

Web Table B: Genes induced in response to starvation/pheromone (transient).

Transient genes are induced within 1 h of nitrogen removal, and their levels decrease during the following 2-3 h.

| Metabolic response | | |
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| Allantoin metabolism | | |
| | SPAC1F7.09C | putative allantoinase (EC 3.5.3.4) |
| | SPAC19G12.04 | putative ureidoglycolate hydrolase |
| | SPCC1223.09 | uricase |
| Salvage pathway | | |
| | SPCC1672.03C | putative guanine deaminase |
| | SPBC1683.03C | MFS transporter |
| <i>pcd1</i> | SPAC1556.04C | putative cytidine deaminase |
| | SPAC1805.16C | putative purine nucleoside phosphorylase |
| | SPAC1002.17C | probable uracil phosphoribosyltransferase |
| | SPAC1399.04C | putative uracil phosphoribosyltransferase |
| | SPBC16G5.02C | ribokinase; pfkB family carbohydrate kinase |
| | SPBC1683.06C | putative inosine-uridine preferring nucleoside hydrolase |
| | SPCC162.11C | putative uridine kinase |
| | SPBC800.11 | putative inosine-uridine preferring nucleoside hydrolase |
| | SPBC3D6.06C | putative ribose-phosphate pyrophosphokinase |
| | SPBPB2B2.05 | putative GMP synthase |
| Degradation of other nitrogen sources | | |
| | SPAPB24D3.03 | putative agmatinase precursor |
| | SPBC8E4.03 | putative agmatinase precursor |
| | SPAC11D3.09 | arginase family protein; putative agmatinase precursor |
| | SPAC186.03 | L-asparaginase precursor |
| | SPAC869.01 | putative aminotransferase |
| | SPAC27F1.05C | probable aminotransferase |
| | SPBC1773.03C | aminotransferase class III |
| | SPAC19D5.07 | 4-aminobutyrate aminotransferase (GABA transaminase) |
| | SPCC1450.07C | putative d-amino acid oxidase |
| | SPAC922.07C | probable aldehyde dehydrogenase |
| | SPAC1002.12C | probable succinate-semialdehyde dehydrogenase |
| | SPAC869.04 | formamidase-like protein |
| | SPCC550.07 | acetamidase |
| | SPAC922.03 | probable 1-aminocyclopropane-1-carboxylate deaminase |
| Others-metabolic | | |
| <i>isp7</i> | SPAC25B8.13C | putative iron/ascorbate oxidoreductase |
| | SPCC1494.01 | putative iron/ascorbate oxidoreductase |
| | SPAC1F7.12 | oxidoreductase similar to pyridoxal reductase |
| | SPAC922.06 | probable oxidoreductase, short chain dehydrogenase/reductase family |
| | SPAC30D11.01C | putative family 31 glucosidase |
| | SPAC3A11.10C | putative microsomal dipeptidase precursor |
| | SPAC521.03 | putative short chain dehydrogenase |
| | SPAC19G12.03 | possible polysaccharide deacetylase |
| | SPBC1861.05 | pfkB family carbohydrate kinase;with Pfam-B_2675 2 |
| | SPAC806.06C | putative Nicotinamide mononucleotide (NMN) adenylyltransferase; by similarity to <i>S. cerevisiae</i> YLR328W |
| | SPAC1039.03 | putative esterase/lipase |
| | SPCC576.02 | putative hydantoin racemase |

| | | |
|-------------------------|---------------|---|
| | SPAC1399.05C | putative involvement in maltose fermentation |
| | SPBPB2B2.06C | putative 5' nucleotidase family protein; possibly involved in the degradation of external UDP-glucose |
| | SPAC1039.06 | putative metal activated pyridoxal enzyme |
| | SPAC14C4.09 | putative Glucanase; by similarity to <i>Penicillium purpurogenum</i> mutanase |
| | SPAC14C4.09 | putative Glucanase; by similarity to <i>Penicillium purpurogenum</i> mutanase |
| | SPBC1683.11C | isocitrate lyase (EC 4.1.3.1) |
| | SPAC1039.02 | membrane protein; similar to <i>S. cerevisiae</i> YHR202W; putative esterase; contains Pfam-B_34335; contains Pfam-B_34336; which co-occur in 5' nucleotidase |
| | SPAC2E1P3.04 | peroxisomal copper amine oxidase |
| | SPCC11E10.01 | cystathionine beta-lyase |
| | SPAC1039.07C | aminotransferase class-III pyridoxal-phosphate; putative 2,2-dialkylglycine decarboxylase |
| | SPAC1039.08 | serine acetyltransferase |
| | SPAC1F7.10 | putative hydantoin racemase |
| Transporters | | |
| | SPCC285.04 | putative transthyretin precursor |
| | SPBC1683.05 | NCS1 allantoin transporter |
| | SPCC417.10 | putative MFS allantoin transporter |
| | SPAC1039.04 | MFS transporter of unknown specificity |
| | SPBC1683.12 | MFS transporter of unknown specificity |
| | SPAC3H1.06C | MFS transporter of unknown specificity |
| | SPAC1399.02 | MFS transporter of unknown specificity |
| | SPBC1271.09 | MFS transporter of unknown specificity |
| <i>fnx1</i> | SPBC12C2.13C | MFS multidrug efflux transporter |
| | SPAC17C9.16C | MFS multidrug efflux transporter |
| | SPCC965.13 | MFS amiloride efflux transporter; car1 homologue |
| | SPAC29B12.14C | NCS1 uracil transporter |
| | SPCC285.05 | purine transporter |
| | SPAC1399.01C | purine permease |
| <i>fur4</i> | SPAC1399.03 | uracil permease |
| | SPBC887.17 | uracil permease |
| | SPAP7G5.06 | amino acid permease |
| | SPCPB1C11.02 | putative amino acid permease |
| | SPBPB2B2.01 | putative amino acid permease |
| | SPAC11D3.08C | APC amino acid transporter |
| | SPAC1039.01 | APC amino acid transporter |
| | SPAC869.03C | SSS urea transporter |
| | SPAC323.07C | conserved protein; UPF0013; putative membrane transporter |
| Sequence orphans | | |
| | SPAC11D3.16C | hypothetical protein; sequence orphan |
| | SPBC800.14C | hypothetical protein; sequence orphan; contains 4 predicted transmembrane helices |
| | SPAC630.07C | hypothetical protein; sequence orphan |
| | SPCC191.05C | hypothetical protein; sequence orphan |
| | SPCC191.06 | hypothetical protein; sequence orphan |
| | SPBC1347.11 | hypothetical protein; sequence orphan |
| | SPBC651.04 | hypothetical protein; sequence orphan |
| | SPCC1322.10 | hypothetical protein; sequence orphan; S-T protein; similar to cell-surface proteins; similar to proteoglycans |
| | SPBC1289.15 | low similarity to seripauperin (PAU) family of possible cell wall mannoproteins |
| Stress response | | |
| <i>hos3</i> | SPCC417.02 | protein necessary for growth under high osmotic stress |

| Transcriptional regulation | | |
|-----------------------------------|--------------|---|
| | SPAC1039.05C | C2H2 zinc finger protein |
| | SPAC11D3.17 | putative transcription factor btd |
| | SPBC1773.12 | putative transcriptional regulator, zinc-finger, binuclear cluster domain |
| Cell cycle regulators | | |
| <i>puc1</i> | SPBC19F5.01C | cyclin |
| Others | | |
| | SPAC20G4.03C | serine/threonine protein kinase; probably regulates initiation of translation by phosphorylation of eIF2alpha |
| | SPAC977.13C | putative hydrolase pseudogene |
| | SPAC1002.18 | hypothetical protein, conserved in other yeasts |
| | SPBC3E7.12C | very putative chitin synthase regulatory factor |
| | SPAC2F3.05C | aldo/keto reductase family oxidoreductase |
| | SPBC215.11C | putative oxidoreductase; aldo-keto family |
| | SPBC9B6.03 | hypothetical zinc finger protein |
| | SPCC576.04 | putative receptor-associated protein |
| | SPAC11D3.03C | conserved hypothetical protein |
| | SPBC839.02 | hypothetical protein; possibly fungal specific |
| | SPCC18.01C | hypothetical protein; SUN family; serine-rich; contains predicted N-terminal signal sequence |
| | SPBP35G2.11C | protein containing 3 ZZ domain zinc finger domains |
| | SPCC965.06 | putative potassium channel subunit |
| | SPCC63.08C | putative serine/threonine protein kinase; <i>S. cerevisiae</i> homologue <i>APG1</i> is involved in autophagy |
| | SPBC800.11 | putative inosine-uridine preferring nucleoside hydrolase |