

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).

The screenshot shows the CGD homepage with a yellow header bar containing links for Home, Search, GBrowse, JBrowse, Sequence, GO, Tools, Literature, Download, and Community. Below the header is a search bar with the placeholder "search our site" and a blue "go" button. To the left of the search bar is a small image of a fluorescence micrograph showing blue spots. The main content area features a section titled "New and Noteworthy" with a sub-section about *C. lusitaniae* strain CBS 6936 sequence and BLAST datasets. There are also sections for "About CGD" and "Meetings & Courses".

The screenshot shows the "CGD Quick Search Result" page for the query "aqy1". It includes a link to "Go to Advanced Search Page". The results are organized by species:

- Candida albicans Search Results for : aqy1**
 - 1 Gene names (gene name/alias/ORF name)
 - 0 Biochemical pathways
 - 0 General Descriptions
 - 0 Phenotypes [Expanded Phenotype Search]
 - 1 Ortholog or Best Hit
- Candida glabrata Search Results for : aqy1**
 - 1 Gene names (gene name/alias/ORF name)
 - 0 Biochemical pathways
 - 0 General Descriptions
 - 0 Phenotypes [Expanded Phenotype Search]
 - 3 Ortholog or Best Hit
- Candida parapsilosis Search Results for : aqy1**
 - 0 Gene names (gene name/alias/ORF name)
 - 0 Biochemical pathways
 - 0 General Descriptions
 - 0 Phenotypes [Expanded Phenotype Search]
 - 3 Ortholog or Best Hit
- Candida dubliniensis Search Results for : aqy1**
 - 0 Gene names (gene name/alias/ORF name)
 - 0 Biochemical pathways
 - 0 General Descriptions
 - 0 Phenotypes [Expanded Phenotype Search]
 - 2 Ortholog or Best Hit

- 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.

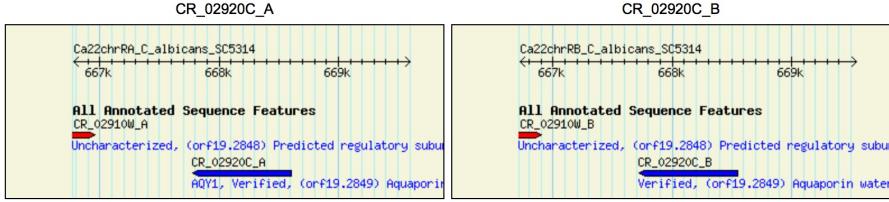
Explore the *C. albicans* AQY1 Locus Summary page:

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

C. albicans AQY1/CR_02920C Summary

Summary Locus History Literature Gene Ontology Phenotype Homologs Protein

AQY1 BASIC INFORMATION [View References]

| | |
|--|--|
| Standard Name | AQY1 ¹ |
| Systematic Name, Reference Strain | CR_02920C_A (<i>C. albicans</i> SC5314) |
| Assembly 19/21 Identifier | orf19.2849 |
| Alias | orf19.10368, IPF24496.1 ² , IPF10705.1 ² , Contig4-2389_0006 ³ , orf6.4943 ⁴ , CA2873 ² , CaO19.2849 ⁵ , orf19.2849, CR_02920C_B, |
| CR_02920C | |
| Feature Type | ORF, Verified |
| Description | Aquaporin water channel; osmotic shock resistance, WT freeze tolerance; virulent in mice; flucytosine repressed; flow model/RPMI/Spider/rat catheter biofilm induced; required for RPMI biofilm formation; Bcr1-induced in a/a RPMI biofilms (1, 6, 7, 8, 9, 10, 11) |
| Literature | Literature Guide View |
| Allele Name | CR_02920C_B |
| Allelic Variation | Synonymous variation between alleles Sequence variation between alleles within 100 bp upstream of feature start coordinates |
| CUG Codons | CR_02920C_A: 0 CR_02920C_B: 0 |
| Systematic Names Used in Other Strains | CAWG_01628 (<i>C. albicans</i> WO-1) |
| Orthologous genes in <i>Candida</i> species | <i>C. dubliniensis</i> CD36 Ortholog(s) : Cd36_27990 <i>C. parapsilosis</i> CDC317 Ortholog(s) : CPAR2_800150 View ortholog cluster : 12 genes among 12 <i>Candida</i> -related species/strains |
| Ortholog(s) in non-CGD species | <i>A. nidulans</i> (AN10902) ; <i>N. crassa</i> (NCU08052) ; <i>S. cerevisiae</i> (AQY1) |
| Best hit(s) in non-CGD species | <i>S. pombe</i> (SPAC977.17) |
| Best hits in <i>Candida</i> species | <i>C. glabrata</i> CBS138 best hit(s) : CAGLOA01221g |
| Chromosomal Location | GBrowse for <i>C. albicans</i> SC5314 Assembly 22 Click on map for expanded view |
|  | |
| JBrowse |  |
| View all AQY1 GO evidence and references | |
| GO Annotations | |
| Molecular Function Manually curated | water channel activity (ISS, IDA) |
| Biological Process Manually curated | cellular response to freezing (IMP) cellular response to osmotic stress (IMP) single-species biofilm formation on inanimate substrate (IMP) |
| Computational | ascospore formation (IEA with <i>S. cerevisiae</i> : AQY1) transmembrane transport (IEA with <i>S. cerevisiae</i> : AQY1) water transport (IEA with <i>S. cerevisiae</i> : AQY1) |
| Cellular Component Manually curated High-throughput Computational | membrane (ISS) plasma membrane (IDA) endoplasmic reticulum (IEA with <i>S. cerevisiae</i> : AQY1) |

- 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*: Last Reviewed on: 2011-10-25 Molecular Function | Biological Process | Cellular Component

Jump to: Top | Computational | High-throughput

| 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. <i>Yeast</i> 18(15):1391-6 CGP CURATED Paper PubMed Access Full Text | 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. <i>Appl Environ Microbiol</i> 71(10):6434-7 CGP CURATED Paper PubMed Access Full Text | 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. <i>Yeast</i> 18(15):1391-6 CGP CURATED Paper PubMed Access Full Text | 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 α/α biofilms. <i>Eukaryot Cell</i> 12(6):875-88 CGP CURATED Paper PubMed Access Full Text | 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. <i>Yeast</i> 18(15):1391-6 CGP CURATED Paper PubMed Access Full Text | 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. <i>Proteomics</i> 9(20):4770-86 CGP CURATED Paper PubMed Access Full Text | 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

| 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 CGP Paper | 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 CGP Paper | 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 CGP Paper | 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. <i>Eukaryot Cell</i> 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. <i>Eukaryot Cell</i> 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 penetrability 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. <i>Eukaryot Cell</i> 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. <i>BMC Microbiol</i> 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. <i>Yeast</i> 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. <i>Appl Environ Microbiol</i> 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. <i>Appl Environ Microbiol</i> 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. <i>Yeast</i> 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. <i>Yeast</i> 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. <i>Yeast</i> 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. <i>PLoS Pathog</i> 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. <i>Yeast</i> 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. <i>Yeast</i> 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**

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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)

| Sequence ID | Organism | Source | Status |
|------------------|---|--------------|-----------------|
| AQY1/CR_02920C_A | <i>Candida albicans</i> SC5314 | CGD | VERIFIED |
| Cd36_27990 | <i>Candida dubliniensis</i> CD36 | CGD | UNCHARACTERIZED |
| CPAR2_800150 | <i>Candida parapsilosis</i> CDC317 | CGD | UNCHARACTERIZED |
| AQY1/YPR192W | <i>Saccharomyces cerevisiae</i> S288C | SGD | VERIFIED |
| CAWG_01628 | <i>Candida albicans</i> WO-1 | EnsemblFungi | |
| CLUG_01034 | <i>Candida lusitaniae</i> ATCC 42720 | EnsemblFungi | |
| CORT_0A00270 | <i>Candida orthopsis</i> Co 90-125 | EnsemblFungi | |
| LELG_00007 | <i>Lodderomyces elongisporus</i> NRRL YB-4239 | EnsemblFungi | |
| DEHA2F27104g | <i>Debaromyces hansenii</i> 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

0.2 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)

| Sequence | Identity (%) | Sequence |
|----------------|--------------|--|
| 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% | -MT-----IDDIEQQ |
| 5 CORT_0A00270 | 79.3% | -MTEAT---SP-----PNEIEAQ |
| 6 LELG_00007 | 80.4% | -MTAAGSIAEPT-----PNEIEAQ |
| 7 DEHA2F27104g | 19.4% | -MDSTLGSDSLPEKRTTIDSEGLNHRNPERFEGENRLSPDLEAQ |
| 8 CLUG_01034 | 75.0% | -MT-----ASDVEAQ |
| 9 YPR192W | 45.9% | MSSNDSNDTDQHTRLDP-----GVDDAYI |

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

C. albicans Aqy1p/Cr_02920cp Protein Information

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Aqy1p PROTEIN INFORMATION [View References]

| | |
|-------------------------------|---|
| Standard Name | Aqy1p [†] |
| Systematic Name | Cr_02920cp_a |
| Allele Name | Cr_02920cp_b |
| Description | Aquaporin water channel; osmotic shock resistance, WT freeze tolerance; virulent in mice; flucytosine repressed; flow model/RPMI/Spider/rat catheter biofilm induced; required for RPMI biofilm formation; Bcr1-induced in a/a RPMI biofilms (1, 2, 3, 4, 5, 6, 7) |
| Experimental Observations | View peptides from PeptideAtlas |
| Structural Information | |
| Top PDB Hit: | 2W2E |
| Source | |
| Quality | |
| Structure | View all PDB BLAST hits View Top PDB Hit Information (Link-out) Komagataella pastoris; 1.15 Angstrom Crystal Structure Of P.Pastoris Aquaporin, Aqy1, In A Closed Conformation At Ph 3.5 68% identical to Aqy1p; P-value = 3.00e-98 (View Alignment) Click on image to access PDB interactive viewer (Link-out) |



Conserved Domains

Domains/Motifs Page

Click on image for expanded interactive view

CR_02920cp_A

ORF CR_02920cp_A

AQY1, Verified, aquaporin water channel

HMM Domains

GDSR_1.20.1080_10
IPR023711: Aquaporin-like
PF00230
IPR000425: MIP Major intrinsic protein
TIGR00851
IPR000425: MIP Family channel proteins Major intrinsic protein

Profile/Motif Hits

PR00783
IPR000425: MINTRINSICP Major intrinsic protein
PR00783
IPR000425: MINTRINSICP Major intrinsic protein

Signal Peptide

Transmembrane Domains

Length = 273 aa; MW = 29.3 kDa; [Physicochemical Properties Page](#)

Sequence Detail

Download in FASTA format

```

1  MVAESSSSIDN TPNDVVAQRP VYEPKYDDSV NVSPLKNHMI AFLGEFFGTF
51  IFLWVAFVIA QIANQDPTIP DKGSQPMQLI MISFGFGFGV MMGVFMFFRV
101 SGGNLNPAVT LTLVLAQAVP PIRGLFMMVA QMIAAGMAAG AASAMTPGPI
151 AFTNGLGGGA SKARGVFLEA FGTCILCLTV LMMAVEKSRA TFMAPFVIGI
201 SLFLGHLLCV YYTGAGLNPA RSFGPCVAAR SFPVYHWIYW VGPILGSVIA
251 FAIWKIFKIL KYETCNPGQD SDA*

```

Homologs

BLAST Aqy1p against other *Candida* sequences

External Sequence Database

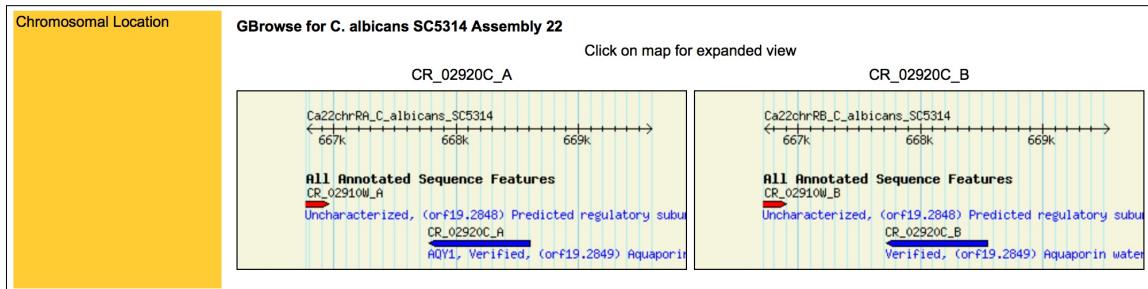
None

REFERENCES CITED ON THIS PAGE [[View Complete Literature Guide for Aqy1p](#)]

1) Carbrey JM, et al. (2001) Aquaporin in *Candida*: characterization of a functional water channel protein. *Yeast* 18(15):1391-6

CCO CURATED Data PubMed Access Full Text

- What is the chromosomal location of AQY1 and its neighboring genes? From the **Summary** tab, click on the **GBrowse** thumbnail for either allele A or B.



- 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.

Sequence Information

Ca22chrRA_C_albicans_SC5314:668602 to 667781 | **GBrowse**
Note: this feature is encoded on the Crick strand.

| | | | |
|-------------------------|--|-------------------------|---|
| Last Update | Coordinates: 2016-01-21 Sequence: 2014-06-24 | | |
| Subfeature Details | Relative Coordinates | Chromosomal Coordinates | Most Recent Update |
| CDS | 1 to 822 | 668,602 to 667,781 | Coordinates Sequence 2016-01-21 2014-06-24 |
| Retrieve Sequences | -- C. albicans SC5314 Assembly 22 -- <input type="button" value="View"/> | | |
| Sequence Analysis Tools | -- C. albicans SC5314 Assembly 22 -- <input type="button" value="View"/> | | |
| Maps & Displays | Flanking Features Table <input type="button" value="View"/> | | |

- 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

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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 | AQY1 Literature Curation Summary |
|--|---|
| Virulence-related ■ Animal Model ■ Sensitivity/response to drugs/other treatments | Curated References for AQY1: 16 References Not Yet Curated: 0 References for Curation: 0 |
| Related Genes/Proteins ■ Cross-species Expression ■ Fungal Related Genes/Proteins | 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 |
| Nucleic Acid Information ■ DNA/RNA Sequence Features ■ RNA Levels and Processing | |
| Research Aids and Literature ■ Strains/Constructs | Reference |
| Proteome-wide Analysis ■ Large-scale protein detection | Srikantha T, et al. (2013) Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of <i>Candida albicans</i> alpha/beta biofilms. <i>Eukaryot Cell</i> 12(6):875-88 |
| Gene Product Information ■ Protein Domains/ Motifs ■ Protein Physical Properties ■ Substrates/Ligands/Cofactors | C. <i>albicans</i> BCR1 BRG1 C1_05890W_A ICHK1 CR_06500C_A CSA1 CSA2 EAP1 ECE1 GCA1 GCA2 GSL1 HAP3 HWP1 MORE |
| Life Cycle ■ Biofilms | Bonhomme J, et al. (2011) Contribution of the glycolytic flux and hypoxia adaptation to efficient biofilm formation by <i>Candida albicans</i> . <i>Mol Microbiol</i> 80(4):995-1013 |
| Curated Literature ■ Alias ■ Reviews ■ List of all Curated References | C. <i>albicans</i> AAF1 ABC1 ACS1 ADH1 ADH5 ADK1 AHP1 ALP1 ALS3 ALT1 AMS1 ARE2 ARG1 ARG4 MORE |
| Regulation ■ Transcriptional Regulation | Vylkova S, et al. (2011) The fungal pathogen <i>Candida albicans</i> autoinduces hyphal morphogenesis by raising extracellular pH. <i>MBio</i> 2(3):e00055-11 |
| Genetics/Cell Biology ■ Cell Growth and Metabolism ■ Cellular Location ■ Function/Process ■ Genetic Interactions ■ Mutants/Phenotypes ■ Signal Transduction | C. <i>albicans</i> AAH1 ABP1 ADH1 ALS4 ARE2 ASR2 ATO2 BCR1 BIO2 BMT3 C1_00160C_A C1_01360C_A C1_02700C_A C1_03510C_A MORE |
| Related Species ■ <i>Candida albicans</i> | Cabezon V, et al. (2009) Analysis of <i>Candida albicans</i> plasma membrane proteome. <i>Proteomics</i> 9(20):4770-86 |
| Genome-wide Analysis ■ Genome-wide Analysis ■ Genomic expression study ■ Large-scale phenotype analysis | C. <i>albicans</i> ADH1 AFG3 AGC1 ALI1 ALO1 AOX2 ATP1 ATP17 ATP18 ATP19 ATP2 ATP20 ATP3 ATP4 MORE |
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