

Yeast Iron Map. Jo, Kim, Oh *et al.* (2009). Novel insights into iron metabolism by integrating deletome and transcriptome analysis in an iron deficiency model of the yeast *Saccharomyces cerevisiae*

Go to map 

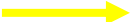
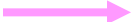
Cellular Component (click to view on map)

Cell wall	Mitochondrion 3
Cellular bud	Nucleolus
Cytoplasm	Nucleus
Endoplasmic Reticulum	Other
Endosome	Peroxisome
Endosome and cytoplasmic membrane-bounded vesicle	Plasma membrane
Golgi apparatus	Ribosome
Membrane	Unknown
Mitochondrion 1	Vacuole 1
Mitochondrion 2	Vacuole 2

Pathway (click to view on map)

Biotine biosynthesis	Glycolytic pathways
<i>De novo</i> biosynthesis of purine nucleotides	Heme biosynthesis
<i>De novo</i> biosynthesis of pyrimidine ribonucleotides	Histidine biosynthesis
Electron transport chain	Leucine, isoleucine and valine biosynthesis
Ergosterol pathway	Lysine biosynthesis
Galactose metabolism	Sulfur amino acid biosynthesis
Glutamate biosynthesis	TCA cycle

Legend

Functional data - gene deletion induces sensitivity to BPS		Expression data - gene is up regulated in BPS	
Functional data - gene deletion induces resistance to BPS		Expression data - gene is down regulated in BPS	
Physical interaction (PI)		Transcriptional regulation expected (TRE)	
Metal transport (MT/PMT)		Indirect regulation expected (IRE)	
Metal transfer expected (MTE)		Pathway sequence / step (PS)	
Transcriptional down regulation (TRD)		Unknown pathway sequence / step (UPS)	
Indirect transcriptional down regulation (ITRD)		Regulatory stimulus (REG)	
Transcriptional up regulation (TRU)		Involved in FeS cluster assembly (FeS)	
Indirect transcriptional up regulation (ITRU)		Translational activator (TLA)	
Transcriptional regulation (TR)		Activation by phosphorylation (AP)	
		Genes within respiratory chain complex, or involved in maturation or assembly (RC)	

Novel insights into iron metabolism by integrating deletome and transcriptome analysis in an iron deficiency model of the yeast *Saccharomyces cerevisiae*
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