

# 10 MINUTES SALT STRESS

UP	DOWN	LOCUS	X	DEFINITION	OBS
CELL GROWTH,	CELL DIVISION AND	DNA SYNTHESIS (		DNA synthesis and replication)	
YFR027W	EC01	2		involved in sister chromatid cohesion during replication	
CELL GROWTH,	CELL DIVISION AND	DNA SYNTHESIS (pheromone resp,		mating-type det., sex-specific prot.)	
YGL032C	AGA2	1		a-agglutinin binding subunit	
YNL145W	MFA2	2		mating pheromone a-factor 2	
YNR044W	AGA1	2		a-agglutinin anchor subunit	
YJR117W		2		zinc metallo-protease	
	YDR103W	STE5	6	pheromone signal transduction pathway protein	
	YER020W	GPA2	6	guanine nucleotide-binding regulatory protein	
	YHL025W	SNF6	7	global transcription activator	
CELL GROWTH,	CELL DIVISION AND	DNA SYNTHESIS ;(budding, cell polarity,		and filament formation)	
YDL135C	RD11	2		rho GDP dissociation inhibitor with activity toward Rho1p	
YLL050C	COF1	2		cofilin, actin binding and severing protein	
YDL188C	PPH22	2		protein ser/thr phosphatase PP2A-2	
	YKL129C	MYO3	6	myosin type I	
	YNL197C	WHI3	6	involved in regulation of cell size	
	YER114C	BOT2	6	budding protein	
	YER020W	GPA2	6	guanine nucleotide-binding regulatory protein	
	YHR103W	SBE22	6	strong similarity to budding protein SBE2	
	YHR030C	SLT2	6	ser/thr protein kinase of MAP kinase family	
	YKR048C	NAP1	6	nucleosome assembly protein I	
	YDR388W	RVS167	6	reduced viability upon starvation protein	
	YGR009C	SEC9	7	protein transport protein	
	YMR016C	SOK2	7	glycogen accum. and heat shock resist.	
	YER109C	FLO8	7	required for diploid filamentous growth	
CELL GROWTH,	CELL DIVISION AND	DNA SYNTHESIS ;(cell cycle control and mitosis)			
YFR027W	EC01	2		involved in sister chromatid cohesion during replication	
YDL188C	PPH22	2		protein ser/thr phosphatase PP2A-2	
	YHR030C	SLT2	6	ser/thr protein kinase of MAP kinase family	
	YNL225C		6	involved in cytokinesis	
	YER123W	YCK3	6	casein kinase, isoform 3	
	YKR072C	SIS2	6	involved in cell cycle-specific gene expression	
	YER173W	RAD24	7	cell cycle checkpoint protein	
	YKR048C	NAP1	6	nucleosome assembly protein I	
CELL GROWTH,	CELL DIVISION AND	DNA SYNTHESIS ;(cell growth)			
YDL188C	PPH22	2		protein ser/thr phosphatase PP2A-2	
	YBR212W	NGR1	6	glucose-repressible RNA-binding protein	
	YNL197C	WHI3	6	involved in regulation of cell size	
	YER170W	ADK2	6	adenylate kinase, mitochondrial	
	YER020W	GPA2	6	guanine nucleotide-binding regulatory protein	
	YHR030C	SLT2	6	ser/thr protein kinase of MAP kinase family	
	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,	CELL DIVISION AND	DNA SYNTHESIS ;(cytokinesis)			
YLR286C	CTS1	1		endochitinase	
	YNL154C	YCK2	6	casein kinase I isoform	
	YNL225C		6	involved in cytokinesis	
	YHR135C	YCK1	7	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane H+-ATPase Pmalp in vitro	
CELL GROWTH,	CELL DIVISION AND	DNA SYNTHESIS ;(meiosis)			
YDR461W	MFA1	1		mating pheromone a-factor 1	
CELL GROWTH,	CELL DIVISION AND	DNA SYNTHESIS ;(recombination and DNA repair)			
	YGL025C	PGD1	6	mediator complex subunit; Hpr1p and Pgd1p may cooperate to initiate c/some breaks; INVOLVED IN POSITIVE AND NEGATIVE REG. OF TRANSCRIPTION; COMPONENT OF RNA POL HOLOENZYME AND MEDIATOR SUBCOMPLEX;	
	YER173W	RAD24	7	cell cycle checkpoint protein	
CELL GROWTH,	CELL DIVISION AND	DNA SYNTHESIS ;(sporulation and germination)			
YNL225C		6		involved in cytokinesis	
CELL RESCUE,	DEFENSE, CELL DEATH	AND AGEING(		DNA repair (direct, base excision and nucleot. excision rep.)	
YDR311W	TFB1	6		TFIIH subunit (transcription initiation factor), 75 kD	
YDL088C	ASM4	6		suppressor of temperature-sensitive mutations in Pol3p	
YIL128W	MET18	6		involved in NER repair and RNA polymerase II transcription	
CELL RESCUE,	DEFENSE, CELL DEATH	AND AGEING(stress response)			
YAL005C	SSA1	1		heat shock protein of HSP70 family, cytosolic	
	YNL160W	YGP1	1	Secreted glycoprotein produced in response to nutrient limitation; homologous to the sporulation-specific SPS100 gene	
	YDR033W		2	strong similarity to putative heat shock protein YRO2	
	YER057C		2	Heat-shock inducible Inhibitor of cell Growth	
	YMR186W	HSC82	1	heat shock protein	
	YDR155C	CPH1	2	cyclophilin (peptidylprolyl isomerase)	
	YDL022W		2	glycerol phosphate dehydrogenase; induced by osmotic stress	
	YIL011W		6	strong similarity to members of the Srp1p/Tiplp family	
	YNL154C	YCK2	6	casein kinase I isoform	
	YCR095C		7	transcribed in late exponential-phase cells	
	YHR135C	YCK1	7	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane H+-ATPase Pmalp in vitro	
	YLL039C	UBI4	7	ubiquitin;disruption of the PHO85 gene inappropriately triggers the derepression of stress response genes, HSP12 and UBI4	
	YOR010C	TIR2	6	cold shock induced protein	
	YLL024C	SSA2	6	heat shock protein of HSP70 family, cytosolic	
	YGL021W	ALK1	6	DNA damage-responsive protein	
	YHR030C	SLT2	6	ser/thr protein kinase of MAP kinase family	

UP	DOWN	LOCUS	X	DEFINITION	OBS
	YKL088W		6	similarity to C.tropicalis hal3 protein, to C-term. of Sis2p and to hypothetical protein YOR054c	
	YEL030W		7	heat shock protein of HSP70 family	
	YKL163W	PIR3	7	member of the Pirlp/Pir2p/Pir3p family	
	YDR077W	SED1	7	abundant cell surface glycoprotein	
	YBL075C	SSA3	7	heat shock protein of HSP70 family, cytosolic	
CELL RESCUE, DEFENSE,		CELL DEATH		AND AGEING(detoxification)	
	YHR053C	CUPIA	2	glucose starvation through the interaction of Hsflp with a heat	
	YHR055C	CUP1B	2	Copper metallothionein	
	YNL239W	LAP3	2	member of the GAL regulon	
	YER185W		7	strong similarity to Rtmlp	
CELLULAR BIOGENESIS (biogenesis of cell wall)					cell surface prot. with GPI anchor
	YLR110C		2	strong similarity to Flo1p	
	YML048W	EFF2	2	involved in glucose repression	
	YDL188C	PPH22	2	protein ser/thr phosphatase PP2A-2	
	YEL030W		7	heat shock protein of HSP70 family	
	YCL007C	CWH36	7	affects the mannoprotein layer of the cell wall	
	YLR249W	YEP3	7	translation elongation factor eEF3;found only in fungi	
CELLULAR BIOGENESIS (biogenesis of chromosome structure)					
	YKR048C	NAP1	6	nucleosome assembly protein I	
CELLULAR BIOGENESIS (biogenesis of mitochondria)					
	YIL051C	MMD1	1	required for maintenance of mitochondrial DNA	
CELLULAR ORGANIZATION (org. of centrosome)					
	YNL225C		6	involved in cytokinesis	
	YER161C	SPT2	6	multifunctional HMG-like chromatin protein	
CELLULAR ORGANIZATION (org. of cytoskeleton)					
	YLL050C	COF1	2	cofilin, actin binding and severing protein	
	YLR429W	CRN1	2	coronin, an actin-binding protein originally identified in Dictyostelium	
	YKL129C	MYO3	6	myosin type I	
	YBR172C	SMY2	6	kinesin-related protein	
	YDR388W	RVS167	6	reduced viability upon starvation protein	
CELLULAR ORGANIZATION (org. of intracellular transport vesicles)					
	YPL218W	SAR1	2	GTP-binding protein of the ARF family	
	YIL109C	SEC24	2	component of COPII coat of ER-Golgi vesicles	
	YAL030W	SNC1	6	strong similarity to synaptic vesicle-associated membrane protein	
CELLULAR ORGANIZATION( ER organization )					
	YCL043C	PD11	1	protein disulfide-isomerase precursor	
	YPR113W	PI51	2	CDP diacylglycerol--inositol 3-phosphatidyltransferase	
	YIL109C	SEC24	2	component of COPII coat of ER-Golgi vesicles	
	YJR117W		2	zinc metallo-protease	
	YDR086C	SSS1	6	ER protein-translocase complex subunit	
	YNR016C	ACCI	7	acetyl-CoA carboxylase	
CELLULAR ORGANIZATION( organization of Golgi )					
	YPR113W	PI51	2	CDP diacylglycerol--inositol 3-phosphatidyltransferase	
	YIL109C	SEC24	2	component of COPII coat of ER-Golgi vesicles	
	YGL203C	KEK1	6	carboxypeptidase (YSC-alpha)	
	YER123W	YCK3	6	casein kinase, isoform 3	
CELLULAR ORGANIZATION( peroxisomal organization )					
	YCR005C	CIT2	6	citrate (si)-synthase, peroxisomal	
CELLULAR ORGANIZATION(cell wall organization)					
	YGL032C	AGA2	1	a-agglutinin binding subunit	
	YGR282C	BGL2	2	endo-beta-1,3-glucanase of the cell wall	
	YOR010C	TIR2	6	cold shock induced protein	
	YLL024C	SSA2	6	heat shock protein of HSP70 family, cytosolic	
	YKL163W	PIR3	7	member of the Pirlp/Pir2p/Pir3p family	
CELLULAR ORGANIZATION(extracellular/secretion protein)					
	YGL032C	AGA2	1	a-agglutinin binding subunit	
	YDR461W	MFA1	1	mating pheromone a-factor 1	
	YNL160W	YGP1	1	Secreted glycoprotein produced in response to nutrient limitation; homologous to the sporulation-specific SPS100 gene	
	YLR286C	CTS1	1	endochitinase	
	YNL145W	MFA2	2	mating pheromone a-factor 2	
	YJR121W	ATP2	1	F1F0-ATPase complex, F1 beta subunit	
	YGR183C	QCR9	1	ubiquinol--cytochrome-c reductase subunit 9	
	YMR189W	GCV2	1	glycine decarboxylase P subunit	
	YKL141W	SDH3	2	cytochrome b560 subunit of respiratory complex II	
	YDL198C	SHM1	2	member of the mitochondrial carrier family (MCF)	
	YDR529C	QCR7	2	ubiquinol--cytochrome-c reductase subunit 7	
	YDL178W	SDH4	2	succinate dehydrogenase membrane anchor subunit for sdh2p	
	YDR377W		2	ATP synthase complex, subunit f	
	YFL018C	LPD1	6	dihydrolipoamide dehydrogenase precursor	
	YGR222W	PET54	6	splicing protein and translational activator, mitochondrial	
	YER170W	ADK2	6	adenylate kinase, mitochondrial	
	YHR037W	PUT2	6	l-pyrroline-5-carboxylate dehydrogenase	
	YLR348C	DIC1	7	dicarboxylate carrier protein	
CELLULAR ORGANIZATION(nuclear organization)					
	YER009W	NTF2	1	nuclear transport factor	
	YPL037C	EGD1	1	GAL4 DNA-binding enhancer protein	
	YFR034C	PHO4	2	transcription factor	
	YLR293C	GSP1	2	GTP-binding protein of the ras superfamily	
	YJL130C	URA2	2	multifunctional pyrimidine biosynthesis protein	
	YKL074C	MUD2	6	pre-mRNA splicing factor	
	YMR229C	FMI1	6	processing of pre-ribosomal RNA	
	YER146W	LSM5	6	similarity to human snRNP E	
	YML074C	NPI46	6	proline cis-trans isomerase	
	YDR311W	TFB1	6	TFIIH subunit (transcription initiation factor), 75 kD	

UP	DOWN	LOCUS	X	DEFINITION	OBS
	YDR390C	UBA2	6	E1-like (ubiquitin-activating) enzyme	
	YCL054W		6	transcriptional silencing protein	
	YER172C	BRR2	6	RNA helicase-related protein	
	YER161C	SPT2	6	multifunctional HMG-like chromatin protein	
	YDR228C	PFC11	6	component of pre-mRNA 3'-end processing factor CF I	
	YDR443C	SCA1	6	DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcomplex subunit	
	YIL063C	YRB2	6	involved in nuclear protein export	
	YKR072C	SIS2	6	involved in cell cycle-specific gene expression	
	YIL128W	MET18	6	involved in NER repair and RNA polymerase II transcription	
	YDR432W	NPL3	6	nucleolar protein	
	YDR176W	NGG1	6	general transcriptional adaptor or co-activator	
	YER123W	YCK3	6	casein kinase, isoform 3	
	YKR048C	NAP1	6	nucleosome assembly protein I	
	YDR088C	SLU7	6	pre-mRNA splicing factor affecting 3' splice site choice	
	YDR310C	SUM1	6	suppressor of SIR mutations	
	YGL025C	PGD1		mediator complex subunit;Hprlp 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;	
	YBR198C	TAF90	6	TFIID subunit (TBP-associated factor), 90 kD	
	YHL025W	SNF6	7	global transcription activator	
	YLL008W	DRS1	7	RNA helicase of the DEAD box family	
	YDR213W		7	transcriptional activator of lysine pathway genes	
	YMR016C			regulatory protein in the PKA signal transduction pathway;alteration in Sok2p production affect glycogen accumulation and heat shock resistance	
	YNL112W	DBP2	7	ATP-dependent RNA helicase of DEAD box family	
	YHL020C	OPT1	7	negative regulator of phospholipid biosynthesis pathway	
	YLL039C	UBI4	7	ubiquitin;disruption of the PHO85 gene inappropriately triggers the derepression of stress response genes, HSP12 and UBI4	
CELLULAR ORGANIZATION(organ. of cytoplasm)					
	YER009W	NTF2	1	nuclear transport factor binds Ran	
	YAL005C	SSA1	1	heat shock protein of HSP70 family, cytosolic	
	YMR186W	HSC82	1	heat shock protein	
	YKR059W	TIF1	2	translation initiation factor 4A	
	YLR293C	GSP1	2	GTP-binding protein of the ras superfamily	
	YBL076C	ILS1	2	isoleucyl-tRNA synthetase	
	YCR053W	THR4	2	threonine synthase (o-p-homoserine p-lyase)	
	YNL244C	SUI1	2	translation initiation factor 3 (eIF3)	
	YJR009C	TDH2	2	glyceraldehyde-3-phosphate dehydrogenase 2	
	YNL239W	LAP3	2	member of the GAL regulon	
	YBR249C	ARO4	2	2-dehydro-3-deoxyphosphoheptonate aldolase, tyrosine-inhibited	
	YLL024C	SSA2	6	heat shock protein of HSP70 family, cytosolic	
	YGR261C	YKS5	6	AP-3 complex subunit, beta3-adaptin, 91 KD	
	YIL107C	PFK26	6	6-phosphofructose-2-kinase, isozyme 1	
	YDL058W	USO1	6	intracellular protein transport protein	
	YMR303C	ADH2	6	alcohol dehydrogenase II	
	YGR254W	ENO1	7	enolase I (2-phosphoglycerate dehydratase)	
	YGR087C	PDC6	7	pyruvate decarboxylase 3	
	YBL075C	SSA3	7	heat shock protein of HSP70 family, cytosolic	
CELLULAR ORGANIZATION(organiz. of plasma membrane)					
	YDR345C	HXT3	1	low-affinity hexose transporter	
	YNR044W	AGA1	2	a-agglutinin anchor subunit	
	YNL239W	LAP3	2	member of the GAL regulon	
	YNL154C	YCK2	6	casein kinase I isoform	
	YER123W	YCK3	6	casein kinase, isoform 3	
	YFR009W	GCN20	7	positive effector of Gcn2p	
	YHR135C	YCK1	7	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane H+-ATPase Pma1p in vitro	
	YMR011W	HXT2	7	high-affinity hexose transporter	
	YHR096C	HXT5	7	Protein with strong similarity to hexose transporters, member of sugar permease family	
	YDR077W	SED1	7	abundant cell surface glycoprotein	
	YGR009C	SEC9	7	protein transport protein	
CELLULAR ORGANIZATION(vacuolar and lysosomal organization)					
	YJL053W	PEP8	1	vacuolar protein sorting/targeting protein	
	YPL154C	PEP4	1	aspartyl protease	
	YLR447C	VMA6	2	H+-ATPase V0 domain 36 KD subunit, vacuolar	
	YHR026W	PPA1	2	H+-ATPase 23 KD subunit, vacuolar	
	YGL006W	PMCL	6	Ca2+-transporting P-type ATPase	
	YDR495C	VPS3	6	vacuolar sorting protein	
	YEL051W	VMA8	7	H+-ATPsynthase V1 domain 32 KD subunit, vacuolar	
CELLULAR ORGANIZATION(mitochondrial organization)					
	YJR121W	ATP2	1	FlFO-ATPase complex, Fl beta subunit	
	YGR183C	QCR9	1	ubiquinol--cytochrome-c reductase subunit 9	
	YMR189W	GCY2	1	glycine decarboxylase P subunit	
	YKL141W	SDH3	2	cytochrome b560 subunit of respiratory complex II	
	YDL198C	SHM1	2	member of the mitochondrial carrier family (MCF)	
	YDR529C	QCR7	2	ubiquinol--cytochrome-c reductase subunit 7	
	YDR178W	SDH4	2	succinate dehydrogenase membrane anchor subunit for sdh2p	
	YDR377W		2	ATP synthase complex, subunit f	
ENERGY (tricarboxylic-acid pathway)					
	YDR178W	SDH4		succinate dehydrogenase membrane anchor subunit for sdh2p	succinate:ubiquinone reductase
	YFL018C	LPD1	6	dihydrolipoamide dehydrogenase precursor	
ENERGY(metabolism of energy reserves)					
	YLR258W	GSY2	6	UDP-glucose--starch glucosyltransferase, isoform 2	

UP	DOWN	LOCUS	X	DEFINITION	OBS
ENERGY(fermentation)					
	YLR044C	PDC1	2	pyruvate decarboxylase, isozyme 1;expression decreases 10-20 fold on low glucose or ethanol	
	YKR096W		6	similarity to mitochondrial aldehyde dehydrogenase Ald1p	
	YMR303C	ADH2	6	alcohol dehydrogenase II	
	YGR087C	PDC6	7	pyruvate decarboxylase 3	
ENERGY(glycolysis)					
	YJR009C	TDH2	2	glyceraldehyde-3-phosphate dehydrogenase 2	
	YGR254W	ENO1	7	enolase I (2-phosphoglycerate dehydratase)	
ENERGY(glyoxylate cycle)					
	YCR005C	CIT2	6	citrate (si)-synthase, peroxisomal	
ENERGY(pentose-phosphate)					
	YGR256W	GND2	7	phosphogluconate dehydrogenase	
ENERGY(respiration)					
	YJR121W	ATP2	1	F1F0-ATPase complex, F1 beta subunit	
	YGR183C	QCR9	1	ubiquinol--cytochrome-c reductase subunit 9	
	YLR044C	PDC1	2	pyruvate decarboxylase, isozyme 1;expression decreases 10-20 fold on low glucose or ethanol	
	YKL141W	SDH3	2	cytochrome b560 subunit of respiratory complex II	
	YDR529C	QCR7	2	ubiquinol--cytochrome-c reductase subunit 7	
	YDR178W	SDH4	2	succinate dehydrogenase membrane anchor subunit for sdh2p	
	YDR377W		2	ATP synthase complex, subunit f	
INTRACELLULAR TRANSPORT (vesicular transport (Golgi network, etc.))					
	YHR135C	YCK1	7	casein kinase I isoform;phosphorylates together with YCK2 the plasma membrane H+-ATPase Pmalp in vitro	
INTRACELLULAR TRANSPORT (cellular import)					
	YDR345C	HXT3	1	low-affinity hexose transporter	
	YLL050C	COF1	2	cofilin, actin binding and severing protein	
	YGR261C	YKS5	6	AP-3 complex subunit, beta3-adaptin, 91 KD	
	YMR011W	HXT2	7	high-affinity hexose transporter	
	YHR096C	HXT5	7	Protein with strong similarity to hexose transporters, member of sugar permease family	
INTRACELLULAR TRANSPORT (cytoskeleton-dependent transport)					
	YKL129C	MYO3	6	myosin type I	
	YBR172C	SMY2	6	kinesin-related protein	
INTRACELLULAR TRANSPORT (extracellular transport)					
	YBR162W-A	YSY6	6	secretory pathway protein	
	YGR009C	SEC9	7	protein transport protein	
INTRACELLULAR TRANSPORT (mitochondrial transport)					
	YJR121W	ATP2	1	F1F0-ATPase complex, F1 beta subunit	
	YDL198C	SHM1	2	member of the mitochondrial carrier family (MCF)	
	YLR034C		2	strong similarity to SMF2 protein(PROBABLE MANGANESE TRANSPORTER)	heavy metal transporter fam.
	YLL024C	SSA2	6	heat shock protein of HSP70 family, cytosolic	
	YLR348C	DIC1	7	dicarboxylate carrier protein	
INTRACELLULAR TRANSPORT (nuclear transport)					
	YER009W	NTF2	1	nuclear transport factor	
	YAL005C	SSA1	1	heat shock protein of HSP70 family, cytosolic	
	YLR293C	GSP1	2	GTP-binding protein of the ras superfamily	
	YIL063C	YRB2	6	involved in nuclear protein export	
	YDR432W	NPL3	6	nucleolar protein	
INTRACELLULAR TRANSPORT (other intracellular transport activities)					
	YDR086C	SSS1	6	ER protein-translocase complex subunit	
INTRACELLULAR TRANSPORT (vacuolar transport)					
	YLR447C	VMA6	2	H+-ATPase V0 domain 36 KD subunit, vacuolar	
	YGL006W	PMCL	6	Ca2+-transporting P-type ATPase	
	YEL051W	VMA8	7	H+-ATPsynthase V1 domain 32 KD subunit, vacuolar	
INTRACELLULAR TRANSPORT (vesicular transport(Golgi network, etc.))					
	YPL218W	SAR1	2	GTP-binding protein of the ARF family	guanine nucleotide exchange
	YIL109C	SEC24	2	component of COPII coat of ER-Golgi vesicles	
	YAL030W	SNC1	6	strong similarity to synaptic vesicle-associated membrane protein	
	YLL024C	SSA2	6	heat shock protein of HSP70 family, cytosolic	
	YDL058W	USO1	6	intracellular protein transport protein	
	YGR009C	SEC9	7	protein transport protein	
IONIC HOMEOSTATIS (homeostasis of other ions)					
	YJR121W	ATP2	1	F1F0-ATPase complex, F1 beta subunit	
	YLR447C	VMA6	2	H+-ATPase V0 domain 36 KD subunit, vacuolar	
	YGL006W	PMCL	6	Ca2+-transporting P-type ATPase	
	YLR348C	DIC1	7	dicarboxylate carrier protein	
	YEL051W	VMA8	7	H+-ATPsynthase V1 domain 32 KD subunit, vacuolar	
METABOLISM (aa metabolism; aa biosyn.)					
	YPR035W	GLN1	1	glutamate--ammonia ligase	
	YAL004W		1	opposite to SSA1;Protein of unknown function, probable non-coding ORF;strong similarity to A.klebsiana glutamate dehydrogenase	
	YIL074C		2	strong similarity to E.coli phosphoglycerate dehydrogenase	
	YER081W		2	strong similarity to phosphoglycerate dehydrogenases	
	YDR158W	HOM2	2	aspartate-semialdehyde dehydrogenase	
	YCR053W	THR4	2	threonine synthase (o-p-homoserine p-lyase)	
	YHR025W	THR1	2	homoserine kinase	
	YLR303W	MET25	2	O-acetylhomoserine sulfhydrylase	
	YHL011C	PRS3	2	ribose-phosphate pyrophosphokinase	
	YBR249C	ARO4	2	2-dehydro-3-deoxyphosphoheptonate aldolase, tyrosine-inhibited	
	YDR508C	GNP1	6	high-affinity glutamine permease	
	YFL018C	LPD1	6	dihydrolipoamide dehydrogenase precursor	
	YHR037W	PUT2	6	1-pyrroline-5-carboxylate dehydrogenase	

UP	DOWN	LOCUS	X	DEFINITION	OBS
METABOLISM (aa metabolism; aa degradation)					
	YMR189W	GCV2	1	glycine decarboxylase P subunit	
METABOLISM (aa metabolism; regulation of aa metab.)					
	YDR213W		7	transcriptional activator of lysine pathway genes	
METABOLISM (aa transport)					
	YDR508C	GNP1	6	high-affinity glutamine permease	
METABOLISM (metabolism of cyclic and unusual nucleotides)					
	YCL050C	APA1	2	ATP adenyllyltransferase I	
METABOLISM (nitrogen and sulfur metabolism)					
	YDR353W		1	thioredoxin reductase (NADPH)	
METABOLISM (nucleotide metabolism)					
	YER170W	ADK2	6	adenylate kinase, mitochondrial	
METABOLISM (nucleotide metabolism, deoxyribonucleotide metabolism)					
	YDR353W		1	thioredoxin reductase (NADPH)	
METABOLISM (nucleotide metabolism; pyrimidine-ribonucleotide metab.)					
	YHL011C	PRS3	2	ribose-phosphate pyrophosphokinase	
	YJL130C	URA2	2	multifunctional pyrimidine biosynthesis protein	
	YKL216W	URA1	2	dihydroorotate dehydrogenase	
METABOLISM (nucleotide metabolism; purine-ribonucleotide metab.)					
	YLR359W	ade13	1	adenylosuccinate lyase	
	YLR058C	SHM2	2	serine hydroxymethyltransferase, cytoplasmic	
	YAR015W	ADE1	2	phosphoribosylamidoimidazole-succinocarboxamide synthase	
	YHL011C	PRS3	2	ribose-phosphate pyrophosphokinase	
	YOR128C	ADE2	2	phosphoribosylaminoimidazole carboxylase	
	YMR217W	GUA1	2	GMP synthase (glutamine-hydrolyzing)	
	YKL216W	URA1	2	dihydroorotate dehydrogenase	
	YHL011C	PRS3	2	ribose-phosphate pyrophosphokinase	
	YJL130C	URA2	2	multifunctional pyrimidine biosynthesis protein	
	YPR062W		6	cytosine deaminase	
METABOLISM (other nucleotide metabolism activities)					
	YPL037C	EGD1	1	GAL4 DNA-binding enhancer protein	
METABOLISM (regulation of aa metabolism)					
	YGL202W	ARO8	2	aromatic amino acid aminotransferase I	
METABOLISM(carbohydrate metabolism and transport)					
	YMR011W	HXT2	7	high-affinity hexose transporter	
METABOLISM(carbohydrate metabolism and utilization)					
	YLR286C	CTS1	1	endochitinase	
	YLR044C	PDC1	2	pyruvate decarboxylase, isozyme 1;expression decreases 10-20 fold on low glucose or ethanol	
	YGR282C	BGL2	2	endo-beta-1,3-glucanase of the cell wall	
	YJR009C	TDH2	2	glyceraldehyde-3-phosphate dehydrogenase 2	
	YPR113W	PI51	2	CDP diacylglycerol--inositol 3-phosphatidyltransferase	
	YDL022W		2	glycerol phosphate dehydrogenase; induced by osmotic stress	
	YDR178W	SDH4	2	succinate dehydrogenase membrane anchor subunit for sdh2p	
	YNL037C	IDH1	2	isocitrate dehydrogenase (NAD+) subunit 1, mitochondrial	
	YML048W	EFF2	2	involved in glucose repression	
	YDL188C	PPH22	2	protein ser/thr phosphatase PP2A-2	
	YBR149W		2	similarity to Gcylp and aldose reductases	
	YLR258W	GSY2	6	UDP-glucose--starch glucosyltransferase, isoform 2	
	YIL107C	PFK26	6	6-phosphofructose-2-kinase, isozyme 1	
	YKR096W		6	similarity to mitochondrial aldehyde dehydrogenase Ald1p	
	YDR443C	SCA1	6	DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcomplex subunit	
	YDR176W	NGG1	6	general transcriptional adaptor or co-activator	
	YCR005C	CIT2	6	citrate (si)-synthase, peroxisomal	
	YMR303C	ADH2	6	alcohol dehydrogenase II	
	YHL025W	SNF6	7	global transcription activator	
	YGR254W	ENO1	7	enolase I (2-phosphoglycerate dehydratase)	
	YHR096C	HXT5	7	Protein with strong similarity to hexose transporters, member of sugar permease family	
	YGR087C	PDC6	7	pyruvate decarboxylase 3	
	YGR256W	GND2	7	phosphogluconate dehydrogenase	
	YLR348C	DIC1	7	dicarboxylate carrier protein	
METABOLISM( f.a.,sterol,lipid)					
	YLR058C	SHM2	2	serine hydroxymethyltransferase, cytoplasmic	
	YCL043C	PDI1	1	protein disulfide-isomerase precursor	
	YNR016C	ACC1	7	acetyl-CoA carboxylase	
	YHL020C	OPF1	7	negative regulator of phospholipid biosynthesis pathway	
METABOLISM(phosphate metabolism, regulation of phosphate utilization)					
	YFR034C	PHO4	2	transcription factor	Phosphate regulon
	YLR348C	DIC1	7	dicarboxylate carrier protein	
PROTEIN DESTINATION (protein modification; glycosylation, acylation, myristylation,etc.)					
	YPL154C	PEP4	1	aspartyl protease	
	YCL043C	PDI1	1	protein disulfide-isomerase precursor	
	YJR117W		2	zinc metallo-protease	
	YGL203C	KEX1	6	carboxypeptidase (YSC-alpha)	
	YDR390C	UBA2	6	E1-like (ubiquitin-activating) enzyme	
	YNL186W		6	derepression of telomeric silencing;predicted to encode a ubiquitin-processing protease; has similarity to UBIQUITIN C-TERMINAL HYDROLASE	
	YDR495C	VPS3	6	vacuolar sorting protein	
PROTEIN DESTINATION (proteolysis; lysosomal and vacuolar)					
	YPL154C	PEP4	1	aspartyl protease	
PROTEIN DESTINATION(assembly of protein complexes)					
	YLL050C	COF1	2	cofilin, actin binding and severing protein	
	YLR447C	VMA6	2	H+-ATPase V0 domain 36 KD subunit, vacuolar	
	YDR377W		2	ATP synthase complex, subunit f	
	YDR495C	VPS3	6	vacuolar sorting protein	

UP	DOWN	LOCUS	X	DEFINITION	OBS
	YKR048C	NAP1	6	nucleosome assembly protein I	
	YLL008W	DRS1	7	RNA helicase of the DEAD box family	
PROTEIN DESTINATION(protein folding and stabilization)					
	YAL005C	SSA1	1	heat shock protein of HSP70 family, cytosolic	
	YCL043C	PDI1	1	protein disulfide-isomerase precursor	
	YDR155C	CPH1	2	cyclophilin (peptidylprolyl isomerase)	
	YLR449W		6	strong similarity to peptidylprolyl isomerase Fpr3p	
	YML074C	NPI46	6	proline cis-trans isomerase	
	YLL024C	SSA2	6	heat shock protein of HSP70 family, cytosolic	
	YEL030W		7	heat shock protein of HSP70 family	
PROTEIN DESTINATION (proteolysis;cytoplasmic degradation)					
	YLR167W	UBI3	2	aka RPS37; UBI3;ubiquitin	
	YNL239W	LAP3	2	member of the GAL regulon	
	YDR390C	UBA2	6	E1-like (ubiquitin-activating) enzyme	
	YER098W	UBP9	6	ubiquitin carboxyl-terminal hydrolase	
	YLL039C	UBI4	7	ubiquitin;disruption of the PHO85 gene inappropriately triggers the derepression of stress response genes, HSP12 and UBI4	
PROTEIN DESTINATION(protein targeting, sorting and translocation)					
	YJL053W	PEP8	1	vacuolar protein sorting/targeting protein	
	YAL005C	SSA1	1	heat shock protein of HSP70 family, cytosolic	
	YBR162W-A	YSY6	6	secretory pathway protein	
	YDR086C	SSS1	6	ER protein-translocase complex subunit	
	YDR432W	NPL3	6	nucleolar protein	
	YDR495C	VPS3	6	vacuolar sorting protein	
PROTEIN SYNTHESIS (other protein synthesis activities)					
	YBR121C	GRS1	2	Glycyl-tRNA synthase; glycine--tRNA ligase	
PROTEIN SYNTHESIS (ribosomal protein)					
	YDL191W	SOS1	1	RPL35A	
	YDR025W	RPS18A	1	aka (RPS18A); ribosomal protein S11.e	
	YBL087C	RPL17A	1	ribosomal protein L23.e	
	YJL190C	RPS24A	1	RPS22A and RPS22B code for nearly identical proteins	
	YLR333C	RPS31	1	aka RPS31B;ribosomal protein S25.e.c12	
	YDR064W	RPS13C	2	ribosomal protein	
	YPL090C		2	ribosomal protein S6.e	
	YBR084C-A	RPL19B	2	aka YL14A; (RPL23A); (RPL19A);ribosomal protein L19.e	
	YOL127W	RPL25	2	ribosomal protein	
	YOR234C	RPL37B	2	ribosomal protein L35a.e.c15	
	YGL147C	RPL9A	2	ribosomal protein L9.e	
	YLR325C		2	putative ribosomal protein	
	YNL069C	RP23	2	aka RP23; ribosomal protein	
	YKL156W	RPS27A	2	ribosomal protein S27.e	
	YHR203C	RPS7A	2	ribosomal protein S4.e.c8	
	YPL081W		2	ribosomal protein	
	YNL178W	RPS3	2	ribosomal protein S3.e	
	YMR242C		2	ribosomal protein, duplicate=20B	
	YLR448W	RPL16B	6	cytoplasmic ribosomal large subunit	
	YOL039W	RPLA2	6	aka (RPL44); (RPA2); RPLA2;acidic ribosomal protein P2.beta	
	YJL191W	CRY2	7	ribosomal protein S14.e.B	
	YDL081C	RPLA1	7	aka;acidic ribosomal protein a1;(RPA1); L12eIIA; RPLA1;RPF1A;plays a role in the elongation step	
	YDR382W	RPL45	7	aka RPL45; YPA1; L12eIA; RPLA4; acidic ribosomal protein	
	YER117W	RPL17B	7	aka RPL20B;ribosomal protein L17.e	
	YDL184C	RPL47A	7	ribosomal protein	
PROTEIN SYNTHESIS (translational control )					
	YGR222W	PET54	6	splicing protein and translational activator, mitochondrial	
	YFR009W	GCN20	7	positive effector of Gcn2p	
PROTEIN SYNTHESIS (tRNA synthases)					
	YBL076C	ILS1	2	isoleucyl-tRNA synthetase	
PROTEIN SYNTHESIS translation(initiation, elongation, termination)					
	YJL138C	TIF2	2	translation initiation factor eIF4A	
	YKR059W	TIF1	2	translation initiation factor 4A	
	YNL244C	SUI1	2	translation initiation factor 3 (eIF3)	
	YNL014W		6	translation elongation factor eEF3 homolog	
	YNL163C		6	translation elongation factor eEF4	
	YLR249W	YEF3	7	translation elongation factor eEF3;found only in fungi	
RETROTRANSPOSONS AND PLASMID PROTEINS					
	YCL019W	TY2B	2	Ty transposon B protein;POL polyprotein	
	YNL054W	VAC7	6	TY1A protein	
	YJR026W		7	TY1A protein	
SIGNAL TRANSDUCTION (morphogenesis, key kinases)					
	YHR030C	SLT2	6	ser/thr protein kinase of MAP kinase family	
SIGNAL TRANSDUCTION (nutritional response pathway;other nutritional-response activities)					
	YPL203W		6	cAMP-dependent protein kinase 2, catalytic chain	
	YER020W	GPA2	6	guanine nucleotide-binding regulatory protein	
SIGNAL TRANSDUCTION (osmosensing)					
	YDL022W	gpd1	2	glycerol phosphate dehydrogenase; induced by osmotic stress	
	YHR030C	SLT2	6	ser/thr protein kinase of MAP kinase family	
SIGNAL TRANSDUCTION (other signal transduction activities)					
	YMR016C		7	regulatory protein in the PKA signal transduction pathway;alteration in Sok2p production affect glycogen accumulation and heat shock resistance	
SIGNAL TRANSDUCTION (pheromone response generation)					
	YDR461W	MFAL	1	mating pheromone a-factor 1	
	YDR103W	STE5	6	pheromone signal transduction pathway protein	
	YER020W	GPA2	6	guanine nucleotide-binding regulatory protein	
SIGNAL TRANSDUCTION (unspecified signal transduction; second messenger formation)					
	YDL135C	RD11	2	rho GDP dissociation inhibitor with activity toward Rho1p	
TRANSCRIPTION ( mRNA 5'-3' end processing and mRNA degradation )					

18 up and 7 down

UP	DOWN	LOCUS	X	DEFINITION	OBS
	YDR228C	PFC11	6	component of pre-mRNA 3'-end processing factor CF I	
TRANSCRIPTION ( transcriptional control )					
	YNL186W		6	derepression of telomeric silencing;predicted to encode a ubiquitin-processing protease; has similarity to UBIQUITIN C-TERMINAL HYDROLASE	
	YGL025C	PGD1	6	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;	
	YMR016C		7	regulatory protein in the PKA signal transduction pathway;alteration in Sok2p production affect glycogen accumulation and heat shock resistance	
TRANSCRIPTION ( tRNA transcription and processing )					
	YHR163W	SOL3	1	weak multicopy suppressor of los1-1	
	YDR088C	SLU7	6	pre-mRNA splicing factor affecting 3' splice site choice	
TRANSCRIPTION (mRNA transcription and splicing)					
	YKL074C	MUD2	6	pre-mRNA splicing factor	
	YGR222W	PET54	6	splicing protein and translational activator, mitochondrial	
	YER146W	LSM5	6	similarity to human snRNP E	
	YDR311W	TFB1	6	TFIIH subunit (transcription initiation factor), 75 kD	
	YDR390C	UBA2	6	E1-like (ubiquitin-activating) enzyme	
	YER172C	BRR2	6	RNA helicase-related protein	
	YDR443C	SCA1	6	DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcomplex subunit	
	YNL186W		6	derepression of telomeric silencing;predicted to encode a ubiquitin-processing protease; has similarity to UBIQUITIN C-TERMINAL HYDROLASE	
	YDR176W	NGG1	6	general transcriptional adaptor or co-activator	
	YGL025C	PGD1	6	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;	
	YBR198C	TAF90	6	TFIID subunit (TBP-associated factor), 90 kD	
	YDR213W		7	transcriptional activator of lysine pathway genes	
	YMR016C		7	regulatory protein in the PKA signal transduction pathway;alteration in Sok2p production affect glycogen accumulation and heat shock resistance	
TRANSCRIPTION (mRNA transcription, synthesis and control)					
	YPL037C	EGD1	1	GAL4 DNA-binding enhancer protein	
	YFR034C	PHO4	2	transcription factor	
	YCL054W		6	transcriptional silencing protein	
	YER161C	SPT2	6	multifunctional HMG-like chromatin protein	
	YKR072C	SIS2	6	involved in cell cycle-specific gene expression	
	YIL128W	MET18	6	involved in NER repair and RNA polymerase II transcription	
	YPL203W		6	cAMP-dependent protein kinase 2, catalytic chain	
	YDL070W	BDF2	6	similarity to bromodomain protein Bdf1p	
	YER164W		6	transcriptional regulator	
	YDR310C	SUM1	6	suppressor of SIR mutations	
	YHL025W	SNF6	7	global transcription activator	
	YHL020C	OPI1	7	negative regulator of phospholipid biosynthesis pathway	
TRANSCRIPTION (other transcription activities)					
	YDL051W	YLA1	2	RNA binding protein	
	YBR212W	NGR1	6	glucose-repressible RNA-binding protein	
TRANSCRIPTION (RNA transport)					
	YLR293C	GSP1	2	GTP-binding protein of the ras superfamily	
	YDR432W	NPL3	6	nucleolar protein	
TRANSCRIPTION (rRNA transcription, rRNA processing)					
	YMR229C	FMI1	6	processing of pre-ribosomal RNA	
	YLR059C	YNT20	6	suppressor of rna12/yme2	
	YDR432W	NPL3	6	nucleolar protein	
	YLL008W	DRS1	7	RNA helicase of the DEAD box family	
	YNL112W	DBP2	7	ATP-dependent RNA helicase of DEAD box family	
TRANSPORT FACILITATION ( other cation transporters (Na ,K ,Ca ,NH4 ,etc.))					
	YLR447C	VMA6	2	H+-ATPase V0 domain 36 KD subunit, vacuolar	
	YHR026W	PPA1	2	H+-ATPase 23 KD subunit, vacuolar	
	YGL006W	PMCL	6	Ca2+-transporting P-type ATPase	
	YEL051W	VMA8	7	H+-ATPsynthase V1 domain 32 KD subunit, vacuolar	
TRANSPORT FACILITATION (ABC transporters)					
	YNL014W		6	translation elongation factor eEF3 homolog	
	YFR009W	GCN20	7	positive effector of Gcn2p	
TRANSPORT FACILITATION (anion transport; Cl, PO4, SO4,etc.)					
	YLR348C	DIC1	7	dicarboxylate carrier protein	
TRANSPORT FACILITATION (other transporters)					
	YDR086C	SSS1	6	ER protein-translocase complex subunit	
TRANSPORT FACILITATION (transport ATPases)					
	YJR121W	ATP2	1	F1F0-ATPase complex, F1 beta subunit	
	YLR447C	VMA6	2	H+-ATPase V0 domain 36 KD subunit, vacuolar	
	YHR026W	PPA1	2	H+-ATPase 23 KD subunit, vacuolar	
	YGL006W	PMCL	6	Ca2+-transporting P-type ATPase	
	YEL051W	VMA8	7	H+-ATPsynthase V1 domain 32 KD subunit, vacuolar	
TRANSPORT FACILITATION(aa transporters)					
	YDR508C	GNP1	6	high-affinity glutamine permease	
TRANSPORT FACILITATION(sugar and carbohydrate transporters)					
	YDR345C	HXT3	1	low-affinity hexose transporter	
	YDL198C	SHM1	2	member of the mitochondrial carrier family (MCF)	
	YMR011W	HXT2	7	high-affinity hexose transporter	
	YHR096C	HXT5	7	Protein with strong similarity to hexose transporters, member of sugar permease family	
	YLR348C	DIC1	7	dicarboxylate carrier protein	

UP	DOWN	LOCUS	X	DEFINITION	OBS
					25 up and 98 down
UNCLASSIFIED					
		YDR276C		1	
		YML053C		1	
		YDR544C		1 strong similarity to subtelomeric encoded proteins	
		YBL081W		1 hypothetical protein	
		YBR134W		1 questionable ORF	
		YDR154C		1 questionable ORF	
		YGL128C		1 weak similarity to rat cysteine string protein	
		YJR115W		1 similarity to hypothetical protein YBL043w	
		YFR027W		1 hypothetical protein	
		YEL059W		2 hypothetical protein	
		YCL019W		2	
		YGR200C		2 weak similarity to rape guanine nucleotide regulatory protein	
		YDR233C		2 similarity to hypothetical protein YDR233c	
		YOR248W		2 questionable ORF	
		YDL015C		2 similarity to rat synaptic glycoprotein SC2	
		YDR209C		2 questionable ORF	
		YKL030W		2 questionable ORF	
		YHR133C		2 similarity to hypothetical protein YNL156c	
		YDR533C		2	
		YKR065C		2 hypothetical protein	
		YLR064W		2 similarity to hypothetical protein YLR064w	
		YMR002W		2 similarity to hypothetical S.pombe and C.elegans proteins	
		YHR143W		2 weak similarity to a-agglutinin core protein AGA1	
		YDR417C		2 questionable ORF	
		YIL082W-A		2 no mips info	
		YNL124W		6 similarity to hypothetical S. pombe protein	
		YEL041W		6 strong similarity to Utr1p	
		YDR486C		6 weak similarity to Snf7p	
		YKL105C		6 similarity to YMR086w	
		YOR382W		6 hypothetical protein	
		YDR296W		6 hypothetical protein	
		YML133C		6 hypothetical protein Y'.2	
		YGL020C		6 hypothetical protein	
		YLR161W		6 identical to hypothetical proteins YLR161w and YLR159w	
		YMR316W		6 similarity to YOR385w and YNL165w	
		YDR407C		6 weak similarity to Myo1p	
		YCL041C		6 questionable ORF	
		YGR130C		6 weak similarity to myosin heavy chain proteins	
		YDL189W		6 hypothetical protein	
		YPL238C		6 questionable ORF	
		YHR131C		6 similarity to hypothetical protein YNL144c	
		YLR068W		6 hypothetical protein	
		YEL033W		6 weak similarity to Sauroleishmania mitochondrial hypothetical ORF-5 protein	
		YER190W		6 strong similarity to subtelomeric encoded proteins	
		YLR003C		6 hypothetical protein	
		YLR162W		6 hypothetical protein	
		YCR016W		6 hypothetical protein	
	ARP1	YDL167C		6 protein of unknown function	
		YCR033W		6 similarity to mouse nuclear receptor co-repressor N-Cor	
		YDR496C		6 similarity to hypothetical human and C.elegans proteins	
		YIL096C		6 hypothetical protein	
		YGR069W		6 questionable ORF	
		YEL043W		6 weak similarity to Mad1p	
		YGR265W		6 questionable ORF	
		YDR413C		6 weak similarity to NADH dehydrogenase	
		YNL115C		6 weak similarity to S.pombe hypothetical protein SPAC23C11	
		YLR095C		6 hypothetical protein	
		YJL225C		6 strong similarity to members of the Sir1p/Tip1p family	
		YGR103W		6 similarity to zebrafish essential for embryonic development gene pescadillo	
		YBL046W		6 weak similarity to hypothetical protein YOR054c	
		YLR051C		6 similarity to human acidic 82 kDa protein	
		YGR272C		6 similarity to hypothetical S.pombe protein SPAC12G12.02	
		YOR309C		6 questionable orf	
		YFL034W		6 similarity to hypothetical S. pombe protein and to C.elegans F35D11 protein	
		YLR339C		6 questionable ORF	
		YDR326C		6 strong similarity to YHR080c, similarity to YFL042c and YLR072w	
		YNR025C		6 questionable ORF	
		YNL075W		6 similarity to YHR088w and C.elegans hypothetical protein F44G4.1	
		YMR014W		6 weak similarity to S.pombe hypothetical protein SPAC4F10	
		YGR163W		6 GTP-binding protein	
		YER066C-A		6 hypothetical protein	
		YDR295C		6 unknown	
		YKL225W		6 strong similarity to Gin11p, YKL225w and other subtelomeric encoded proteins	
		YDR230W		6 questionable ORF	
		YNL170W		6 questionable ORF	
		YCR030C		6 weak similarity to S.pombe hypothetical protein SPBC4C3.06	
		YIL019W		6 weak similarity to S.pombe hypothetical protein SPAC3F10	
	UBP7	YIL156W		6 questionable ORF	
		YNL217W		6 weak similarity to E.coli bis(5'-nucleosyl)-tetrphosphatase	
		YHR177W		6 weak similarity to Spombe pac2 protein	
		YIL152W		6 hypothetical protein	
		YKR033C		6 questionable ORF	
		YFL067W		6 similarity to mouse period clock protein	

UP	DOWN	LOCUS	X	DEFINITION	OBS
	YPL027W		6	hypothetical protein	
	YJL019W		6	hypothetical protein	
	YHL050C		6	strong similarity to subtelomeric encoded proteins	
	YDR104C		7	hypothetical protein	
	YKR078W		7	similarity to Vps5p	
	YBL113C		7	Y' short ORF no intron	
	YDR316W		7	putative methyltransferase	
	YHR095W		7	hypothetical protein	
	YER106W		7	hypothetical protein	
	YMR251W		7	strong similarity to YKR076w and YGR154c	
	YDR365C		7	weak similarity to Streptococcus M protein	
	YGR017W		7	hypothetical protein	
	YFL023W		7	similarity to repeat structures in a Plasmodium falciparum protein (MESA) that binds human erythrocyte	
	YNL120C		7	questionable ORF	
	YOR359W		7	hypothetical protein	
	YKR040C		7	questionable ORF	
	YDR412W		7	questionable ORF	
	YDR398W		7	similarity to human KIAA0007 gene	
	YGR296W		7	strong similarity to subtelomeric encoded proteins	
	YNL187W		7	hypothetical protein	
	YHR214W-A		7	strong similarity to hypothetical protein YAR068w	
	YHR219W		7	strong similarity to subtelomeric encoded proteins	
	YNL179C		7	hypothetical protein	
	YLR334C		7	questionable orf	
	YLR467W		7	strong similarity to subtelomeric encoded proteins	
	YLR466W		7	protein of unknown function	
	YNL013C		7	questionable orf	
	YBR190W		7	questionable ORF	
	YFR008W		7	weak similarity to human centromere protein E	
	YMR290W-A		7	questionable ORF	
	YHR126C		7	hypothetical protein	
	YER181C		7	questionable ORF	
	YAR010C		6	no info	
	YML045W		6	no info	
	YCRX05W		6	no info	
	YIR043C		6	no info	
	YFR001W		6	weak similarity to rabbit triadin Spp41p	
	YMR046C		7	no info	
	YKL082C		7	weak similarity to C.elegans hypothetical protein	
	YCRX16C		7	no info	
CLASSIFICATION NOT YET CLEAR-CUT					
	YEL026W		2	strong similarity to high mobility group-like protein Nhp2p	
	YOL030W				transglycosylation in cell wall?
	YMR099C		2	similarity to P.ciliare possible apospory-associated protein	
	YGR279C		2	glucanase gene family member	
	YGR262C		7	ser/thr protein kinase	