

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. At the top right, there is a search bar with the word "go" inside it, which is highlighted with a purple arrow. The main content area has a heading "New and Noteworthy" followed by a brief text about the availability of C. lusitaniae strain CBS 6936 sequence and BLAST datasets. Below this, there are two sidebar sections: "About CGD" and "Meetings & Courses". On the left side of the main content area, there is a large image showing GFP-labeled Dam1 Complex proteins in DAPI-stained nuclei.

The screenshot shows the CGD Quick Search Result page for the query "aqy1". The results are organized into four sections based on species: *Candida albicans*, *Candida glabrata*, *Candida parapsilosis*, and *Candida dubliniensis*. Each section provides a summary of the number of hits for different categories: Gene names, Biochemical pathways, General Descriptions, and Phenotypes. For example, under *Candida albicans*, there is 1 hit for Gene names and 0 hits for Biochemical pathways.

Species	Gene names (gene name/alias/ORF name)	Biochemical pathways	General Descriptions	Phenotypes [Expanded Phenotype Search]	Ortholog or Best Hit
<i>Candida albicans</i>	1	0	0	0	1
<i>Candida glabrata</i>	1	0	0	0	3
<i>Candida parapsilosis</i>	0	0	0	0	3
<i>Candida dubliniensis</i>	0	0	0	0	2

- 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.

C. albicans AQY1/CR_02920C Summary

Last curated 2014-06-25
See the [Literature Guide](#) for most recent publications.

[Summary](#) [Locus History](#) [Literature](#) [Gene Ontology](#) [Phenotype](#) [Homologs](#) [Protein](#)

AQY1 BASIC INFORMATION [View References]

Standard Name	AQY1
Systematic Name, Reference Strain	CR_02920C_A (<i>C. albicans</i> SC5314)
Assembly 19/21 Identifier	orf19.2849
Alias	orf19.10368, IPF24496.1, IPF10705.1, Contig4-2389_0006, orf6.4943, CA2873, CaO19.2849, 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_G_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. auris</i> B4441 Ortholog(s) : B9J08_000928 <i>C. parapsilosis</i> CDC317 Ortholog(s) : CPAR2_800150 View ortholog cluster : 15 genes among 15 <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
JBrowse	

GO Annotations

[View all AQY1 GO evidence and references](#)

Molecular Function	<ul style="list-style-type: none"> water channel activity (ISS, IDA) water channel activity (IEA with <i>S. cerevisiae</i>: AQY1)
Biological Process	<ul style="list-style-type: none"> cellular response to freezing (IMP) cellular response to osmotic stress (IMP) single-species biofilm formation on inanimate substrate (IMP) ascospore formation (IEA with <i>S. cerevisiae</i>: AQY1) proteasome-mediated ubiquitin-dependent protein catabolic process (RCA) transmembrane transport (IEA with <i>S. cerevisiae</i>: AQY1) water transport (IEA with <i>S. cerevisiae</i>: AQY1)
Cellular Component	<ul style="list-style-type: none"> membrane (ISS) plasma membrane (IDA) plasma membrane (IEA with <i>S. cerevisiae</i>: AQY1)

[View all AQY1 Phenotype details and references](#)

Mutant Phenotype

Classical genetics

homozygous null

- biofilm formation: abnormal
- flocculation: normal
- freeze-thaw resistance: decreased
- hyphal growth: normal
- invasive growth: normal
- osmotic stress resistance: increased
- viable
- virulence: normal



- Scroll down to Locus Summary Notes.

LOCUS SUMMARY NOTES for AQY1 (Last Updated: 2011-06-20)

- AQY1 encodes an aquaporin water channel (1)
- It is required for wild-type tolerance of freezing (7)
- the mutant shows increased resistance to osmotic shock (1)
- its expression is induced during biofilm formation (9)
- the transcript is repressed by flucytosine (6)
- it is not required for virulence in a mouse model of systemic infection (1)

REFERENCES CITED ON THIS PAGE [View Complete Literature Guide for AQY1]

1) Carbrey JM, et al. (2001) Aquaporin in Candida: characterization of a functional water channel protein. <i>Yeast</i> 18(15):1391-6
Published
2) CandidaDB
3) Berman J (2005) Mapping of ORFs in Assembly 4 to those in Assembly 19.
4) CGD (2005) CGD comparison of orf6 and orf19 predicted protein products.
5) Magliocca D, et al. (2007) Entrez Gene: gene-centered information at NCBI. <i>Nucleic Acids Res</i> 35(Database issue):D26-31
Published
6) Liu TT, et al. (2005) Genome-wide expression profiling of the response to azole, polyene, echinocandins, and pyrimidine antifungal agents in Candida albicans. <i>Antimicrob Agents Chemother</i> 49(1):2226-36
Published
7) Tanghe A, et al. (2005) Aquaporin expression and freeze tolerance in Candida albicans. <i>Appl Environ Microbiol</i> 71(10):6434-7
Published
8) Nett JE, et al. (2009) Time course global gene expression analysis of an in vivo Candida biofilm. <i>J Infect Dis</i> 200(2):307-13
Published
9) Bonhommier J, et al. (2011) Contribution of the glycolytic flux and hypoxia adaptation to efficient biofilm formation by Candida albicans. <i>Mol Microbiol</i> 80(4):995-1013
Published
10) Nobile CJ, et al. (2012) A recently evolved transcriptional network controls biofilm development in Candida albicans. <i>Cell</i> 148(1-2):126-38
Published
11) 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
Published

Send a Message to the CGD Curators

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To cite CGD, please use the following reference: Skrzypek MS, Binkley J, Binkley G, Miyasato SR, Simison M, Sherlock G (2017). The Candida Genome Database (CGD): incorporation of Assembly 22, systematic identifiers and visualization of high throughput sequencing data. *Nucleic Acids Res* 45 (D1): D592-D596; see How to cite CGD.

- 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
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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 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	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	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	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. <i>Eukaryot Cell</i> 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. <i>Yeast</i> 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. <i>Proteomics</i> 9(20):4770-86	IDA : Inferred from Direct Assay Assigned on 2014-06-25	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 <i>Candida albicans</i> 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 <i>Candida albicans</i> 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 <i>Candida albicans</i> 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 <i>Candida albicans</i> 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 <i>Candida</i> : 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 <i>Candida albicans</i> . <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 <i>Candida albicans</i> . <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 <i>Candida</i> : 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 <i>Candida</i> : 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 <i>Candida</i> : 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 <i>Candida albicans</i> . <i>PLoS Pathog</i> 3(6):e92
homozygous diploid, classical genetics	Description: null	CAI-4	viable			Carbrey JM, et al. (2001) Aquaporin in <i>Candida</i> : 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 <i>Candida</i> : 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**

?

Summary Locus History Literature Gene Ontology Phenotype Homologs Protein

AQY1 HOMOLOG INFORMATION

Ortholog Cluster From CGOB View CGOB cluster and synteny information

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 orthopsisilosis</i> Co 90-125	EnsemblFungi	
LELG_00007	<i>Lodderomyces elongisporus</i> NRRL 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](#))

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

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)

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)

```

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 LEGL_00007 80.4% -----MTAAGSIAEPT-----PNEIEAQ
7 DEHA2F27104g 19.4% -----MDSTLGSDSLPEKERTTIDSEGLNHRNPFRFEGENRLSPDLEAQ
8 CLUG_01034 75.0% -----MT-----ASDVEAQ
9 YPR192W 45.9% MSSNDSNNDTDKQHTRLDPT-----GVDDAYI

```

- Explore the **Protein** tab. What is known about the structure and physicochemical properties of this protein? How is it expected to fold?

C. albicans Aqy1p/Cr_02920cp Protein Information

?

[Summary](#) [Locus History](#) [Literature](#) [Gene Ontology](#) [Phenotype](#) [Homologs](#) **Protein**

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: Predicted Structure from AlphaFold (Link-out)

Top PDB Hit: **2W2E** View all PDB BLAST hits

Source: Komagataella pastoris; 1.15 Ångstrom Crystal Structure Of *P.Pastoris* Aquaporin, Aqy1, In A Closed Conformation At Ph 3.5

Quality: 68% identical to Aqy1p; P-value = 3.00e-98 (View Alignment)

Structure: Click on image to access PDB interactive viewer (Link-out)



Sequence Detail: Length = 273 aa; MW = 29.3 kDa; Physicochemical Properties Page
[Download](#) in FASTA format

```

1 MVAESSSIDN TPNDVEAQRP VYEPKYDDSV NVSPLKNHMI AFLGEFFGTF
5 IFLWVAFVIA QIANQDPTIP DKGSQDMQLI MISFGFGFVG MMGVPMFPRV
101 SGGNLNPATV LTIVLQAQAVP PIRGLPFMVVA QMIAAGMAAG AASAMTPGPI
151 AFTNGLGGA SKARGVFLEA FGTCLCLTV LMMAVEKSRRA TPMAPFVICI
201 SLFLGHLLIV YTGAGLNPA RSGFPCVAAR SFPVYHWIYW VGPILGSVIA
251 FAIWKIFKIL KYETCNPQGD SDA*

```

Homologs: BLAST Aqy1p against other *Candida* sequences

- What is the chromosomal location of AQY1 and its neighboring genes? From the **Summary** tab, view the **Sequence Information** section and retrieve sequence with or without flanking sequence and/or introns.

Sequence Information Ca22chrRA_C_albicans_SC5314:668602 to 667781 | [JBrowse](#)
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	2016-01-21	2014-06-24

Retrieve Sequences: DNA + flanking intergenic seq for CR_02920C_A [View](#)

Sequence Analysis Tools: C. albicans SC5314 Assembly 22 -- [View](#)

Maps & Displays: Flanking Features Table [View](#)

Allele Location Ca22chrRB_C_albicans_SC5314:668545 to 667724 | [JBrowse](#)
Allele CR_02920C_B **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	668,545 to 667,724	2016-01-21	2014-06-24

- 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	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	AQY1 Literature Curation Summary		
Virulence-related	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		
Related Genes/Proteins			
Nucleic Acid Information			
Research Aids and Literature			
Proteome-wide Analysis			
Gene Product Information			
Life Cycle			
Curated Literature			
Regulation			
Genetics/Cell Biology			
Related Species			
Genome-wide Analysis			
	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 <i>Candida albicans</i> alpha/beta biofilms. <i>Eukaryot Cell</i> 12(6):875-88	<i>C. albicans</i>	[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 <i>Candida albicans</i> . <i>Mol Microbiol</i> 80(4):995-1013	<i>C. albicans</i>	[AAF1] [ABC1] [ACS1] [ADH1] [ADH5] [ADK1] [AHP1] [ALP1] [ALS3] [ALT1] [AMS1] [ARE2] [ARG1] [ARG4] [MORE]
	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	<i>C. albicans</i>	[ACH1] [ACS1] [ARG1] [ARG3] [ARG4] [ATO1] [ATO10] [ATO2] [ATO5] [ATO6] [ATO7] [ATO9] [C2_02650C_A] [C4_06910W_A] [MORE]
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	Cabeson V, et al. (2009) Analysis of <i>Candida albicans</i> plasma membrane proteome. <i>Proteomics</i> 9(20):4770-86	<i>C. albicans</i>	[ADH1] [AFG3] [AGC1] [AL1] [AL01] [AOX2] [ATP1] [ATP17] [ATP18] [ATP19] [ATP2] [ATP20] [ATP3] [ATP4] [MORE]
	Cottier F and Muhlschlegel FA (2009) Sensing the environment: response of <i>Candida albicans</i> to the X factor. <i>FEMS Microbiol Lett</i> 295(1):1-9	<i>C. albicans</i>	[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 <i>Candida albicans</i> strains are associated with keratomycosis virulence. <i>Mol Vis</i> 15:1476-84	<i>C. albicans</i>	[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 <i>Candida</i> biofilm. <i>J Infect Dis</i> 200(2):307-13	<i>C. albicans</i>	[AAH1] [AGP2] [ALD6] [ALS1] [AOX2] [ARG1] [ARG8] [BGL2] [C1_10570C_A] [CAN1] [CAT8] [CDC21] [CDG1] [CDR2] [MORE]
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	Trunk K, et al. (2009) Depletion of the culin Cdc53p induces morphogenetic changes in <i>Candida albicans</i> . <i>Eukaryot Cell</i> 8(5):756-67	<i>C. albicans</i>	[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 <i>Candida albicans</i> . <i>PLoS Pathog</i> 3(6):e92	<i>C. albicans</i>	[AAH1] [AAP1] [AAT21] [ABC1] [ABD1] [ABP140] [ABZ21] [ACC1] [ACF2] [ACO1] [ACO2] [ACP12] [ACS2] [MORE]