

90 MINUTES SALT STRESS

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
CELL GROWTH, YHR166C	CELL DIVISION AND	DNA SYNTHESIS (cell cycle control and mitosis) COMPONENT OF ANAPHASE-PROMOTING COMPLEX (APC); REQUIRED FOR CLB2P DEGRADATION AND FOR THE METAPHASE-ANAPHASE TRANSITION	CDC23	1		322
YLR178C	TFS1	CDC25-dependent nutrient- and ammonia-response cell cycleregulator, suppressor of CDC25 mutations;controls the phosphorylation of two 31 kDa proteins whose phosphorylation and dephosphorylation are strongly correlated with cell-cycle arrest and proliferation		1		
YOR028C	CIN5	YAP4,HAL6;transcriptional activator		1		
YNL007C	SIS1	heat shock protein;autoregulates its own transcription via the heat shock element (HSE)		2		
	YNL064C	YDJ1	6	mitochondrial and ER import protein		
	YJL080C	SCP160	6	required for maintenance of exact ploidy		
CELL GROWTH, YHR139C	CELL DIVISION AND	DNA SYNTHESIS ;(sporulation and germination) Sporulation specific protein involved in spore wall formation, first appears at 12h of sporulation	SPS100	1		98
YNR019W	ARE2	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)		1		
YDR055W		strong similarity to SPS2 protein		1		
YNL192W	CHS1	chitin synthase I		2		
YLR399C	BDF1	sporulation protein		2		
	YOL139C	CDC33	5	translation initiation factor eIF4E		
	YLR300W	EXG1	6	exo-beta-1,3-glucanase (I/II), major isoform		
	YBR078W	ECM33	6	involved in cell wall biogenesis and architecture		
CELL GROWTH, YHR086W	CELL DIVISION AND	DNA SYNTHESIS ;(meiosis) MRE2,MUD15;meiotic recombination protein	NAM8	1		94
YKR046C		meiotically induced, hypothetical protein		1		
YDR055W		strong similarity to SPS2 protein		1		
YBL058W	SHP1	potential regulatory subunit for Glc7p		2		
	YDR461W	MFA1	6	mating pheromone a-factor 1		
	YBR078W	ECM33	6	involved in cell wall biogenesis and architecture		89
CELL GROWTH, YHR086W	CELL DIVISION AND	DNA SYNTHESIS ;(recombination and DNA repair) MRE2,MUD15;meiotic recombination protein	NAM8	1		
YGR180C	RNR4	ribonucleotide reductase small subunit		1		
YER176W	HEL1	DNA dependent ATPase/DNA helicase B		2		
	YGL025C	PGD1	7	mediator complex subunit;Hpr1p and Pgd1p may cooperate to initiate chromosome breaks; INVOLVED IN BOTH POSITIVE AND NEGATIVE REGULATION OF TRANSCRIPTION;COMPONENT OF RNA POLYMERASE HOLOENZYME AND MEDIATOR SUBCOMPLEX;		
CELL GROWTH, YAL040C	CELL DIVISION AND	DNA SYNTHESIS ;(cell growth) DAF1,WHI1,FUN10;cyclin, G1/S-specific	CLN3	1		73
YJR090C	GRR1	required for glucose repression and for glucose and cation transport		2		
YOR027W	STI1	stress-induced protein;related to MAP kinase kinases		2		
YDL134C	PPH21	protein ser/thr phosphatase PP2A-1		2		
	YLR300W	EXG1	6	exo-beta-1,3-glucanase (I/II), major isoform		
	YNL154C	YCK2	6	casein kinase I isoform		
	YHR135C	YCK1	7	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane H+-ATPase Pmalp in vitro		
CELL GROWTH, YAL040C	CELL DIVISION AND	DNA SYNTHESIS ;(budding, cell polarity, and filament formation) DAF1,WHI1,FUN10;cyclin, G1/S-specific	CLN3	1		166
YJR090C	GRR1	required for glucose repression and for glucose and cation transport		2		
YDL134C	PPH21	protein ser/thr phosphatase PP2A-1		2		
YBL058W	SHP1	potential regulatory subunit for Glc7p		2		
	YJL158C		6	member of the Pirlp/Hsp150p/Pir3p family		
	YDL135C	RD11	6	rho GDP dissociation inhibitor with activity toward Rho1p		
	YNL154C	YCK2	6	casein kinase I isoform		
	YHR135C	YCK1	7	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane H+-ATPase Pmalp in vitro		
	YMR016C		7	regulatory protein in the PKA signal transduction pathway;alteration in Sok2p production affect glycogen accumulation and heat shock resistance		
	YGR214W	YST1	7	aka RPS0A;YST1; NAB1A; (NAB1);40S ribosomal protein p40 homolog A		
CELL GROWTH, YAL040C	CELL DIVISION AND	DNA SYNTHESIS ;(DNA synthesis and replication) DAF1,WHI1,FUN10;cyclin, G1/S-specific	CLN3	1		82
YGR180C	RNR4	ribonucleotide reductase small subunit		1		
YER176W	HEL1	DNA dependent ATPase/DNA helicase B		2		322
CELL GROWTH, YPL018W	CELL DIVISION AND	DNA SYNTHESIS ;(cell cycle control and mitosis) Protein important for chromosome segregation	CTF19	1		
YAL040C	CLN3	DAF1,WHI1,FUN10;cyclin, G1/S-specific		1		
YJR090C	GRR1	required for glucose repression and for glucose and cation transport		2		
YDL134C	PPH21	protein ser/thr phosphatase PP2A-1		2		
YBL058W	SHP1	potential regulatory subunit for Glc7p		2		
CELL GROWTH, YNL192W	CELL DIVISION AND	DNA SYNTHESIS ;(cytokinesis) chitin synthase I	CHS1	2		30
	YNL154C	YCK2	6	casein kinase I isoform		
	YHR135C	YCK1	7	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane H+-ATPase Pmalp in vitro		
CELL GROWTH, YNL192W	CELL DIVISION AND	DNA SYNTHESIS (pheromone response, mating-type determination, sex-specific prote chitin synthase I	CHS1	2		156
	YIL015W	BAR1	5	barrierpepsin precursor		
	YLR300W	EXG1	6	exo-beta-1,3-glucanase (I/II), major isoform		
	YNL145W	MFA2	6	mating pheromone a-factor 2		
	YNR044W	AGA1	6	a-agglutinin anchor subunit		
	YGL032C	AGA2	6	a-agglutinin binding subunit		

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
	YLR441C	RPS1A	7	aka RPS10A); (PLC1); RP10A; ribosomal protein S3a.e		
CELL GROWTH, CELL DIVISION AND				DNA SYNTHESIS (other cell growth, cell division and DNA synthesis activities)	11	
YGL091C		NBP35	2	nucleotide-binding protein		
CELLULAR BIOGENESIS (biogenesis				of cytoskeleton)	17	
YHR166C		CDC23	1	COMPONENT OF ANAPHASE-PROMOTING COMPLEX (APC); REQUIRED FOR CLB2P DEGRADATION		
CELLULAR BIOGENESIS (biogenesis				of mitochondria)	26	
YMR012W		CLU1	6	ranslation initiation factor eIF3 (p135 subunit)		
CELLULAR BIOGENESIS (biogenesis				of cell wall)	102	
YGR008C		STF2	1	ATPase stabilizing factor, binds to F0-ATPase and facilitates binding of		
YER176W		HEL1	2	inhibitor and 9 kDa protein to F1-ATPase		
YNR030W		ECM39	2	DNA dependent ATPase/DNA helicase B		
	YBR078W	ECM33	6	involved in cell wall biogenesis and architecture		
	YLR249W	YEF3	7	involved in cell wall biogenesis and architecture		
				translation elongation factor eEF3;found only in fungi		
CELLULAR ORGANIZATION(organ. of cytoplasm)					562	
167 ORFs involved in cellular organization						
CELLULAR ORGANIZATION(extracellular/secretion protein)					20	
YNL160W		YGP1	1	Secreted glycoprotein produced in response to nutrient limitation; homologous		
YGL104C				to the sporulation-specific SPS100 gene		
	YIL015W	BAR1	5	similarity to glucose transport proteins		
	YDR461W	MFA1	6	barrierpepsin precursor		
	YLR300W	EXG1	6	mating pheromone a-factor 1		
	YNL145W	MFA2	6	exo-beta-1,3-glucanase (I/II), major isoform		
	YGL032C	AGA2	6	mating pheromone a-factor 2		
CELLULAR ORGANIZATION(organiz. of plasma membrane)					142	
YOR348C		PUT4	1	a-agglutinin binding subunit		
YDR536W		STL1	1	Proline and gamma-aminobutyrate (GABA) permease, required for high-affinity		
YHR094C		HXT1	1	proline transport;member of the amino acid permease family, a subfamily of		
YBR021W		FUR4	1	the major facilitator superfamily (MFS)		
YBR068C		BAP2	1	has 28% identity to Hxt2p and Gal2p; has 31% identity to Hxt4p over 183		
YMR058W		FET3	1	amino acids;has 12 predicted transmembrane domains		
YLR120C		YAP3	1	HOR4 Low-affinity hexose transporter and member of sugar permease family,		
YOR153W		PDR5	1	induced by glucose only at high concentration		
YHR096C		HXT5	1	Uracil permease, member of the uracil/allantoin permease family of the major		
YNL192W		CHS1	2	facilitator superfamily (MFS)		
YMR011W		HXT2	2	leucine permease, high-affinity (S1)		
YDR345C		HXT3	2	cell surface ferroxidase, high affinity		
YGR055W		MUP1	2	aspergillopepsin		
YDR046C		BAP3	2	1 aspergillopepsin		
	YHR161C			pleiotropic drug resistance protein		
	YER056C	FCY2	6	Protein with strong similarity to hexose transporters, member of sugar		
	YNR044W	AGA1	6	permease family		
	YNL154C	YCK2	6	chitin synthase I		
	YHR135C	YCK1	7	high-affinity hexose transporter		
CELLULAR ORGANIZATION(nuclear organization)					726	
YHR166C		CDC23	1	high affinity methionine permease		
YGR246C		BRF1	1	valine transporter		
YGL166W		CUP2	1	Yeast Adaptor Protein, member of AP180 protein family		
YOR028C		CIN5	1	purine-cytosine permease		
YGR180C		RNR4	1	a-agglutinin anchor subunit		
YAL019W		FUN30	1	casein kinase I isoform		
YMR037C		MSN2	2	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane		
YNL007C		SIS1	2	H+-ATPase Pmalp in vitro		
YNL112W		DBP2	2	COMPONENT OF ANAPHASE-PROMOTING COMPLEX (APC); REQUIRED FOR CLB2P DEGRADATION		
YOR098C		NUP1	2	AND FOR THE METAPHASE-ANAPHASE TRANSITION		
YFLO31W		HAC1	2	TFIIIB is comprised of TATA-binding protein (TBP/Spt15p), Brf (TFIIIB70), and		
YER176W		HEL1	2	Tfc5p (TFIIIB90);transcription factor for POL 3 transcription		
YKL125W		RRN3	2	copper-dependent transcription factor		
YLR399C		BDF1	2	YAP4,HAL6;transcriptional activator		
YGL091C		NBP35	2	ribonucleotide reductase small subunit		
YDL140C		RPO21	2	similarity to helicases of the Snf2/Rad54 family		
YNR038W		DBP6	2	stress responsive regulatory protein		
	YER110C			heat shock protein;autoregulates its own transcription via the heat shock		
	YDL014W	NOP1	6	element (HSE)		
	YFR034C	PHO4	6	ATP-dependent RNA helicase of DEAD box family		
	YML074C	NPI46	6	nuclear pore protein		
	YHL034C	SBP1	6	transcription factor		
	YOR310C	NOP5	6	DNA dependent ATPase/DNA helicase B		
	YLR256W	HAP1	6	RNA polymerase I specific transcription factor		
	YJL080C	SCP160	6	required for maintenance of exact ploidy		
	YBR009C	HHF1	6	histone H4		
	YPL037C	EGD1	6	GAL4 DNA-binding enhancer protein		
	YJL130C	URA2	7	multifunctional pyrimidine biosynthesis protein		
	YNL220W	ADE12	7	adenylosuccinate synthetase		
	YGL122C	NAB2	7	nuclear poly(A)-binding protein		

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
	YER165W	PAB1	7	mRNA polyadenylate-binding protein		
	YLR197W	SIK1	7	involved in pre-rRNA processing		
	YHR089C	GAR1	7	nucleolar rRNA processing protein		
	YMR016C			regulatory protein in the PKA signal transduction pathway;alteration in Sok2p		
		SOK2	7	production affect glycogen accumulation and heat shock resistance		
	YGL025C	PGD1		mediator complex subunit;Hprlp and Pgdlp may cooperate to initiate chromosome		
			7	breaks; INVOLVED IN BOTH POSITIVE AND NEGATIVE REGULATION OF		
				TRANSCRIPTION;COMPONENT OF RNA POLYMERASE HOLOENZYME AND MEDIATOR SUBCOMPLEX;		
	YIR023W	DAL81	7	transcriptional activator for allantoin and GABA catabolic genes;positive		
				regulator of multiple nitrogen catabolic genes		
	YLL039C	UBI4	7	ubiquitin;disruption of the PHO85 gene inappropriately triggers the		
			7	derepression of stress response genes, HSP12 and UBI4		
CELLULAR ORGANIZATION(cell wall organization)						30
	YHR139C	SPS100	1	Sporulation specific protein involved in spore wall formation, first appears		
			1	at 12h of sporulation		
	YKL096W	CWP1	1	YJUL Mannoprotein of the cell wall, member of the PAU1 family		
	YNL066W	SUN4	6	cell wall protein with homology to beta-glucosidase		
	YGL032C	AGA2	6	a-agglutinin binding subunit		
	YER011W	TIR1	7	cold-shock induced protein of the Tirlp,Tiplp family;gene expression is		
				induced by glucose, cold shock, and anaerobiosis		
CELLULAR ORGANIZATION(mitochondrial organization)						345
	YKL150W	MCR1	1	NADH-cytochrome b5 reductase		
				Trehalose-6-phosphate phosphatase, component of the trehalose-6-phosphatase		
	YDR074W	TPS2	1	synthase/phosphatase complex;aka HOG2;like DDR2, CCT1 and HSP12 regulated		
			1	through the MSN2/STRE pathway		
	YDR258C	HSP78	1	Heat shock protein of ClpB family of ATP-dependent proteases, mitochondrial		
				Cytochrome-c isoform 2, predominant isoform during anaerobic growth each of		
	YEL039C	CYC7	1	the three STRE elements in the 5' regulatory region can induce the stress		
			1	response		
	YOR065W	CYT1	1	Cytochrome c1, has an inner membrane space (IMS) sorting signal that does not		
			1	require Imp1p for cleavage		
	YEL024W	RIP1	1	Ubiquinol cytochrome-c reductase iron-sulfur protein (Rieske iron-sulfur		
			1	protein), component of ubiquinol cytochrome-c reductase complex		
	YKL142W	MRP8	1	YKL3 Mitochondrial ribosomal protein of the small subunit		
	YHR008C	SOD2	1	superoxide dismutase (Mn) precursor, mitochondrial		
				putative methylene tetrahydrofolate reductase;predicted protein function as		
	YGL125W		1	ribosomal protein of the large subunit, mitochondrial		
	YGR008C	STF2	1	ATPase stabilizing factor, binds to F0-ATPase and facilitates binding of		
			1	inhibitor and 9 kDa protein to F1-ATPase		
	YHR001W-A	QCR10	1	ubiquinol--cytochrome-c reductase 8.5 kDa subunit		
	YNL037C	IDH1	2	isocitrate dehydrogenase (NAD+) subunit 1, mitochondrial		
	YMR145C		2	Protein with similarity to rotenone-insensitive NADH-ubiquinone		
			2	oxidoreductase Ndi1p		
	YNR001C	CIT1	2	citrate (si)-synthase, mitochondrial;derepression requires Hap2p/Hap3p/Hap4p		
	YGL187C	COX4	2	cytochrome-c oxidase chain IV		
	YKL085W	MDH1	2	malate dehydrogenase precursor, mitochondrial		
	YDR529C	QCR7	2	ubiquinol--cytochrome-c reductase subunit 7		
				Homolog of E. coli DnaJ protein, involved in mitochondrial biogenesis and		
	YFL016C	MDJ1	2	protein folding;heat shock protein - chaperone		
	YER141W	COX15	2	Protein required for cytochrome oxidase assembly		
	YJL166W	QCR8	2	ubiquinol--cytochrome-c reductase chain VIII		
	YDR035W	ARO3	2	2-dehydro-3-deoxyphosphoheptonate aldolase, phenylalanine-inhibited		
	YER061C	CEM1	2	beta-keto-acyl-ACP synthase, mitochondrial		
	YDR456W	NHX1	2	NA+-H+ antiporter		
	YOL059W	GPD2	2	glycerol-3-phosphate dehydrogenase (NAD+), mitochondrial		
	YLR259C	HSP60	6	heat shock protein - chaperone, mitochondrial		
	YAL044C	GCV3	6	glycine decarboxylase, subunit H		
	YMR083W	ADH3	7	alcohol dehydrogenase III;in yeast there are three isozymes of alcohol		
			7	dehydrogenase		
CELLULAR ORGANIZATION(vacuolar and lysosomal organization)						49
	YPL154C	PEP4		aspartyl protease		
	YMR297W	PRC1	1	Carboxypeptidase Y (CPY) (yscY), serine-type protease		
	YJL172W	CPS1	1	Gly-X carboxypeptidase yscS precursor, involved in nitrogen metabolism		
				CVT1 Protease B (yscB) (PrB) (cerevisin), serine protease of the subtilisin		
	YEL060C	PRB1	1	family with broad proteolytic specificity		
	YDL128W	VCK1	2	Ca2+-transport (H+/Ca2+ exchange) protein, vacuolar		
	YPR036W	VMA13	2	H+-ATPase V1 domain 54 KD subunit, vacuolar		
CELLULAR ORGANIZATION(peroxisomal organization)						38
	YLR251W		2	similarity to peroxisomal rat membrane protein PMP22		
CELLULAR ORGANIZATION(ER organization)						117
	YMR015C	ERG5	1	C-22 sterol desaturase		
	YGL055W	OLE1	1	stearoyl-CoA desaturase		
	YBR036C	CSG2	1	calcium dependent regulatory protein		
	YHR190W	ERG9	2	farnesyl-diphosphate farnesyltransferase;squalene synthetase		
	YCR070W	SCC3	2	cyclophilin homolog;peptidyl-prolyl cis-trans isomerase precursor		
	YKL065C		2	Yeast endoplasmic reticulum 25 kDa transmembrane protein		
	YNL064C	YDJ1	6	mitochondrial and ER import protein		
	YJL080C	SCP160	6	required for maintenance of exact ploidy		
CELLULAR ORGANIZATION(organization of Golgi)						66
	YER039C		2	strong similarity to K.lactis golgi uridine diphosphate-N-acetylglucosamine		
			2	transporter		

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
CELLULAR ORGANIZATION	YDL192W	ARF1	7	small GTP-binding protein of the ARF family (org. of intracellular transport vesicles)		42
CELLULAR ORGANIZATION	YGL200C	EMP24	6	component of the COPII-coated vesicles, 24 kDa (org. of cytoskeleton)		nd
CELL RESCUE, DEFENSE, CELL DEATH	YBR009C	HHF1	6	histone H4 AND AGEING(stress response)		153
	YFL014W	HSP12	1	heat shock protein of 12kDa, induced by heat, osmotic stress, oxidative stress and stationary phase;regulated by HOG1 high-osmolarity signal transduction pathway ;stress-induced transcription is decreased severely with msn2 msn4 double mutant		
	YDL022W	GPD1	1	glycerol phosphate dehydrogenase; induced by osmotic stress		
	YER062C	HOR2	1	Msn2p- and Msn4p-dependent ;target gene for HOG-mitogen activated protein		
	YNL160W	YGP1	1	to the sporulation-specific SPS100 gene		
	YGR088W	CTT1	1	Catalase T (cytosolic)		
	YML070W		1	Putative dihydroxyacetone kinase		
YOL052C-A				Stress protein induced by DNA damage, heat shock, osmotic shock and oxidative stress;three stress response elements (STRE) are present in the promoter		
		DDR2	1	;stress-induced transcription stimulation requires functional Msn2p and Msn4p Trehalose-6-phosphate phosphatase, component of the trehalose-6-phosphatase synthase/phosphatase complex;aka HOG2;like DDR2, CCT1 and HSP12 regulated through the MSN2/STRE pathway		
YDR074W		TPS2	1	Heat shock protein 26kD, expressed during entry to stationary phase and		
	YBR072W	HSP26	1	induced by osmotic stress		
YDR258C		HSP78	1	Heat shock protein of ClpB family of ATP-dependent proteases, mitochondrial		
YBR169C		SSE2	1	Heat shock protein of the HSP70 family, present at low level at 23 deg but greatly induced after shift to 37 deg		
YEL039C		CYC7	1	Cytochrome-c isoform 2, predominant isoform during anaerobic growth each of the three STRE elements in the 5' regulatory region can induce the stress response		
YHR104W			1	aldose reductase;induced by osmotic stress		
YBR126C		TPS1	1	CIF1,GGS1,BYP1,fdp1,glc6,TSS1;induced by heat, osmotic and oxidative stress;gene disruption lethal;Msn2p, Mns4p are required for transcriptional activation;promoter contains the stress-regulated CCCCT element (STRE)		
YDR513W		TTR1	1	Glutaredoxin (thioltransferase) (glutathione reductase)		
YMR251W-A			1	Protein involved in responsiveness to hyperosmolarity; akaHOR7;very highly transcribed in late exponential-phase cells		
YLL026W		HSP104	1	Heat shock protein required for thermotolerance, importantfor reactivation of mRNA splicing after heat shock		
YMR173W			1	FSP Stress protein induced by heat shock, DNA damage, or osmotic stress;divergently transcribed from ALD2 and the promoter has putative stress response elements(STRES)		
YBR054W		YRO2	1	Homolog to HSP30 heat shock protein Yro1p		
YER143W			2	induced in response to DNA alkylation damage		
YMR037C		MSN2	2	stress responsive regulatory protein		
YCL035C			2	glutaredoxin		
YER103W		SSA4	2	Heat shock protein of HSP70 family, cytoplasmic heat-induced form not expressed under optimal conditions		
YFL016C		MDJ1	2	Homolog of E. coli DnaJ protein, involved in mitochondrial biogenesis and protein folding;heat shock protein - chaperone		
YML016C		PPZ1	2	ser/thr phosphatase required for normal osmoregulation		
YDR456W		NHX1	2	NA+H+ antiporter		
YDR155C		CPH1	2	cyclophilin (peptidylprolyl isomerase)		
	YGR234W	YHB1	5	flavo-hemoglobin		
	YLR259C	HSP60	6	heat shock protein - chaperone, mitochondrial		
	YNL064C	YDJ1	6	mitochondrial and ER import protein		
	YJL158C		6	member of the Pir1p/Hsp150p/Pir3p family		
	YNL154C	YCK2	6	casein kinase I isoform		
	YHR135C	YCK1	6	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane		
	YIL011W		7	H+-ATPase Pmalp in vitro		
	YER011W	TIR1	7	strong similarity to members of the Srplp/Tiplp family cold-shock induced protein of the Tirlp,Tiplp family;gene expression is induced by glucose, cold shock, and anaerobiosis		
	YLL039C	UBI4	7	ubiquitin;disruption of the PHO85 gene inappropriately triggers the derepression of stress response genes, HSP12 and UBI4		
CELL RESCUE, DEFENSE, CELL DEATH				AND AGEING(detoxification)		96
YOR273C			1	Protein with similarity to members of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family;members of family 1 of the multidrug permeases all have 12 predicted membrane-spanning regions		
YOR273C			1	Protein with similarity to members of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family;members of family 1 of the multidrug permeases all have 12 predicted membrane-spanning regions		
YHR055C		CUP1B	1	Copper metallothionein		
YGR088W		CTT1	1	Catalase T (cytosolic)		
YHR053C		CUP1	1	Copper metallothionein; transcriptionally activated in response to heat shock and glucose starvation through the interaction of Hsflp with a heat		
YBL064C			1	Protein with similarity to Tsalp;strong similarity to thiol-specific antioxidant enzyme		
YDR513W		TTR1	1	Glutaredoxin (thioltransferase) (glutathione reductase)		
YEL065W			1	probably multidrug resistance protein		
YHL040C			1	similarity to C.carbonum toxin pump		
YOR153W		PDR5	1	pleiotropic drug resistance protein		

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
YNR001C		CIT1	2	citrate (si)-synthase, mitochondrial;derepression requires Hap2p/Hap3p/Hap4p		
YKL085W		MDH1	2	malate dehydrogenase precursor, mitochondrial		
YEL047C			2	soluble fumarate reductase, cytoplasmic		
YOR142W		LSC1	2	succinate-CoA ligase alpha subunit		
	YJL200C		6	strong similarity to aconitate hydratase		
INTRACELLULAR	TRANSPORT (cellular			import)		100
YCL040W		GLK1	1	induction by high salt is defective in msn2 msn4 double mutants and in hog1 single mutants;three stress response elements (STRE) are present in the promoter		
YOR348C		PUT4	1	Proline and gamma-aminobutyrate (GABA) permease, required for high-affinity proline transport;member of the amino acid permease family, a subfamily of the major facilitator superfamily (MFS)		
YHR094C		HXT1	1	HOR4 Low-affinity hexose transporter and member of sugar permease family, induced by glucose only at high concentration		
YBR021W		FUR4	1	Uracil permease, member of the uracil/allantoin permease family of the major facilitator superfamily (MFS)		
YBR068C		BAP2	1	leucine permease, high-affinity (S1)		
YMR058W		FET3	1	cell surface ferroxidase, high affinity		
YHR096C		HXT5	1	Protein with strong similarity to hexose transporters, member of sugar permease family		
YJR090C		GRR1	2	required for glucose repression and for glucose and cation transport		
YMR011W		HXT2	2	high-affinity hexose transporter		
YDR345C		HXT3	2	low-affinity hexose transporter		
YGR055W		MUP1	2	high affinity methionine permease		
YDR046C		BAP3	2	valine transporter		
	YHR161C		5	Yeast Adaptor Protein, member of AP180 protein family		
	YER056C	FCY2	6	purine-cytosine permease		
	YNL154C	YCK2	6	casein kinase I isoform		
INTRACELLULAR	TRANSPORT (extracellular transport)					36
YJL044C		GYP6	1	GTPase-activating protein for Ypt6(gtp binding protein(RAS fam.) involved in the secretory pathway		
YNL036W		NCE3	1	Protein involved in a non-classical protein export pathway for proteins that lack standard secretory signal sequences		
INTRACELLULAR	TRANSPORT (other intracellular transport activities)					25
YJR059W		PTK2	1	involved in polyamine uptake		
YNL183C		NPR1	2	ser/thr protein kinase		
INTRACELLULAR	TRANSPORT (mitochondrial transport)					79
YLR034C			1	strong similarity to SMF2 protein(PROBABLE MANGANESE TRANSPORTER)		
YER053C			1	strong similarity to mitochondrial phosphate carrier protein		
	YNL064C	YDJ1	6	mitochondrial and ER import protein		
INTRACELLULAR	TRANSPORT (nuclear transport)					48
YOR098C		NUP1	2	nuclear pore protein		
	YER110C		5	binds with high affinity to yeast ribosomal proteins;RAN-binding protein;		
INTRACELLULAR	TRANSPORT (vesicular transport (Golgi network, etc.))					nd
YPR028W		YIP2	2	Ypt-interacting protein		
YNL006W			2	required for transport of permeases from the golgi to the plasma membrane		
	YNL064C	YDJ1	6	mitochondrial and ER import protein		
	YGL200C	EMP24	6	component of the COPII-coated vesicles, 24 kDa		
	YDL192W	ARF1	7	small GTP-binding protein of the ARF family		
	YHR135C	YCK1	7	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane H+-ATPase Pmalp in vitro		
INTRACELLULAR	TRANSPORT (vacuolar transport)					45
YDL128W		VCX1	2	Ca2+-transport (H+/Ca2+ exchange) protein, vacuolar		
YPR036W		VMAL3	2	H+-ATPase V1 domain 54 KD subunit, vacuolar		
IONIC HOMEOSTATIS (homeostasis of metal ions)						55
YGL166W		CUP2	1	copper-dependent transcription factor		
YNR060W		FRE4	1	Protein with similarity to ferric reductases Fre1p and Fre2p		
YMR058W		FET3	1	cell surface ferroxidase, high affinity		
YOR153W		PDR5	1	pleiotropic drug resistance protein		
IONIC HOMEOSTATIS (homeostasis of other ions)						66
YDR038C		ENA5	1	P-type ATPase involved in Na+ efflux		
YDR039C		ENA2	1	P-type ATPase involved in Na+ efflux		
YER053C			1	strong similarity to mitochondrial phosphate carrier protein		
YDR040C		ENA1	2	PMR2,(SED3),HOR6;P-type ATPase involved in Na+ efflux		
YNR013C			2	similarity to Pho87p and YJL198w		
YDL128W		VCX1	2	Ca2+-transport (H+/Ca2+ exchange) protein, vacuolar		
YPR036W		VMAL3	2	H+-ATPase V1 domain 54 KD subunit, vacuolar		
YDR456W		NHX1	2	NA+-H+ antiporter		
MAJOR FACILITATOR SUPERFAMILY MEMBER						nk
YOR273C				Protein with similarity to members of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family;members of family 1 of the multidrug permeases all have 12 predicted membrane-spanning regions		
YOR348C		PUT4	1	Proline and gamma-aminobutyrate (GABA) permease, required for high-affinity proline transport;member of the amino acid permease family, a subfamily of the major facilitator superfamily (MFS)		
YOR161C			1	Protein of unknown function, member of the major facilitator superfamily (MFS)		
YBR021W		FUR4	1	Uracil permease, member of the uracil/allantoin permease family of the major facilitator superfamily (MFS)		
YOL119C			1	Protein with weak similarity to mammalian monocarboxylate transporter proteins		
YLL028W			1	Member of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family		

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
YER068C		BAP2	1	leucine permease, high-affinity (S1)		
YMR058W		FET3	1	cell surface ferroxidase, high affinity		
YEL065W			1	probably multidrug resistance protein		
YHL040C			1	similarity to C.carbonum toxin pump		
YHR096C		HXT5	1	Protein with strong similarity to hexose transporters, member of sugar permease family		
YGR065C			2	similarity to P.putida phthalate transporter		
YDR387C			2	similarity to Itr1p and Itr2p and E.coli araE		
YNR013C			2	similarity to Pho87p and YJL198w		
YGL084C			2	strong similarity to hypothetical protein YPL189w		
YDL128W		VCX1	2	Ca2+-transport (H+/Ca2+ exchange) protein, vacuolar		
YMR011W		HXT2	2	high-affinity hexose transporter		
YIL056W			2	similarity to YER064c		
YDR345C		HXT3	2	low-affinity hexose transporter		
YGL104C			2	similarity to glucose transport proteins		
YIL121W			2	similarity to antibiotic resistance proteins		
YDR456W		NHX1	2	NA+-H+ antiporter		
YNR030W		ECM39	2	involved in cell wall biogenesis and architecture		
YGR055W		MUP1	2	high affinity methionine permease		
YDR046C		BAP3	2	valine transporter		
METABOLISM(carbohydrate, f.a.,sterol,lipid)						180
YFL014W		HSP12	1	heat shock protein of 12kDa, induced by heat, osmstress, oxidative stress and stationary phase;regulated by HOG1 high-osmolarity signal transduction pathway ;stress-induced transcription is decreased severely with msn2 msn4 double mutant		
YML131W			1	similarity to human leukotriene b4 12-hydroxydehydrogenase and A.thaliana		
YMR015C		ERG5	1	C-22 sterol desaturase		
YNR019W		ARE2	1	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)		
YOR317W		FAA1	1	Long-chain fatty acid CoA ligase (fatty acid activator 1), can incorporate exogenous myristate into myristoyl-CoA and other fatty acids to the CoA derivatives		
YGL055W		OLE1	1	stearoyl-CoA desaturase		
YLR120C		YAP3	1	aspergillopepsin		
YNL231C			1	weak similarity to Sec14p(phosphatidylinositol transfer protein)		
YOR153W		PDR5	1	pleiotropic drug resistance protein		
YER036C		CSG2	1	calcium dependent regulatory protein		
YOL011W			1	strong similarity to phospholipases		
YHR190W		ERG9	2	farnesyl-diphosphate farnesyltransferase;squalene synthetase		
YNL066W		SUN4	6	cell wall protein with homology to beta-glucosidase		
METABOLISM (f.a.,sterol,lipid metabolism and biosynthesis)						96
YPL117C		IDI1	2	isopentenyl-diphosphate delta-isomerase		
YKL091C			2	strong similarity to Sec14p		
YER061C		CEM1	2	beta-keto-acyl-ACP synthase, mitochondrial		
YPL028W		ERG10	2	acetyl-CoA C-acetyltransferase, cytosolic		
YFL031W		HAC1	2	transcription factor		
YER019W			2	putative neutral sphingomyelinase		
YER055C		HIS1	6	ATP phosphoribosyltransferase		
YLR058C		SHM2	7	serine hydroxymethyltransferase, cytoplasmic		
METABOLISM(lipid and f.a. transport)						17
YER053C			1	strong similarity to mitochondrial phosphate carrier protein		
YNR013C			2	similarity to Pho87p and YJL198w		
YBR106W		PHO88	6	involved in phosphate transport		
YOR317W		FAA1	1	Long-chain fatty acid CoA ligase (fatty acid activator 1), can incorporate exogenous myristate into myristoyl-CoA and other fatty acids to the CoA derivatives		
YOR153W		PDR5	1	pleiotropic drug resistance protein		
METABOLISM (breakdown of lipids and phospholipids)						16
YOL011W			1	strong similarity to phospholipases		
METABOLISM(carbohydrate metabolism and utilization)						260
YDL022W		GPD1	1	glycerol phosphate dehydrogenase; induced by osmotic stress		
YCL040W		GLK1	1	induction by high salt is defective in msn2 msn4 double mutants and in hog1 single mutants;three stress response elements (STRE) are present in the promoter		
YER062C		HOR2	1	DL-glycerol phosphate phosphatase;induction under the diauxic transition is Msn2p- and Msn4p-dependent ;target gene for HOG-mitogen activated protein kinase pathway		
YGR043C			1	Protein with strong similarity to Tal1p (a transaldolase);one of a group of 16 genes (OM45, ALD2, SOL4, YNL200C, YGR043C, YKL026C, YBL064C, HSP26, YGR236C,YOR215C, CTT1, YDL204W, HSP30, HSP42, YER150W, and YNL194C) that are coordinately induced early in the diauxic shift; stress response elements (STRE) are present in the promoter		
YML100W		TSL1	1	Component of the trehalose-6-phosphate synthase/phosphatase complex,		
YML070W			1	alternate third subunit with Tps3p		
YBR117C		TKL2	1	Putative dihydroxyacetone kinase		
YHR094C		HXT1	1	TKL1p/Tkl2p required for biosynthesis of erythrose-4 -phosphate which is needed for biosynthesis of aromatic amino acids		
YDR074W		TPS2	1	HOR4 Low-affinity hexose transporter and member of sugar permease family, induced by glucose only at high concentration		
YHR104W			1	Trehalose-6-phosphate phosphatase, component of the trehalose-6-phosphatase synthase/phosphatase complex;aka HOG2;like DDR2, CCT1 and HSP12 regulated through the MSN2/STRE pathway		
YMR105C		PGM2	1	aldose reductase;induced by osmotic stress		
			1	GAL5 Phosphoglucomutase, major isozyme, interconverts Glc-1-P and Glc-6-P		

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
YBR126C		TPS1		CIF1,GGS1,BYP1,fdp1,glc6,TSS1;induced by heat, osmotic and oxidative stress;gene_disruption lethal;Msn2p, Mns4p are required for transcriptional activation;promoter contains the stress-regulated CCCCT element (STRE)		
YDL124W			1	similarity to aldose reductases		
YIL053W		RHR2	1	GPP1 DL-glycerol phosphate phosphatase		
YAL061W			1	Protein with similarity to alcohol/sorbitol dehydrogenase, member of the zinc-containing alcohol dehydrogenase family		
YOL136C		PFK27	1	6-Phosphofructose-2-kinase, isozyme 2		
YAL060W			1	Protein with similarity to alcohol/sorbitol dehydrogenase, member of the zinc-containing alcohol dehydrogenase family		
YKL035W			1	UTP--glucose-1-phosphate uridylyltransferase		
YDR368W		YPR1	1	strong similarity to members of the aldo/keto reductase family		
YNL241C		ZWF1	1	Glucose-6-phosphate dehydrogenase		
YJR096W			1	similarity to Corynebacterium 2,5-diketo-D-gluconic acid reductase and aldehyde reductases		
YLR044C		PDC1	1	pyruvate decarboxylase, isozyme 1;expression decreases 10-20 fold on low glucose or ethanol		
YHR096C		HXT5	1	Protein with strong similarity to hexose transporters, member of sugar permease family		
YNL037C		IDH1	2	isocitrate dehydrogenase (NAD+) subunit 1, mitochondrial		
YNR001C		CIT1	2	citrate (si)-synthase, mitochondrial;derepression requires Hap2p/Hap3p/Hap4p		
YKL085W		MDH1	2	malate dehydrogenase precursor, mitochondrial		
YDR516C			2	Protein with similarity to Glk1p		
YCR036W		RBK1	2	ribokinase		
YNL192W		CHS1	2	chitin synthase I		
YJR090C		GRR1	2	required for glucose repression and for glucose and cation transport		
YFR053C		HXK1	2	hexokinase I		
YLR134W		PDC5	2	pyruvate decarboxylase, isozyme 2		
YBR149W			2	similarity to Gcy1p and aldose reductases		
YGR256W		GND2	2	phosphogluconate dehydrogenase		
YKL060C		FBA1	2	fructose-bisphosphate aldolase		
YMR311C		GLC8	2	regulatory subunit for protein ser/thr phosphatase Glc7p		
YDR345C		HXT3	2	low-affinity hexose transporter		
YDL134C		PPH21	2	protein ser/thr phosphatase PP2A-1		
YFR015C		GSY1	2	UDP glucose--starch glucosyltransferase, isoform 1		
YOR142W		LSC1	2	succinate-CoA ligase alpha subunit		
YOL059W		GPD2	2	glycerol-3-phosphate dehydrogenase (NAD+), mitochondrial		
	YLR300W	EXG1	6	exo-beta-1,3-glucanase (I/II), major isoform		
	YMR083W	ADH3	7	alcohol dehydrogenase III;in yeast there are three isozymes of alcohol dehydrogenase		
METABOLISM(carbohydrate metabolism and transport)						41
	YDR387C		2	similarity to Itr1p and Itr2p and E.coli araE		
	YMR011W	HXT2	2	high-affinity hexose transporter		
	YER039C		2	strong similarity to K.lactis golgi uridine diphosphate-N-acetylglucosamine transporter		
METABOLISM (regulation of aa metabolism)						33
	YHR137W		1	Aromatic amino acid aminotransferase II		
		YIR023W	DAL81	7	transcriptional activator for allantoin and GABA catabolic genes;positive regulator of multiple nitrogen catabolic genes	
METABOLISM (aa metabolism)						202
	YBR068C	BAP2	1	leucine permease, high-affinity (S1)		
	YLR375W	STP3	1	involved in pre-tRNA splicing and in uptake of branched-chain amino acids;Zinc finger		
	YGL125W		1	putative methylene tetrahydrofolate reductase;predicted protein function as ribosomal protein of the large subunit, mitochondrial		
	YDR046C	BAP3	2	valine transporter		
METABOLISM (aa metabolism; aa biosyn.)						116
	YPL111W	CAR1	1	Arginase, present in a complex with ornithine carbamyltransferase where it acts as a allosteric regulator ;expression is induced by intracellular accumulation of arginine		
	YBR117C	TKL2	1	TKL1p/TKL2p required for biosynthesis of erythrose-4 -phosphate which is needed for biosynthesis of aromatic amino acids		
	YMR250W		1	Protein with similarity to glutamate decarboxylase		
	YLR438W	CAR2	1	CARGB; Ornithine aminotransferase		
	YAL004W		1	opposite to SSA1;Protein of unknown function, probable non-coding ORF;strong similarity to A.klebsiana glutamate dehydrogenase		
	YGR019W	UGA1	1	4-aminobutyrate aminotransferase (GABA transaminase)		
	YIR034C	LYS1	1	saccharopine dehydrogenase		
	YOR303W	CPA1	2	arginine-specific carbamoylphosphate synthase, small chain		
	YDR035W	ARO3	2	2-dehydro-3-deoxyphosphoheptonate aldolase, phenylalanine-inhibited		
	YHR018C	ARG4	2	arginosuccinate lyase		
	YGL026C	TRP5	2	tryptophan synthase		
	YER090W	TRP2	2	anthranilate synthase component I		
	YGR055W	MUP1	2	high affinity methionine permease		
	YER055C	HIS1	6	ATP phosphoribosyltransferase		
	YER091C	MET6	6	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
	YLR172C	DPH5	6	diphthamide methyltransferase		
	YJR148W	TWT2	6	branched chain amino acid aminotransferase, cytosolic		
	YPR035W	GLN1	7	glutamate--ammonia ligase		
	YLR180W	SAM1	7	S-adenosylmethionine synthetase 1		
METABOLISM (aa metabolism; aa degradation)						36

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
				Glyoxalase I, converts methylglyoxal and glutathione into S-D-lactoylglutathione;approx. 80% and 50% repressed in msn2 and msn4 disruptants respectively under osmotic stress;promoter contains two STRE;regulated by HOG (high osmolarity glycerol)-MAP (mitogen-activated protein) kinase pathway in osmotic stress response		
YML004C		GLO1				
			1			
YJR025C		BNA1		3-hydroxyanthranilic acid dioxygenase		
YBR006W			1	Protein with similarity to aldehyde dehydrogenase		
	YDR502C	SAM2	5	S-adenosylmethionine synthetase 2		
	YAL044C	GCV3	6	glycine decarboxylase, subunit H		
	YHR216W	PUR5	6	IMP dehydrogenase		
	YJR148W	TWT2	6	branched chain amino acid aminotransferase, cytosolic		
	YLR180W	SAM1	7	S-adenosylmethionine synthetase 1		
METABOLISM (aa transport)						23
				Proline and gamma-aminobutyrate (GABA) permease, required for high-affinity proline transport;member of the amino acid permease family, a subfamily of the major facilitator superfamily (MFS)		
YOR348C		PUT4				
			1			
YBR068C		BAP2		leucine permease, high-affinity (S1)		
YLR375W		STP3		involved in pre-tRNA splicing and in uptake of branched-chain amino acids;Zinc finger		
			1			
YGR055W		MUP1		high affinity methionine permease		
YDR046C		BAP3		valine transporter		
METABOLISM(phosphate)						31
				strong similarity to mitochondrial phosphate carrier protein		
YER053C			1			
YNR013C			2	similarity to Pho87p and YJL198w		
METABOLISM(phosphate metabolism, regulation of phosphate utilization)						8
	YFR034C	PHO4	6	transcription factor		
	YBR106W	PHO88	6	involved in phosphate transport		
METABOLISM (nucleotide metabolism, deoxyribonucleotide metabolism)						12
				Glutaredoxin (thioltransferase) (glutathione reductase)		
YDR513W		TTR1	1			
YGL157W			1	similarity to V.vinifera dihydroflavonol 4-reductase		
YGR180C		RNR4	1	ribonucleotide reductase small subunit		
YBR014C			2	similarity to glutaredoxin		
METABOLISM (nucleotide metabolism; pyrimidine-ribonucleotide metab.)						28
				Uracil permease, member of the uracil/allantoin permease family of the major facilitator superfamily (MFS)		
YBR021W		FUR4				
			1			
	YML106W	URA5	6	orotate phosphoribosyltransferase		
	YKL216W	URA1	6	dihydroorotate dehydrogenase		
	YJL130C	URA2	7	multifunctional pyrimidine biosynthesis protein		
	YIR023W	DAL81	7	transcriptional activator for allantoin and GABA catabolic genes;positive regulator of multiple nitrogen catabolic genes		
METABOLISM (nucleotide metabolism; purine-ribonucleotide metab.)						45
				adenosine deaminase		
YNL141W		AAH1	6			
YML056C			6	strong similarity to IMP dehydrogenases		
YAR075W			6	strong similarity to IMP dehydrogenases		
YHR128W		FUR1	6	uracil phosphoribosyltransferase		
YLR432W			6	strong similarity to IMP dehydrogenases, Pur5p and YML056c		
YKR080W		MTD1	7	methylenetetrahydrofolate dehydrogenase (NAD+)		
				phosphoribosylamine-glycine ligase and phosphoribosylformylglycinamide		
YGL234W		ADE5.7	7	cyclo-ligase		
			7			
YNL220W		ADE12	7	adenylosuccinate synthetase		
YLR359W		ade13	7	adenylosuccinate lyase		
YLR058C		SHM2	7	serine hydroxymethyltransferase, cytoplasmic		
YDR399W			7	hypoxanthine guanine phosphoribosyl transferase		
YMR120C		ade17	7	5-aminoimidazole-4-carboxamide ribotide transformylase		
METABOLISM (metabolism of cyclic and unusual nucleotides)						8
YOR360C		PDE2	1	SRA5;high affinity 3',5'-cyclic-nucleotide phosphodiesterase		
METABOLISM (nucleotide metabolism, regulation of)						13
YGL248W		PDE1	2	low affinity 3',5'-cyclic-nucleotide phosphodiesterase		
	YER056C	FCY2	6	purine-cytosine permease		
METABOLISM (nucleotide metabolism, nucleotide transport)						13
	YER056C	FCY2	6	purine-cytosine permease		
METABOLISM (other nucleotide metabolism activities)						7
YDL125C		YHI1	2	similarity to protein kinase C inhibitor-I		
	YLR150W	MPT4	6	specific affinity for guanine-rich quadruplex nucleic acids		
	YPL037C	EGD1	6	GAL4 DNA-binding enhancer protein		
METABOLISM (nitrogen and sulfur metabolism)						38
				Arginase, present in a complex with ornithine carbamyltransferase where it acts as a allosteric regulator ;expression is induced by intracellular accumulation of arginine		
YPL111W		CAR1				
			1			
YJL172W		CPS1		Gly-X carboxypeptidase yscS precursor, involved in nitrogen metabolism		
YPL135W		ISU1		strong similarity to nitrogen fixation protein		
YGR019W		UGA1		4-aminobutyrate aminotransferase (GABA transaminase)		
YJL060W			1	Protein with similarity to kynurenine aminotransferase		
YNL183C		NPRI	2	ser/thr protein kinase		
	YPR035W	GLN1	7	glutamate--ammonia ligase		
	YIR023W	DAL81	7	transcriptional activator for allantoin and GABA catabolic genes;positive regulator of multiple nitrogen catabolic genes		
METABOLISM(other vitamin, cofactors and prosthetic group activities)						7
YGL157W			1	similarity to V.vinifera dihydroflavonol 4-reductase		
YGL125W			1	putative methylene tetrahydrofolate reductase;predicted protein function as ribosomal protein of the large subunit, mitochondrial		
YGR144W		THI4	1	involved in thiamine biosynthesis and DNA repair		
METABOLISM(vitamins, cofactors and prosthetic groups)						80
				Protein induced by osmotic stress;similar to dihydroflavonol 4-reductase from plants		
YOL151W		GRE2	1			
YJR025C		BNA1	1	3-hydroxyanthranilic acid dioxygenase		
YBL033C		RIB1	2	GTP cyclohydrolase II		
PROTEIN DESTINATION (protein modification; glycosylation, acylation, myristylation,etc.)						

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
YHR166C		CDC23	1	COMPONENT OF ANAPHASE-PROMOTING COMPLEX (APC); REQUIRED FOR CLB2P DEGRADATION AND FOR THE METAPHASE-ANAPHASE TRANSITION		
YPL154C		PEP4	1	aspartyl protease		
YEL060C		PRB1	1	CVT1 Protease B (yscB) (PrB) (cerevisin), serine protease of the subtilisin family with broad proteolytic specificity		
YKL035W			1	UTP--glucose-1-phosphate uridylyltransferase		
YER039C			2	strong similarity to K.lactis golgi uridine diphosphate-N-acetylglucosamine transporter		
	YNL186W			derepression of telomeric silencing;predicted to encode a ubiquitin-processing protease; has similarity to UBIQUITIN C-TERMINAL HYDROLASE		
PROTEIN DESTINATION(proteolysis)	UBP10		7			144
YHR113W			2	similarity to vacuolar aminopeptidase Apelp		
	YIL015W	BAR1	5	barrierpepsin precursor		
PROTEIN DESTINATION (proteolysis;cytoplasmic degradation)						93
YHR166C		CDC23	1	COMPONENT OF ANAPHASE-PROMOTING COMPLEX (APC); REQUIRED FOR CLB2P DEGRADATION AND FOR THE METAPHASE-ANAPHASE TRANSITION		
	YLR167W	RPS31	7	aka RPS37; UBI3;ubiquitin		
	YIL148W	RPL40A	7	ubiquitin		
	YDL192W	ARF1	7	small GTP-binding protein of the ARF family		
	YKR094C	RPL40B	7	aka CEP52B; UBI2;ubiquitin		
	YGR214W	YST1	7	aka RPS0A;YST1; NAB1A; (NAB1);40S ribosomal protein p40 homolog A		
	YLL039C	UBI4	7	ubiquitin;disruption of the PHO85 gene inappropriately triggers the derepression of stress response genes, HSP12 and UBI4		
	YLR048W	NAB1B	7	Ribosomal protein S0B; 40S ribosomal protein p40 homolog B		
PROTEIN DESTINATION (proteolysis; lysosomal and vacuolar)						17
YPL154C		PEP4	1	aspartyl protease		
YMR297W		PRC1	1	Carboxypeptidase Y (CPY) (yscY), serine-type protease		
YJL172W		CPS1	1	Gly-X carboxypeptidase yscS precursor, involved in nitrogen metabolism		
YEL060C		PRB1	1	CVT1 Protease B (yscB) (PrB) (cerevisin), serine protease of the subtilisin family with broad proteolytic specificity		
PROTEIN DESTINATION (other protein destination activities)						6
YDR258C		HSP78	1	Heat shock protein of ClpB family of ATP-dependent proteases, mitochondrial		
PROTEIN DESTINATION(protein folding and stabilization)						54
YDR171W		HSP42		heat shock protein; three stress response elements (STRE) are present in the promoter;induction by high salt is defective in msn2 msn4 double mutants and in hog1 single mutants;has 3 AGGGG elements, sequences which are also found in other stationary phase responsive genes		
YCR070W		SCC3	2	cyclophilin homolog;peptidyl-prolyl cis-trans isomerase precursor		
YPL016C		MDJ1	2	Homolog of E. coli DnaJ protein, involved in mitochondrial biogenesis and protein folding;heat shock protein - chaperone		
YDR155C		CPH1	2	cyclophilin (peptidylprolyl isomerase)		
	YLR259C	HSP60	6	heat shock protein - chaperone, mitochondrial		
	YML074C	NPI46	6	proline cis-trans isomerase		
	YLR449W	FPR4	6	strong similarity to peptidylprolyl isomerase Fpr3p		
PROTEIN DESTINATION(assembly of protein complexes)						87
YLR327C			2	strong similarity to Stf2p(ATPase stabilizing factor)		
YER141W		COX15	2	Protein required for cytochrome oxidase assembly		
YNR038W		DBP6	2	RNA helicase required for 60S ribosomal subunit assembly		
	YHR161C		5	Yeast Adaptor Protein, member of AP180 protein family		
PROTEIN DESTINATION(protein targeting, sorting and translocation)						123
YOR285W			2	Protein with similarity to Drosophila melanogaster heat shock protein 67B2		
YBL069W		AST1	2	PMAL protein targeting protein;Protein involved in targeting of plasma membrane [H+]ATPase		
YER110C			5	binds with high affinity to yeast ribosomal proteins;RAN-binding protein;		
YNL064C		YDJ1	6	mitochondrial and ER import protein		
PROTEIN SYNTHESIS translation(initiation, elongation, termination)						63
YNL007C		SIS1	2	heat shock protein;autoregulates its own transcription via the heat shock element (HSE)		
	YOL139C	CDC33	5	translation initiation factor eIF4E		
	YNL014W		6	translation elongation factor eEF3 homolog		
	YMR012W	CLU1	6	translation initiation factor eIF3 (p135 subunit)		
PROTEIN SYNTHESIS translation(initiation, elongation, termination)...continued						
	YMR146C	TIF34	6	translation initiation factor eIF3, p39 subunit		
	YDR429C		6	translation initiation factor eIF3 (p33 subunit)		
	YLR256W	HAP1	6	transcription factor		
	YJL138C	TIF2	6	translation initiation factor eIF4A		
	YJR047C	ANB1	7	translation initiation factor eIF5A.2		
	YER165W	PAB1	7	mRNA polyadenylate-binding protein		
	YLR249W	YEF3	7	translation elongation factor eEF3;found only in fungi		
	YMR260C	TIF11	7	translation initiation factor eIF1a		
	YDL081C	RPLA1	7	aka;acidic ribosomal protein a1;(RPA1); L12eIIA; RPLA1;RPP1A;plays a role in the elongation step		
PROTEIN SYNTHESIS (ribosomal proteins)						137
				there are 137 known ribosomal ORFs. 50 cytoplasmic, small ribosomal proteins (down regulated). 47 cytoplasmic, large ribosomal proteins (downregulated). 2 mitochondrial small subunits upregulated		
PROTEIN SYNTHESIS (other protein synthesis activities)						12
	YBR121C	GRS1	5	Glycyl-tRNA synthase; glycine--tRNA ligase		
	YNL209W	SSB2	6	heat shock protein of HSP70 family, cytosolic		
PROTEIN SYNTHESIS (translational control)						28
YBL058W		SHP1	2	potential regulatory subunit for Glc7p		
RETROTRANSPOSONS AND PLASMID PROTEINS						113

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
YOR344C		TYE7	2	TY2A protein		
	YAL003W	EFB1	6	translation elongation factor eEF1beta		
SIGNAL TRANSDUCTION (nutritional response pathway;other nutritional-response activities)						9
YLR178C		TFS1		CDC25-dependent nutrient- and ammonia-response cell cycleregulator, suppressor of CDC25 mutations;controls the phosphorylation of two 31 kDa proteins whose phosphorylation and dephosphorylation are strongly correlated with cell-cycle arrest and proliferation		
YJR059W		PTK2	1	involved in polyamine uptake		
SIGNAL TRANSDUCTION (pheromone response generation)						34
	YDR461W	MFA1	6	mating pheromone a-factor 1		
SIGNAL TRANSDUCTION (other pheromone response activities)						18
	YDR461W	MFA1	6	mating pheromone a-factor 1		
SIGNAL TRANSDUCTION (other signal transduction activities)						37
YFL031W		HAC1	2	transcription factor		
YJL164C		SRA3	2	cAMP-dependent protein kinase 1, catalytic chain		
	YLR150W	MPT4	6	specific affinity for guanine-rich quadruplex nucleic acids		
	YMR016C			regulatory protein in the PKA signal transduction pathway;alteration in Sok2p		
		SOK2	7	production affect glycogen accumulation and heat shock resistance		
SIGNAL TRANSDUCTION (unspecified signal transduction; second messenger formation)						2
YER019W			2	putative neutral sphingomyelinase		
	YDL135C	RDI1	6	rho GDP dissociation inhibitor with activity toward Rholp		
SIGNAL TRANSDUCTION (osmosensing)						17
				heat shock protein of 12kDa, induced by heat, osmstress, oxidative stress and stationary phase;regulated by HOG1 high-osmolarity signal transduction pathway ;stress-induced transcription is decreased severely with msn2 msn4		
YFL014W		HSP12		double mutant		
YDL022W		GPD1	1	glycerol phosphate dehydrogenase; induced by osmotic stress		
TRANSCRIPTION (transcriptional control)						314
YGL166W		CUP2	1	copper-dependent transcription factor		
YOR028C		CIN5	1	YAP4,HAL6;transcriptional activator		
YMR037C		MSN2	2	stress responsive regulatory protein		
YER130C			2	similarity to Msn2p and weak similarity to Msn4p		
YFL031W		HAC1	2	transcription factor		
YLR399C		BDF1	2	sporulation protein		
YER169W		RPH1	2	regulator of PHR1(DEOXYRIBODIPYRIMIDINE PHOTOLYASE, INVOLVED IN LIGHT-DEPENDENT REPAIR OF PYRIMIDINE DIMERS)		
YJL164C		SRA3	2	cAMP-dependent protein kinase 1, catalytic chain		
	YNL186W			derepression of telomeric silencing;predicted to encode a ubiquitin-		
		UBP10	7	processing protease; has similarity to UBIQUITIN C-TERMINAL HYDROLASE		
	YMR016C			regulatory protein in the PKA signal transduction pathway;alteration in Sok2p		
		SOK2	7	production affect glycogen accumulation and heat shock resistance		
	YGL025C	PGD1		mediator complex subunit;Hpr1p and Pgd1p may cooperate to initiate chromosome breaks; INVOLVED IN BOTH POSITIVE AND NEGATIVE REGULATION OF		
			7	TRANSCRIPTION;COMPONENT OF RNA POLYMERASE HOLOENZYME AND MEDIATOR SUBCOMPLEX;		
	YIR023W	DAL81	7	transcriptional activator for allantoin and GABA catabolic genes;positive regulator of multiple nitrogen catabolic genes		
TRANSCRIPTION (mRNA transcription and splicing)						
YHR086W		NAM8	1	MRE2,MUD15;meiotic recombination protein		
TRANSCRIPTION (mRNA transcription and synthesis)						401
YGL166W		CUP2	1	copper-dependent transcription factor		
YOR028C		CIN5	1	YAP4,HAL6;transcriptional activator		
YMR037C		MSN2	2	stress responsive regulatory protein		
YER130C			2	similarity to Msn2p and weak similarity to Msn4p		
YFL031W		HAC1	2	transcription factor		
YLR399C		BDF1	2	sporulation protein		
YER169W		RPH1	2	regulator of PHR1(DEOXYRIBODIPYRIMIDINE PHOTOLYASE, INVOLVED IN LIGHT-DEPENDENT REPAIR OF PYRIMIDINE DIMERS)		
YDL140C		RPO21	2	DNA-directed RNA polymerase II, 215 KD subunit		
YJL164C		SRA3	2	cAMP-dependent protein kinase 1, catalytic chain		
	YMR290C		5	helicase associated with Set1p		
	YNL186W			derepression of telomeric silencing;predicted to encode a ubiquitin-		
		UBP10	7	processing protease; has similarity to UBIQUITIN C-TERMINAL HYDROLASE		
	YMR016C			regulatory protein in the PKA signal transduction pathway;alteration in Sok2p		
		SOK2	7	production affect glycogen accumulation and heat shock resistance		
	YGL025C	PGD1		mediator complex subunit;Hpr1p and Pgd1p may cooperate to initiate chromosome breaks; INVOLVED IN BOTH POSITIVE AND NEGATIVE REGULATION OF		
			7	TRANSCRIPTION;COMPONENT OF RNA POLYMERASE HOLOENZYME AND MEDIATOR SUBCOMPLEX;		
	YIR023W	DAL81	7	transcriptional activator for allantoin and GABA catabolic genes;positive regulator of multiple nitrogen catabolic genes		
TRANSCRIPTION (mRNA transcription, synthesis and control)						533
YJL115W		ASF1	6	anti-silencing protein		
YFR034C		PHO4	6	transcription factor		
YLR256W		HAP1	6	transcription factor		
YBR009C		HHF1	6	histone H4		
YPL037C		EGD1	6	GAL4 DNA-binding enhancer protein		
TRANSCRIPTION (mRNA 5'-3' end processing and mRNA degradation)						36
YGL122C		NAB2	7	nuclear poly(A)-binding protein		
YER165W		PAB1	7	mRNA polyadenylate-binding protein		
TRANSCRIPTION(rRNA, tRNA)						

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
		BRF1		TFIIIB is comprised of TATA-binding protein (TBP/Spt15p), Brf (TFIIIB70), and Tfc5p (TFIIIB90);transcription factor for POL 3 transcription		
YGR246C						
TRANSCRIPTION (rRNA transcription, rRNA processing)						54
YNL112W		DBP2	2	ATP-dependent RNA helicase of DEAD box family		
YKL125W		RRN3	2	RNA polymerase I specific transcription factor		
YNR038W		DBP6	2	RNA helicase required for 60S ribosomal subunit assembly		
	YDL014W	NOP1	6	fibrillarlin		
	YHL034C	SBP1	6	single-strand nucleic acid binding protein		
	YOR310C	NOP5	6	required for pre-18S rRNA processing		
	YLR197W	SIK1	7	involved in pre-rRNA processing		
	YHR089C	GAR1	7	nucleolar rRNA processing protein		
TRANSCRIPTION (tRNA transcription and processing)						37
YGR248W		SOL4	1	Protein of unknown function;strong similarity to Sol3p(similarity to glucose-6-phosphate dehydrogenase)		
YLR375W		STP3	1	involved in pre-tRNA splicing and in uptake of branched-chain amino acids;Zinc finger		
YNR034W		SOL1	2	multicopy suppressor of los1-1		
TRANSCRIPTION (tRNA transcription; tRNA modification)						12
	YGL105W	ARC1	6	protein with specific affinity for G4 quadruplex nucleic acids		
TRANSCRIPTION (RNA transport)						27
	YGL122C	NAB2	7	nuclear poly(A)-binding protein		
TRANSCRIPTION (chromatin modification)						30
	YMR290C		5	helicase associated with Set1p		
YMR027W			2	high level expression reduced Ty3 transposition		
YNR047W			2	similarity to ser/thr protein kinases		
	YMR305C	SCW10	6	member of the glucanase gene family		
	YNL002C	RLP7	6	strong similarity to mammalian ribosomal L7 proteins		
TRANSCRIPTION (other transcription activities)						60
YDR043C			1	weak similarity to K.marxianus Mig1 and other regulatory proteins;zinc finger		
YNL037C		IDH1	2	isocitrate dehydrogenase (NAD+) subunit 1, mitochondrial		
TRANSPORT FACILITATION(drug transporters)						35
YOR273C			1	Protein with similarity to members of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family;members of family 1 of the multidrug permeases all have 12 predicted membrane-spanning regions		
YBR052C			1	Protein with similarity to Ycp4p, S. pombe obr1, and E. coli trp repressor binding protein;strong similarity to S.pombe brefeldin A resistance protein		
YEL065W			1	probably multidrug resistance protein		
YHL040C			1	similarity to C.carbonum toxin pump		
YIL121W			2	similarity to antibiotic resistance proteins		
TRANSPORT FACILITATION(sugar and carbohydrate transporters)						44
YDR536W		STL1	1	has 28% identity to Hxt2p and Gal2p; has 31% identity to Hxt4p over 183 amino acids;has 12 predicted transmembrane domains		
YHR094C		HXT1	1	HOR4 Low-affinity hexose transporter and member of sugar permease family, induced by glucose only at high concentration		
YHR096C		HXT5	1	Protein with strong similarity to hexose transporters, member of sugar permease family		
YDR387C			2	similarity to Itr1p and Itr2p and E.coli araE		
YMR011W		HXT2	2	high-affinity hexose transporter		
YER039C			2	strong similarity to K.lactis golgi uridine diphosphate-N-acetylglucosamine transporter		
YDR345C		HXT3	2	low-affinity hexose transporter		
YGL104C			2	similarity to glucose transport proteins		
TRANSPORT FACILITATION(aa transporters)						25
YOR348C		PUT4	1	Proline and gamma-aminobutyrate (GABA) permease, required for high-affinity proline transport;member of the amino acid permease family, a subfamily of the major facilitator superfamily (MFS)		
YBR068C		BAP2	1	leucine permease, high-affinity (S1)		
YGR055W		MUP1	2	high affinity methionine permease		
YDR046C		BAP3	2	valine transporter		
TRANSPORT FACILITATION(purine and pyrimidine transporters)						15
YBR021W		FUR4	1	Uracil permease, member of the uracil/allantoin permease family of the major facilitator superfamily (MFS)		
YER056C		FCY2	6	purine-cytosine permease		
TRANSPORT FACILITATION (anion transport; Cl, PO4, SO4,etc.)						15
YER053C			1	strong similarity to mitochondrial phosphate carrier protein		
YNR013C			2	similarity to Pho87p and YJL198w		
TRANSPORT FACILITATION (other transporters)						55
YOL119C			1	Protein with weak similarity to mammalian monocarboxylate transporter proteins		
YER053C			1	strong similarity to mitochondrial phosphate carrier protein		
YGR065C			2	similarity to P.putida phthalate transporter		
YKL146W			2	strong similarity to S.pombe hypothetical protein C3H1.09C		
TRANSPORT FACILITATION (ABC transporters)						28
YOR153W		PDR5	1	pleiotropic drug resistance protein		
YNL014W			6	translation elongation factor eEF3 homolog		
TRANSPORT FACILITATION (other cation transporters (Na ,K ,Ca ,NH4 ,etc.))						37
YOR153W		PDR5	1	pleiotropic drug resistance protein		
YDL128W		VCK1	2	Ca2+-transport (H+/Ca2+ exchange) protein, vacuolar		
YPR036W		VMA13	2	H+-ATPase V1 domain 54 KD subunit, vacuolar		
YDR456W		NHX1	2	NA+-H+ antiporter		
TRANSPORT FACILITATION (transport ATPases)						44
YDR038C		ENA5	1	P-type ATPase involved in Na+ efflux		
YDR039C		ENA2	1	P-type ATPase involved in Na+ efflux		
YDR040C		ENA1	2	PMR2,(SED3),HOR6;P-type ATPase involved in Na+ efflux		
YPR036W		VMA13	2	H+-ATPase V1 domain 54 KD subunit, vacuolar		

UP	DOWN	LOCUS	X	DEFINITION	Gene	OBS
TRANSPORT FACILITATION (metal ion transporters (Cu, Fe, etc.)						21
YMR058W		FET3	1	cell surface ferroxidase, high affinity		
UNCLASSIFIED PROTEINS						2593
152	22			173 unknown ORFs		
CLASSIFICATION NOT YET CLEAR-CUT						151
	YOR374W		1	Aldehyde dehydrogenase		
	YKL039W	PTM1	1	Protein with strong similarity to Yh1017p, member of the major facilitator superfamily (MFS)		