

Cold Stress

Metabolite	Affy Probe ID	correlation	EC	Yeast Gene ID	Gene Symbol	Annotation
Arginine	1774813_at	0.830492823	6.1.1.19	YHR091C	MSR1	Nuclear-encoded mitochondrial protein
Citric acid	1769943_at	-0.829813097	4.2.1.3	YJL200C	ECM25	Hypothetical ORF
Fructose	1770167_at	0.983643136	2.7.1.1	YGL253W	HXK2	Hexokinase isoenzyme 2
Fructose	1770506_at	0.942699545	3.2.1.26	YIL162W	SUC2	Suc2p
Fructose	1775391_s_at	0.908667563	3.2.1.20	YIL172C	VTH1	Hypothetical ORF
Fructose	1778617_at	0.944075395	3.2.1.20	YJL216C	HXT9	Protein of unknown function
Fructose-6-phosphate	1770167_at	0.976879131	2.7.1.1	YGL253W	HXK2	Hexokinase isoenzyme 2
Fructose-6-phosphate	1774340_at	0.867796391	3.1.3.46	YJL155C	FBP26	Fructose-2
Fructose-6-phosphate	1774445_at	0.881481431	2.7.1.11	YGR240C	PFK1	phosphofructokinase alpha subunit
Fructose-6-phosphate	1776768_at	0.957430871	3.1.3.11	YLR377C	FBP1	Fructose-1
Fumaric acid	1779688_at	-0.873349669	1.3.5.1	YLR164W	MAS1	YLR164Wp is homologous to TIM18p
						Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1
Glucose	1770001_at	0.918002771	2.7.1.2	YDR516C	EMI2	
Glucose	1770167_at	0.96378365	2.7.1.1	YGL253W	HXK2	Hexokinase isoenzyme 2
Glucose	1775391_s_at	0.948887214	3.2.1.20	YIL172C	VTH1	Hypothetical ORF
Glucose	1775738_at	0.827385156	3.2.1.22	YBR184W	YPC1	Hypothetical ORF
Glucose	1778617_at	0.964795956	3.2.1.20	YJL216C	HXT9	Protein of unknown function
						Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1
Glucose-6-phosphate	1770001_at	0.923989404	2.7.1.2	YDR516C	EMI2	115 kD regulatory subunit of trehalose-6-
Glucose-6-phosphate	1773683_at	0.909520111	2.4.1.15	YMR261C	TPS3	phosphate synthase 123 kD regulatory subunit of trehalose-6-
Glucose-6-phosphate	1774756_at	0.919204856	2.4.1.15	YML100W	TSL1	phosphate synthase
Glucose-6-phosphate	1775976_at	0.8829882	2.7.1.1	YFR053C	HXK1	Hexokinase isoenzyme 1
Glucose-6-phosphate	1776427_at	0.940897388	1.1.1.49	YNL241C	ZWF1	Glucose-6-phosphate dehydrogenase
Glucose-6-phosphate	1779150_at	0.909031401	2.7.1.2	YCL040W	GLK1	Glucose phosphorylation Probable regulator of glucose influx into the cell
Glucose-6-phosphate	1779408_at	0.889433862	2.4.1.15	YBR126C	TPS1	& into glycolytic pathway putative alanine transaminase (glutamyl pyruvic
Glutamic acid	1769691_at	0.842801861	2.6.1.2	YLR089C	GAA1	transaminase) Acetylglutamate synthase (glutamate N-
Glutamic acid	1773952_at	-0.899469259	2.3.1.35	YJL071W	ARG2	acetyltransferase)
Glutamic acid	1774739_at	-0.828322746	2.6.1.9	YIL116W	HIS5	Histidinol-phosphate aminotransferase

Glutamic acid	1775518_at	-0.918376151	6.3.5.1	YHR074W	QNS1	Glutamine-dependent NAD Synthetase
Glutamic acid	1776080_at	0.915883073	6.1.1.17	YGL245W	RAI1	Glutamyl-tRNA synthetase (GluRS)
Glutamic acid	1776272_at	-0.855008611	2.3.1.35	YMR062C	ECM40	Mitochondrial ornithine acetyltransferase putative alanine transaminase (glutamyl pyruvic transaminase)
Glutamic acid	1778563_at	0.876694182	2.6.1.2	YDR111C	FOB1	Multifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase) that catalyzes the two first reactions of the pyrimidine pathway Utilizes NADP+ as the preferred coenzyme.
Glutamic acid	1779682_at	-0.802185116	6.3.5.5	YJL130C	URA2	Activated by K+.
Glyceric acid	1771943_at	-0.959520478	1.2.1.3	YER073W	ALD5	Glucose repressed. Utilizes NADP+ or NAD+ as a coenzyme equally well. (sold by SIGMA under the catalogue number A5550
Glyceric acid	1776624_at	0.923020599	1.2.1.3	YOR374W	ALD4	Utilizes NADP+ as the preferred coenzyme.
Glyceric acid	1778325_at	0.821755486	1.2.1.3	YPL061W	ALD6	Activated by Mg2+.
Isoleucine	1779000_at	-0.844282111	2.6.1.42	YHR208W	BAT1	BAT1 highly expressed during logarithmic phase and is repressed during stationary phase
Lysine	1770279_at	-0.815146015	1.5.1.7	YIR034C	LYS1	saccharopine dehydrogenase
Lysine	1771061_at	0.891393503	6.1.1.6	YNL073W	MSK1	mitochondrial lysine-tRNA synthetase
Lysine	1779238_at	-0.878603734	6.1.1.6	YDR037W	KRS1	lysyl-tRNA synthetase
Malic acid	1769857_at	-0.945839494	1.1.1.37	YKL085W	MDH1	mitochondrial malate dehydrogenase
Malic acid	1770087_at	0.874182769	4.2.1.2	YPL262W	FUM1	Fumarase
Malic acid	1774081_at	-0.952654406	1.1.1.37	YOL126C	MDH2	cytosolic malate dehydrogenase
Proline	1778412_at	0.850564806	1.5.1.2	YER023W	PRO3	Delta 1-pyrroline-5-carboxylate reductase
Serine	1771458_at	0.914220116	3.1.3.3	YGR208W	SER2	phosphoserine phosphatase
Serine	1774806_at	0.87678734	2.1.2.1	YBR263W	SHM1	Serine hydroxymethyltransferase
Serine	1776401_at	0.895707658	2.1.2.1	YLR058C	SHM2	serine hydroxymethyltransferase
Serine	1776603_at	0.807343484	4.3.1.19	YER086W	ILV1	Threonine deaminase
Serine	1776877_at	0.951394922	6.1.1.11	YDR023W	SES1	seryl-tRNA synthetase
Serine	1778479_at	0.924259607	4.3.1.19	YCL064C	CHA1	catabolism of hydroxy amino acids
Trehalose	1776531_at	-0.828380305	3.1.3.12	YDR074W	TPS2	Trehalose-6-phosphate phosphatase

Heat Stress

Metabolite	Affy Probe ID	correlation		Yeast Gene		Annotation
		coefficient, r	EC	ID	Gene Symbol	
Adenosine-5-monophosphate	1771215_at	0.937044153	3.1.3.7	YOL064C	MET22	Bisphosphate-3'-nucleotidase
Adenosine-5-monophosphate	1776097_at	0.83462906	2.7.6.1	YHL011C	PRS3	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase
Adenosine-5-monophosphate	1778594_at	0.8087759	3.1.4.17	YOR360C	PDE2	low-Km (high-affinity) cAMP phosphodiesterase
Alanine	1776171_at	0.899683824	6.1.1.7	YOR335C	ALA1	Cytoplasmic alanyl-tRNA synthetase
Alanine	1778563_at	-0.874481904	2.6.1.2	YDR111C	FOB1	putative alanine transaminase (glutamyl pyruvic transaminase)
Arginine	1774813_at	0.830492823	6.1.1.19	YHR091C	MSR1	Nuclear-encoded mitochondrial protein
Asparagine	1777566_s_at	0.805893491	3.5.1.1	YLR155C	ASP3-1	Cell-wall L-asparaginase II
Citric acid	1769943_at	-0.829813097	4.2.1.3	YJL200C	ECM25	Hypothetical ORF
Fructose	1770167_at	0.983643136	2.7.1.1	YGL253W	HXK2	Hexokinase isoenzyme 2
Fructose	1770506_at	0.942699545	3.2.1.26	YIL162W	SUC2	Suc2p
Fructose	1775391_s_at	0.908667563	3.2.1.20	YIL172C	VTH1	Hypothetical ORF
Fructose	1778617_at	0.944075395	3.2.1.20	YJL216C	HXT9	Protein of unknown function
Fructose-6-phosphate	1770167_at	0.976879131	2.7.1.1	YGL253W	HXK2	Hexokinase isoenzyme 2
Fructose-6-phosphate	1774340_at	0.867796391	3.1.3.46	YJL155C	FBP26	Fructose-2
Fructose-6-phosphate	1774445_at	0.881481431	2.7.1.11	YGR240C	PFK1	phosphofructokinase alpha subunit
Fructose-6-phosphate	1776768_at	0.957430871	3.1.3.11	YLR377C	FBP1	Fructose-1
Fumaric acid	1779688_at	-0.873349669	1.3.5.1	YLR164W	MAS1	YLR164Wp is homologous to TIM18p
Glucose	1775738_at	0.823555683	3.2.1.22	YBR184W	YPC1	Hypothetical ORF
Glucose	1770001_at	0.918002771	2.7.1.2	YDR516C	EMI2	Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1
Glucose	1770167_at	0.96378365	2.7.1.1	YGL253W	HXK2	Hexokinase isoenzyme 2
Glucose	1775391_s_at	0.948887214	3.2.1.20	YIL172C	VTH1	Hypothetical ORF
Glucose	1775738_at	0.827385156	3.2.1.22	YBR184W	YPC1	Hypothetical ORF
Glucose	1778617_at	0.964795956	3.2.1.20	YJL216C	HXT9	Protein of unknown function
Glucose-6-phosphate	1770001_at	0.923989404	2.7.1.2	YDR516C	EMI2	Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1
Glucose-6-phosphate	1773683_at	0.909520111	2.4.1.15	YMR261C	TPS3	115 kD regulatory subunit of trehalose-6-phosphate synthase
Glucose-6-phosphate	1774756_at	0.919204856	2.4.1.15	YML100W	TSL1	123 kD regulatory subunit of trehalose-6-phosphate synthase
Glucose-6-phosphate	1775976_at	0.8829882	2.7.1.1	YFR053C	HXK1	Hexokinase isoenzyme 1
Glucose-6-phosphate	1776427_at	0.940897388	1.1.1.49	YNL241C	ZWF1	Glucose-6-phosphate dehydrogenase
Glucose-6-phosphate	1779150_at	0.909031401	2.7.1.2	YCL040W	GLK1	Glucose phosphorylation

Glucose-6-phosphate	1779408_at	0.889433862	2.4.1.15	YBR126C	TPS1	Probable regulator of glucose influx into the cell & into glycolytic pathway
Glutamic acid	1769938_at	0.882082785	6.3.2.17	YKL132C	RMA1	probable folyl-polyglutamate synthetase
Glutamic acid	1772615_at	0.854638933	6.3.5.4	YPR145W	ASN1	Asparagine synthetase
Glutamic acid	1773117_at	-0.882215795	1.5.1.12	YHR037W	PUT2	delta-1-pyrroline-5-carboxylate dehydrogenase
Glutamic acid	1773540_at	0.867634604	2.7.2.11	YDR300C	PRO1	Gamma-glutamyl kinase
Glutamic acid	1775174_at	-0.813191195	6.3.2.17	YMR113W	FOL3	Dihydrofolate synthetase
Glutamic acid	1776650_at	0.846207249	2.6.1.1	YKL106W	AAT1	Mitochondrial aspartate aminotransferase
Glutamic acid	1777344_at	-0.845307957	2.6.1.42	YJR148W	BAT2	BAT1 highly expressed during logarithmic phase and is repressed during stationary phase
Glutamic acid	1778563_at	-0.85141935	2.6.1.2	YDR111C	FOB1	putative alanine transaminase (glutamyl pyruvic transaminase)
Glutamic acid	1779000_at	0.920530026	2.6.1.42	YHR208W	BAT1	BAT1 highly expressed during logarithmic phase and is repressed during stationary phase
Glutamic acid	1779734_at	0.815487462	6.3.5.2	YMR217W	GUA1	GMP synthase
Glutamic acid	1769691_at	0.842801861	2.6.1.2	YLR089C	GAA1	putative alanine transaminase (glutamyl pyruvic transaminase)
Glutamic acid	1773952_at	-0.899469259	2.3.1.35	YJL071W	ARG2	Acetylglutamate synthase (glutamyl N-acetyltransferase)
Glutamic acid	1774739_at	-0.828322746	2.6.1.9	YIL116W	HIS5	Histidinol-phosphate aminotransferase
Glutamic acid	1775518_at	-0.918376151	6.3.5.1	YHR074W	QNS1	Glutamine-dependent NAD Synthetase
Glutamic acid	1776080_at	0.915883073	6.1.1.17	YGL245W	RAI1	Glutamyl-tRNA synthetase (GluRS)
Glutamic acid	1776272_at	-0.855008611	2.3.1.35	YMR062C	ECM40	Mitochondrial ornithine acetyltransferase
Glutamic acid	1778563_at	0.876694182	2.6.1.2	YDR111C	FOB1	putative alanine transaminase (glutamyl pyruvic transaminase)
Glutamic acid	1779682_at	-0.802185116	6.3.5.5	YJL130C	URA2	Multifunctional carbamoylphosphate synthetase (CPSase)-
Glutamine	1772615_at	0.873616227	6.3.5.4	YPR145W	ASN1	aspartate transcarbamylase (ATCase) that catalyzes the two first reactions of the pyrimidine pathway
Glyceric acid	1771943_at	-0.959520478	1.2.1.3	YER073W	ALD5	Asparagine synthetase
Glyceric acid	1776624_at	0.923020599	1.2.1.3	YOR374W	ALD4	Utilizes NADP+ as the preferred coenzyme. Activated by K+.
Glyceric acid	1778325_at	0.821755486	1.2.1.3	YPL061W	ALD6	Glucose repressed. Utilizes NADP+ or NAD+ as a coenzyme equally well. (sold by SIGMA under the catalogue number A5550)
Homoserine	1777312_at	0.915289263	2.7.1.39	YHR025W	THR1	Utilizes NADP+ as the preferred coenzyme. Activated by Mg2+.
Isoleucine	1777344_at	-0.916418773	2.6.1.42	YJR148W	BAT2	homoserine kinase
Isoleucine	1779139_at	0.936411589	6.1.1.5	YBL076C	ILS1	BAT1 highly expressed during logarithmic phase and is repressed during stationary phase
						Cytoplasmic isoleucine-tRNA synthetase

Isoleucine	1779000_at	-0.844282111	2.6.1.42	YHR208W	BAT1	BAT1 highly expressed during logarithmic phase and is repressed during stationary phase
Lysine	1770279_at	-0.815146015	1.5.1.7	YIR034C	LYS1	saccharopine dehydrogenase
Lysine	1771061_at	0.891393503	6.1.1.6	YNL073W	MSK1	mitochondrial lysine-tRNA synthetase
Lysine	1779238_at	-0.878603734	6.1.1.6	YDR037W	KRS1	lysyl-tRNA synthetase
Malic acid	1769857_at	-0.945839494	1.1.1.37	YKL085W	MDH1	mitochondrial malate dehydrogenase
Malic acid	1770087_at	0.874182769	4.2.1.2	YPL262W	FUM1	Fumarase
Malic acid	1774081_at	-0.952654406	1.1.1.37	YOL126C	MDH2	cytosolic malate dehydrogenase
Phenylalanine	1773228_at	-0.98286093	6.1.1.20	YPR047W	MSF1	alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
Phenylalanine	1776650_at	0.894019205	2.6.1.1	YKL106W	AAT1	Mitochondrial aspartate aminotransferase
Phenylalanine	1779336_at	0.869285556	6.1.1.20	YFL022C	FRS2	Beta (small) subunit of cytoplasmic phenylalanyl-tRNA synthetase
Proline	1774658_at	0.955230036	6.1.1.15	YHR020W	DED81	Protein required for cell viability
Proline	1776689_at	-0.854809048	6.1.1.15	YER087W	ILV1	Hypothetical ORF
Proline	1778412_at	-0.897808151	1.5.1.2	YER023W	PRO3	Delta 1-pyrroline-5-carboxylate reductase
Proline	1778412_at	0.850564806	1.5.1.2	YER023W	PRO3	Delta 1-pyrroline-5-carboxylate reductase
Serine	1771458_at	0.813592041	3.1.3.3	YGR208W	SER2	phosphoserine phosphatase
Serine	1776603_at	0.881509564	4.3.1.19	YER086W	ILV1	Threonine deaminase
Serine	1776877_at	0.807363439	6.1.1.11	YDR023W	SES1	seryl-tRNA synthetase
Serine	1779478_at	0.976823382	4.2.1.20	YGL026C	TRP5	tryptophan synthetase
Serine	1771458_at	0.914220116	3.1.3.3	YGR208W	SER2	phosphoserine phosphatase
Serine	1774806_at	0.87678734	2.1.2.1	YBR263W	SHM1	Serine hydroxymethyltransferase
Serine	1776401_at	0.895707658	2.1.2.1	YLR058C	SHM2	serine hydroxymethyltransferase
Serine	1776603_at	0.807343484	4.3.1.19	YER086W	ILV1	Threonine deaminase
Serine	1776877_at	0.951394922	6.1.1.11	YDR023W	SES1	seryl-tRNA synthetase
Serine	1778479_at	0.924259607	4.3.1.19	YCL064C	CHA1	catabolism of hydroxy amino acids
Threonine	1769828_at	-0.940356164	6.1.1.3	YKL194C	MST1	mitochondrial threonine-tRNA synthetase
Threonine	1772625_at	0.806506445	4.1.2.5	YEL046C	GLY1	L-threonine aldolase that catalyzes cleavage of L-allo-threonine and L-threonine to glycine
Threonine	1774604_at	0.801698067	6.1.1.3	YIL078W	THS1	Threonyl-tRNA synthetase
Threonine	1776603_at	0.926368306	4.3.1.19	YER086W	ILV1	Threonine deaminase
Trehalose	1776531_at	-0.828380305	3.1.3.12	YDR074W	TPS2	Trehalose-6-phosphate phosphatase
Valine	1777344_at	-0.928940739	2.6.1.42	YJR148W	BAT2	BAT1 highly expressed during logarithmic phase and is repressed during stationary phase
Valine	1779000_at	0.92053668	2.6.1.42	YHR208W	BAT1	BAT1 highly expressed during logarithmic phase and is repressed during stationary phase