

Supplemental Materials: AYbRAH: a curated ortholog database for yeasts and fungi spanning 600 million years of evolution

October 8, 2018

Contents

| | | |
|----------|---|----------|
| 1 | Comparison of AYbRAH orthology assignments to published ortholog databases | 2 |
| 2 | Sample webpages for homolog groups | 6 |

1 Comparison of AYbRAH orthology assignments to published ortholog databases

Table S1: **Comparison of manually curated acetyl-Coenzyme A synthetase orthologs in AYbRAH to highly cited ortholog databases.** N/A indicates genomes that do not have orthology relationships in the public database but have been assigned orthology with AYbRAH. Omission indicates genomes that have annotations in the public ortholog database but do not have an annotation for the given gene. PANTHER is the only database that can distinguish between the three ACS ortholog groups; ACS3 is assigned to a different PANTHER family despite the shared ancestry of all the orthologs. KEGG can only differentiate between ACS1 and ACS3 ortholog groups, while all other database orthology assignments are polyphyletic. EggNOG includes FOG07524 and FOG07525 in the ACS ortholog group, which both have predicted acetoacetate-CoA ligase activity.

| AYbRAH Annotation | | Ortholog DB | spo | ang | ncr | yli | ppa | pic | kla | sce |
|-------------------|----------|-------------|----------------|-----------|----------------|----------------|-----------|------------|------------|-----------------|
| ACS1 | FOG00404 | PANTHER | PTHR24095:SF14 | N/A | PTHR24095:SF14 | PTHR24095:SF14 | N/A | N/A | N/A | PTHR24095:SF14 |
| ACS2 | FOG00405 | | | | | | N/A | N/A | N/A | PTHR24095:SF245 |
| ACS3 | FOG00406 | | | N/A | PTHR43347:SF3 | | | | | |
| ACS1 | FOG00404 | KEGG | K01895 | K01895 | K01895 | K01895 | K01895 | K01895 | K01895 | K01895 |
| ACS2 | FOG00405 | | | | | | K01895 | K01895 | K01895 | K01895 |
| ACS3 | FOG00406 | | | K01908 | K01908 | | | | | |
| ACS1 | FOG00404 | OrthoMCL | OG5_126680 | N/A | OG5_126680 | OG5_126680 | N/A | OG5_126680 | OG5_126680 | OG5_126680 |
| ACS2 | FOG00405 | | | | | | N/A | OG5_126680 | OG5_126680 | OG5_126680 |
| ACS3 | FOG00406 | | | N/A | OG5_126680 | | | | | |
| ACS1 | FOG00404 | OrthoDB | EOG8HQC0H | EOG8HQC0H | EOG8HQC0H | EOG8HQC0H | EOG8HQC0H | EOG8HQC0H | EOG8HQC0H | EOG8HQC0H |
| ACS2 | FOG00405 | | | | | | EOG8HQC0H | EOG8HQC0H | EOG8HQC0H | EOG8HQC0H |
| ACS3 | FOG00406 | | | omission | EOG8HQC0H | | | | | |
| ACS1 | FOG00404 | EggNOG | KOG1175 | KOG1175 | KOG1175 | KOG1175 | KOG1175 | KOG1175 | KOG1175 | KOG1175 |
| ACS2 | FOG00405 | | | | | | KOG1175 | KOG1175 | KOG1175 | KOG1175 |
| ACS3 | FOG00406 | | | KOG1175 | KOG1175 | | | | | |
| HYP | FOG07524 | | | KOG1175 | KOG1175 | | | | | |
| HYP | FOG07525 | | | KOG1175 | KOG1175 | | | | | |

Table S2: **Comparison of manually curated Type II NADH dehydrogenase (NDH2) orthologs in AYbRAH to highly cited ortholog databases.** N/A indicates genomes that do not have orthology relationships in the public database but have been assigned orthology with AYbRAH. Omission indicates genomes that have annotations in the public ortholog database but do not have an annotation for the given gene. PANTHER is able to distinguish between most orthologs in the NDH2 family, with the exception of NDE1 and NDE2; NDE0 is in a different PANTHER family than the rest of the NDH2 genes. KEGG is the only other database that can differentiate between some NDH2 genes; the genes are split between the older NDI0/NDE0 ortholog group and more recent NDE1/NDI1 ortholog group. PANTHER and EggNOG contain additional genes not included in other ortholog databases, which may represent ancient paralogs having lower sequence similarities than other NDH2 paralogs. AIF1, which can localize to the mitochondria in *S. cerevisiae*, is in the same subfamily as NDE0 in PANTHER; the other inconsistency is an *Aspergillus niger* gene (FOG07265) paralogous to a characterized external NADH dehydrogenase in *Neurospora crassa* (FOG07264) in EggNOG (Carneiro et al., 2007).

| AYbRAH annotation | Ortholog Database | spo | ang | ncr | yli | ppa | pic | kla | sce | |
|-------------------|-------------------|-----|---------------|----------------|---------------|---------------|-----------|------------|---------------|----------------|
| NDI0 FOG00837 | PANTHER | | N/A | PTHR43706:SF11 | | | | | | |
| NDE0 FOG00838 | | | N/A | PTHR42913:SF2 | PTHR42913:SF2 | N/A | | N/A | | |
| AIF1 FOG11982 | | | | | | | N/A | | PTHR42913:SF2 | |
| NDE1 FOG00839 | | | PTHR43706:SF1 | N/A | PTHR43706:SF1 | PTHR43706:SF1 | N/A | N/A | N/A | PTHR43706:SF1 |
| NDE2 FOG00845 | | | | | | | | N/A | | PTHR43706:SF1 |
| NDI1 FOG00846 | | | | | | | | | N/A | PTHR43706:SF10 |
| NDI0 FOG00837 | KEGG | | omission | K03885 | | | | | | |
| NDE0 FOG00845 | | | omission | K03885 | K03885 | K03885 | | K03885 | | |
| NDE1 FOG00845 | | | K17871 | K17871 | omission | K17871 | K17871 | K17871 | K17871 | |
| NDE2 FOG00845 | | | | | | | | | K17871 | |
| NDI1 FOG00845 | | | | | | | | K17871 | K17871 | |
| NDI0 FOG00837 | OrthoMCL | | N/A | OG5_126960 | | | | | | |
| NDE0 FOG00838 | | | N/A | OG5_126960 | OG5_126960 | N/A | | OG5_126960 | | |
| NDE1 FOG00839 | | | OG5_126960 | N/A | OG5_126960 | OG5_126960 | N/A | OG5_126960 | OG5_126960 | |
| NDE2 FOG00845 | | | | | | | | | OG5_126960 | |
| NDI1 FOG00846 | | | | | | | | OG5_126960 | OG5_126960 | |
| NDI0 FOG00837 | OrthoDB | | EOG8P8D18 | EOG8P8D18 | | | | | | |
| NDE0 FOG00838 | | | EOG8P8D18 | EOG8P8D18 | EOG8P8D18 | EOG8P8D18 | | EOG8P8D18 | | |
| NDE1 FOG00839 | | | EOG8P8D18 | EOG8P8D18 | EOG8P8D18 | EOG8P8D18 | EOG8P8D18 | EOG8P8D18 | EOG8P8D18 | |
| NDE2 FOG00845 | | | | | | | | | EOG8P8D18 | |
| NDI1 FOG00846 | | | | | | | | EOG8P8D18 | EOG8P8D18 | |
| NDI0 FOG00837 | EggNOG | | KOG2495 | KOG2495 | | | | | | |
| NDE0 FOG00838 | | | KOG2495 | KOG2495 | KOG2495 | KOG2495 | | KOG2495 | | |
| NDE1 FOG00839 | | | KOG2495 | KOG2495 | KOG2495 | KOG2495 | KOG2495 | KOG2495 | KOG2495 | |
| NDE2 FOG00845 | | | | | | | | | KOG2495 | |
| NDI1 FOG00846 | | | | | | | | KOG2495 | KOG2495 | |
| HYP FOG07265 | | | | KOG2495 | | | | | | |

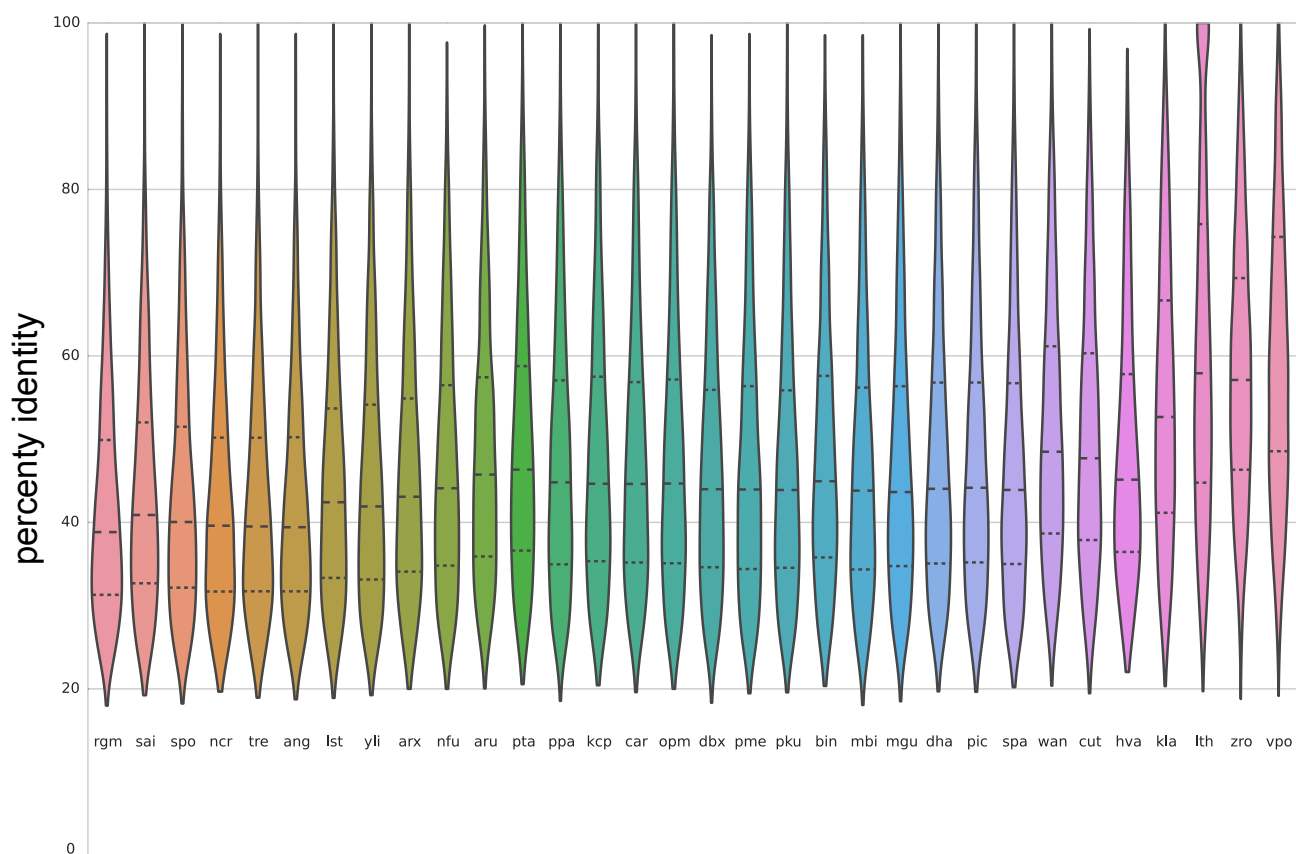


Figure S1: Distributions of BLASTP percent identities for proteins identified as orthologous to *Saccharomyces cerevisiae* in AYbRAH.

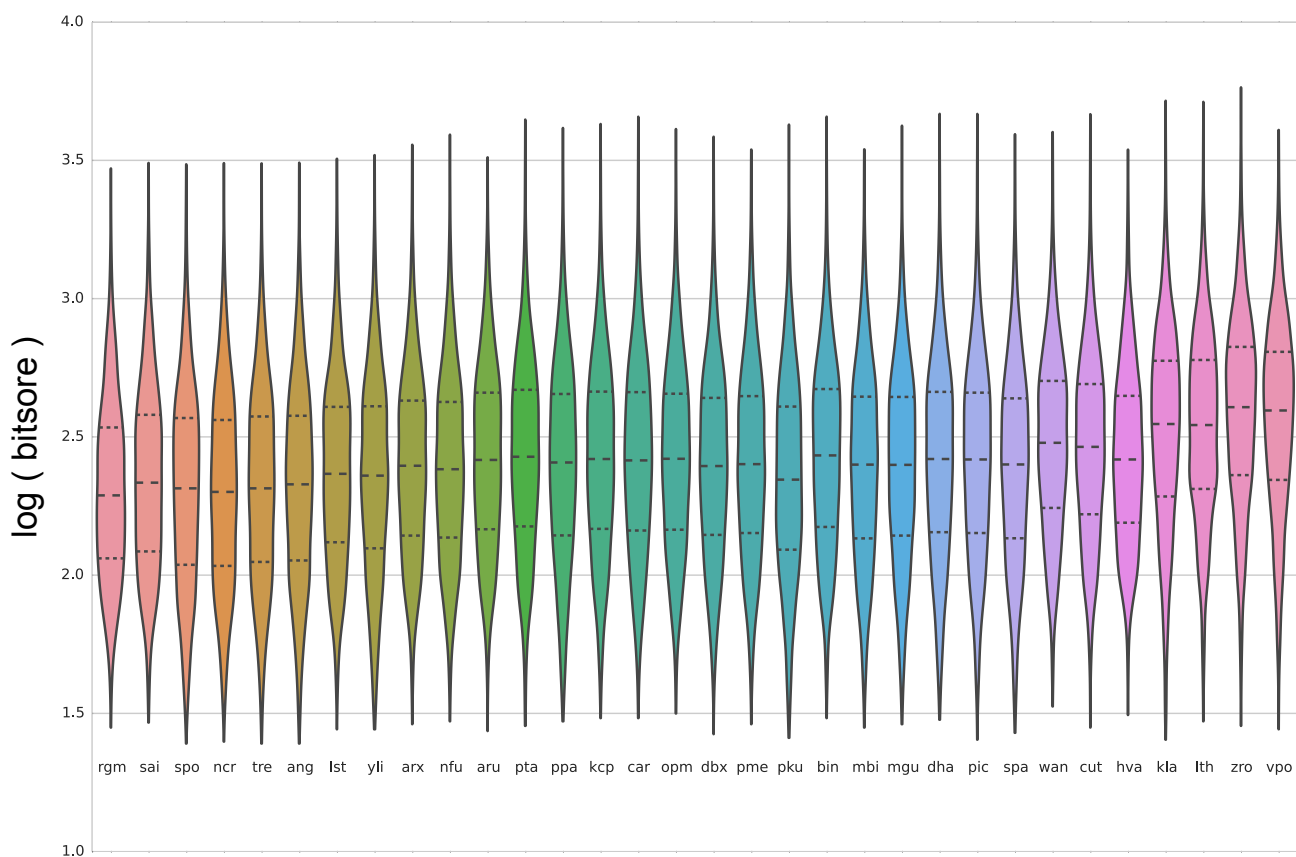


Figure S2: Distributions of logarithm BLASTP bitscores for proteins orthologous to *Saccharomyces cerevisiae* in AYbRAH.

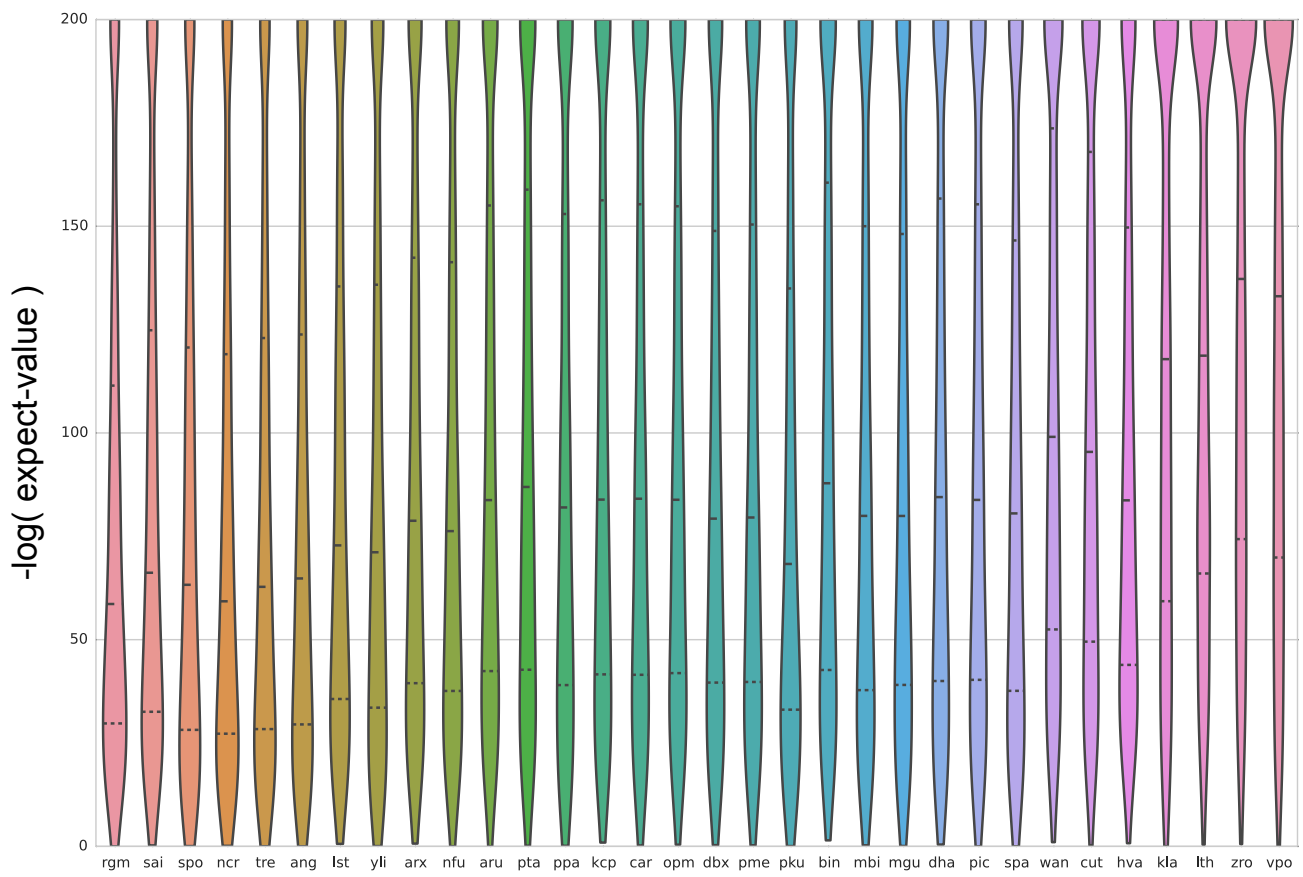


Figure S3: Distributions of negative logarithm of BLASTP expect-values for proteins orthologous to *Saccharomyces cerevisiae* in AYbRAH.

2 Sample webpages for homolog groups



[Home](#)

[HOG00227](#) [HAD-like hydrolase superfamily, DOG/GPP family](#)

[HOG00229](#)

[HOG00230](#) [acetyl-CoA hydrolase/transferase family](#)

[FASTA](#)

[MAFFT sequence alignment](#)

[Phyml trees](#)

[Gblocks](#)

[Phobius predictions](#)

FOG00404
EOG8HQC0H
ACS1
sce:ACS1

Genes: 34

Protein description

Acetyl-coA synthetase isoform expressed with non-fermentable carbon sources. Spo gene expressed with fermentable carbon sources.

SGD Description

Acetyl-coA synthetase isoform; along with Acs2p, acetyl-coA synthetase isoform is the nuclear source of acetyl-coA for histone acetylation; expressed during growth on nonfermentable carbon sources and under aerobic conditions

PomBase Description

acetyl-CoA ligase (predicted)

AspGD Description

Putative acetyl-CoA synthase

References

[Armitt S, et al. \(1976 Feb\)](#). Analysis of acetate non-utilizing (acu) mutants in *Aspergillus nidulans*.

[Payton M, et al. \(1976 May\)](#). Agar as a carbon source and its effect on the utilization of other carbon sources by acetate non-utilizing (acu) mutants of *Aspergillus nidulans*.

[Frenkel EP, et al. \(1977 Jan 25\)](#). Purification and properties of acetyl coenzyme A synthetase from bakers' yeast.

[Hynes MJ, et al. \(1977 Sep\)](#). Induction of the acetamidase of *Aspergillus nidulans* by acetate metabolism.

[Midelfort CF, et al. \(1978 Oct 25\)](#). The stereochemical course of acetate activation by yeast acetyl-CoA synthetase.

- [Bal J, et al. \(1979 Dec\)](#). Allele specific and locus non-specific suppressors in *Aspergillus nidulans*.
- [Kelly JM, et al. \(1981 Apr\)](#). The regulation of phosphoenolpyruvate carboxykinase and the NADP-linked malic enzyme in *Aspergillus nidulans*.
- [Sandeman RA, et al. \(1989 Jul\)](#). Isolation of the *facA* (acetyl-coenzyme A synthetase) and *acuE* (malate synthase) genes of *Aspergillus nidulans*.
- [Connerton IF, et al. \(1990 Mar\)](#). Comparison and cross-species expression of the acetyl-CoA synthetase genes of the Ascomycete fungi, *Aspergillus nidulans* and *Neurospora crassa*.
- [Lloyd AT, et al. \(1991 Nov\)](#). Codon usage in *Aspergillus nidulans*.
- [Sandeman RA, et al. \(1991 Sep\)](#). Molecular organisation of the malate synthase genes of *Aspergillus nidulans* and *Neurospora crassa*.
- [Birch PR, et al. \(1992\)](#). Nucleotide sequence of a gene from *Phanerochaete chrysosporium* that shows homology to the *facA* gene of *Aspergillus nidulans*.
- [Maconochie MK, et al. \(1992 Aug\)](#). The *acu-1* gene of *Coprinus cinereus* is a regulatory gene required for induction of acetate utilisation enzymes.
- [De Virgilio C, et al. \(1992 Dec\)](#). Cloning and disruption of a gene required for growth on acetate but not on ethanol: the acetyl-coenzyme A synthetase gene of *Saccharomyces cerevisiae*.
- [Kujau M, et al. \(1992 Mar\)](#). Characterization of mutants of the yeast *Yarrowia lipolytica* defective in acetyl-coenzyme A synthetase.
- [Saleeba JA, et al. \(1992 Nov\)](#). Characterization of the *amdA*-regulated *aciA* gene of *Aspergillus nidulans*.
- [Steensma HY, et al. \(1993 Apr\)](#). Genetic and physical localization of the acetyl-coenzyme A synthetase gene *ACS1* on chromosome I of *Saccharomyces cerevisiae*.
- [Martínez-Blanco H, et al. \(1993 Aug 25\)](#). Characterisation of the gene encoding acetyl-CoA synthetase in *Penicillium chrysogenum*: conservation of intron position in plectomycetes.
- [Gouka RJ, et al. \(1993 Jan\)](#). Development of a new transformant selection system for *Penicillium chrysogenum*: isolation and characterization of the *P. chrysogenum* acetyl-coenzyme A synthetase gene (*facA*) and its use as a homologous selection marker.
- [Sealy-Lewis HM, et al. \(1994 Jan\)](#). A new selection method for isolating mutants defective in acetate utilisation in *Aspergillus nidulans*.
- [Van den Berg MA, et al. \(1995 Aug 1\)](#). *ACS2*, a *Saccharomyces cerevisiae* gene encoding acetyl-coenzyme A synthetase, essential for growth on glucose.
- [Kratzer S, et al. \(1995 Aug 8\)](#). Carbon source-dependent regulation of the acetyl-coenzyme A synthetase-encoding gene *ACS1* from *Saccharomyces cerevisiae*.
- [van den Berg MA, et al. \(1996 Nov 15\)](#). The two acetyl-coenzyme A synthetases of *Saccharomyces cerevisiae* differ with respect to kinetic properties and transcriptional regulation.
- [de Jong-Gubbels P, et al. \(1997 Aug 1\)](#). The *Saccharomyces cerevisiae* acetyl-coenzyme A synthetase encoded by the *ACS1* gene, but not the *ACS2*-encoded enzyme, is subject to

glucose catabolite inactivation.

[Clutterbuck AJ, et al. \(1997 Jun\)](#). The validity of the *Aspergillus nidulans* linkage map.

[Todd RB, et al. \(1998 Apr 1\)](#). FacB, the *Aspergillus nidulans* activator of acetate utilization genes, binds dissimilar DNA sequences.

[Stemple CJ, et al. \(1998 Dec\)](#). The facC gene of *Aspergillus nidulans* encodes an acetate-inducible carnitine acetyltransferase.

[Papadopoulou S, et al. \(1999 Sep 1\)](#). The *Aspergillus niger* acuA and acuB genes correspond to the facA and facB genes in *Aspergillus nidulans*.

[Dessen P, et al. \(2000 Feb 22\)](#). The PAUSE software for analysis of translational control over protein targeting: application to *E. nidulans* membrane proteins.

[Brock M, et al. \(2000 Mar\)](#). Methylcitrate synthase from *Aspergillus nidulans*: implications for propionate as an antifungal agent.

[Jones IG, et al. \(2001 Feb\)](#). ADHII in *Aspergillus nidulans* is induced by carbon starvation stress.

[Lodi T, et al. \(2001 Sep\)](#). Three target genes for the transcriptional activator Cat8p of *Kluyveromyces lactis*: acetyl coenzyme A synthetase genes KIACS1 and KIACS2 and lactate permease gene KIJEN1.

[Hynes MJ, et al. \(2002 Jan\)](#). Regulation of the acuF gene, encoding phosphoenolpyruvate carboxykinase in the filamentous fungus *Aspergillus nidulans*.

[Kumar A, et al. \(2002 Mar 15\)](#). Subcellular localization of the yeast proteome.

[Flipphi M, et al. \(2002 May 15\)](#). Characteristics of physiological inducers of the ethanol utilization (alc) pathway in *Aspergillus nidulans*.

[Flipphi M, et al. \(2003 Apr 4\)](#). Onset of carbon catabolite repression in *Aspergillus nidulans*. Parallel involvement of hexokinase and glucokinase in sugar signaling.

[Zeeman AM, et al. \(2003 Jan 15\)](#). The acetyl co-enzyme A synthetase genes of *Kluyveromyces lactis*.

[Sickmann A, et al. \(2003 Nov 11\)](#). The proteome of *Saccharomyces cerevisiae* mitochondria.

[Flipphi M, et al. \(2003 Sep\)](#). Relationships between the ethanol utilization (alc) pathway and unrelated catabolic pathways in *Aspergillus nidulans*.

[Brock M, et al. \(2004 Aug\)](#). On the mechanism of action of the antifungal agent propionate.

[Sims AH, et al. \(2004 Feb\)](#). Use of expressed sequence tag analysis and cDNA microarrays of the filamentous fungus *Aspergillus nidulans*.

[Jogl G, et al. \(2004 Feb 17\)](#). Crystal structure of yeast acetyl-coenzyme A synthetase in complex with AMP.

[Takasaki K, et al. \(2004 Mar 26\)](#). Fungal ammonia fermentation, a novel metabolic mechanism that couples the dissimilatory and assimilatory pathways of both nitrate and ethanol. Role of acetyl CoA synthetase in anaerobic ATP synthesis.

[Zhang YQ, et al. \(2004 Oct\)](#). Connection of propionyl-CoA metabolism to polyketide biosynthesis in *Aspergillus nidulans*.

[David H, et al. \(2006\)](#). Metabolic network driven analysis of genome-wide transcription data from *Aspergillus nidulans*.

[Mogensen J, et al. \(2006 Aug\)](#). Transcription analysis using high-density micro-arrays of *Aspergillus nidulans* wild-type and *creA* mutant during growth on glucose or ethanol.

[Takahashi H, et al. \(2006 Jul 21\)](#). Nucleocytoplasmic acetyl-coenzyme A synthetase is required for histone acetylation and global transcription.

[Hynes MJ, et al. \(2006 May\)](#). Regulatory genes controlling fatty acid catabolism and peroxisomal functions in the filamentous fungus *Aspergillus nidulans*.

[Salazar M, et al. \(2009 Dec\)](#). Uncovering transcriptional regulation of glycerol metabolism in *Aspergilli* through genome-wide gene expression data analysis.

[Shimizu M, et al. \(2009 Jan\)](#). Proteomic analysis of *Aspergillus nidulans* cultured under hypoxic conditions.

[Flipphi M, et al. \(2009 Mar\)](#). Biodiversity and evolution of primary carbon metabolism in *Aspergillus nidulans* and other *Aspergillus* spp.

[Hynes MJ, et al. \(2010 Jul\)](#). ATP-citrate lyase is required for production of cytosolic acetyl coenzyme A and development in *Aspergillus nidulans*.

[Oh YT, et al. \(2010 Mar\)](#). Proteomic analysis of early phase of conidia germination in *Aspergillus nidulans*.

[Wendland J, et al. \(2011 Dec\)](#). Genome evolution in the eremothecium clade of the *Saccharomyces* complex revealed by comparative genomics.

[Saykhedkar S, et al. \(2012 Jul 26\)](#). A time course analysis of the extracellular proteome of *Aspergillus nidulans* growing on sorghum stover.

[Georgakopoulos P, et al. \(2012 Nov\)](#). SAGA complex components and acetate repression in *Aspergillus nidulans*.

[Nakamura T, et al. \(2012 Sep\)](#). Impaired coenzyme A synthesis in fission yeast causes defective mitosis, quiescence-exit failure, histone hypoacetylation and fragile DNA.

[Carpny A, et al. \(2014 Aug\)](#). Absolute proteome and phosphoproteome dynamics during the cell cycle of *Schizosaccharomyces pombe* (Fission Yeast).

[Beckley JR, et al. \(2015 Dec\)](#). A Degenerate Cohort of Yeast Membrane Trafficking DUBs Mediates Cell Polarity and Survival.

[Malecki M, et al. \(2016 Nov 25\)](#). Functional and regulatory profiling of energy metabolism in fission yeast.

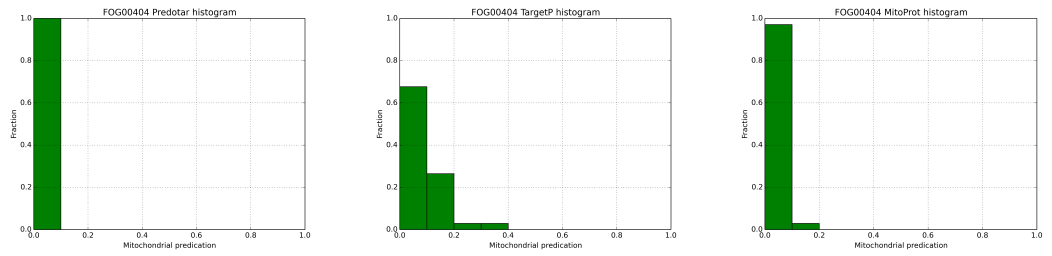
Mitochondrial localization predications

[Predotar](#)

[TargetP](#)

[MitoProt](#)

Mitochondrial localization predictions



[Raw data](#)

[Phobius transmembrane predictions](#)

24 genes with posterior transmembrane prediction > 50%

FOG00405
EOG8HQC0H
ACS2
sce:ACS2

Genes: 26

Protein description

Acetyl-coA synthetase isoform expressed with fermentable carbon sources

Parent

paralog:FOG00404

SGD Description

Acetyl-coA synthetase isoform; along with Acs1p, acetyl-coA synthetase isoform is the nuclear source of acetyl-coA for histone acetylation; mutants affect global transcription; required for growth on glucose; expressed under anaerobic conditions

References

[Frenkel EP, et al. \(1977 Jan 25\)](#). Purification and properties of acetyl coenzyme A synthetase from bakers' yeast.

[Midelfort CF, et al. \(1978 Oct 25\)](#). The stereochemical course of acetate activation by yeast acetyl-CoA synthetase.

[De Virgilio C, et al. \(1992 Dec\)](#). Cloning and disruption of a gene required for growth on acetate but not on ethanol: the acetyl-coenzyme A synthetase gene of *Saccharomyces cerevisiae*.

[Van den Berg MA, et al. \(1995 Aug 1\)](#). ACS2, a *Saccharomyces cerevisiae* gene encoding acetyl-coenzyme A synthetase, essential for growth on glucose.

[Kratzer S, et al. \(1995 Aug 8\)](#). Carbon source-dependent regulation of the acetyl-coenzyme A synthetase-encoding gene ACS1 from *Saccharomyces cerevisiae*.

[van den Berg MA, et al. \(1996 Nov 15\)](#). The two acetyl-coenzyme A synthetases of *Saccharomyces cerevisiae* differ with respect to kinetic properties and transcriptional regulation.

[de Jong-Gubbels P, et al. \(1997 Aug 1\)](#). The *Saccharomyces cerevisiae* acetyl-coenzyme A synthetase encoded by the ACS1 gene, but not the ACS2-encoded enzyme, is subject to glucose catabolite inactivation.

[Lodi T, et al. \(2001 Sep\)](#). Three target genes for the transcriptional activator Cat8p of *Kluyveromyces lactis*: acetyl coenzyme A synthetase genes KIACS1 and KIACS2 and lactate permease gene KIJEN1.

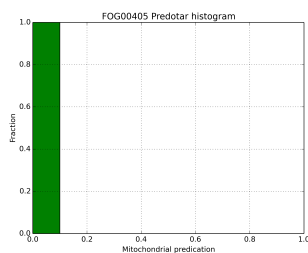
[Peng J, et al. \(2003 Aug\)](#). A proteomics approach to understanding protein ubiquitination.

[Zeeman AM, et al. \(2003 Jan 15\)](#). The acetyl co-enzyme A synthetase genes of *Kluyveromyces lactis*.

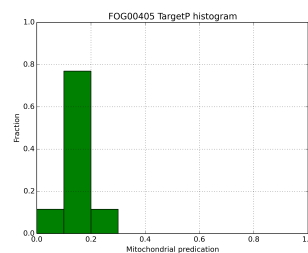
[Takahashi H, et al. \(2006 Jul 21\)](#). Nucleocytosolic acetyl-coenzyme a synthetase is required for histone acetylation and global transcription.

Mitochondrial localization predications

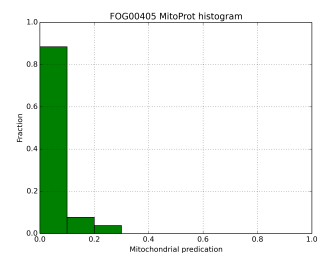
[Predotar](#)



[TargetP](#)



[MitoProt](#)



[Raw data](#)

[Phobius transmembrane predictions](#)

16 genes with posterior transmembrane prediction > 50%

FOG00406
EOG8HQC0H
ACS3
sce:absent

Genes: 3

Protein description

Uncharacterized acetyl-coA synthetase paralog

Parent

paralog:FOG00404

AspGD Description

Putative acetyl-CoA synthase

References

[Zhang YQ, et al. \(2004 Oct\)](#). Connection of propionyl-CoA metabolism to polyketide biosynthesis in *Aspergillus nidulans*.

[Salazar M, et al. \(2009 Dec\)](#). Uncovering transcriptional regulation of glycerol metabolism in *Aspergilli* through genome-wide gene expression data analysis.

[Flipphi M, et al. \(2009 Mar\)](#). Biodiversity and evolution of primary carbon metabolism in *Aspergillus nidulans* and other *Aspergillus* spp.

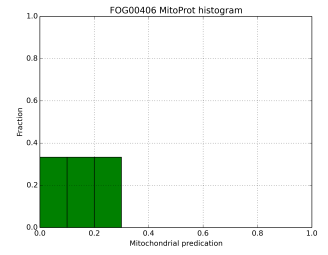
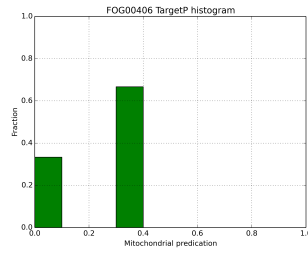
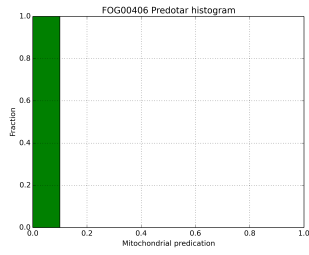
[Lee MK, et al. \(2014 May\)](#). NsdD is a key repressor of asexual development in *Aspergillus nidulans*.

Mitochondrial localization predications

[Predotar](#)

[TargetP](#)

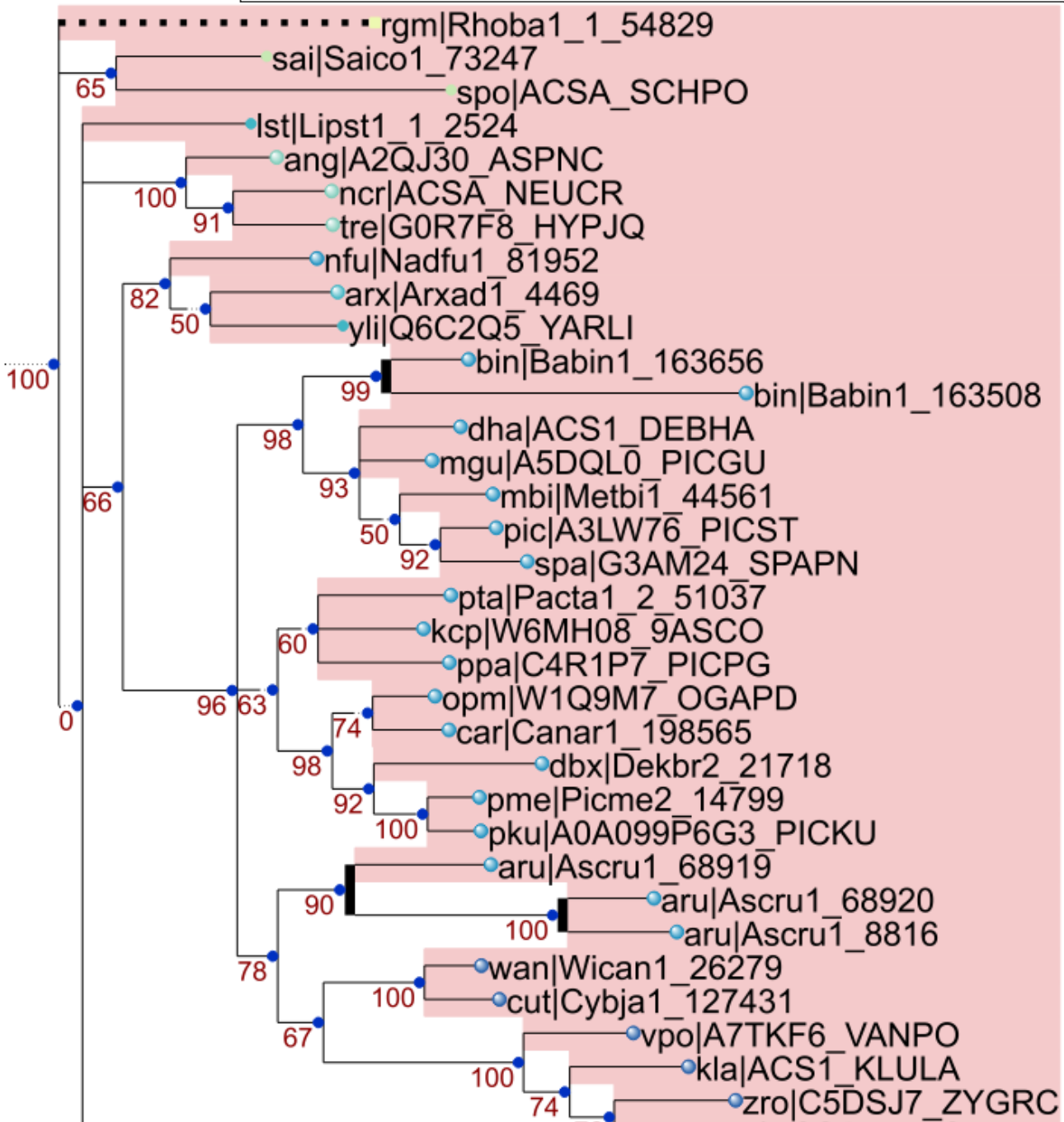
[MitoProt](#)

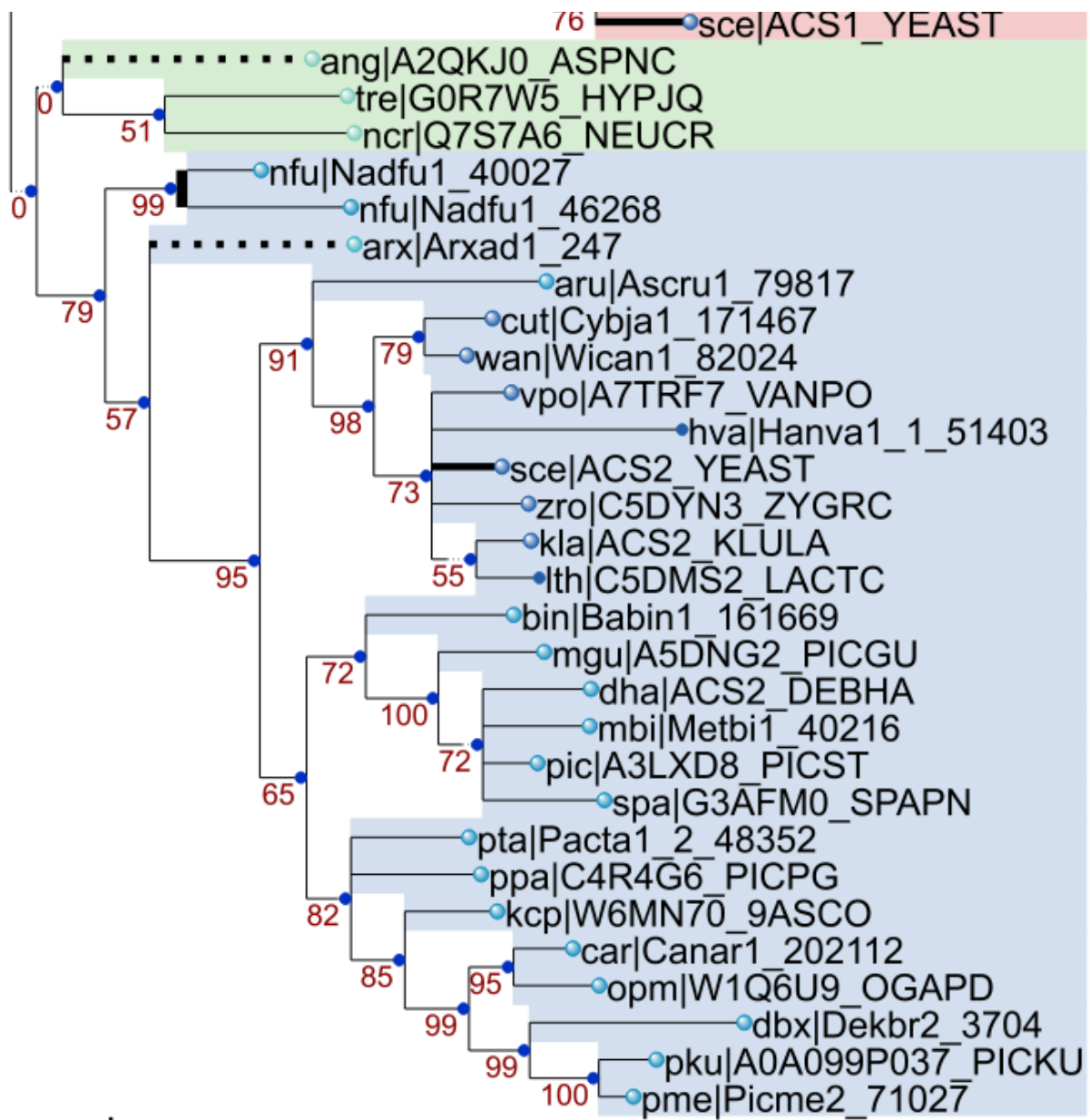


[Raw data](#)

[Phobius transmembrane predictions](#)

3 genes with posterior transmembrane prediction > 50%





0.32

[Home](#)

[HOG00398](#) [FMC1 family](#)

[HOG00399](#)

[HOG00403](#) [SUN family](#)

[FASTA](#)

[MAFFT sequence alignment](#)

[Phyml trees](#)

[Gblocks](#)

[Phobius predictions](#)

FOG00837
EOG8P8D18
NDI0
sce:absent

Genes: 6

Protein description

Internal NADH dehydrogenase, orthologous to NDH2 in *E. coli*

Features

NADH

AspGD Description

Ortholog(s) have NADPH dehydrogenase activity, role in spore germination and mitochondrial inner membrane localization

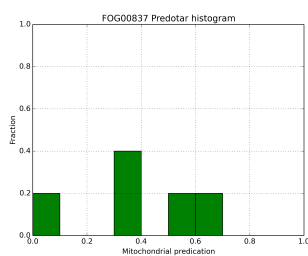
References

[Dinamarco TM, et al. \(2010 Dec\)](#). The roles played by *Aspergillus nidulans* apoptosis-inducing factor (AIF)-like mitochondrial oxidoreductase (AifA) and NADH-ubiquinone oxidoreductases (NdeA-B and NdiA) in farnesol resistance.

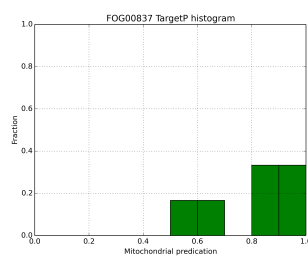
[Dinamarco TM, et al. \(2011 Oct\)](#). Farnesol-induced cell death in the filamentous fungus *Aspergillus nidulans*.

Mitochondrial localization predictions

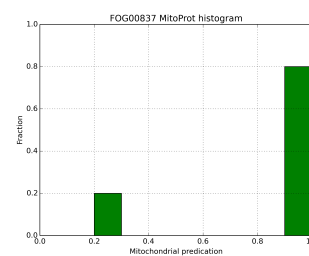
[Predotar](#)



[TargetP](#)



[MitoProt](#)



[Raw data](#)

Mitochondrial localization predications

[Phobius transmembrane predictions](#)

2 genes with posterior transmembrane prediction > 50%

FOG00838
EOG8P8D18
NDE0
sce:absent

Genes: 22

Protein description

External NADH and NADPH dehydrogenase

Features

NADH;NADPH

Parent

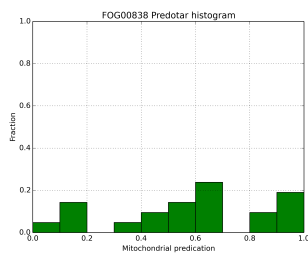
paralog:FOG00837

AspGD Description

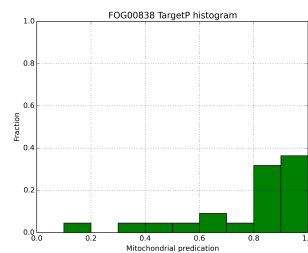
NADH-ubiquinone oxidoreductase; respiratory-chain NADH dehydrogenase

Mitochondrial localization predications

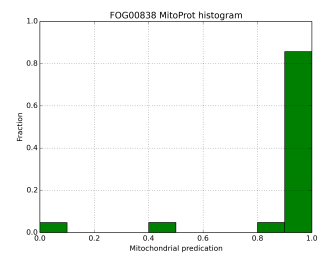
[Predotar](#)



[TargetP](#)



[MitoProt](#)



[Raw data](#)

[Phobius transmembrane predictions](#)

21 genes with posterior transmembrane prediction > 50%

FOG00839
EOG8P8D18
NDE1
sce:absent

Genes: 33

Protein description

External NADH and NADPH dehydrogenase, spo ortholog may have translate sites than enable internal NADH dehydrogenase

Features

NADH;NADPH

Parent

paralog:FOG00838

PomBase Description

mitochondrial NADH dehydrogenase (ubiquinone) Nde2 (predicted)

AspGD Description

NADH-ubiquinone oxidoreductase; respiratory-chain NADH dehydrogenase

References

[Kerscher SJ, et al. \(1999 Jul\)](#). A single external enzyme confers alternative NADH:ubiquinone oxidoreductase activity in *Yarrowia lipolytica*.

[Todd BL, et al. \(2006 Apr\)](#). Sterol regulatory element binding protein is a principal regulator of anaerobic gene expression in fission yeast.

[Harris SD, et al. \(2009 Mar\)](#). Morphology and development in *Aspergillus nidulans*: a complex puzzle.

[Dinamarco TM, et al. \(2010 Dec\)](#). The roles played by *Aspergillus nidulans* apoptosis-inducing factor (AIF)-like mitochondrial oxidoreductase (AifA) and NADH-ubiquinone oxidoreductases (NdeA-B and NdiA) in farnesol resistance.

[Arita Y, et al. \(2011 May\)](#). Microarray-based target identification using drug hypersensitive fission yeast expressing ORFeome.

[Dinamarco TM, et al. \(2011 Oct\)](#). Farnesol-induced cell death in the filamentous fungus *Aspergillus nidulans*.

[Lando D, et al. \(2012\)](#). The *S. pombe* histone H2A dioxygenase Ofd2 regulates gene expression during hypoxia.

[Cary A, et al. \(2014 Aug\)](#). Absolute proteome and phosphoproteome dynamics during the cell cycle of *Schizosaccharomyces pombe* (Fission Yeast).

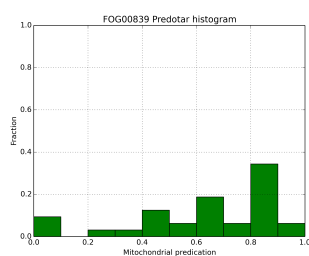
[Guo L, et al. \(2016 Oct 13\)](#). Global Fitness Profiling Identifies Arsenic and Cadmium Tolerance Mechanisms in Fission Yeast.

[Dudin O, et al. \(2017 Apr\)](#). A systematic screen for morphological abnormalities during fission yeast sexual reproduction identifies a mechanism of actin aster formation for cell fusion.

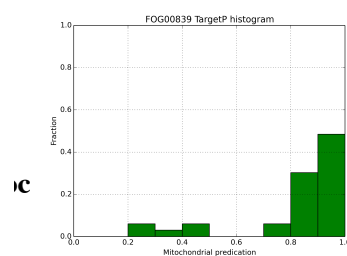
[Lee J, et al. \(2017 Feb 20\)](#). Chromatin remodeller Fun30^{>Fft3} induces nucleosome disassembly to facilitate RNA polymerase II elongation.</sup>

Mitochondrial localization predications

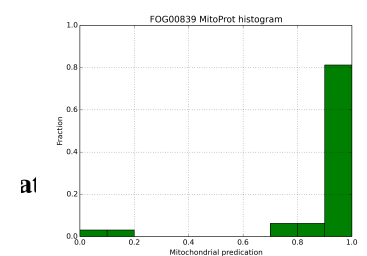
[Predotar](#)



[TargetP](#)



[MitoProt](#)



[Raw data](#)

[Phobius transmembrane predictions](#)

31 genes with posterior transmembrane prediction > 50%

FOG00840
EOG8P8D18
NDE1.2
sce:absent

Genes: 1

Protein description

External NADH and NADPH dehydrogenase, spo ortholog may have translate sites than enable internal NADH dehydrogenase

Parent

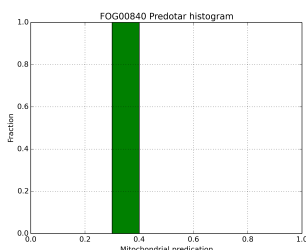
paralog:FOG00839

PomBase Description

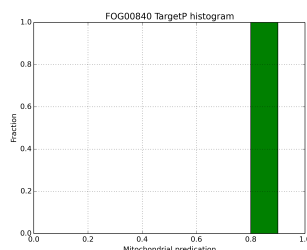
mitochondrial NADH dehydrogenase (ubiquinone) Nde1 (predicted)

Mitochondrial localization predictions

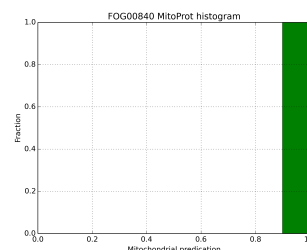
[Predotar](#)



[TargetP](#)



[MitoProt](#)



[Raw data](#)

[Phobius transmembrane predictions](#)

1 genes with posterior transmembrane prediction > 50%

FOG00841
EOG8P8D18
NDE1
sce:NDE1

Genes: 2

Protein description

External NADH dehydrogenase, loss of NADPH activity

Parent

ortholog:FOG00839

SGD Description

Mitochondrial external NADH dehydrogenase; type II NAD(P)H:quinone oxidoreductase that catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p provide cytosolic NADH to the mitochondrial respiratory chain; NDE1 has a paralog, NDE2, that arose from the whole genome duplication

References

[Small WC, et al. \(1998 Aug\)](#). Identification of a cytosolically directed NADH dehydrogenase in mitochondria of *Saccharomyces cerevisiae*.

[Luttik MA, et al. \(1998 Sep 18\)](#). The *Saccharomyces cerevisiae* NDE1 and NDE2 genes

encode separate mitochondrial NADH dehydrogenases catalyzing the oxidation of cytosolic NADH.

[Kerscher SJ, et al. \(2000 Aug 15\)](#). Diversity and origin of alternative NADH:ubiquinone oxidoreductases.

[Overkamp KM, et al. \(2000 May\)](#). In vivo analysis of the mechanisms for oxidation of cytosolic NADH by *Saccharomyces cerevisiae* mitochondria.

[Joseph-Horne T, et al. \(2001 Apr 2\)](#). Fungal respiration: a fusion of standard and alternative components.

[Grandier-Vazeille X, et al. \(2001 Aug 21\)](#). Yeast mitochondrial dehydrogenases are associated in a supramolecular complex.

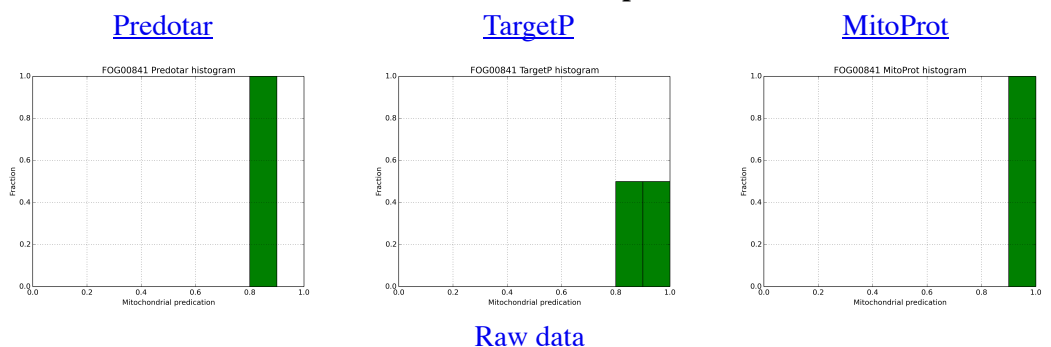
[Davidson JF, et al. \(2001 Dec\)](#). Mitochondrial respiratory electron carriers are involved in oxidative stress during heat stress in *Saccharomyces cerevisiae*.

[Bakker BM, et al. \(2001 Jan\)](#). Stoichiometry and compartmentation of NADH metabolism in *Saccharomyces cerevisiae*.

[Pählman IL, et al. \(2002 Aug 2\)](#). Kinetic regulation of the mitochondrial glycerol-3-phosphate dehydrogenase by the external NADH dehydrogenase in *Saccharomyces cerevisiae*.

[Sickmann A, et al. \(2003 Nov 11\)](#). The proteome of *Saccharomyces cerevisiae* mitochondria.

Mitochondrial localization predications



[Phobius transmembrane predictions](#)

2 genes with posterior transmembrane prediction > 50%

FOG00842

NDI2
sce:absent

Genes: 1

Features
NADH

Parent
paralog:FOG00839

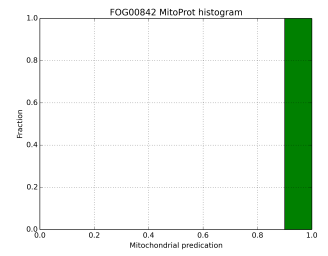
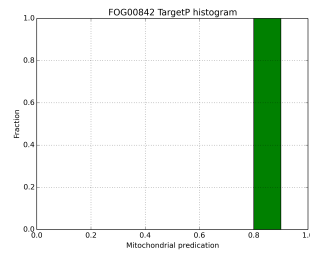
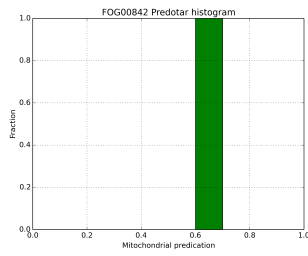
Mitochondrial localization predications

[Predotar](#)

[TargetP](#)

[MitoProt](#)

Mitochondrial localization predictions



[Raw data](#)

[Phobius transmembrane predictions](#)

0 genes with posterior transmembrane prediction > 50%

FOG00843

NDE1.3
sce:absent

Genes: 2

Protein description

External NADH and NADPH dehydrogenase

Parent

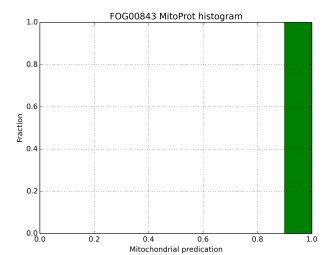
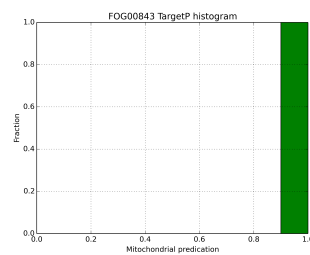
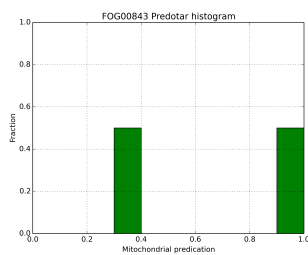
paralog:FOG00841

Mitochondrial localization predictions

[Predotar](#)

[TargetP](#)

[MitoProt](#)



[Raw data](#)

[Phobius transmembrane predictions](#)

2 genes with posterior transmembrane prediction > 50%

FOG00844

NDE1.4
sce:absent

Genes: 1

Protein description

External NADH and NADPH dehydrogenase

Parent

paralog:FOG00843

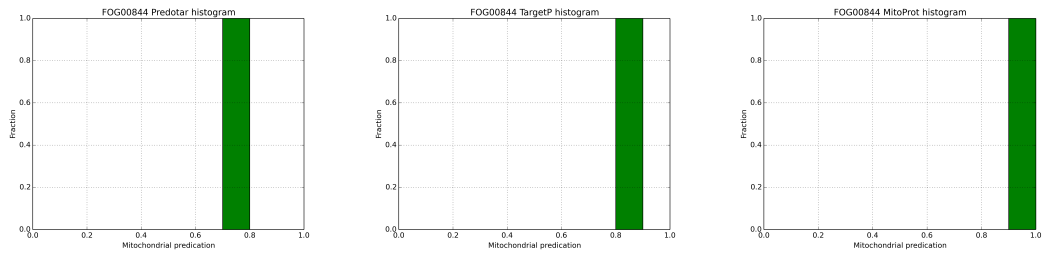
Mitochondrial localization predictions

[Predotar](#)

[TargetP](#)

[MitoProt](#)

Mitochondrial localization predictions



[Raw data](#)

[Phobius transmembrane predictions](#)

1 genes with posterior transmembrane prediction > 50%

FOG00845
EOG8P8D18
NDE2
sce:NDE2

Genes: 1

Protein description

External NADH dehydrogenase

Features

NADH

Parent

ohnolog:FOG00841

SGD Description

Mitochondrial external NADH dehydrogenase; catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p are involved in providing the cytosolic NADH to the mitochondrial respiratory chain; NDE2 has a paralog, NDE1, that arose from the whole genome duplication

References

[Zhu QS, et al. \(1988 Jan 5\)](#). Direct interaction between yeast NADH-ubiquinone oxidoreductase, succinate-ubiquinone oxidoreductase, and ubiquinol-cytochrome c oxidoreductase in the reduction of exogenous quinones.

[Shankar CS, et al. \(1996 Sep\)](#). Mitochondrial NADH dehydrogenase activity and ability to tolerate acetaldehyde determine faster ethanol production in *Saccharomyces cerevisiae*.

[Luttik MA, et al. \(1998 Sep 18\)](#). The *Saccharomyces cerevisiae* NDE1 and NDE2 genes encode separate mitochondrial NADH dehydrogenases catalyzing the oxidation of cytosolic NADH.

[Kerscher SJ, et al. \(2000 Aug 15\)](#). Diversity and origin of alternative NADH:ubiquinone oxidoreductases.

[Overkamp KM, et al. \(2000 May\)](#). In vivo analysis of the mechanisms for oxidation of cytosolic NADH by *Saccharomyces cerevisiae* mitochondria.

[Grandier-Vazeille X, et al. \(2001 Aug 21\)](#). Yeast mitochondrial dehydrogenases are associated in a supramolecular complex.

[Davidson JF, et al. \(2001 Dec\)](#). Mitochondrial respiratory electron carriers are involved in oxidative stress during heat stress in *Saccharomyces cerevisiae*.

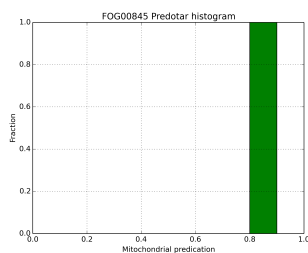
[Bakker BM, et al. \(2001 Jan\)](#). Stoichiometry and compartmentation of NADH metabolism in *Saccharomyces cerevisiae*.

[Pählman IL, et al. \(2002 Aug 2\)](#). Kinetic regulation of the mitochondrial glycerol-3-phosphate dehydrogenase by the external NADH dehydrogenase in *Saccharomyces cerevisiae*.

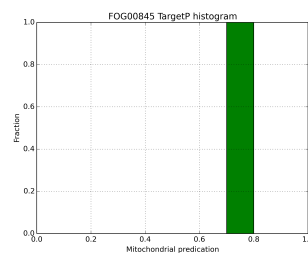
[Sickmann A, et al. \(2003 Nov 11\)](#). The proteome of *Saccharomyces cerevisiae* mitochondria.

Mitochondrial localization predications

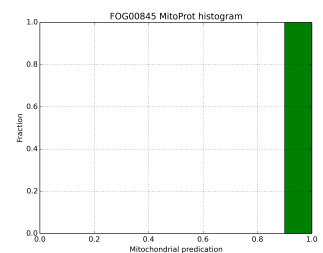
[Predotar](#)



[TargetP](#)



[MitoProt](#)



[Raw data](#)

[Phobius transmembrane predictions](#)

1 genes with posterior transmembrane prediction > 50%

FOG00846
EOG8P8D18
NDI1
sce:NDI1

Genes: 9

Protein description

Internal NADH dehydrogenase

Features

NADH

Parent

paralog:FOG00839

SGD Description

NADH:ubiquinone oxidoreductase; transfers electrons from NADH to ubiquinone in the respiratory chain but does not pump protons, in contrast to the higher eukaryotic multisubunit respiratory complex I; phosphorylated; involved in Mn and H₂O₂ induced apoptosis; upon apoptotic stress, Ndi1 is activated in the mitochondria by N-terminal cleavage, and the truncated protein translocates to the cytoplasm to induce apoptosis; homolog of human AMID

References

[De Vries S, et al. \(1992 Feb 1\)](#). Primary structure and import pathway of the rotenone-insensitive NADH-ubiquinone oxidoreductase of mitochondria from *Saccharomyces cerevisiae*.

[Small WC, et al. \(1998 Aug\)](#). Identification of a cytosolically directed NADH dehydrogenase in mitochondria of *Saccharomyces cerevisiae*.

[Luttik MA, et al. \(1998 Sep 18\)](#). The *Saccharomyces cerevisiae* NDE1 and NDE2 genes encode separate mitochondrial NADH dehydrogenases catalyzing the oxidation of cytosolic NADH.

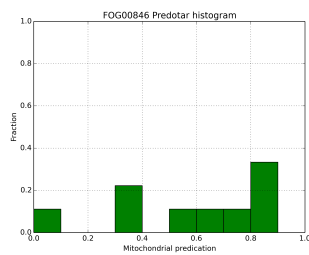
[Grandier-Vazeille X, et al. \(2001 Aug 21\)](#). Yeast mitochondrial dehydrogenases are associated in a supramolecular complex.

[Reinders J, et al. \(2007 Nov\)](#). Profiling phosphoproteins of yeast mitochondria reveals a role of phosphorylation in assembly of the ATP synthase.

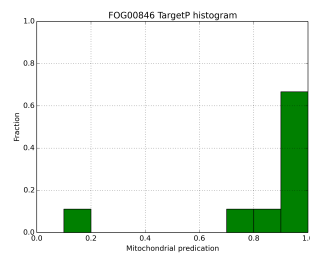
[Renvois  M, et al. \(2014 Jun 25\)](#). Quantitative variations of the mitochondrial proteome and phosphoproteome during fermentative and respiratory growth in *Saccharomyces cerevisiae*.

Mitochondrial localization predications

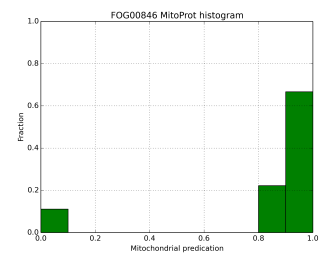
[Predotar](#)



[TargetP](#)



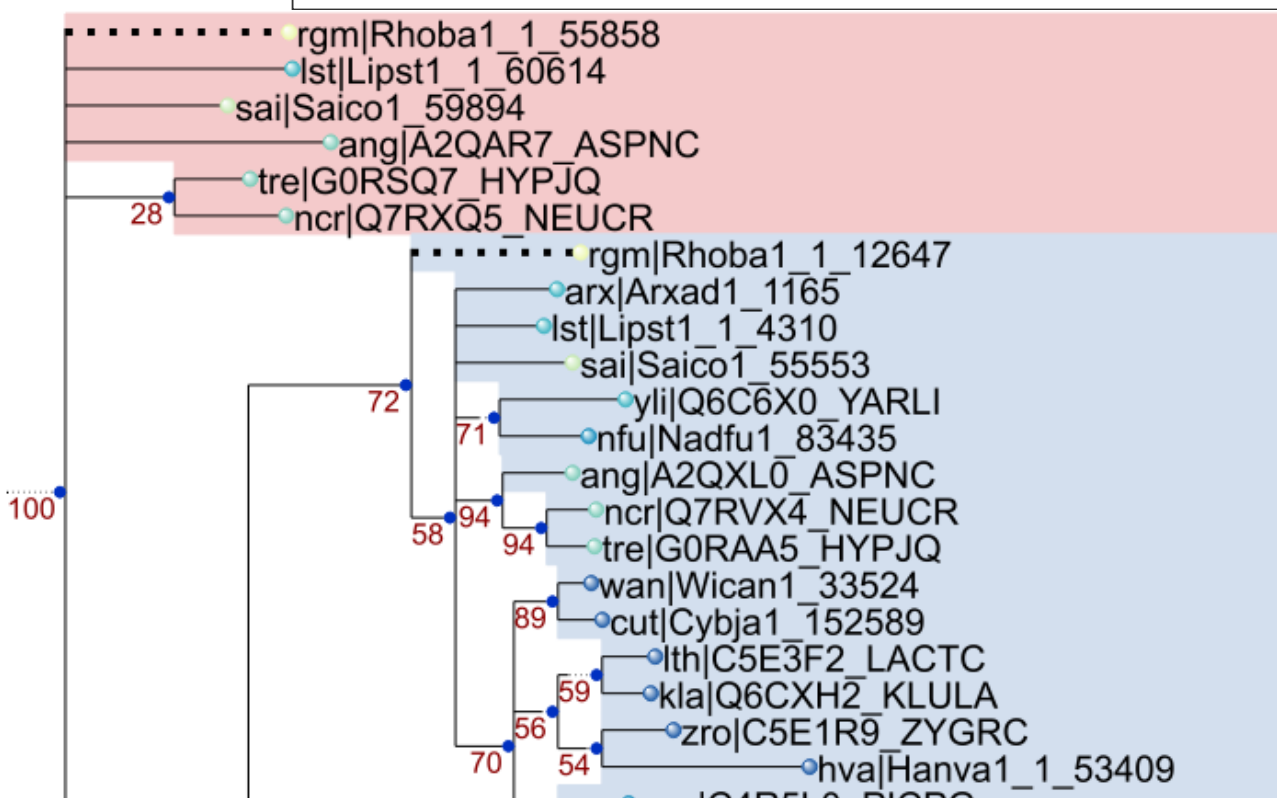
[MitoProt](#)

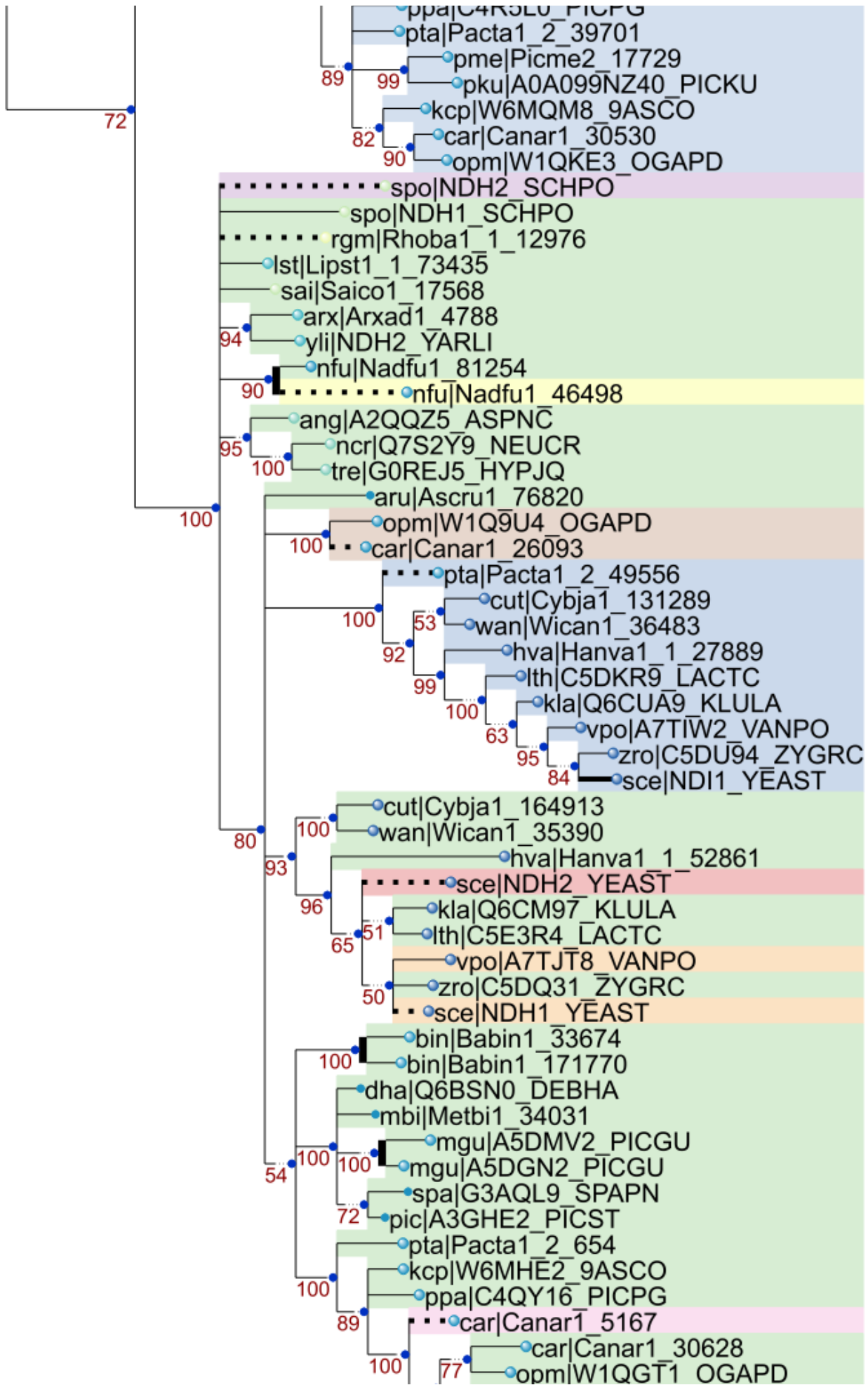


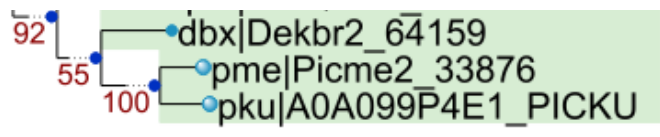
[Raw data](#)

[Phobius transmembrane predictions](#)

9 genes with posterior transmembrane prediction > 50%







1.11

References

Patrícia Carneiro, Margarida Duarte, and Arnaldo Videira. The external alternative NAD(P)H dehydrogenase NDE3 is localized both in the mitochondria and in the cytoplasm of *Neurospora crassa*. *Journal of Molecular Biology*, 368(4):1114–1121, 2007.