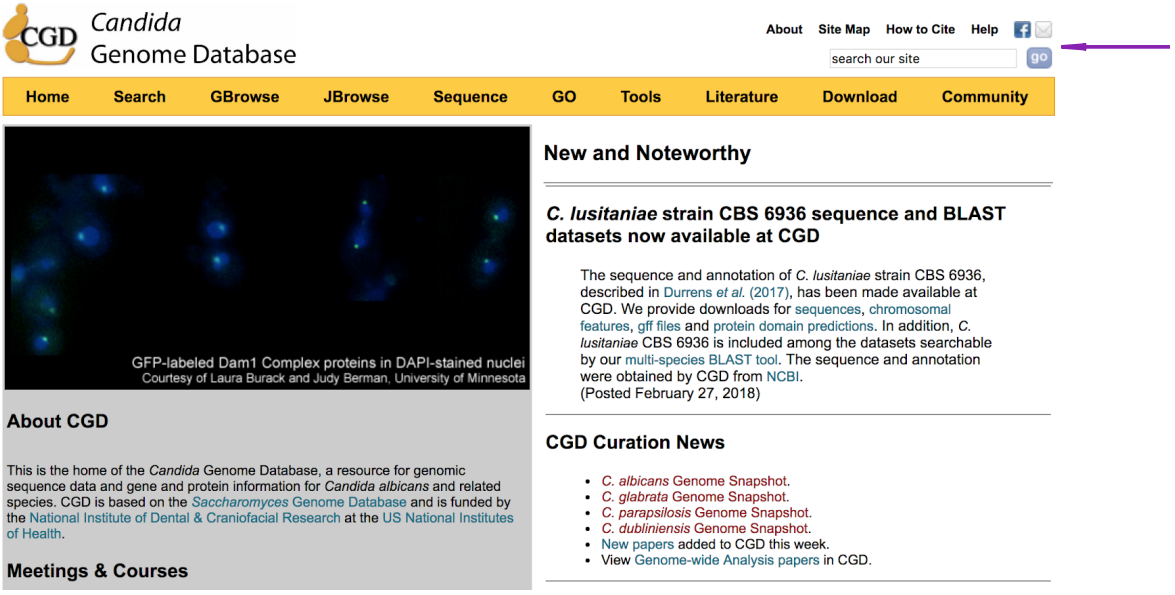
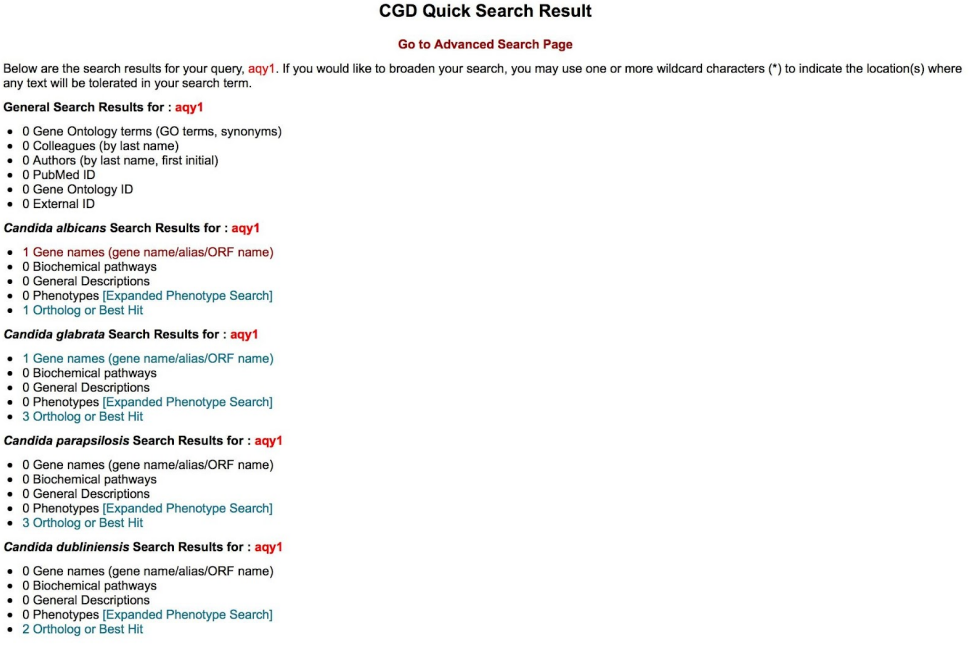
Searching CGD and Navigating Gene Pages

Explore gene-specific information in CGD using Quick search and Locus Summary page for aquaporin (**AQY1**)

- Open the CGD home page (http://www.candidagenome.org).

- Enter your query into the "search our site" box above the banner. Looking for a particular gene, you can enter a standard gene name (**AQY1**), a systematic name (**CR_02920C**), an alias or a systematic name from previous genome assemblies (**orf19.2849, orf6.4943, CA2873**), or an identifier from some of the external resources (NCBI's Gene ID: **3642587**, as an example).

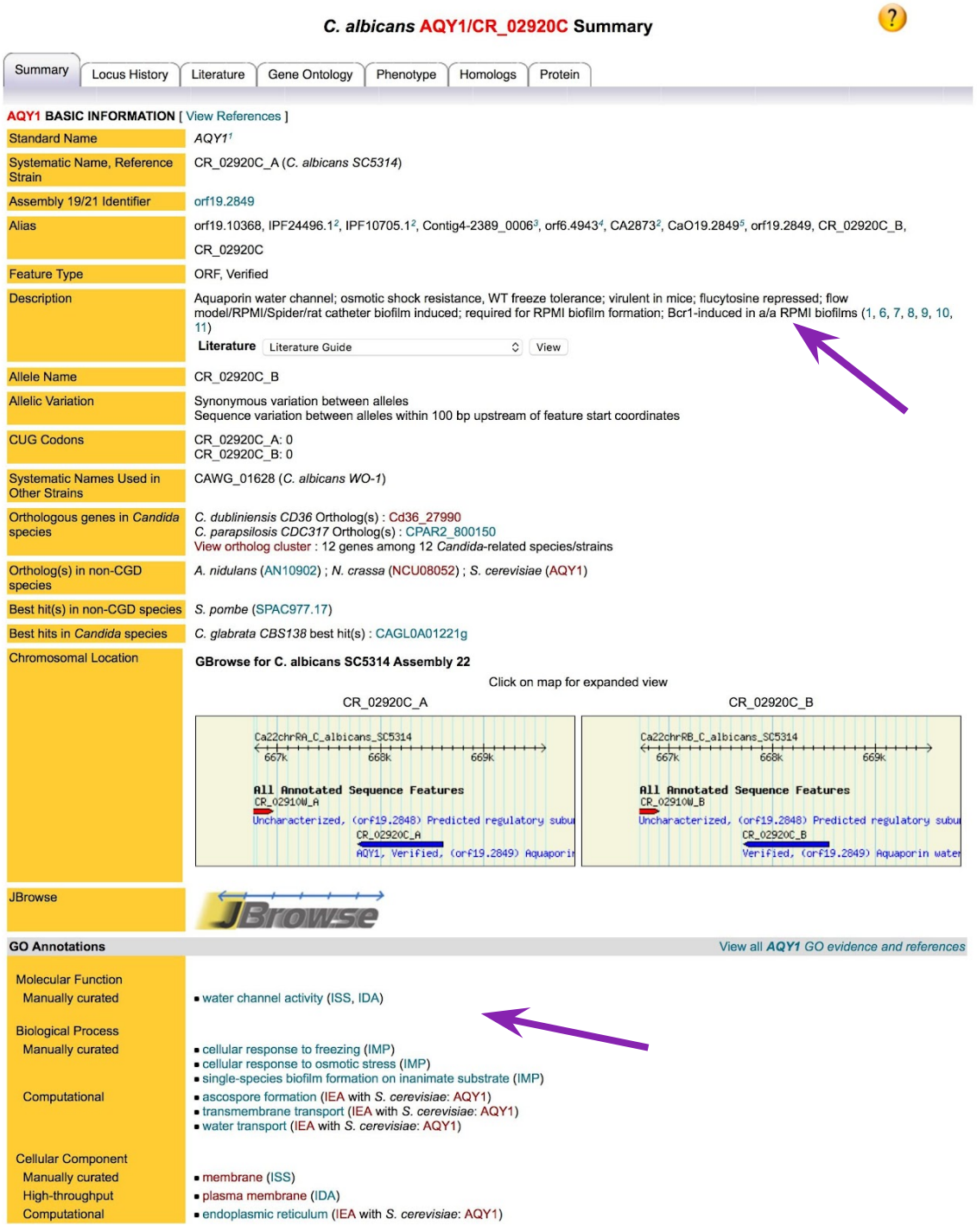




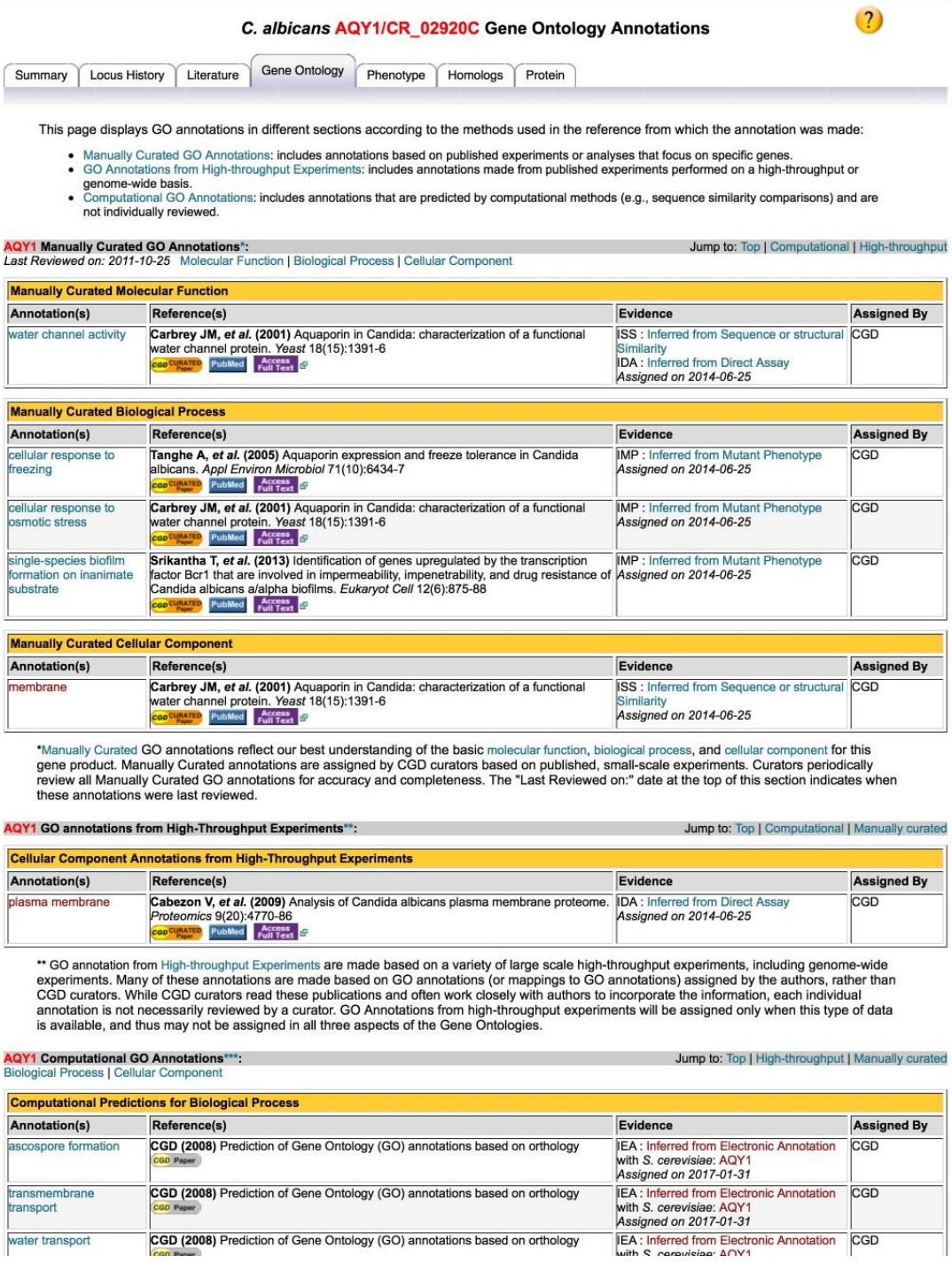
- If your query produces multiple hits, such as a gene name that is used in several *Candida* species represented in CGD, you will get a "CGD Quick Search Result" page that lists the type and number of hits, general and broken down by species. Positive hits are hyperlinked to either their respective Locus Summary pages, or to an intermediate list of individual hits. We will explore other search options later, but for now, select **1 Gene names (gene name/alias/ORF name)** under "*Candida albicans* Search Results" to open the Locus Summary page.

Explore the *C. albicans* AQY1 Locus Summary page:

- On the **Summary** tab, visit the Description and GO Annotations section. Scroll down to Locus Summary Notes.



- Open the **Gene Ontology** tab to see more information, including evidence and references. Hyperlinked phrases lead to definitions.



C. albicans AQY1/CR_02920C Gene Ontology Annotations

Summary | Locus History | Literature | Gene Ontology | Phenotype | Homologs | Protein

This page displays GO annotations in different sections according to the methods used in the reference from which the annotation was made:

- Manually Curated GO Annotations: includes annotations based on published experiments or analyses that focus on specific genes.
- GO Annotations from High-throughput Experiments: includes annotations made from published experiments performed on a high-throughput or genome-wide basis.
- Computational GO Annotations: includes annotations that are predicted by computational methods (e.g., sequence similarity comparisons) and are not individually reviewed.

AQY1 Manually Curated GO Annotations*: Jump to: Top | Computational | High-throughput
Last Reviewed on: 2011-10-25 Molecular Function | Biological Process | Cellular Component

Manually Curated Molecular Function

Annotation(s)	Reference(s)	Evidence	Assigned By
water channel activity	**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. *Yeast* 18(15):1391-6	ISS : Inferred from Sequence or structural Similarity IDA : Inferred from Direct Assay *Assigned on 2014-06-25*	CGD

Manually Curated Biological Process

Annotation(s)	Reference(s)	Evidence	Assigned By
cellular response to freezing	**Tanghe A, *et al.* (2005)** Aquaporin expression and freeze tolerance in Candida albicans. *Appl Environ Microbiol* 71(10):6434-7	IMP : Inferred from Mutant Phenotype *Assigned on 2014-06-25*	CGD
cellular response to osmotic stress	**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. *Yeast* 18(15):1391-6	IMP : Inferred from Mutant Phenotype *Assigned on 2014-06-25*	CGD
single-species biofilm formation on inanimate substrate	**Srikantha T, *et al.* (2013)** Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of Candida albicans a/alpha biofilms. *Eukaryot Cell* 12(6):875-88	IMP : Inferred from Mutant Phenotype *Assigned on 2014-06-25*	CGD

Manually Curated Cellular Component

Annotation(s)	Reference(s)	Evidence	Assigned By
membrane	**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. *Yeast* 18(15):1391-6	ISS : Inferred from Sequence or structural Similarity *Assigned on 2014-06-25*	CGD

*Manually Curated GO annotations reflect our best understanding of the basic molecular function, biological process, and cellular component for this gene product. Manually Curated annotations are assigned by CGD curators based on published, small-scale experiments. Curators periodically review all Manually Curated GO annotations for accuracy and completeness. The "Last Reviewed on:" date at the top of this section indicates when these annotations were last reviewed.

AQY1 GO annotations from High-Throughput Experiments:** Jump to: Top | Computational | Manually curated

Cellular Component Annotations from High-Throughput Experiments

Annotation(s)	Reference(s)	Evidence	Assigned By
plasma membrane	**Cabezon V, *et al.* (2009)** Analysis of Candida albicans plasma membrane proteome. *Proteomics* 9(20):4770-86	IDA : Inferred from Direct Assay *Assigned on 2014-06-25*	CGD

** GO annotation from High-throughput Experiments are made based on a variety of large scale high-throughput experiments, including genome-wide experiments. Many of these annotations are made based on GO annotations (or mappings to GO annotations) assigned by the authors, rather than CGD curators. While CGD curators read these publications and often work closely with authors to incorporate the information, each individual annotation is not necessarily reviewed by a curator. GO Annotations from high-throughput experiments will be assigned only when this type of data is available, and thus may not be assigned in all three aspects of the Gene Ontologies.

AQY1 Computational GO Annotations*:** Jump to: Top | High-throughput | Manually curated
Biological Process | Cellular Component

Computational Predictions for Biological Process

Annotation(s)	Reference(s)	Evidence	Assigned By
ascospore formation	**CGD (2008)** Prediction of Gene Ontology (GO) annotations based on orthology	IEA : Inferred from Electronic Annotation with *S. cerevisiae*: AQY1 *Assigned on 2017-01-31*	CGD
transmembrane transport	**CGD (2008)** Prediction of Gene Ontology (GO) annotations based on orthology	IEA : Inferred from Electronic Annotation with *S. cerevisiae*: AQY1 *Assigned on 2017-01-31*	CGD
water transport	**CGD (2008)** Prediction of Gene Ontology (GO) annotations based on orthology	IEA : Inferred from Electronic Annotation with *S. cerevisiae*: AQY1	CGD

- What are the phenotypes caused by mutations in this gene? In the Summary tab, find the Mutant Phenotype section. Open the **Phenotype** tab for more details, including experimental settings and references.

C. albicans AQY1/CR_02920C_A Phenotypes

Summary | Locus History | Literature | Gene Ontology | Phenotype | Protein

This page lists all curated single mutant phenotypes associated with AQY1. Click on a term in the phenotype column to see other genes associated with that term or download all data. Browse phenotype terms

Jump to: Download Data

13 Single Mutant Phenotype(s) for AQY1/CR_02920C_A

Experiment type	Mutant Information	Strain background	Phenotype	Details	Virulence Model	References
heterozygous diploid, classical genetics	Description: repressible Allele: aqy1::FRT/aqy1::FRT ADH1/adh1::pTET-AQY1-GFP::SATR	SC5314	biofilm formation: abnormal	Condition: RPMI medium 29 degrees C with rocking for 48 hr Details: mutant has minor defects in vertical orientation of hyphae and reduced extracellular matrix, complete permeability to Sypro Ruby and human PMNs and decreased fluconazole resistance		**Srikantha T, *et al.* (2013)** Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of Candida albicans a/alpha biofilms. Eukaryot Cell 12(6):875-88
heterozygous diploid, classical genetics	Description: repressible Allele: ADH1/adh1::pTET-AQY1-GFP::SATR (tet repressed)	P37005	biofilm formation: abnormal	Condition: RPMI medium 29 degrees C with rocking for 48 hr Details: decreased Sypro Ruby and human PMN penetrability, decreased resistance to fluconazole		**Srikantha T, *et al.* (2013)** Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of Candida albicans a/alpha biofilms. Eukaryot Cell 12(6):875-88
homozygous diploid, classical genetics	Description: null Allele: a/alpha aqy1::FRT/aqy1::FRT	SC5314	biofilm formation: abnormal	Condition: RPMI medium 29 degrees C with rocking for 48 hr Details: mutants have reduced vertical orientation of hyphae, an abnormal extracellular matrix, complete penetrabity to Sypro Ruby and human PMNs and increased sensitivity to fluconazole		**Srikantha T, *et al.* (2013)** Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of Candida albicans a/alpha biofilms. Eukaryot Cell 12(6):875-88
homozygous diploid, classical genetics	Description: null	SC5314	biofilm formation: abnormal	Details: forms biofilm with altered detachment properties		**Sellam A, *et al.* (2009)** A Candida albicans early stage biofilm detachment event in rich medium. BMC Microbiol 9:25
homozygous diploid, classical genetics	Description: null	CAI-4	flocculation: normal	Condition: liquid YPD medium		**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. Yeast 18(15):1391-6
heterozygous diploid, classical genetics	Description: repressible	Not recorded	freeze-thaw resistance: decreased			**Tanghe A, *et al.* (2005)** Aquaporin expression and freeze tolerance in Candida albicans. Appl Environ Microbiol 71(10):6434-7
homozygous diploid, classical genetics	Description: null	Not recorded	freeze-thaw resistance: decreased			**Tanghe A, *et al.* (2005)** Aquaporin expression and freeze tolerance in Candida albicans. Appl Environ Microbiol 71(10):6434-7
homozygous diploid, classical genetics	Description: null	CAI-4	hyphal growth: normal	Condition: solid Spider medium		**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. Yeast 18(15):1391-6
homozygous diploid, classical genetics	Description: null	CAI-4	invasive growth: normal	Condition: solid YPD medium		**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. Yeast 18(15):1391-6
homozygous diploid, classical genetics	Description: null	CAI-4	osmotic stress resistance: increased	Details: greater-than-wild type resistance to both hyper- and hypoosmotic shock		**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. Yeast 18(15):1391-6
heterozygous diploid, large-scale survey (haploinsufficient phenotype assay, barcode deletion set)	Description: null	SC5314	viable			**Xu D, *et al.* (2007)** Genome-wide fitness test and mechanism-of-action studies of inhibitory compounds in Candida albicans. PLoS Pathog 3(6):e92
homozygous diploid, classical genetics	Description: null	CAI-4	viable			**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. Yeast 18(15):1391-6
homozygous diploid, classical genetics	Description: null	CAI-4	virulence: normal	Details: organ colonization is also normal	mouse intravenous infection	**Carbrey JM, *et al.* (2001)** Aquaporin in Candida: characterization of a functional water channel protein. Yeast 18(15):1391-6

- What are the orthologs in other *Candida* species? Return to Summary tab and find Orthologous Genes and Best Hits among items listed in Basic Information section with links to their source databases. Open the **Homologs** tab to see a Phylogenetic Tree and multiple sequence alignments.

C. albicans AQY1/CR_02920C Homology Information

Summary | Locus History | Literature | Gene Ontology | Phenotype | Homologs | Protein

AQY1 HOMOLOG INFORMATION

Ortholog Cluster
From CGOB
Download cluster sequence files:
Proteins (multi-FASTA format)
Coding (multi-FASTA format)
Genomic (multi-FASTA format)
Genomic +/- 1000 BP (multi-FASTA format)

View CGOB cluster and synteny information

Sequence ID	Organism	Source	Status
AQY1/CR_02920C_A	*Candida albicans* SC5314	CGD	VERIFIED
Cd36_27990	*Candida dubliniensis* CD36	CGD	UNCHARACTERIZED
CPAR2_800150	*Candida parapsilosis* CDC317	CGD	UNCHARACTERIZED
AQY1/YPR192W	*Saccharomyces cerevisiae* S288C	SGD	VERIFIED
CAWG_01628	*Candida albicans* WO-1	EnsemblFungi	
CLUG_01034	*Candida lusitaniae* ATCC 42720	EnsemblFungi	
CORT_0A00270	*Candida orthopsilosis* Co 90-125	EnsemblFungi	
LELG_00007	*Lodderomyces elongisporus* NRLL YB-4239	EnsemblFungi	
DEHA2F27104g	*Debaryomyces hansenii* CBS767	EnsemblFungi	

Best hits in CGD species: *C. glabrata CBS138* best hit: CAGL0A01221g
Orthologs in fungal species: *A. nidulans* (AN10902) ; *N. crassa* (NCU08052)
Best hits in fungal species: *S. pombe* (SPAC977.17)
Reciprocal best hits in other species: *M. musculus* (AQP1) ; *R. norvegicus* (Aqp1) ; *D. discoideum* (wacA)

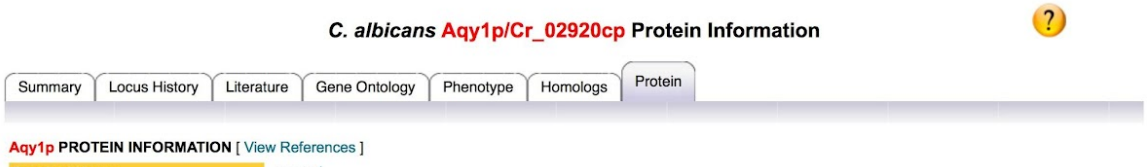
Phylogenetic Tree
Built with SEMPHY
Download tree files:
Unrooted Tree (Newick format)
Rooted Tree (Newick format)
Rooted Tree (phyloXML format)
Rooted, Annotated Tree (phyloXML format)

Tree rooted by midpoint; total tree length = 2.45 subs/site

Protein Sequence Alignment
Built with MUSCLE
Download alignment files:
Protein alignment (Multi-FASTA format)
Protein alignment (ClustalW format)

```
Reference sequence (1): CR_02920C_A
Identities normalized by aligned length.
Colored by: identity >= 80% and property:
     Hydrophobic (A, I, L, M, V)
     Aromatic (F, W, Y)
     Polar (N, Q, S, T)
     Negative charge (D, E)
     Positive charge (H, K, R)
     Backbone change (G, P)
     Cysteine (C)
 1 CR_02920C_A  100.0%  --------MVAESSSIDNT------------------------PNDVEAQ
 2 CAWG_01628   100.0%  --------MVAESSSIDNT------------------------PNDVEAQ
 3 Cd36_27990    98.9%  --------MVAESSSIDNT------------------------ANDVEAQ
 4 CPAR2_800150  81.6%  ----------------------------------------------------
 5 CORT_0A00270  79.3%  --------MTVEAT---SP------------------------IDDIEQQ
 6 LELG_00007    80.4%  --------MTAAGSIAEPT-----------------------PNEIEAQ
 7 DEHA2F27104g  19.4%  ------MDSTLGSDSLEPEKRTTIDSEGLNHRNPERFEGENRLSPDLEAQ
 8 CLUG_01034    75.0%  ----------------MT------------------------ASDVEAQ
 9 YPR192W       45.9%  MSSNDSNDTDKQHTRLDPT-----------------------GVDDAYI
```

- Explore the **Protein** tab. What is known about the structure and physicochemical properties of this protein?



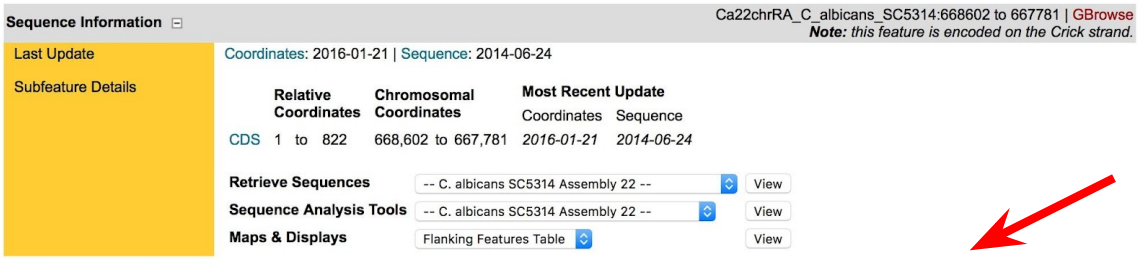
C. albicans Aqy1p/Cr_02920cp Protein Information

Summary | Locus History | Literature | Gene Ontology | Phenotype | Homologs | Protein

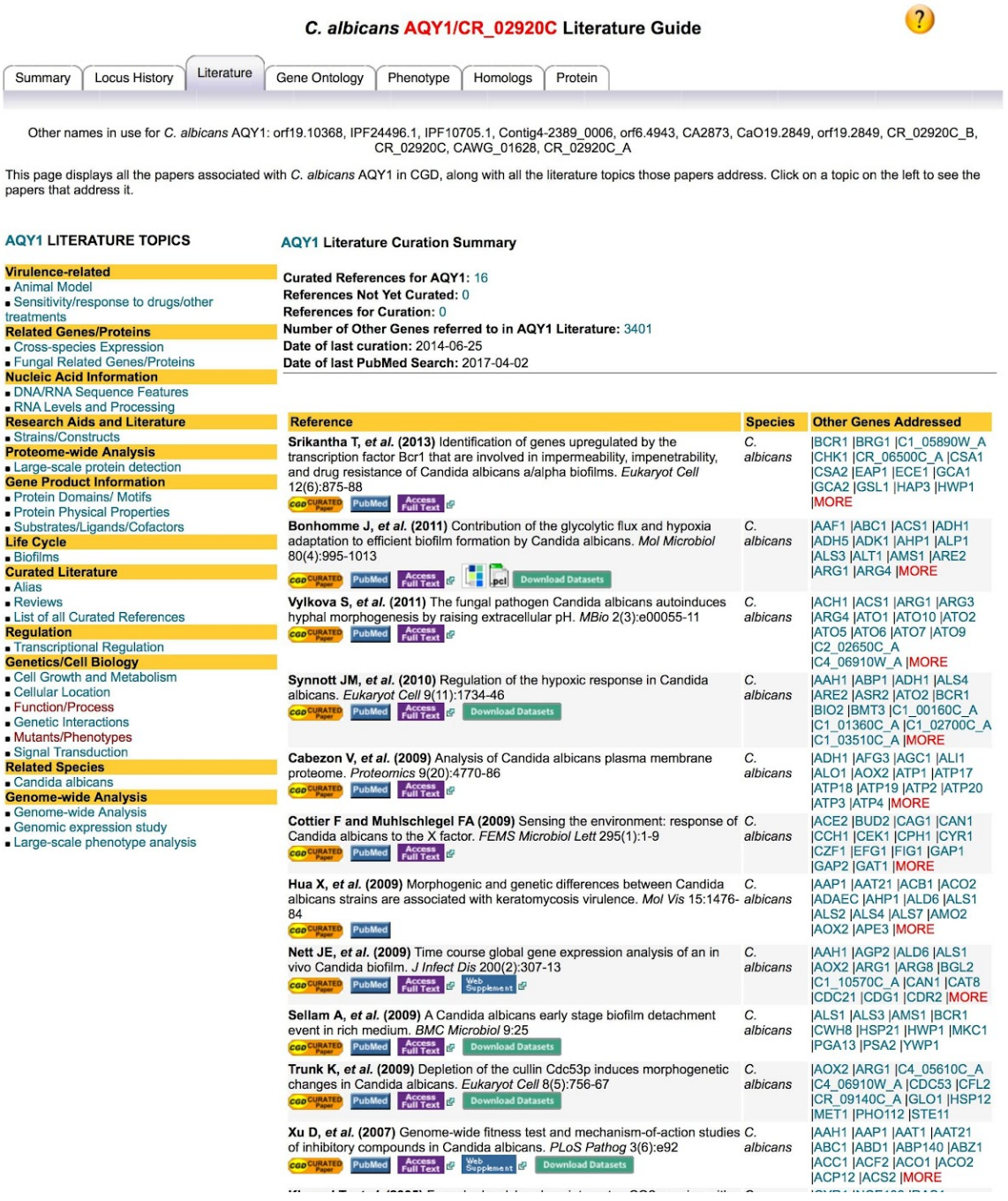
Aqy1p PROTEIN INFORMATION [View References]

- Note the “predicted protein structure,” now available from AlphaFold

- What are the genomic and protein sequences for both AQY1 alleles? On the Summary tab, scroll down to Sequence Information section and explore the Retrieve Sequences pull-down menu. To analyze the AQY1 sequence, in the Sequence Information section, open the Sequence Analysis Tools pull-down menu to run BLAST, design primers, and get restriction maps.



- What literature is available on AQY1? View references at the bottom of AQY1 Locus Summary page and click on Complete Literature Guide, or simply open the **Literature** tab. To filter out papers that deal with a specific topic, such as mutants and phenotypes, click on that topic using the menu on the left side of the page.



C. albicans AQY1/CR_02920C Literature Guide

Summary | Locus History | Literature | Gene Ontology | Phenotype | Homologs | Protein

Other names in use for *C. albicans* AQY1: orf19.10368, IPF24496.1, IPF10705.1, Contig4-2389_0006, orf6.4943, CA2873, CaO19.2849, orf19.2849, CR_02920C_B, CR_02920C, CAWG_01628, CR_02920C_A

This page displays all the papers associated with *C. albicans* AQY1 in CGD, along with all the literature topics those papers address. Click on a topic on the left to see the papers that address it.

AQY1 LITERATURE TOPICS

Virulence-related
- Animal Model
- Sensitivity/response to drugs/other treatments

Related Genes/Proteins
- Cross-species Expression
- Fungal Related Genes/Proteins

Nucleic Acid Information
- DNA/RNA Sequence Features
- RNA Levels and Processing

Research Aids and Literature
- Strains/Constructs

Proteome-wide Analysis
- Large-scale protein detection

Gene Product Information
- Protein Domains/ Motifs
- Protein Physical Properties
- Substrates/Ligands/Cofactors

Life Cycle
- Biofilms

Curated Literature
- Alias
- Reviews
- List of all Curated References

Regulation
- Transcriptional Regulation

Genetics/Cell Biology
- Cell Growth and Metabolism
- Cellular Location
- Function/Process
- Genetic Interactions
- Mutants/Phenotypes
- Signal Transduction

Related Species
- Candida albicans

Genome-wide Analysis
- Genome-wide Analysis
- Genomic expression study
- Large-scale phenotype analysis

AQY1 Literature Curation Summary

Curated References for AQY1: 16
References Not Yet Curated: 0
References for Curation: 0
Number of Other Genes referred to in AQY1 Literature: 3401
Date of last curation: 2014-06-25
Date of last PubMed Search: 2017-04-02

Reference	Species	Other Genes Addressed
Srikantha T, *et al.* (2013) Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of Candida albicans a/alpha biofilms. *Eukaryot Cell* 12(6):875-88	*C. albicans*	|BCR1 |BRG1 |C1_05890W_A |CHK1 |CR_06500C_A |CSA1 |CSA2 |EAP1 |ECE1 |GCA1 |GCA2 |GSL1 |HAP3 |HWP1 |MORE
Bonhomme J, *et al.* (2011) Contribution of the glycolytic flux and hypoxia adaptation to efficient biofilm formation by Candida albicans. *Mol Microbiol* 80(4):995-1013	*C. albicans*	|AAF1 |ABC1 |ACS1 |ADH1 |ADH5 |ADK1 |AHP1 |ALP1 |ALS3 |ALT1 |AMS1 |ARE2 |ARG1 |ARG4 |MORE
Vylkova S, *et al.* (2011) The fungal pathogen Candida albicans autoinduces hyphal morphogenesis by raising extracellular pH. *MBio* 2(3):e00055-11	*C. albicans*	|ACH1 |ACS1 |ARG1 |ARG3 |ARG4 |ATO1 |ATO10 |ATO2 |ATO5 |ATO6 |ATO7 |ATO9 |C2_02650C_A |C4_06910W_A |MORE
Synnott JM, *et al.* (2010) Regulation of the hypoxic response in Candida albicans. *Eukaryot Cell* 9(11):1734-46	*C. albicans*	|AAH1 |ABP1 |ADH1 |ALS4 |ARE2 |ASR2 |ATO2 |BCR1 |BIO2 |BMT3 |C1_00160C_A |C1_01360C_A |C1_02700C_A |C1_03510C_A |MORE
Cabezon V, *et al.* (2009) Analysis of Candida albicans plasma membrane proteome. *Proteomics* 9(20):4770-86	*C. albicans*	|ADH1 |AFG3 |AGC1 |ALI1 |ALO1 |AOX2 |ATP1 |ATP17 |ATP18 |ATP19 |ATP2 |ATP20 |ATP3 |ATP4 |MORE
Cottier F and Muhlschlegel FA (2009) Sensing the environment: response of Candida albicans to the X factor. *FEMS Microbiol Lett* 295(1):1-9	*C. albicans*	|ACE2 |BUD2 |CAG1 |CAN1 |CCH1 |CEK1 |CPH1 |CYR1 |CZF1 |EFG1 |FIG1 |GAP1 |GAP2 |GAT1 |MORE
Hua X, *et al.* (2009) Morphogenic and genetic differences between Candida albicans strains are associated with keratomycosis virulence. *Mol Vis* 15:1476-84	*C. albicans*	|AAP1 |AAT21 |ACB1 |ACO2 |ADAEC |AHP1 |ALD6 |ALS1 |ALS2 |ALS4 |ALS7 |AMO2 |AOX2 |APE3 |MORE
Nett JE, *et al.* (2009) Time course global gene expression analysis of an in vivo Candida biofilm. *J Infect Dis* 200(2):307-13	*C. albicans*	|AAH1 |AGP2 |ALD6 |ALS1 |AOX2 |ARG1 |ARG8 |BGL2 |C1_10570C_A |CAN1 |CAT8 |CDC21 |CDG1 |CDR2 |MORE
Sellam A, *et al.* (2009) A Candida albicans early stage biofilm detachment event in rich medium. *BMC Microbiol* 9:25	*C. albicans*	|ALS1 |ALS3 |AMS1 |BCR1 |CWH8 |HSP21 |HWP1 |MKC1 |PGA13 |PSA2 |YWP1
Trunk K, *et al.* (2009) Depletion of the cullin Cdc53p induces morphogenetic changes in Candida albicans. *Eukaryot Cell* 8(5):756-67	*C. albicans*	|AOX2 |ARG1 |C4_05610C_A |C4_06910W_A |CDC53 |CFL2 |CR_09140C_A |GLO1 |HSP12 |MET1 |PHO112 |STE11
Xu D, *et al.* (2007) Genome-wide fitness test and mechanism-of-action studies of inhibitory compounds in Candida albicans. *PLoS Pathog* 3(6):e92	*C. albicans*	|AAH1 |AAP1 |AAT1 |AAT21 |ABC1 |ABD1 |ABP140 |ABZ1 |ACC1 |ACF2 |ACO1 |ACO2 |ACP12 |ACS2 |MORE