

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

Note: this will need refinement as more updated ortholog tables become available.

<i>S. cerevisiae</i>	<i>S. pombe</i>	<i>S. pombe</i> Annotation
YML004C	SPBC12C2.12C	lactoylglutathione lyase
YKL035W	SPCC1322.04	putative UTP-glucose-1-phosphate uridylyltransferase
YNL200C	SPAC15A10.05C	hypothetical protein
YPR149W	SPBC1685.13	possibly involved in non-classical protein export pathway
YLL026W	SPBC16D10.08C	putative chaperonin; heat shock protein
YDL124W	SPAC19G12.09	putative aldose reductase
YJL141C	SPAC1E11.03	serine/threonine protein kinase; yeast yak1 homolog
YML042W	SPAC212.04C	hypothetical protein; duplicated in <i>S. pombe</i> telomeric region
YMR090W	SPBC216.03	protein with similarity to malate dehydrogenases
YHR087W	SPBC21C3.19	hypothetical protein
YNL115C	SPAC23C11.06C	contains 5 predicted transmembrane helices
YIL124W	SPAC23D3.11	putative 1-acyl dihydroxyacetone phosphate reductase
YBR026C	SPAC26F1.04C	hypothetical protein
YJR096W	SPAC2F3.05C	aldo/keto reductase family oxidoreductase
YHR138C	SPCC338.12	putative proteinase inhibitor
YML128C	ish1	stress response gene
YGL037C	SPBC365.20C	putative pyrazinamidase/nicotinamidase
YDR258C	SPBC4F6.17C	yeast chaperonin hsp78 homolog
YLR149C	SPCC4G3.03	WD repeat protein
YJR008W	SPAC4H3.04C	hypothetical protein; UPF0103 family
YKR009C	SPAC4H3.08	putative short chain dehydrogenase
YNL305C	SPCC576.04	putative receptor-associated protein
YKL151C	SPCC61.03	conserved hypothetical protein
YIR038C	SPAC688.04C	glutathione-S-transferase 3
YPL196W	SPAC8C9.16C	hypothetical protein
YBR056W	exg3	glucan 1,3-beta-glucosidase
YIR037W	gpx1	glutathione peroxidase
YCL035C	grx1	thioltransferase
YBR072W	hsp16	heat shock protein 16
YFL014W	hsp9	heat shock protein 9
YEL060C	isp6	sexual differentiation protein; putative subtilase-type proteinase
YER142C	mag1	DNA-3-methyladenine glycosylase; base excision repair
YDR001C	ntp1	neutral trehalase
YDR032C	obr1	brefeldin a resistance protein
YBL049W	SPAPJ691.02	hypothetical zinc binding protein yipee-like
YPL203W	pkal: tpk: git6	CAMP-dependent protein kinase catalytic subunit
YJR104C	sod1	Cu,Zn-superoxide dismutase
YBR126C	tps1	alpha,alpha-trehalose-phosphate synthase
YEL012W	ubc8	ubiquitin conjugating enzyme
YDR406W	bfr1: hba2	MFS brefeldin A efflux transporter
YBR256C	SPCC1450.13C	riboflavin synthase alpha chain
YLL023C	SPBC1539.04	hypothetical protein
YOL032W	SPBC21H7.06C	conserved hypothetical protein
YOR120W	SPAC26F1.07	probable oxidoreductase
YBR290W	SPAC328.07C	putative metal homeostatis protein

YNR007C	SPBC3B9.06C	putative autophagy protein
YGL157W	SPAC513.07	putative cinnamoyl-coa reductase
YIL033C	cgs1	CAMP-dependent protein kinase regulatory chain
YMR261C	SPACUNK4.16C	putative alpha-trehalose-phosphate synthase