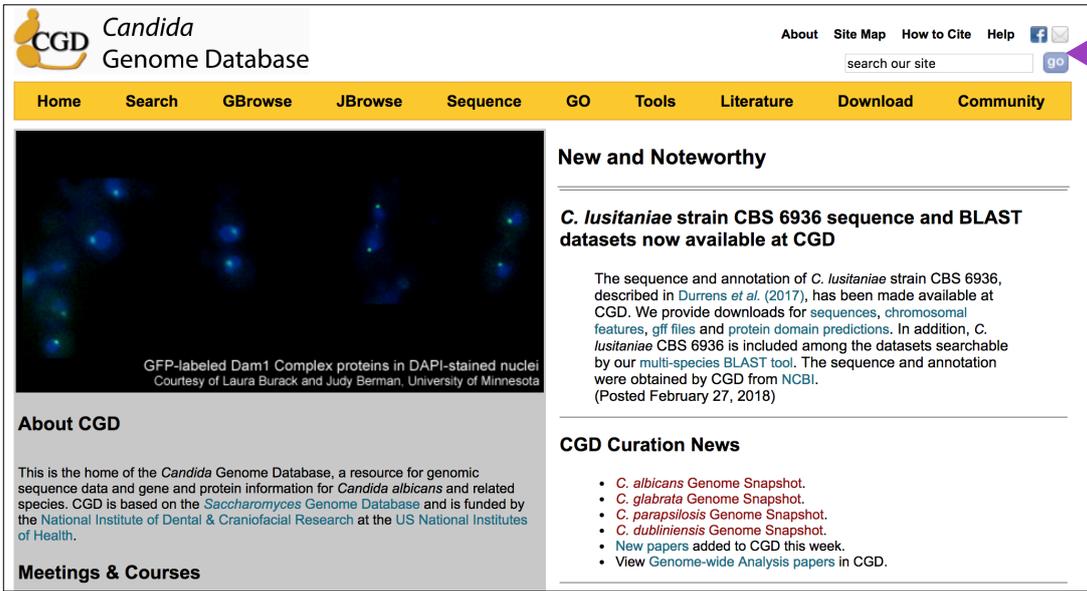


# Searching CGD and Navigating Gene Pages

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).



**Candida Genome Database**

About Site Map How to Cite Help

search our site go

Home Search GBrowse JBrowse Sequence GO Tools Literature Download Community

### New and Noteworthy

#### C. lusitaniae strain CBS 6936 sequence and BLAST datasets now available at CGD

The sequence and annotation of *C. lusitaniae* strain CBS 6936, described in Durrens *et al.* (2017), has been made available at CGD. We provide downloads for sequences, chromosomal features, gff files and protein domain predictions. In addition, *C. lusitaniae* CBS 6936 is included among the datasets searchable by our multi-species BLAST tool. The sequence and annotation were obtained by CGD from NCBI. (Posted February 27, 2018)

#### CGD Curation News

- *C. albicans* Genome Snapshot.
- *C. glabrata* Genome Snapshot.
- *C. parapsilosis* Genome Snapshot.
- *C. dubliniensis* Genome Snapshot.
- New papers added to CGD this week.
- View Genome-wide Analysis papers in CGD.

**About CGD**

This is the home of the *Candida* Genome Database, a resource for genomic sequence data and gene and protein information for *Candida albicans* and related species. CGD is based on the *Saccharomyces* Genome Database and is funded by the National Institute of Dental & Craniofacial Research at the US National Institutes of Health.

**Meetings & Courses**

### CGD Quick Search Result

[Go to Advanced Search Page](#)

Below are the search results for your query, *aqy1*. If you would like to broaden your search, you may use one or more wildcard characters (\*) to indicate the location(s) where any text will be tolerated in your search term.

**General Search Results for : *aqy1***

- 0 Gene Ontology terms (GO terms, synonyms)
- 0 Colleagues (by last name)
- 0 Authors (by last name, first initial)
- 0 PubMed ID
- 0 Gene Ontology ID
- 0 External ID

***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 <sup>1</sup>
Systematic Name, Reference Strain	CR_02920C_A ( <i>C. albicans</i> SC5314)
Assembly 19/21 Identifier	orf19.2849
Alias	orf19.10368, IPF24496.1 <sup>2</sup> , IPF10705.1 <sup>2</sup> , Contig4-2389_0006 <sup>3</sup> , orf6.4943 <sup>4</sup> , CA2873 <sup>2</sup> , CaO19.2849 <sup>5</sup> , 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) <b>Literature</b> <input type="text" value="Literature Guide"/> <input type="button" value="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 <a href="#">View ortholog cluster</a> : 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) : CAGL0A01221g
Chromosomal Location	<b>GBrowse for <i>C. albicans</i> SC5314 Assembly 22</b> Click on map for expanded view <div style="display: flex; justify-content: space-around;"> <div style="text-align: center;"> <p>CR_02920C_A</p> </div> <div style="text-align: center;"> <p>CR_02920C_B</p> </div> </div>
JBrowse	
<b>GO Annotations</b>	<a href="#">View all AQY1 GO evidence and references</a>
Molecular Function Manually curated	<ul style="list-style-type: none"> <li>water channel activity (ISS, IDA)</li> </ul>
Biological Process Manually curated	<ul style="list-style-type: none"> <li>cellular response to freezing (IMP)</li> <li>cellular response to osmotic stress (IMP)</li> <li>single-species biofilm formation on inanimate substrate (IMP)</li> </ul>
Computational	<ul style="list-style-type: none"> <li>ascospore formation (IEA with <i>S. cerevisiae</i>: AQY1)</li> <li>transmembrane transport (IEA with <i>S. cerevisiae</i>: AQY1)</li> <li>water transport (IEA with <i>S. cerevisiae</i>: AQY1)</li> </ul>
Cellular Component Manually curated	<ul style="list-style-type: none"> <li>membrane (ISS)</li> <li>plasma membrane (IDA)</li> </ul>
High-throughput	
Computational	<ul style="list-style-type: none"> <li>endoplasmic reticulum (IEA with <i>S. cerevisiae</i>: AQY1)</li> </ul>

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

**Manually Curated Cellular Component**

Annotation(s)	Reference(s)	Evidence	Assigned By
membrane	<a href="#">Carbrey JM, et al. (2001)</a> Aquaporin in Candida: characterization of a functional water channel protein. <i>Yeast</i> 18(15):1391-6 <a href="#">CGD Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>	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	<a href="#">Cabezon V, et al. (2009)</a> Analysis of Candida albicans plasma membrane proteome. <i>Proteomics</i> 9(20):4770-86 <a href="#">CGD Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>	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	<a href="#">CGD (2008)</a> Prediction of Gene Ontology (GO) annotations based on orthology <a href="#">CGD Paper</a>	IEA : Inferred from Electronic Annotation with <i>S. cerevisiae</i> : AQY1 Assigned on 2017-01-31	CGD
transmembrane transport	<a href="#">CGD (2008)</a> Prediction of Gene Ontology (GO) annotations based on orthology <a href="#">CGD Paper</a>	IEA : Inferred from Electronic Annotation with <i>S. cerevisiae</i> : AQY1 Assigned on 2017-01-31	CGD
water transport	<a href="#">CGD (2008)</a> Prediction of Gene Ontology (GO) annotations based on orthology <a href="#">CGD Paper</a>	IEA : Inferred from Electronic Annotation with <i>S. cerevisiae</i> : 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		<b>Srikantha T, et al. (2013)</b> Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of <i>Candida albicans</i> a/alpha biofilms. <i>Eukaryot Cell</i> 12(6):875-88 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
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		<b>Srikantha T, et al. (2013)</b> Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of <i>Candida albicans</i> a/alpha biofilms. <i>Eukaryot Cell</i> 12(6):875-88 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
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		<b>Srikantha T, et al. (2013)</b> Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of <i>Candida albicans</i> a/alpha biofilms. <i>Eukaryot Cell</i> 12(6):875-88 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
homozygous diploid, classical genetics	Description: null	SC5314	biofilm formation: abnormal	Details: forms biofilm with altered detachment properties		<b>Sellam A, et al. (2009)</b> A <i>Candida albicans</i> early stage biofilm detachment event in rich medium. <i>BMC Microbiol</i> 9:25 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a> <a href="#">Access Full Text</a>
homozygous diploid, classical genetics	Description: null	CAI-4	flocculation: normal	Condition: liquid YPD medium		<b>Carbrey JM, et al. (2001)</b> Aquaporin in <i>Candida</i> : characterization of a functional water channel protein. <i>Yeast</i> 18(15):1391-6 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
heterozygous diploid, classical genetics	Description: repressible	Not recorded	freeze-thaw resistance: decreased			<b>Tanghe A, et al. (2005)</b> Aquaporin expression and freeze tolerance in <i>Candida albicans</i> . <i>Appl Environ Microbiol</i> 71(10):6434-7 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
homozygous diploid, classical genetics	Description: null	Not recorded	freeze-thaw resistance: decreased			<b>Tanghe A, et al. (2005)</b> Aquaporin expression and freeze tolerance in <i>Candida albicans</i> . <i>Appl Environ Microbiol</i> 71(10):6434-7 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
homozygous diploid, classical genetics	Description: null	CAI-4	hyphal growth: normal	Condition: solid Spider medium		<b>Carbrey JM, et al. (2001)</b> Aquaporin in <i>Candida</i> : characterization of a functional water channel protein. <i>Yeast</i> 18(15):1391-6 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
homozygous diploid, classical genetics	Description: null	CAI-4	invasive growth: normal	Condition: solid YPD medium		<b>Carbrey JM, et al. (2001)</b> Aquaporin in <i>Candida</i> : characterization of a functional water channel protein. <i>Yeast</i> 18(15):1391-6 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
homozygous diploid, classical genetics	Description: null	CAI-4	osmotic stress resistance: increased	Details: greater-than-wild type resistance to both hyper- and hypoosmotic shock		<b>Carbrey JM, et al. (2001)</b> Aquaporin in <i>Candida</i> : characterization of a functional water channel protein. <i>Yeast</i> 18(15):1391-6 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
heterozygous diploid, large-scale survey (haploinsufficient phenotype assay, barcode deletion set)	Description: null	SC5314	viable			<b>Xu D, et al. (2007)</b> Genome-wide fitness test and mechanism-of-action studies of inhibitory compounds in <i>Candida albicans</i> . <i>PLoS Pathog</i> 3(6):e92 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a> <a href="#">Access Full Text</a> <a href="#">Web Supplement</a>
homozygous diploid, classical genetics	Description: null	CAI-4	viable			<b>Carbrey JM, et al. (2001)</b> Aquaporin in <i>Candida</i> : characterization of a functional water channel protein. <i>Yeast</i> 18(15):1391-6 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>
homozygous diploid, classical genetics	Description: null	CAI-4	virulence: normal	Details: organ colonization is also normal	mouse intravenous infection	<b>Carbrey JM, et al. (2001)</b> Aquaporin in <i>Candida</i> : characterization of a functional water channel protein. <i>Yeast</i> 18(15):1391-6 <a href="#">CCO</a> <a href="#">CURATE</a> <a href="#">Paper</a> <a href="#">PubMed</a> <a href="#">Access Full Text</a>

- 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
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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	<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 lusitanae</i> ATCC 42720	EnsemblFungi	
CORT_0A00270	<i>Candida orthopsilosis</i> Co 90-125	EnsemblFungi	
LELG_00007	<i>Lodderomyces elongisporus</i> NRLL YB-4239	EnsemblFungi	
DEHA2F27104g	<i>Debaryomyces 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**

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%	-----MTVEAT---SP-----IDDIEQQ
5	CORT_0A00270	79.3%	-----MTAAGSIAEPT-----PNEIEAQ
6	LELG_00007	80.4%	-----MDSTLGSDSLPEKRTTIDSEGLNHRNPERFEGENRLSPDLEAQ
7	DEHA2F27104g	19.4%	-----MT-----ASDVEAQ
8	CLUG_01034	75.0%	-----MT-----ASDVEAQ
9	YPR192W	45.9%	MSSNDSNDRKQHTRLDPT-----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
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Literature
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Homologs
Protein

**Aqy1p PROTEIN INFORMATION** [ [View References](#) ]

Standard Name	Aqy1p <sup>1</sup>
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	<a href="#">View peptides from PeptideAtlas</a>
<b>Structural Information</b>	<a href="#">View all PDB BLAST hits</a> <a href="#">View Top PDB Hit Information (Link-out)</a> <i>Komagataella pastoris</i> ; 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 ( <a href="#">View Alignment</a> ) Click on image to access PDB interactive viewer (Link-out)
<b>Conserved Domains</b>	<a href="#">Domains/Motifs Page</a> <div style="text-align: center; background-color: yellow; border: 1px solid black; padding: 2px; margin: 5px 0;">             Click on image for expanded interactive view           </div>
<b>Sequence Detail</b>	Length = 273 aa; MW = 29.3 kDa; <a href="#">Physicochemical Properties Page</a> <div style="background-color: yellow; border: 1px solid black; padding: 2px; margin: 5px 0;">             Download in FASTA format           </div> <pre> 1  MVAESSIDN TPNDVEAQRP VYEPKYDDSV NVSPLKNHMI AFLGEFFGTF 51  IFLWVAFVIA QIANQDPTIP DRGSDPMQLI MISFGFGFV MMGVFMFRRV 101 SGGNLNPAVT LTLVLAQAVP PIRGLFMVA QMIAGMAAAG AASAMTPGPI 151 AFTNGLGGA SKARGVLEA FGTCILCLTV LMMAVEKSRA TFMAPFVIGI 201 SLFLGHLICV YTGAGLNPA RSGFGVAAAR SFPVYHVIYW VGPILGSVIA 251 FAIWKIPKIL KYETCNPQGD SDA*           </pre>
Homologs	<a href="#">BLAST Aqy1p against other <i>Candida</i> sequences</a>
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

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- 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.

**Chromosomal Location**

**GBrowse for C. albicans SC5314 Assembly 22** Click on map for expanded view

CR\_02920C\_A

**All Annotated Sequence Features**

CR\_02910M\_A

Uncharacterized, (orf19.2848) Predicted regulatory subunit

CR\_02920C\_A

AQY1, Verified, (orf19.2849) Aquaporin water channel

CR\_02920C\_B

**All Annotated Sequence Features**

CR\_02910M\_B

Uncharacterized, (orf19.2848) Predicted regulatory subunit

CR\_02920C\_B

Verified, (orf19.2849) Aquaporin water channel

- 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	
			Coordinates	Sequence
CDS	1 to 822	668,602 to 667,781	2016-01-21	2014-06-24

**Retrieve Sequences** -- C. albicans SC5314 Assembly 22 -- View

**Sequence Analysis Tools** -- C. albicans SC5314 Assembly 22 -- View

**Maps & Displays** Flanking Features Table 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 ?

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
<b>Srikantha T, et al. (2013)</b> Identification of genes upregulated by the transcription factor Bcr1 that are involved in impermeability, impenetrability, and drug resistance of Candida albicans <i>a/alpha</i> biofilms. <i>Eukaryot Cell</i> 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
<b>Bonhomme J, et al. (2011)</b> Contribution of the glycolytic flux and hypoxia adaptation to efficient biofilm formation by Candida albicans. <i>Mol Microbiol</i> 80(4):995-1013 	C. albicans	AAF1  ABC1  ACS1  ADH1  ADH5  ADK1  AHP1  ALP1  ALS3  ALT1  JAMS1  JARE2  JARG1  JARG4  MORE
<b>Vylkova S, et al. (2011)</b> The fungal pathogen Candida albicans autoinduces hyphal morphogenesis by raising extracellular pH. <i>MBio</i> 2(3):e00055-11 	C. albicans	ACH1  ACS1  ARG1  ARG3  JARG4  JATO1  JATO10  JATO2  JATO5  JATO6  JATO7  JATO9  C2_02650C_A  C4_06910W_A  MORE
<b>Synnot JM, et al. (2010)</b> Regulation of the hypoxic response in Candida albicans. <i>Eukaryot Cell</i> 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
<b>Cabezon V, et al. (2009)</b> Analysis of Candida albicans plasma membrane proteome. <i>Proteomics</i> 9(20):4770-86 	C. albicans	ADH1  AFG3  AGC1  AL11  ALO1  AOX2  ATP1  ATP17  ATP18  ATP19  ATP2  ATP20  ATP3  ATP4  MORE
<b>Cottier F and Mulschlegel FA (2009)</b> Sensing the environment: response of Candida albicans to the X factor. <i>FEMS Microbiol Lett</i> 295(1):1-9 	C. albicans	ACE2  BUD2  CAG1  CAN1  CCH1  CEK1  CPH1  CYR1  CFZ1  EFG1  FIG1  GAP1  GAP2  GAT1  MORE
<b>Hua X, et al. (2009)</b> Morphogenic and genetic differences between Candida albicans strains are associated with keratomycosis virulence. <i>Mol Vis</i> 15:1476-84 	C. albicans	AAP1  AAT21  ACB1  ACO2  ADAEAC  JHP1  JALD6  JALS1  JALS2  JALS4  JALS7  JAMO2  JAOX2  JPE3  MORE
<b>Nett JE, et al. (2009)</b> Time course global gene expression analysis of an in vivo Candida biofilm. <i>J Infect Dis</i> 200(2):307-13 	C. albicans	AAH1  AGP2  ALD6  ALS1  AOX2  ARG1  ARG8  BGL2  C1_10570C_A  CAN1  CAT8  CDC21  CDG1  CDR2  MORE
<b>Sellam A, et al. (2009)</b> A Candida albicans early stage biofilm detachment event in rich medium. <i>BMC Microbiol</i> 9:25 	C. albicans	ALS1  ALS3  JAMS1  BCR1  CWH8  HSP21  HWP1  JMKC1  PGA13  PSA2  YWP1
<b>Trunk K, et al. (2009)</b> Depletion of the cutlin Cdc53p induces morphogenetic changes in Candida albicans. <i>Eukaryot Cell</i> 8(5):756-67 	C. albicans	AOX2  ARG1  C4_05610C_A  C4_06910W_A  CDC53  CFL2  CR_09140C_A  GLO1  HSP12  JMET1  PHO112  JSTE11
<b>Xu D, et al. (2007)</b> Genome-wide fitness test and mechanism-of-action studies of inhibitory compounds in Candida albicans. <i>PLoS Pathog</i> 3(6):e92 	C. albicans	AAH1  AAP1  AAT1  AAT21  ABC1  ABD1  ABP140  ABZ1  ACC1  ACF2  ACO1  ACO2  ACP12  ACS2  MORE