

221 orthologs generally induced during stress in both *S. cerevisiae* and *S. pombe*:

Note: this will need refinement as more updated ortholog tables become available.
Assignment of orthologs for ribosomal genes is ambiguous.

<i>S. cerevisiae</i>	<i>S. pombe</i>	<i>S. pombe</i> Annotation
YHR068W	SPBC1271.04C	deoxyhypusine synthase
YGR094W	SPBC1709.02C	valyl-tRNA synthetase, mitochondrial
YHR020W	SPBC19C7.06	prolyl-tRNA synthetase, cytoplasmic
YOL039W	rpp2-2	60S acidic ribosomal protein p2-beta or P2B
YLR333C	rps25-1	40S ribosomal protein S25A/S25.1
YER131W	rps26-1	40S ribosomal protein S26
YKR059W	tif1	eukaryotic initiation factor 4a
YBR031W	rpl4	60s ribosomal protein L2
YDL082W	rpl13	60s ribosomal protein L13/L16
YBR191W	rpl21	60s ribosomal protein L21
YHL033C	rpl7a	60s ribosomal protein L7a (L8)
YJL189W	rpl39	60s ribosomal protein L39
YLR061W	rpl22	60s ribosomal protein L22
YOL127W	rpl25b/rpl23a-2	60s ribosomal protein L25.
YFR031C-A	rpl8-3/rpk5-b/rpkd	60s ribosomal protein L8
YGL103W	rpl28-2	60s ribosomal protein L27a.2/L28A
YKL056C	SPAC1F12.02C	highly conserved eukaryotic protein; translationally controlled tumor protein homolog; TCTP family protein.
YNL096C	rps7	40S ribosomal protein S7
YLR197W	SPBC646.10C	putative U3 snoRNP complex component; involved in 2'-O-methylation of ribosomal RNAs.
YHR021C	rps27	40s ribosomal protein S27
YJL190C	rps15a-1/rps22-1	40S ribosomal protein S15 or S22
YIL133C	rpl13a-2/rpl16-2	60s ribosomal protein L16-B
YHR141C	rpl36a	60s ribosomal protein L36/L42
YLR175W	SPAC29A4.04C	centromere/microtubule binding protein cbf5
YDR447C	rps17-1	40s ribosomal protein S17
YCR031C	rps14-1	40s ribosomal protein S14
YEL026W	snu13	putative pre-mRNA splicing factor; component of the U4/U6.U5 snRNP component; similar to <i>S. cerevisiae</i> SNU13
YGL031C	rpl24	60s ribosomal protein L24-3 (L30)
YLR150W	SPBC16A3.08C	similarity to yeast suppressor protein mpt4 aProtein with specific affinity for guanine-rich quadruplex nucleic acids
YOL040C	rps15-1	40s ribosomal protein S15
YOL120C	rpl18-2	60S ribosomal protein L18
YMR121C	rpl15	60S ribosomal protein L15.2/L15B
YPL198W	rpl7-1	60s ribosomal protein L7
YGR118W	rps23	40s ribosomal protein S23
YLR388W	rps29	40s ribosomal protein S29
YHR010W	rpl27-1/rpl27a	60S ribosomal protein L27A
YHR203C	rps4-3	40s ribosomal protein S4
YOR369C	rps12-1	40s ribosomal protein S12
YDL081C	rpp1-2	60S acidic ribosomal protein P1-alpha or P1B
YGL147C	rpl9-1	60s ribosomal protein L9

YGL135W	rpl1-1/rpl10a-1	60s ribosomal protein L10a.
YGR085C	rpl11-1	60s ribosomal protein L11
YER102W	rps8-2	40s ribosomal protein S8
YBR048W	rps11-1	40s ribosomal protein S11
YJL177W	rpl17	60s ribosomal protein L17
YBR189W	rps9-2/rps9b	40s ribosomal protein S9
YDL191W	rpl35	60s ribosomal protein L35
YER117W	rpl23-2	60s ribosomal protein L23.
YNL302C	rps19-2	40S ribosomal protein S19B/S19.2
YEL054C	rpl12-2	60s ribosomal protein L12
YLR344W	rpl26	60s ribosomal protein L26
YBR084C-A	rpl19-1	60s ribosomal protein L19
YLR048W	SPBC685.06	40s ribosomal protein S0 (p40)
YNL178W	rps3	40s ribosomal protein S3
YLR264W	rps28-2	40s ribosomal protein S28
YOR312C	rpl20-1	60s ribosomal protein L20a
YBL092W	rpl32-2	60s ribosomal protein L32
YOR234C	rpl37-1	60s ribosomal protein L37
YOR063W	rpl3-1	60s ribosomal protein L3
YHR193C	SPBC25H2.05	nascent polypeptide associated complex alpha subunit
YHL015W	rps20	40s ribosomal protein S20
YKR057W	rps21	40s ribosomal protein S21
YJR123W	rps5-2	40s ribosomal protein S5
YGL123W	rps2	40s ribosomal protein S2
YMR143W	rps16-2	40s ribosomal protein S16B
YLR448W	rpl6	60s ribosomal protein L6
YOR095C	SPAC144.12	putative ribose 5-phosphate isomerase
YLR017W	SPAC16C9.02C	putative methylthioadenosine phosphorylase
YML106W	SPBC725.15	orotate phosphoribosyltransferase; pyrimidine synthesis
YDL014W	fib	fibrillarin; putative U3 snoRNP component; required for 35S rRNA processing and methylation; bsimilar to yeast NOP1
YOR340C	rpa43	DNA-directed RNA polymerase I polypeptide
YHR064C	SPAC57A7.12	heat shock protein 70 homolog
YAL003W	tef5	elongation factor 1 beta
YDL051W	sla1	la protein homolog; RNA binding protein; similar to S. cerevisiae LHP1
YKR092C	SPBC1711.05	putative nucleolar chaperone
YML022W	SPAC23A1.03	putative adenine phosphoribosyltransferase (APRT); similar to S. cerevisiae APT1; phosphoribosyl transferases family
YGR162W	tif471	putative eukaryotic translation initiation factor eIF4G
YER156C	SPAC694.04C	putative metal dependent hydrolase
YNL209W	sks2/hsc1	heat-shock protein
YER043C	SPBC8D2.18C	putative adenosylhomocysteinase
YMR217W	SPAP7G5.02C	GMP synthase (glutamine-hydrolyzing)
YDR429C	tif35	eukaryotic translation initiation factor 3 RNA-binding subunit
YBR249C	SPAC24H6.10C	putative phospho-2-dehydro-3-deoxyheptonate aldolase
YJR016C	ilv3	dihydroxy-acid dehydratase; mitochondrial precursor
YJR007W	tif211	eukaryotic translation initiation factor 2 alpha subunit
YGL148W	SPCC1223.14	chorismate synthase
YGR285C	SPBC1778.01C	zuotin like protein; putative zDNA binding; DNAJ domain
YLR056W	SPAC1687.16C	C-5 sterol desaturase

YJL109C	SPBC23E6.04C	hypothetical protein; similar to <i>S. cerevisiae</i> YJL109
YER036C	SPBC16H5.08C	non transporter with ABC binding cassette
YER006W	SPBC26H8.08C	putative GTPase protein; possibly associated with nuclear pore complex by similarity to yeast YER006W
YHR169W	SPBC543.06C	ATP-dependent RNA helicase
YPR169W	SPAC1A6.02	WD domains by similarity; putative spicing factor
YOL124C	SPBC16D10.02	highly conserved hypothetical protein
YMR014W	SPAC4F10.06	hypothetical protein; contains Pfam-B_32523
YDL201W	SPCPB16A4.04C	putative methyltransferase
YPR190C	SPAPB1E7.03	putative DNA directed RNA polymerase III subunit (C74)
YBL024W	SPAC17D4.04	putative methyltransferase possibly cytidine and tRNAs
YJL125C	SPAC9G1.12	putative M1A-tRNA methyltransferase
YNR003C	rpc34	DNA-directed rna polymerase III subunit
YDL055C	SPCC1906.01	mannose-1-phosphate guanyltransferase
YLR372W	SPAC1B2.03C	GNS1/SUR4 family protein; putative fatty acid elongation protein
YPR143W	SPAC227.02C	eukaryotic conserved protein; possible coiled-coil region
YNL141W	SPBC1198.02	adenosine deaminase
YDR449C	SPBC244.02C	HAT repeat protein (context
YBR143C	sup45	translation release factor subunit 1.
YGL078C	SPCC17D1.06	putative ATP-dependent RNA helicase
YPL212C	lps1	pseudouridylate synthase
YOR224C	rpb8	DNA-directed RNA polymerases I, II, and III
YDR341C	SPBC25B2.09C	arginyl-trna synthetase, putative cytoplasmic
YBR162C	SPBP23A10.11C	serine-rich protein; putative cell wall, septation and/or ageing
YPR110C	rpc40/rpa42	DNA-directed rna polymerases I and III polypeptide.
YHR013C	SPAC15E1.08	putative N-terminal acetyltransferase complex subunit; ard1 family; possibly involved in telomeric silencing.
YDR091C	SPBC14F5.06	putative RNase L inhibitor
YCR053W	thrc	threonine synthase
YLR003C	SPBC23G7.07C	hypothetical protein
YOR341W	nuc1/rpa1	DNA-directed RNA polymerase I 190 kd polypeptide
YBL039C	SPAC10F6.03C	probable CTP synthase
YDR101C	SPBC23E6.05	conserved hypothetical protein
YHR089C	gar1	pre-mRNA processing protein
YNL124W	SPBC30D10.15	conserved hypothetical protein
YJR070C	SPAC30C2.02	hypothetical protein
YGR159C	gar2	rrm RNA recognition motif
YNL112W	dbp2	DEAD/DEAH box helicase; putative pre-mRNA splicing factor.
YOL041C	SPAC16E8.06C	putative RNA-binding protein
YJL122W	SPBC2D10.19C	small hypothetical protein; confirmed by EST
YDR465C	SPAC26A3.17C	putative N-methyltransferase
YKR056W	SPAC4G8.07C	putative Uridine methyltransferase that catalyzes the formation of ribothymidine in tRNAs.
YGL029W	SPAC1556.05C	possibly involved in ribosome biogenesis; similar to <i>S. cerevisiae</i> CGR1; predicted coiled-coil region
YNL182C	crb3	damage and replication checkpoint control protein; essential
YOR272W	ytm1	WD repeat protein.
YLR336C	SPAC24C9.11	hypothetical protein; possibly involved in signal transduction.
YGR200C	SPCC895.06	WD repeat protein

YPR112C	pi029	RNA binding protein; 5 rrm RNA recognition motifs
YLR129W	SPBC3D6.12	WD repeat protein; possibly involved in translation.
YGL171W	SPAC22F3.08C	ATP-dependent RNA helicase
YLR401C	SPAC16.04	conserved hypothetical protein
YML093W	SPAC57A7.06	hypothetical protein; GFP fusion nuclear; predicted coiled-coil
YNR053C	SPAC6F6.03C	GTP-binding protein associated; possibly involved in splicing.
YJL050W	SPAC6F12.16C	required for mRNA export from nucleus, member of the DEAD-box RNA helicase family by similarity to yeast mtr4
YPL012W	SPAPB8E5.07C	conserved hypothetical protein; contains Pfam-B_17883
YJR063W	rpa12	DNA-directed RNA polymerase I subunit
YIL091C	SPCC1827.01C	hypothetical helicase
YER110C	kap123	putative importin beta-4 subunit; karyopherin-beta involved in nuclear import of ribosomal proteins
YMR049C	SPBC4F6.13C	WD repeat protein
YPL266W	SPCC16A11.05C	putative pre-mRNA splicing factor
YPL146C	SPAC22F8.09	conserved hypothetical protein; similar to human GLTSCR2; glioma tumor suppressor candidate region protein2
YOL080C	SPBC1604.09C	putative exonuclease
YHR088W	SPAC4F8.04	possible role in RNA processing
YGR195W	SPAC3G9.10C	putative exosome 3'-5' exoribonuclease complex; involved in 3' processing of ribosomal 5.8S rRNA, snoRNAs and U4 snRNA; degradation of poly(A)-mRNAs.
YDR087C	SPBC9B6.07	protein involved in maturation of 25S rRNA.
YCL031C	SPBC776.17	protein involved in pre-rRNA processing and ribosome assembly.
YNL075W	SPAC19A8.07C	U3 snoRNP component; required for pre-rRNA processing.
YHR143W-A	rpc10/rpb12	DNA-directed RNA polymerases I, II, and III 7.3 kd polypeptide.
YKL172W	SPAC17H9.05	nucleolar protein P40-like; involved in pre-rRNA processing and ribosomal subunit assembly.
YNL113W	rpc19/rpa17	putative shared subunit of RNA polymerases I and III.
YGR272C	SPAC12G12.02	hypothetical protein
YKL205W	SPBP8B7.09C	putative pre-tRNA nuclear export receptor
YMR290C	SPAC1F7.02C	probable ATP-dependent RNA helicase
YLL011W	SPBC1A4.07C	WD repeat protein; putative U3 snoRNP complex associated; 18S pre-rRNA maturation.
YHR170W	SPAC16C9.03	putative nonsense-mediated mRNA decay protein
YLR074C	SPAC19B12.11C	C2H2 zinc finger protein
YMR229C	SPCC1183.07	putative rRNA biogenesis protein; multiple S1 RNA binding domain protein
YER082C	SPAC959.03C	conserved hypothetical protein; contains 1 WD-repeat
YGR145W	SPCC330.09	conserved hypothetical protein
YGL099W	SPAC3F10.16C	putative GTP-binding protein
YOR145C	SPAC2C4.11C	conserved hypothetical protein; yeast homologue purifies as part of nuclear pore complex
YCR072C	SPCC18.05C	WD repeat protein; notchless-like
YBR247C	SPBC13G1.09	bystin-family protein.
YPL093W	SPBC651.01C	putative GTP-binding protein
YLR222C	SPCC16A11.02	WD repeat protein; similar to human SAZD
YCL054W	pmt2	pmt2 methyltransferase
YFL002C	SPBC24C6.02	putative ATP dependent RNA helicase

YLL034C	SPBC16E9.10C	AAA ATPase
YOR287C	SPAC823.04	hypothetical protein
YNL255C	SPAC683.02C	hypothetical zinc-finger protein
YLR409C	SPCC1672.07	WD repeat protein
YDR165W	SPCC18.13	WD repeat protein
YNL308C	SPAC22G7.05	hypothetical coiled-coil protein; similar to <i>S. cerevisiae</i> KRI1 which binds protein cell division/spore germination protein
YNL132W	SPAC20G8.09C	hypothetical protein; highly conserved
YMR131C	SPBC1711.07	WD repeat protein; possible nuclear pore complex associated
YJL033W	SPAC1093.05	probable ATP-dependent RNA helicase
YJL069C	SPBC29A3.06	WD repeat protein
YPR137W	SPAC2E1P5.05	putative U3 snoRNP associated WD repeat protein
YNL061W	SPBP8B7.20C	putative nucleolar protein; NOL1/NOP2/sun family
YCL059C	mis3	similar to yeast cell division/spore germination protein Krr1p
YLR435W	SPBC409.15	highly acidic C terminus
YOR056C	SPAC1486.09	protein that may associate with the 26S proteasome.
YLL008W	SPAC30D11.03	ATP dependent RNA helicase
YGL111W	SPBC83.15	conserved protein
YCL037C	SPAC1527.03	putative RNA-bd LA related protein; similar to yeast SRO9
YKR081C	SPAC926.08C	similar to <i>S. cerevisiae</i> YKR081C; contains Pfam-B_20446
YPL086C	SPAC29A4.20	putative subunit of elongator/RNAPII holoenzyme; putative histone acetyltransferase.
YNL110C	SPCC1827.05C	protein with rrm, RNA recognition motif
YEL055C	pol5	DNA polymerase V
YER127W	SPAC18B11.06	putative U3 snoRNP component; pre-rRNA processing.
YGR245C	SPBC106.14C	possibly required for actin cytoskeletal organisation.
YJL010C	SPAC6G9.02C	RNA binding protein
YGR103W	SPBC19F5.05C	pescadillo-like hypothetical protein.
YOL077C	SPBC800.06	required for biogenesis of the 60S ribosomal subunit.
YPL211W	SPCC320.11C	putative protein involved in 60S ribosome subunit biogenesis
YHR148W	SPAC19D5.05C	putative U3 snoRNP component; pre-rRNA processing.
YPR144C	SPBC1604.06C	conserved hypothetical protein.
YOR294W	SPBC29A3.16	putative regulator of ribosome synthesis.
YKL009W	SPBC11G11.03	putative 60S acidic ribosomal protein
YLR009W	rpl24-3	60S ribosomal protein L24C (L30)
YNL248C	rpa49	DNA-directed RNA polymerase I 49 kD polypeptide
YDL060W	SPAC23H4.15	hypothetical protein; contains Pfam-B_1475 and Pfam-B_6211
YDR161W	SPBC16D10.01C	protein that interacts with protein phosphatase 2C
YKR060W	SPAC8F11.04	hypothetical protein; similar to <i>S. cerevisiae</i> YKR060W
YOR004W	SPCC18.12C	tRNA synthetase class II (D K N), cytoplasmic
YHR065C	SPAC823.08C	putative ATP-dependent RNA helicase
YPL043W	SPBC4F6.14	RNA binding ribonucleoprotein
YPR041W	SPAC2F7.05C	eukaryotic translation initiation factor 5
YGR280C	SPAC1952.02	similar to <i>S. cerevisiae</i> YGR280C and SPAC890.05.
YDL167C	SPAC17H9.04C	RNA-binding / Ran zinc finger protein
YOR206W	SPAC1142.04	possible nuclear pore complex; putative coiled-coil regions
YHR066W	SPAC1B9.03C	similarity to yeast mating protein SSF1
YNL313C	SPAC19B12.01	similar to <i>S. cerevisiae</i> YNL313C protein of unknown function.
YDL213C	SPBC365.04C	RNA binding protein
YDR083W	SPAC56F8.09	ribosomal RNA processing.