TABLES.CHR2_ORFS.TXT

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NOTE: Please set terminal width to 132 characters/line and edit (VMS eve) to read properly !!!!

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The content of this file is part of the data unraveled by a consortium of European laboratories supported by the Commission of the European Union in the framework of sequencing yeast chromosome II.

H. Feldmann et al. (1994) ' Complete sequence of yeast chromosome II', submitted

The dataset was developed in collaboration of
H.W. Mewes
Martinsried Institute for Protein Sequences (MIPS)
Max-Planck-Institut fuer Biochemie, 85152 Martinsried, Germany
Telephone:+49 89 8578 2656 FAX +49 89 8578 2655
e-mail mewes@ehpmic.mips.biochem.mpg.de
e-mail mewes@mips.embnet.org
and
Horst Feldmann
Institut fuer Physiologische Chemie, Universitaet Muenchen,
Schillerstrasse 44, 80336 Muenchen, Germany
Telephone:+49 89 5996 451 FAX +49 89 5996 316
e-mail feldmann@dec1.bio.med.uni-muenchen.de

>>> The data may be used for scientific purposes under the condition that the proper reference is given. <<<

We have made every effort to ensure liability of the data and cannot be responsible for the consequences to users of any errors resulting from its use.

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Table 3. Yeast chromosome II: Open reading frames

System. ORF nomencl.	MIPS working nomencl.	Coordinates begin	end	ORF length	Gene name	Function	Put. TM spans
YBL108w	YBL0801w	2223	2525	101		/ Homolog to YKL223w; YCR103c /	

YBL107c	YBL0805c	4010	4597	196			
YBL106c	YBL0806c	4896	7925	1010		Probable ß-transducin, mouse mgl1 homolog	5
YBL105c	YBL0807c	8290	11742	1151	PKC1	Protein kinase-C like protein, ser/thr-specific (EC 2.7.1.37)	2
YBL104c	YBL0808c	12366	15140	925			1
YBL103c	YBL0810c	16628	17575	316		Probable cytochrome c subunit, copper binding	
YBL102w	YBL0812	18138	18782	215			4
YBL101c	YBL0814c	18989	22219	1077			
YBL000	YBL0821w	23968	25281	438	TY2A		
YBL000	YBL0822w	23968	29278	1770t	TY2B		
YBL100c	YBL0826c ov	31025	31336	104			2
YBL099w	YBL0827w	31086	32720	545	ATP1	Mitochondrial ATPase, alpha chain precursor (EC 3.6.1.34)	
YBL098w	YBL0828w	33178	34557	460			2
YBL097w	YBL0830w	34944	37127	728			
YBL096c	YBL0834c ov	37212	37517	102			2
YBL095w	YBL0835w	37312	38121	270			2
YBL094c	YBL0836c ov	37803	38132	110			2
YBL093c	YBL0837c	38294	38953	220	ROX3	Essential nuclear protein involved in CYC7 expression	
YBL092w	YBL0838w	40013	40402	130i	[RPL32.e]	Probable ribosomal protein L32.e	
YBL091c	YBL0701c	41401	42447	349		Probable IF2-associated glycoprotein	
YBL090w	YBL0702w	42860	43390	177§			
YBL089w	YBL0703w	43459	44985	509§			10
YBL088c	YBL0706c	45057	53417	2787		Probable phosphatidylinositol kinase, homolog of DRR1 (S. cerevisiae)	10
YBL087c	YBL0713c	53859	54773	137i	RPL17A	Probable ribosomal protein L23.e or YL17a	
YBL086c	YBL0714c	55240	56637	466			
YBL085w	YBL0717w	57911	60850	980	BOB1	BEM1-binding protein	
YBL084c	YBL0718c	61207	63480	758	CDC27	Cell division control protein CDC27	
YBL083c	YBL0719c ov	63751	64173	141			
YBL082c	YBL0720c	63789	65162	458			10
YBL081w	YBL0722w	65901	67004	368			
YBL080c	YBL0724c	67108	68730	541	PET112	Factor essential for maintenance of rho+ mitochondrial DNA	1
YBL079w	YBL0725w	69294	73799	1502			6
YBL078c	YBL0732c	74416	74766	117			
YBL077w	YBL0733w ov	74933	75361	143			
YBL076c	YBL0734c	75082	78297	1072	ILS1	Isoleucyl tRNA synthetase (EC 6.1.1.5)	
YBL075c	YBL0610c	78538	80484	649	SSA3	Heat shock protein, 70 kDa	
YBL074c	YBL0611c	80761	81825	355	AAR2	MATa1-mRNA splicing factor	
YBL073w	YBL0612w ov	81682	81990	103			2
YBL072c	YBL0613c	82562	83161	200i	RPS8	Ribosomal protein S8.e	
YBL071c	YBL0615c	84262	84567	102			1
YBL070c	YBL0616c ov	84644	84961	106			3
YBL069w	YBL0617w	84777	85760	328		/ Homology to quinone oxidoreductase (E. coli) /	

YBL068w YBL0619w	86367	87431	355	[PRPS3]	Probable ribose-phosphate pyrophosphokinase	1
YBL067c YBL0621c	87859	89922	688			
YBL066c YBL0501c	90948	94118	1057		Probable regulatory Zn-finger protein	3
YBL065w YBL0502w ov	93966	94307	114			2
YBL064c YBL0503c	94377	95159	261		Homolog to thiol-specific antioxidant	
YBL063w YBL0504w	95889	99221	1111	KIP1	Kinesin-related protein	
YBL062w YBL0505w ov	99311	99688	126			2
YBL061c YBL0506c	99322	101409	696	SKT5	Probable Ca++ binding membrane protein (prenylated)	
YBL060w YBL0507w	101935	103995	687			
YBL059w YBL0508w	104597	105247	193i			2
YBL058w YBL0509w	105440	106708	423			
YBL057c YBL0510c	106807	107448	214			
YBL056w YBL0511w	107766	109169	468		Probable phosphoprotein (ser/thr) phosphatase	
YBL055c YBL0512c	109580	110833	418			
YBL054w YBL0513w	111593	113167	525		Homolog to myb transforming proteins	
YBL053w YBL0514w ov	113339	113710	124			1
YBL052c YBL0515c	113386	115878	831		/ Homology to human HLA-associated protein I /	
YBL051c YBL0516c	116760	118763	668		/ Homology to RNP-binding proteins /	
YBL050w YBL0517w	119129	120120	292i	SEC17	Transport vesicle fusion protein (SNAP protein)	
YBL049w YBL0518w	120832	121245	138§			
YBL048w YBL0519w	121303	121611	103§			3
YBL047c YBL0520c	121902	126044	1381		USO1 homolog (S. cerevisiae), cytoskeletal-related transport protein, Ca++ binding	1
YBL046w YBL0402w	126428	127750	441			
YBL045c YBL0403c	128150	129520	457	COR1	Ubiquinol-cytochrome c reductase (EC 1.10.2.2)	
YBL044w YBL0404w	130002	130367	122			
YBL043w YBL0405w	130692	131462	257			
YBL042c YBL0406c	132348	134264	639		Homolog to FUR4 , uracil transport protein (S.cerevisiae)	12
YBL041w YBL0407w	135251	135973	241	PRS3	Proteasome subunit 3 (multicatalytic endopeptidase complex, EC 3.4.99.46)	
YBL040c YBL0408c	136119	136872	219i	ERD2	ER lumen protein retaining receptor	6
YBL039c YBL0410c	137996	139732	579	URA7	Cytidine triphosphate synthase (EC 6.3.4.2)	3
YBL038w YBL0411w	140191	140886	232	[MRPL16]	Probable mitochondrial ribosomal protein L16	
YBL037w YBL0412w	141213	144287	1025		/ Homology to mouse alpha adaptin protein(s) /	4
YBL036c YBL0413c	144454	145224	257		Homolog to twitching motility protein (P. aeroginosa)	
YBL035c YBL0414c	145500	147614	705		/ Homology to human DNA polymerase alpha, chain B /	1
YBL034c YBL0416c	147855	152393	1513			
YBL033c YBL0417c	152663	153697	345	[RIB1]	Probable GTP cyclohydrolase II	
YBL032w YBL0418w	154188	155330	381			
YBL031w YBL0420w	155703	156716	338			
YBL030c YBL0421c	157048	158001	318	AAC2	Mitochondrial ATP/ADP carrier	4
YBL029w YBL0423w	160138	161265	376			

YBL028c	YBL0424c	161525	161842	106			
YBL027w	YBL0425w	162427	163377	189i	RPL19	Ribosomal protein L19.e	
YBL026w	YBL0425aw	164627	165039	95i		Probable snRNP-related protein	
YBL025w	YBL0426w	165485	165919	145			
YBL024w	YBL0437w	166538	168589	684		Probable proliferating-cell nucleolar antigen (human p120)	
YBL023c	YBL0438c	168927	171530	868	MCM2	Minichromosome maintenance protein, transcription factor	
YBL022c	YBL0440c	171881	175279	1133	PIM1	Mitochondrial ATP-dependent lon-like serine proteinase precursor	
YBL021c	YBL0441c	175667	176098	144	HAP3	Nuclear factor regulating respiratory and catabolite genes	
YBL020w	YBL0442w	176405	178126	574		/ Homology to AP endonuclease /	12
YBL019w	YBL0443w	178357	179916	520			1
YBL018c	YBL0301c	180005	180478	133i§			
YBL017c	YBL0302c	180851	185587	1579	PEP1	Carboxypeptidase Y sorting precursor (transmembrane protein)	3
YBL016w	YBL0303w	186455	187513	353	FUS3	Protein kinase with a positive role in the cell cycle and in cell fusion (EC 2.7.1.-)	
YBL015w	YBL0304w	188126	189703	526	ACH1	Acetyl-CoA hydrolase (EC 3.1.2.1)	
YBL014c	YBL0311c	193071	195752	894			
YBL013w	YBL0313w	196060	197238	393		Probable met-tRNA formyltransferase, mitochondrial	
YBL012c	YBL0314c ov	197412	197810	133			2
YBL011w	YBL0315w	197541	199817	759		/ Homolog to YKR067w /	3-6
YBL010c	YBL0316c	200113	200952	280			
YBL009w	YBL0317w	201197	203224	676			
YBL008w	YBL0318w	203656	206175	840	HIR1	Regulator of histone gene transcription	
YBL007c	YBL0321c	206638	210369	1244	SLA1	Cytoskeleton assembly control protein	
YBL006c	YBL0322c	210699	211133	145			
YBL005w	YBL0323w	211474	214401	976	PDR3	Pleiotropic drug resistance protein 3	2
YBL000	YBL0324w	215334	216653	440	TY1A		
YBL000	YBL0325w	215334	220599	1755t	TY1B		
YBL004w	YBL0101w	221640	229118	2493			12
YBL003c	YBL0103c	229401	229796	132	HTA2	Histone H2A.2	
YBL002w	YBL0104w	230496	230888	131	HTB2	Histone H2B.2	
YBL001c	YBL0105c	231159	231470	104			
YBR001c	YBR0106c	232947	235286	780	NTH2	a,a-trehalase (EC 3.2.1.28)	
YBR002c	YBR0107c	235714	236571	286			
YBR003w	YBR0109w	236812	238230	473	COQ1	Hexaprenyl-pyrophosphate synthase precursor (EC 2.5.1.33)	
YBR004c	YBR0110c	238372	239670	433			8
YBR005w	YBR0111w	239909	240547	213			1
YBR006w	YBR0112w	241013	242317	435		Probable aldehyde dehydrogenase (EC 1.2.1.-)	
YBR007c	YBR0113c	242811	245018	736			
YBR008c	YBR0120c	246568	248211	548		Probable benomyl/methotrexate resistance protein	13
YBR009c	YBR0122c	249375	249683	103	HHF1	Histone H4	
YBR010w	YBR0201w	250330	250737	136	HHT1	Histone H3	
YBR011c	YBR0202c	251114	251974	287	IPP1	Inorganic pyrophosphatase (EC 3.6.1.1)	

YBR012c	YBR0205c	253149	253565	139			
YBR000	YBR0206w	253868	255187	440	TY1A		
YBR000	YBR0207w	253868	259136	1756t	TY1B		
YBR013c	YBR0209c	259494	259880	129			1
YBR014c	YBR0219c	260729	261337	203		Glutaredoxin homolog	1
YBR015c	YBR0220c	261714	263504	597	TPP1	'Type II transmembrane protein'	1-3
YBR016w	YBR0222w	264248	264631	128			1
YBR017c	YBR0224c	264951	267704	918		/ Homology to GCN1 (S. cerevisiae), ATP-binding /	
YBR018c	YBR0226c	268431	269528	366	GAL7	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12) 1	
YBR019c	YBR0301c	270257	272353	699	GAL10	UDP-glucose-4-epimerase (EC 5.1.3.2)	
YBR020w	YBR0302w	273022	274605	528	GAL1	Galactokinase (EC 2.7.1.6)	3
YBR021w	YBR0303w	275444	277342	633	FUR4	Uracil transport protein	10-12
YBR022w	YBR0304w	277739	278269	177			
YBR023c	YBR0305c	278432	281926	1165	CHS3	Chitin synthase 3 (EC 2.4.1.16) 8	
YBR024w	YBR0308w	283446	284348	301	[SCO2]	SCO1 protein homolog (S. cerevisiae)	
YBR025c	YBR0309c	284685	285866	394		Probable purine nucleotide-binding protein	
YBR026c	YBR0310c	286881	288020	380§	[MRF1]	Probable (mitochondrial) ssDNA-binding protein	
YBR027c	YBR0311c	288028	288357	110			2
YBR028c	YBR0312c	288429	290003	525		Probable ser/thr-specific protein kinase, homolog to YKR2 and YPK1 (S. cerevisiae)	
YBR029c	YBR0313c	290373	291743	457		/ Homology to cytochrome c oxidase (T. brucei) /	6
YBR030w	YBR0314w	292293	293948	552		/ Homology to SIN3 (S. cerevisiae) (weak) /	
YBR031w	YBR0315w	294167	295252	362	RPL2	Ribosomal protein L2.A	
YBR032w	YBR0317w	295520	295819	100			
YBR033w	YBR0318w	295945	298701	919		Probable regulatory Zn-finger protein, / homolog to YKL251/	5
YBR034c	YBR0320c	298934	299977	348	ODP1	ORF distal from PDX3	1
YBR035c	YBR0321c	300273	300956	228	PDX3	Pyridoxamine-phosphate oxidase (EC 1.4.3.5)	
YBR036c	YBR0404c	303085	304314	410	CSG2	Ca2++ -dependent regulatory protein	10
YBR037c	YBR0406c	304568	305452	295	SCO1	Cytochrome oxidase assembly protein precursor	1
YBR038w	YBR0407w	305898	308786	963	CHS2	Chitin synthase 2 (EC 2.4.1.16)	8
YBR039w	YBR0408w	309576	310508	311	ATP3	Probable H+ -transporting ATPase / Homolog to bovine F(1)-ATPase gamma chain /	
YBR040w	YBR0410w	310969	311862	298			5
YBR041w	YBR0411w	312267	314135	623		Probable AMP-binding protein	4
YBR042c	YBR0412c	314422	315612	397		Probable membrane-bound small GTPase	4
YBR043c	YBR0413c	315882	317948	689		/ Homology to benomyl/methotrexate resistance protein /	11
YBR044c	YBR0414c	318343	320061	573		/ Homology to mitochondrial chaperonin hsp60 /	1
YBR045c	YBR0420c	322375	324093	573			
YBR046c	YBR0421c	324511	325512	334		Homolog to quinone oxidoreductase (E. coli)	2
YBR047w	YBR0422w	325834	326358	175			
YBR048w	YBR0501w	326832	327813	156i	RPS18B	Ribosomal protein S11.e.B	
YBR049c	YBR0502c	328390	330819	810	REB1	DNA-binding regulatory protein	

YBR050c YBR0504c	331187	332200	338			
YBR051w YBR0504awo	331989	332336	116			3
YBR052c YBR0505c	332724	333353	210		Homolog to YCR004, obr1 (S. pombe), trp repressor binding protein (E. coli)	
YBR053c YBR0506c	333679	334752	358			
YBR054w YBR0507w	337102	338133	344	[YRO2]	Homolog to HSP30 heat shock protein YRO1 (S. cerevisiae)	7
YBR055c YBR0508c	338606	341302	899	PRP6	Pre-mRNA splicing factor	
YBR056w YBR0510w	341880	343382	501§		Homolog to glucan-1,3-ß-glucosidase (EC 3.2.1.5; S. cerevisiae)	2
YBR057c YBR0514c	346197	347294	366			
YBR058c YBR0515c	347676	350084	803		/ Homology to human transforming protein (weak) /	
YBR059c YBR0519c	350865	354188	1108		Probable protein kinase	
YBR060c YBR0523c	354656	356515	620	RRR1	Origin recognition complex, 72 kDa subunit	
YBR061c YBR0527c	358791	359720	310		Homolog to ftsJ protein (E. coli) , / YCR054 /	
YBR062c YBR0528c	359980	360324	115			
YBR063c YBR0610c	360975	362186	404		Probable phosphopanthethein-binding protein	1
YBR064w YBR0612w ov	361765	362190	142			3
YBR065c YBR0614c	362589	363680	364			
YBR066c YBR0616c	364042	364701	220		Probable Zn-finger protein	
YBR067c YBR0622c	366107	366736	210	TIP1	Temp. shock-inducible protein precursor SRP1/TIP1	1-2
YBR068c YBR0629c	367865	369691	609		Probable amino acid transport protein	12
YBR069c YBR0710c	370578	372434	619		Probable amino acid transport protein	12
YBR070c YBR0711c	373224	373934	237			3
YBR071w YBR0712w	374411	375043	211			
YBR072w YBR0714w	376030	376671	214	HSP26	Heat shock protein, 30 kDa	
YBR073w YBR0715w	377110	379983	958		Probable RAD protein (S. cerevisiae), DNA repair helicase	3
YBR074w YBR0718w	380284	381522	413		Homolog to aminopeptidase Y (S. cerevisiae)	3
YBR075w YBR0719w	381834	383213	460			3
YBR076w YBR0722w	384374	385390	339			
YBR077c YBR0723c	385807	386292	162			1
YBR078w YBR0727w	387123	388130	226i§		Homolog to sporulation specific protein SPS2 (S. cerevisiae)	
YBR079c YBR0734c	389391	392282	964			
YBR080c YBR0736c	392622	394895	758	SEC18	Vesicular fusion protein	
YBR081c YBR0739c	395261	399256	1332	SPT7	Probable transcription factor, suppressor of Ty transcription	
YBR082c YBR0745c	400636	401128	148i	UBC4	Ubiquitin conjugating enzyme E2, 16 kD subunit (EC 6.2.3.19)	
YBR083w YBR0750w	403174	404631	486	TEC1	Ty transcription activator	
YBR084w YBR0751w	405059	407983	975	MIS1	C1-tetrahydrofolate synthase precursor, mitochondrial	6
YBR085w YBR0753w	409988	410908	307	AAC3	Mitochondrial ATP/ADP carrier	4
YBR086c YBR0809c	414209	417046	946		Probable transmembrane protein	7-9
YBR087w YBR0810w	417770	418831	354		Replication factor RFC3 homolog	3
YBR088c YBR0811c	418998	419771	258	POL30	Proliferating cell nuclear antigen	
YBR089w YBR0811awo	419188	419784	199			2
YBR090c YBR0811bc	420382	421062	108i			1

YBR091c	YBR0812c	421162	421488	109	MRS5	Nuclear protein involved in mitochondrial intron splicing
YBR092c	YBR0813c	421705	423105	467	PHO3	Acidic phosphatase, constitutive (EC 3.1.3.2)
YBR093c	YBR0814c	423555	424955	467	PHO5	Acidic phosphatase, repressible (EC 3.1.3.2)
YBR094w	YBR0821w	426040	428298	753		/ Homology to porcine tubulin-tyrosine ligase /
YBR095c	YBR0822c	428413	429771	453		/ Homology to cyclin B /
YBR096w	YBR0824w	430025	430714	230		
YBR097w	YBR0825w	430955	435316	1454	VPS15	Protein kinase essential for delivery of hydrolases to the vacuole 8
YBR098w	YBR0826w	435519	436931	471		/ Homology to clathrin , heavy chain /
YBR099c	YBR0828c ov	436932	437312	127		3
YBR100w	YBR0829w	437257	437592	112		
YBR101c	YBR0830c	437829	438698	290		/Homology to Ytb/rab interacting protein /
YBR102c	YBR0831c	439070	441328	753		/ Homology to myosin-like protein MLP1 / 1
YBR103w	YBR0832w	441714	443318	535		/ Homology to human LIS-1 protein, C-type lectin / 1
YBR104w	YBR0833w	443672	444658	329	[YMC2]	Mitochondrial carrier protein 4
YBR105c	YBR0834c	444889	445974	362		
YBR106w	YBR0835w	446663	447226	188		
YBR107c	YBR0836c	447801	448535	245		/ Homology to chitin synthase /
YBR108w	YBR0901w	448827	451370	848		Probable transcription factor
YBR109c	YBR0904c	451926	452366	147	CMD1	Calmodulin
YBR110w	YBR0906w	452876	454222	449	ALG1	a-Mannosyltransferase (EC 2.4.1.-) 4
YBR111c	YBR0907c	455185	455877	231	[YSA1]	Homolog to serendipity protein (D. melanogaster)
YBR112c	YBR0908c	456877	459774	966	SSN6	Transcription regulatory protein
YBR113w	YBR0908ewo	459570	460049	160		3
YBR114w	YBR0909w	461252	463621	790	RAD16	Radiation repair protein, putative DNA helicase
YBR115c	YBR0910c	463755	467930	1392	LYS2	a-Aminoadipate reductase (EC 1.2.1.31) 3
YBR116c	YBR0911c ov	468206	468730	175§		2
YBR117c	YBR0912c	468399	470441	681	TKL2	Transketolase 2 (EC 2.2.1.1)
YBR118w	YBR0913w	471675	473048	458	TEF2	Translational elongation factor alpha-1 2
YBR119w	YBR0915w	473342	474324	298i	MUD1	U1snRNP-specific A protein
YBR120c	YBR0916c	474442	474927	162	CBP6	Cytochrome B pre-mRNA processing protein 6
YBR121c	YBR0917c	475371	477371	667	[GRS1]	Probable glycyl-tRNA synthase (EC 2.7.7.6)
YBR122c	YBR0918c	477977	478564	196	MRPL36	Mitochondrial ribosomal protein YmL36
YBR123c	YBR0919c	478749	480695	649	TFC1	Transcription factor TFIIIC, 95 kDa subunit
YBR124w	YBR0920bwo	480511	480867	119		3
YBR125c	YBR0921c	481206	482384	393		Probable phosphoprotein phosphatase (EC 3.1.3.16)
YBR126c	YBR0922c	482912	484396	495	CIF1	a,a-trehalose-phosphate synthase (EC 2.4.1.15) TPS1
YBR127c	YBR1002c	485276	486826	517	ATPvs	H+-transporting ATPase, vacuolar (EC 3.6.1.35)
YBR128c	YBR1003c	487088	488119	344		
YBR129c	YBR1004c	488360	489343	328		
YBR130c	YBR1005c	489599	490873	425		
YBR131w	YBR1006w	491167	493278	704		3

YBR132c	YBR1007c	493659	495446	596	Probable amino acid transport protein	12
YBR133c	YBR1008c	495811	498291	827	/ Homology to DUR1,2 (S. cerevisiae) /	3
YBR134w	YBR1010wov	498247	498645	133		
YBR135w	YBR1011w	498858	499307	150 CKS1	CDC28 kinase complex, regulatory subunit	
YBR136w	YBR1012w	499672	506775	2368	Probable phosphoinosityl PI3 kinase, TOR2 homolog	9
YBR137w	YBR1013w	507048	507584	179		
YBR138c	YBR1014c	507769	509340	524		
YBR139w	YBR1015w	509668	511191	508	Probable serine-type carboxypeptidase (EC 3.4.16.1)	1
YBR140c	YBR1016c	511357	520632	3092 IRA1	GTPase-activating protein of the RAS-cAMP pathway	21
YBR141c	YBR1118c	521032	522042	337		
YBR142w	YBR1119w	522321	524639	773	Probable pre-mRNA splicing RNA-helicase	
YBR143c	YBR1120c	524876	526186	437 SUP1	Ominipotent suppressor protein of nonsense codons	
YBR144c	YBR1121c	527242	527553	104		1
YBR145w	YBR1122w	527766	528818	351 [ADH5]	Alcohol dehydrogenase (EC 1.1.1.1)	
YBR146w	YBR1123w	529264	530097	278 [MRPS9]	Probable mitochondrial ribosomal protein S9	
YBR147w	YBR1124w	530579	531466	296		7
YBR148w	YBR1125w	531880	533706	609		
YBR149w	YBR1127w	533991	535022	344	Probable aldehyde reductase (EC 1.1.1.21)	
YBR150c	YBR1133c	535216	538497	1094	Probable Zn-finger protein	4
YBR151w	YBR1201w	539032	539979	316		
YBR152w	YBR1202w	540380	541252	291		
YBR153w	YBR1203w	541464	542195	244 [RIB7]	Riboflavin biosynthesis protein	
YBR154c	YBR1204c	542369	543013	215 RPB5	RNA polymerases I,II, and III, 27 kDa subunit (ABC27) (EC 2.7.7.6)	
YBR155w	YBR1205w	543775	544929	385	Stress-inducible riboflavin biosynthetic protein homolog	
YBR156c	YBR1206c	545111	547204	698		
YBR157c	YBR1207c	547996	548313	106		
YBR158w	YBR1208w	550552	552198	549	/ Homology to CNTF receptor alpha (C. elegans) /	
YBR159w	YBR1209w	552688	553728	347	/ Homology to 17-ß hydroxysteroid dehydrogenase /	4
YBR160w	YBR1211w	554081	554974	298 CDC28	Cell division control protein (EC2.7.1.-), p34/cdc2+ protein equivalent	
YBR161w	YBR1212w	555638	556765	376	Homolog to suppressor of reduced viability of starvation (SUR1, S. cerevisiae)	2
YBR162c	YBR1213c	557210	558574	455		1
YBR163w	YBR1215w	559727	561481	585§	/ Homology to pre-tRNA processing factor PTA1 (S. cerevisiae) /	
YBR164c	YBR1216c	561882	562430	183 ARF3	GTP-binding ADP-ribosylation factor	3
YBR165w	YBR1217w	562856	563686	277§		1
YBR166c	YBR1218c	563849	565204	452 TYR1	Prephenate dehydrogenase (NADP+) (EC 1.3.1.13)	
YBR167c	YBR1219c	565475	565894	140		
YBR168w	YBR1220w	566375	567613	413		4
YBR169c	YBR1221c	567922	570000	693 SSE2	Heat-shock protein, 70 kDa	
YBR170c	YBR1231c	570351	572090	580 NPL4	Suppressor of SEC63 (S.cerevisiae), novel ER translocation component	

YBR171w YBR1232w	572368	572985	206	HSS1	ER translocation complex subunit SEC66	2
YBR172c YBR1233c	573157	575526	790	SMY2	Kinesin-related protein suppressing myosin defects (MYO2)	
YBR173c YBR1234c	575733	576176	148			
YBR174c YBR1236c ov	576345	576656	104			
YBR175w YBR1237w	576412	577356	315		Probable GTP-binding protein	
YBR176w YBR1238w	577724	578659	312		Probable 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	
YBR177c YBR1239c	578814	580166	451		Probable membrane receptor	
YBR178w YBR1240w ov	580075	580446	124			1
YBR179c YBR1241c	580554	583118	855		Probable purine nucleotide-binding protein	2
YBR180w YBR1242w	583745	585460	572		Probable resistance protein	12
YBR181c YBR1244c	585719	586778	236i	RPS101	Ribosomal protein S6.e	
YBR182c YBR1245c	587513	588868	452		Probable DNA-binding transcription factor, Homolog to SRF/SL-2	1
YBR183w YBR1305w	590119	591066	316		/ Homology to lic-1 protein (H. influenzae) /	6
YBR184w YBR1306w	591367	592935	523			
YBR185c YBR1307c	593130	593963	278			
YBR186w YBR1308w	594557	596164	536		Probable ATP-binding protein, YTA1 related protein	3
YBR187w YBR1310w	596638	597477	280		Probable membrane protein	6
YBR188c YBR1316c	597692	598111	140			
YBR189w YBR1317w	598512	599509	195i	SUP46	Suppressor, ribosomal protein S13	
YBR190w YBR1318w	599970	600278	103		/ Homology to glycosyl hydrolases /	
YBR191w YBR1401w	600274	601141	160i	URP1	Ribosomal protein L21.e	
YBR192w YBR1402w	601656	602786	377	RIM2	Probable carrier protein, mitochondrial	
YBR193c YBR1403c	603089	603757	223			
YBR194w YBR1405w	604042	604410	123			
YBR195c YBR1406c	604621	605886	422	MSI1	Multicopy suppressor of IRA1, probable ß-transducin type	
YBR196c YBR1407c	606243	607904	554	PGI1	Phosphoglucose isomerase (EC 5.3.1.9)	
YBR197c YBR1410c	609210	609860	217			
YBR198c YBR1411c	610134	612527	798		Probable transcription-associated factor protein, probable ß-transducin type	2
YBR199w YBR1412w	612913	614304	464	KTR4	a-1,2-mannosyltransferase homolog	1
YBR200w YBR1413w	614876	616528	551	BEM1	Bud emergence mediator	1
YBR201w YBR1414w	617792	618214	141			2
YBR202w YBR1441w	619777	622311	845		MCM3 protein homolog (S. cerevisiae)	
YBR203w YBR1443w	623173	625944	924			
YBR204c YBR1444c	626262	627386	375		Probable serine-active lipase, peroxisomal (EX 3.1.1.-)	2
YBR205w YBR1445w	627627	628838	404	[KTR3]	a-1,2-mannosyltransferase homolog	1
YBR206w YBR1447w ov	628606	628926	107			1
YBR207w YBR1448w	629151	630545	465		Probable membrane protein	5
YBR208c YBR1449c	630711	636215	1835	DUR1,2	Urea carboxylase (EC 6.3.4.6)	6
YBR209w YBR1451w	636588	636902	105			1
YBR210w YBR1457w	639555	639980	142			3

YBR211c YBR1458c	640166	641137	324		/ Homology to PEP3 protein (S. cerevisiae) /	
YBR212w YBR1459w	641891	643906	672	RBP1	RNA-binding protein, negative growth regulatory protein NGR1	
YBR213w YBR1461w	644373	645194	274	MET8	Effector in the expression of PAPS reductase and sulfite reductase	
YBR214w YBR1501w	645420	647000	527			
YBR215w YBR1503w	647451	649319	623§	HPC2	Cell-cycle regulatory protein, Regulator of S-phase transcription of histone genes	
YBR216c YBR1505c	649584	651605	674			2
YBR217w YBR1506w	651837	652394	186			1
YBR218c YBR1507c	652715	656254	1180	PYC2	Pyruvate carboxylase 2 (EC 6.4.1.1)	
YBR219c YBR1509c ov	656507	657308	127i§			3
YBR220c YBR1510c	657003	658682	560		/ Homolog to E. coli ampG protein /	10
YBR221c YBR1511c	659161	660258	366	PDB1	Pyruvate dehydrogenase (lipoamide), ß chain precursor (EC 1.2.4.1)	
YBR222c YBR1512c	660728	662356	543		Probable AMP-binding protein	3
YBR223c YBR1520c	662671	664302	544			
YBR224w YBR1521w ov	664130	664642	171			5
YBR225w YBR1522w	664632	667331	900			
YBR226c YBR1523c ov	667163	667570	136§			
YBR227c YBR1524c	667580	669139	520§		Homolog to ATP-binding protein clpX (E.coli)	3
YBR228w YBR1525w	669318	670229	304			
YBR229c YBR1526c	670365	673226	954		Homolog to 1,4-a-glucosidase (S.cerevisiae) (EC 3.2.1.3)	3
YBR230c YBR1527c	673557	674055	134i§			2
YBR231c YBR1529c	676187	677095	303			
YBR232c YBR1530c ov	677381	677737	119			3
YBR233w YBR1531w	677433	678671	413		Homolog to human hnRNP complex K protein	
YBR234c YBR1532c	679446	680597	384		/ Homology to MAK11 protein (S. cerevisiae) /	
YBR235w YBR1601w	680906	684265	1120			13
YBR236c YBR1602c	684391	685698	436	ABD1	Protein with mutational synergism related to BEM1	
YBR237w YBR1603w	685974	688520	849	PRP5	Pre-mRNA processing protein, RNA helicase	
YBR238c YBR1608c	689115	691307	731			
YBR239c YBR1622c	692362	693948	529		Probable Zn-finger protein	
YBR240c YBR1624c	694498	695847	450		Probable Zn-finger protein	
YBR241c YBR1625c	696597	698060	488		Probable sugar transport protein	10
YBR242w YBR1627w	698675	699388	238		Probable ATP/GTP-binding protein	
YBR243c YBR1628c	699455	700798	448	TUR1	UDP-N-acetylglucosamin-1-phosphate transferase (EC 2.7.8.-); tunicamycin resistance	13
YBR244w YBR1632w	701533	702018	162		Probable glutathione peroxidase (EC 1.11.1.9)	
YBR245c YBR1633c	702158	705586	1143		Homolog to SNF2/SWI2 DNA-binding regulatory protein	1
YBR246w YBR1634w	705597	706757	387			
YBR247c YBR1635c	707013	708461	483			
YBR248c YBR1640c	708816	710471	552	HIS7	Glutamine amido transferase (EC 2.4.2.-)	2

YBR249c	YBR1701c	710891	712000	370	ARO4	2-deoxy-3-deoxyphosphoheptanoate aldolase (EC 4.1.2.15)	
YBR250w	YBR1702w	713039	714607	523			
YBR251w	YBR1704w	715396	716316	307	[MRPS5]	Probable mitochondrial ribosomal protein S5	
YBR252w	YBR1705w	716617	717057	147	DUT1	Mitochondrial dUTP pyrophosphatase (EC 3.6.1.23)	
YBR253w	YBR1721w	717276	717638	121			
YBR254c	YBR1722c	717745	718269	175		Probable membrane protein	
YBR255w	YBR1723w	718462	720543	694			2
YBR256c	YBR1724c	721395	722108	238	RIB5	Riboflavin synthase a-chain (EC 2.5.1.9)	
YBR257w	YBR1725w	722891	723727	279			
YBR258c	YBR1726c	723743	724168	142			
YBR259w	YBR1727w	724393	726456	688		/ Homology to serine-type carboxypeptidase PCR1 (S. cerevisiae) /	
YBR260c	YBR1728c	726648	728645	666		/ Homology to human bcr (break-poin cluster) protein /	
YBR261c	YBR1729c	728841	729536	232			
YBR262c	YBR1731c	729729	730046	106			
YBR263w	YBR1732w	730045	731739	565	[SHMT1]	Serine hydroxymethyltransferase (EC 2.1.2.1)	1
YBR264c	YBR1733c	731779	732432	218		Probable small GTP-binding protein	
YBR265w	YBR1734w	732588	733547	320		Probable membrane protein	3
YBR266c	YBR1735c ov	733836	734396	187		Probable membrane protein	3
YBR267w	YBR1736w	734143	735027	295		Probable Zn-finger protein (C2H2 type)	
YBR268w	YBR1736aw	735307	735621	105	MRPL37	Probable mitochondrial ribosomal protein L37	
YBR269c	YBR1737c	736193	736582	130			
YBR270c	YBR1738c	736770	738404	545		Probable ATP/GTP-binding protein	1
YBR271w	YBR1739w	738858	740114	419		/ Homology to Clostridium botulinum C1 toxin /	2
YBR272c	YBR1740c	740370	741809	480		/ Homology to MSH1 protein (S. cerevisiae) (weak) /	2
YBR273c	YBR1741c	742070	743377	436			
YBR274w	YBR1742w	743600	745180	527		Probable protein kinase (growth factor & cytokine receptor family)	
YBR275c	YBR1743c	745365	751112	1916	RIF1	RAP1-interacting regulatory protein	6
YBR276c	YBR2013c	751630	754050	807		Probable tyrosine-specific protein phosphatase	5
YBR277c	YBR2014c ov	754225	754623	133			3
YBR278w	YBR2015w	754301	754903	201	DPB3	DNA-directed DNA polymerase, chain C (EC 2.7.7.7)	
YBR279w	YBR2016w	755264	756598	445			
YBR280c	YBR2017c	756794	758719	642		/ Homology to pheromone response pathway component SRM1/PRP20 /	2
YBR281c	YBR2018c	758980	761613	878		Probable G-protein, ß-transducin type	
YBR282w	YBR2019w	762247	762684	146	MRPL27	Mitochondrial ribosomal protein YmL27	
YBR283c	YBR2020c	762953	764422	490		Probable SEC61 protein homolog	12
YBR284w	YBR2021w	765246	767636	797		/ Homology to S. cerevisiae AMP deaminase /	2
YBR285w	YBR2023w	767929	768360	144			
YBR286w	YBR2024w	768625	770316	564		Aminopeptidase Y	
YBR287w	YBR2034w	770577	771857	427			8
YBR288c	YBR2035c	772021	773469	483			
YBR289w	YBR2036w	773673	776387	905	SNF5	General transcriptional activator	

YBR290w	YBR2037w	776597	777559	321		2
YBR291c	YBR2039c	777682	778578	299	Probable mitochondrial carrier protein , uncoupling protein homolog	4
YBR292c	YBR2040c	778711	779079	123		2
YBR293w	YBR2109w	781011	782432	474	Probable multidrug resistance protein	13
YBR294w	YBR2110w	783240	785816	859	Probable sulfate transport protein	12
YBR295w	YBR2112w	786853	790500	1216 PCA1	P-type copper transporting ATPase	10
YBR296c	YBR2113c	790805	792526	574	Homolog to phosphate-repressible phosphate permease	10
YBR297w	YBR2115w	794527	795930	468 MAL3R	Maltose fermentation regulatory protein	
YBR298c	YBR2116c	796638	798479	614 MAL3T	Maltose permease	9
YBR299w	YBR2117w	799355	801106	584 MAL3S	Maltase (EC 3.2.1.20)	
YBR300c	YBR2120c ov	802607	803101	165		1
YBR301w	YBR2120aw	803061	803420	120	YKL224 c homolog	
YBR302c	YBR2121c	804347	805483	379	/ Homolog to YKL219w /	4

NOTES: i, intron-containing ORF; for length and coordinates of intron, see Table 5; §, two alternative ORFs, one spliced according to Fondrat and Kalogeropoulos (1993) and one non-spliced, overlap in this region; in this listing, preference has been given to the longer ORF or to the one with the higher CAI value. ’ov’ indicates overlapping ORFs. [ ] refer to preliminary gene names. Weaker homologies are soecified by / /.