	0.850	50	50	270	85	
	Ssc1	0.521	2	2.6	68	80	1.2
	Sse1	0.521	8	8	96	48	
	Sti1	0.247	1	1.1	25	44	1.7
	Amino acid synthesis	Ade1	0.229	4	4	14	27
Ade3		0.276	2	1.7	12	9	
Ade5,7		0.257	2	1.4	14	4	
Arg4		0.229	1	8.1	41	41	
Gdh1		0.585	10	27	148	55	
Gln1		0.524	11	11	77	104	1.3
His4		0.267	3	3	15	23	1.5
Ilv5		0.801	6	6	152	109	0.7
Lys9		0.332	4	4	32	17	0.52
Met6		0.657	No <i>Nla</i>	22	190	80	0.42
Pro2		0.248	3	3	30	12	
Ser1		0.258	2	1.2	15	8	
Trp5		0.319	5	5	28	12	
Miscellaneous	Act1	0.710	54	54	205	164	0.78
	Adk1	0.531	No <i>Nla</i>		47	43	
	Ald6	0.520	3	3	181	159	
	Atp2	0.424	1	4.1	76	109	1.4
	Bmh1	0.322	46	46	191	137	0.72
	Bmh2	0.384	1	1.4	134	147	
	Cdc48	0.306	2	2.4	32	26	
	Cdc60	0.299	2	0.86	6	2	
	Erg20	0.373	5	5	92	39	
	Gpp1	0.603	16	5	234	158	
	Gsp1	0.621	3	3	115	39	0.34
	Ipp1	0.620	4	4	254	147	0.58
	Lcb1	0.173	0.3	0.8	19	40	
	Mol1	0.423	0	0.45	20	16	
	Pab1	0.488	3	3	41	19	0.47
	Psa1	0.600	15	15	148	56	
	Rnr4	0.497	6	6	44	37	
	Sam1	0.494	5	5	59	21	
	Sam2	0.497	3	15	63	20	
	Sod1	0.376	36	36	631	618	
	Uba1	0.212	2	2	14	20	
	YKL056	0.731	62	62	253	112	0.44
	YLR109	0.549	21	21	930		
YMR116	0.777	41	41	184	40	0.20	

^a CAI, a measure of codon bias, is taken from the YPD. mRNA, number of mRNA molecules per cell from SAGE data (27); adjusted mRNA, number of mRNA molecules per cell based on both SAGE and chip hybridization (30) (see Materials and Methods); Protein (Glu), number of molecules of protein per cell in YNB-glucose; Protein (Eth), number of molecules of protein per cell in YNB-ethanol; E/G ratio, ratio of protein abundance in ethanol to glucose. The E/G ratio is not given if it was close to 1 or if it was not repeatable (NR) in multiple gels. Some gene products (e.g., Tif1 and Tif2 [Tif1,2]) were difficult to distinguish on either a protein or an mRNA basis; these are pooled. No *Nla*, there was no suitable *Nla*III site in the 3' region of the gene, and so there are no SAGE mRNA data; No Met, the mature gene product contains no methionines, and so there are no reliable protein data.

TABLE 2. Functions of proteins listed in Table 1

Name ^a	YPD title lines ^b
Adh1	Alcohol dehydrogenase I; cytoplasmic isozyme reducing acetaldehyde to ethanol, regenerating NAD ⁺
Adh2	Alcohol dehydrogenase II; oxidizes ethanol to acetaldehyde, glucose repressed
Cit2	Citrate synthase, peroxisomal (nonmitochondrial); converts acetyl-CoA and oxaloacetate to citrate plus CoA
Eno1	Enolase 1 (2-phosphoglycerate dehydratase); converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis
Eno2	Enolase 2 (2-phosphoglycerate dehydratase); converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis
Fba1	Fructose bisphosphate aldolase II; sixth step in glycolysis
Hxk1	Hexokinase I; converts hexoses to hexose phosphates in glycolysis; repressed by glucose
Hxk2	Hexokinase II; converts hexoses to hexose phosphates in glycolysis and plays a regulatory role in glucose repression
Icl1	Isocitrate lyase, peroxisomal; carries out part of the glyoxylate cycle; required for gluconeogenesis
Pdb1	Pyruvate dehydrogenase complex, E1 beta subunit
Pdc1	Pyruvate decarboxylase isozyme 1
Pfk1	Phosphofructokinase alpha subunit, part of a complex with Pfk2p which carries out a key regulatory step in glycolysis
Pgi1	Glucose-6-phosphate isomerase, converts glucose-6-phosphate to fructose-6-phosphate
Pyc1	Pyruvate carboxylase 1; converts pyruvate to oxaloacetate for gluconeogenesis
Tal1	Transaldolase; component of nonoxidative part of pentose phosphate pathway
Tdh2	Glyceraldehyde-3-phosphate dehydrogenase 2; converts D-glyceraldehyde 3-phosphate to 1,3-dephosphoglycerate
Tdh3	Glyceraldehyde-3-phosphate dehydrogenase 3; converts D-glyceraldehyde 3-phosphate to 1,3-dephosphoglycerate
Tpi1	Triosephosphate isomerase; interconverts glyceraldehyde-3-phosphate and dihydroxyacetone phosphate
Efb1	Translation elongation factor EF-1β; GDP/GTP exchange factor for Tef1p/Tef2p
Eft1	Translation elongation factor EF-2; contains diphthamide which is not essential for activity; identical to Eft2p
Eft2	Translation elongation factor EF-2; contains diphthamide which is not essential for activity; identical to Eft1p
Prt1	Translation initiation factor eIF3 beta subunit (p90); has an RNA recognition domain
Rpa0 (RPPO)	Acidic ribosomal protein A0
Tif1	Translation initiation factor 4A (eIF4A) of the DEAD box family
Tif2	Translation initiation factor 4A (eIF4A) of the DEAD box family
Yef3	Translation elongation factor EF-3A; member of ATP-binding cassette superfamily
Hsc82	Chaperonin homologous to <i>E. coli</i> HtpG and mammalian HSP90
Hsp60	Mitochondrial chaperonin that cooperates with Hsp10p; homolog of <i>E. coli</i> GroEL
Hsp82	Heat-inducible chaperonin homologous to <i>E. coli</i> HtpG and mammalian HSP90
Hsp104	Heat shock protein required for induced thermotolerance and for resolubilizing aggregates of denatured proteins; important for [psi ⁻]-to-[PSI ⁺] prion conversion
Kar2	Heat shock protein of the endoplasmic reticulum lumen required for protein translocation across the endoplasmic reticulum membrane and for nuclear fusion; member of the HSP70 family
Ssa1	Cytoplasmic chaperone; heat shock protein of the HSP70 family
Ssa2	Cytoplasmic chaperone; member of the HSP70 family
Ssb1	Heat shock protein of HSP70 family involved in the translational apparatus
Ssb2	Heat shock protein of HSP70 family, cytoplasmic
Ssc1	Mitochondrial protein that acts as an import motor with Tim44p and plays a chaperonin role in receiving and folding of protein chains during import; heat shock protein of HSP70 family
Sse1	Heat shock protein of the HSP70 family; multicopy suppressor of mutants with hyperactivated Ras/cyclic AMP pathway
Sti1	Stress-induced protein required for optimal growth at high and low temperature; has tetratricopeptide repeats
Ade1	Phosphoribosylamidoimidazole-succinocarboxamide synthase; catalyzes the seventh step in de novo purine biosynthesis pathway
Ade3	C ₁ tetrahydrofolate synthase (trifunctional enzyme), cytoplasmic
Ade5,7	Phosphoribosylamine-glycine ligase plus phosphoribosylformylglycinamide cyclo-ligase; bifunctional protein
Arg4	Argininosuccinate lyase; catalyzes the final step in arginine biosynthesis
Gdh1	Glutamate dehydrogenase (NADP ⁺); combines ammonia and α-ketoglutarate to form glutamate
Gln1	Glutamine synthetase; combines ammonia to glutamate in ATP-driven reaction
His4	Phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphohydrolase/histidinol dehydrogenase; 2nd, 3rd, and 10th steps of his biosynthesis pathway
Ilv5	Ketol-acid reductoisomerase (acetohydroxy, acid reductoisomerase) (alpha-keto-β-hydroxylacyl) reductoisomerase; second step in Val and Ilv biosynthesis pathway
Lys9	Saccharopine dehydrogenase (NADP ⁺ , L-glutamate forming) (saccharopine reductase), seventh step in lysine biosynthesis pathway
Met6	Homocysteine methyltransferase; (5-methyltetrahydropteroyl triglutamate-homocysteine methyltransferase), methionine synthase, cobalamin independent
Pro2	γ-Glutamyl phosphate reductase (phosphoglutamate dehydrogenase), proline biosynthetic enzyme
Ser1	Phosphoserine transaminase; involved in synthesis of serine from 3-phosphoglycerate
Trp5	Tryptophan synthase, last (5th) step in tryptophan biosynthesis pathway
Act1	Actin; involved in cell polarization, endocytosis, and other cytoskeletal functions
Adk1	Adenylate kinase (GTP:AMP phosphotransferase), cytoplasmic
Ald6	Cytosolic acetaldehyde dehydrogenase
Atp2	Beta subunit of F1-ATP synthase; 3 copies are found in each F1 oligomer
Bmh1	Homolog of mammalian 14-3-3 protein; has strong similarity to Bmh2p
Bmh2	Homolog of mammalian 14-3-3 protein; has strong similarity to Bmh1p
Cdc48	Protein of the AAA family of ATPases; required for cell division and homotypic membrane fusion
Cdc60	Leucyl-tRNA synthetase, cytoplasmic
Erg20	Farnesyl pyrophosphate synthetase; may be rate-limiting step in sterol biosynthesis pathway
Gpp1 (Rhr2)	DL-Glycerol phosphate phosphatase
Gsp1	Ran, a GTP-binding protein of the Ras superfamily involved in trafficking through nuclear pores
Ipp1	Inorganic pyrophosphatase, cytoplasmic
Lcb1	Component of serine C-palmitoyltransferase; first step in biosynthesis of long-chain base component of sphingolipids
Mol1 (Thi4)	Thiamine-repressed protein essential for growth in the absence of thiamine
Pab1	Poly(A)-binding protein of cytoplasm and nucleus; part of the 3'-end RNA-processing complex (cleavage factor I); has 4 RNA recognition domains
Psa1	Mannose-1-phosphate guanyltransferase; GDP-mannose pyrophosphorylase
Rnr4	Ribonucleotide reductase small subunit
Sam1	S-Adenosylmethionine synthetase 1
Sam2	S-Adenosylmethionine synthetase 2
Sod1	Copper-zinc superoxide dismutase
Uba1	Ubiquitin-activating (E1) enzyme
YKL056	Resembles translationally controlled tumor protein of animal cells and higher plants
YLR109 (Ahp1)	Alkyl hydroperoxide reductase
YMR116 (Asc1)	Abundant protein with effects on translational efficiency and cell size, has two WD (WD-40) repeats

^a Accepted name from the *Saccharomyces* genome database and YPD. Names in parentheses represent recent changes.^b Courtesy of Proteome, Inc., reprinted with permission.