

Search for...

[expand all](#) | [collapse all](#)

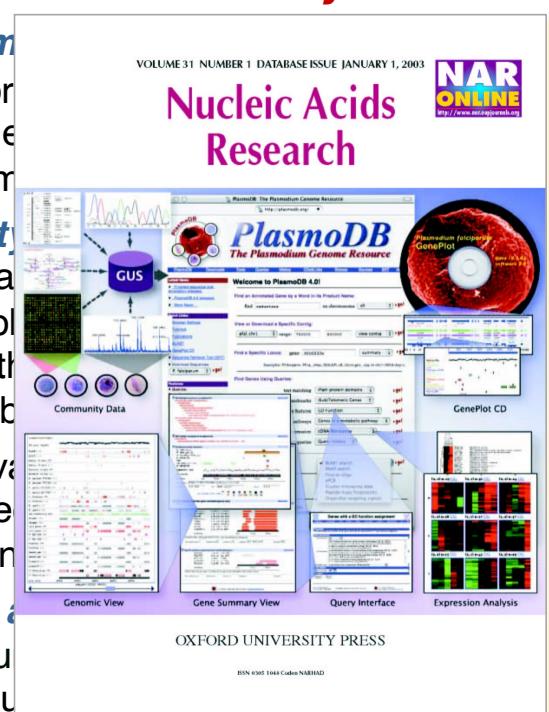
 Filter the searches below...

- ▶ Genes
 - ▶ Organisms
 - ▶ Popset Isolate Sequences
 - ▶ Genomic Sequences



- The philosophy behind VEuPathDB knowledgebases ... ~25 years on!**

 - ❖ **Curated annotation and automated analyses, in a semantically-enriched environment, facilitating data integration for discovery research:** provides annotations for protein structures, functions, locations, pathways, etc ... for diverse eukaryotes, prokaryotes, viruses & vector species. Support for expert knowledge capture from literature.
 - ❖ **Incorporation, integration & analysis of diverse data types:** variation data, field & clinical isolates (with relevant metadata), epigenetic marks, chromatin marks, transcriptomic & proteomic profiling (multiple platforms & single-cell data), subcellular localization, interactomes, pathogenome databases, genomics, metabolomics, comparative genomics, orthology-based analyses.
 - ❖ **Rapid, FAIR data access.** With the wealth of data now available, platform consistency, access & integration are critical for effective sharing and reuse, with data-sharing policies. Support for analysis of users' own data is also provided.
 - ❖ **Robust, sustainable production resources, universal accessibility:** to date (~2800 in 2023); ave 11M page views/mo from 46K unique visitors; 7.3 Tb downloaded/yr (51 Tb to date). Extensive scientific output.
 - ❖ **Provide researchers with the data and tools to ask their own questions!**





Thanks to ...

Search for...

[expand all](#) | [collapse all](#)

Filter the searches below...



▶ Genes

▶ Organisms

▶ Popset Isolate Sequences

▶ Genomic Sequences

▶ Genomic Segments

▶ SNPs

▶ ESTs

▶ Metabolic Pathways

▶ Compounds

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to be named

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Paul Wilkinson⁴

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Steph Wever¹
to be named⁸
to be named⁸

User Interface Dev't

Cristina Aurrecoechea³
Dave Falke³
Sam Kendrick²
Jeremy Myers¹

Ontology Dev't

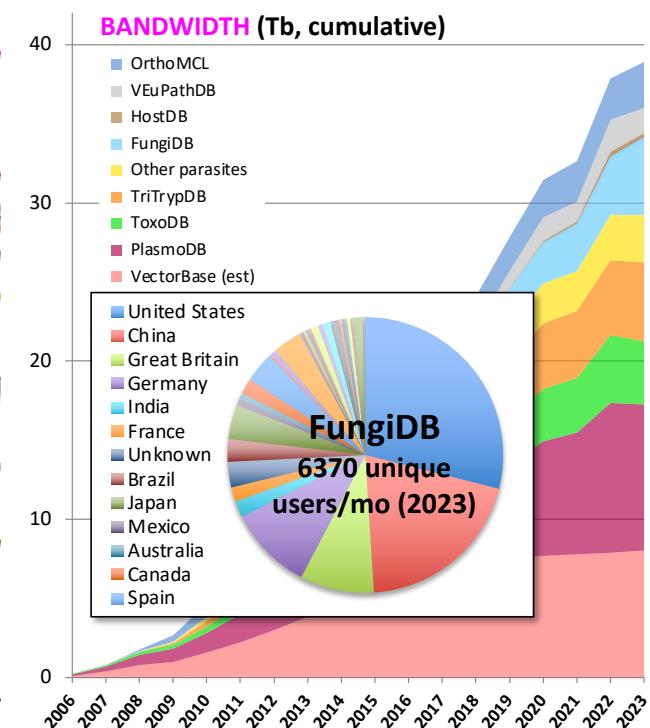
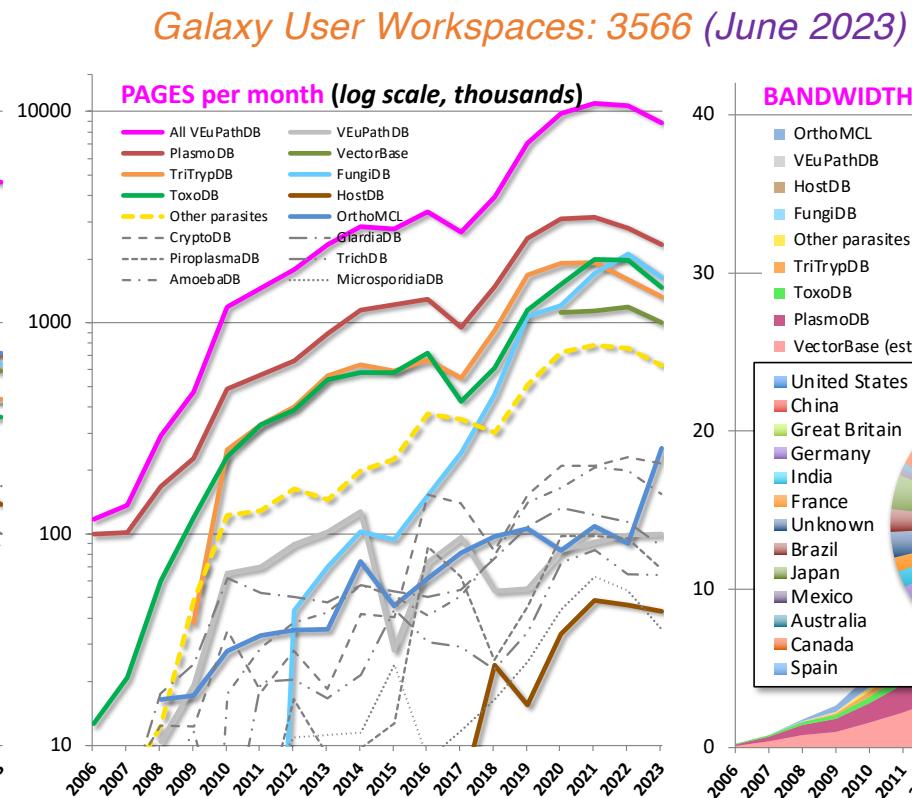
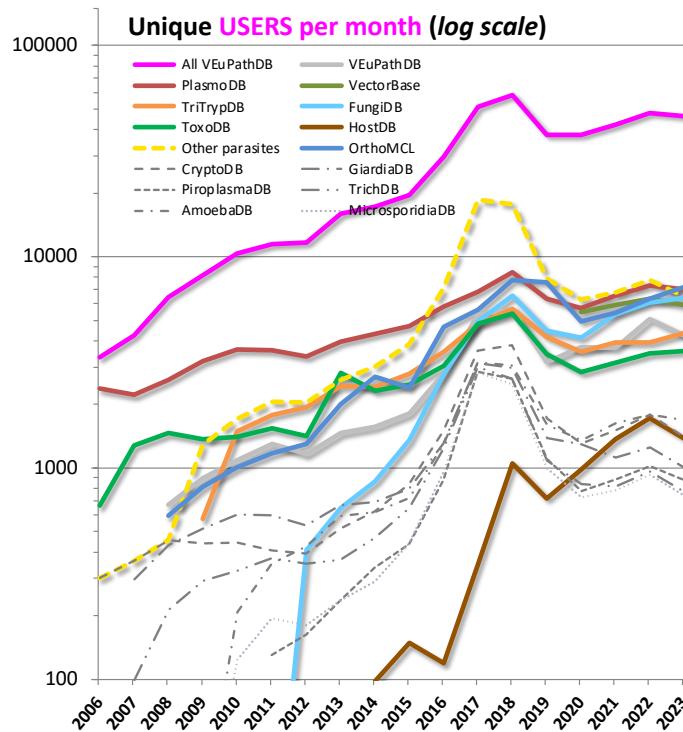
Jie Zheng¹
John Judkins¹
to be named⁸



Usage Statistics (2023)



Registered Users: 29K (June 2023)





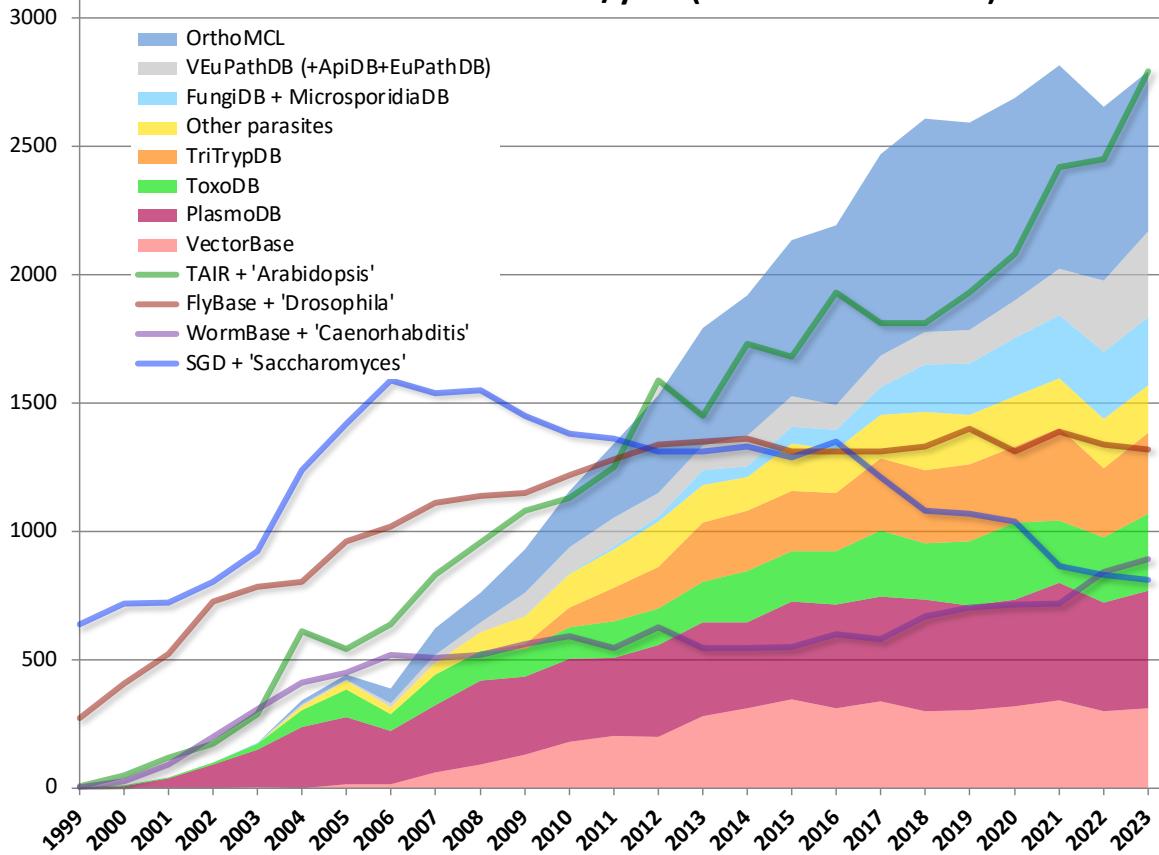
Usage Statistics (2023)

My Strategies Searches Tools My Workspace Data About Help Contact Us

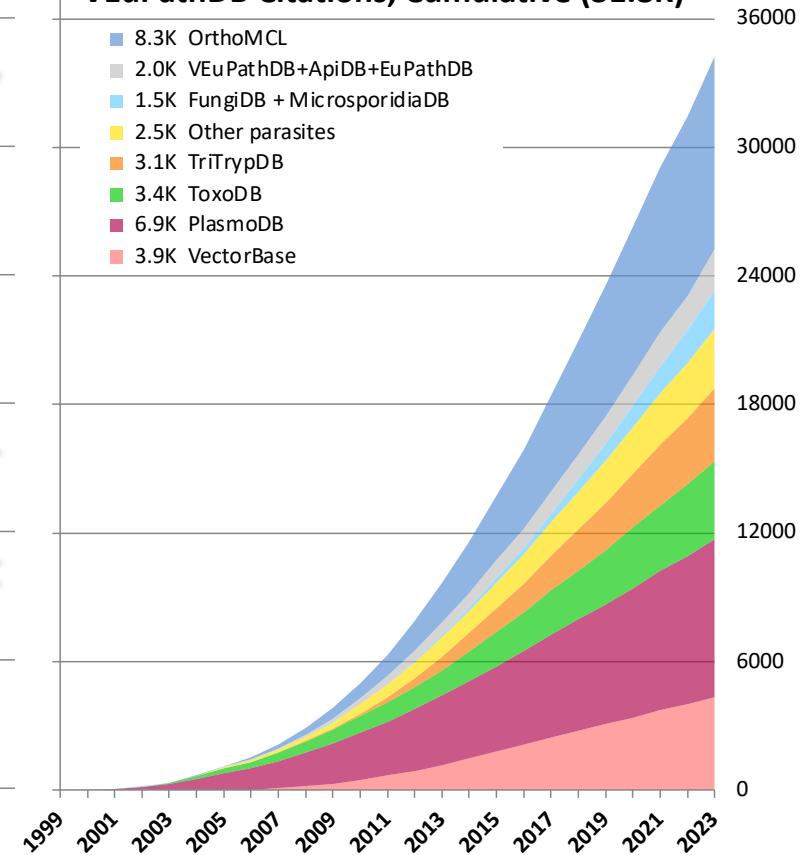
A VEuPathDB Project



VEuPathDB & MODs -- CITATIONS/year (VEuPathDB stacked)



VEuPathDB Citations, Cumulative (31.8K)





Release 65
14 Sept 2023

Fungal & Oomycete Informatics Resources

Site search, e.g. NCU06658 or *reductase or "binding protein"



A VEuPathDB Project

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Search for...

[expand all](#) | [collapse all](#)

Filter the searches below...

Genes

- ▶ Annotation, curation and identifiers
- ▶ Epigenomics
- ▶ Function prediction
- ▶ Gene models
- ▶ Genetic variation
- ▶ Genomic Location
- ▶ Immunology
- ▶ Orthology and synteny
- ▶ Pathways and interactions
- ▶ Phenotype
- ▶ Protein features and properties
- ▶ Protein targeting and localization
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- ▶ Sequence analysis
- ▶ Structure analysis
- ▶ Taxonomy
- ▶ Text
- ▶ Transcriptomics

Organisms

- ▶ Popset Isolate Sequences
- ▶ Genomic Sequences
- ▶ Genomic Segments
- ▶ SNPs
- ▶ ESTs



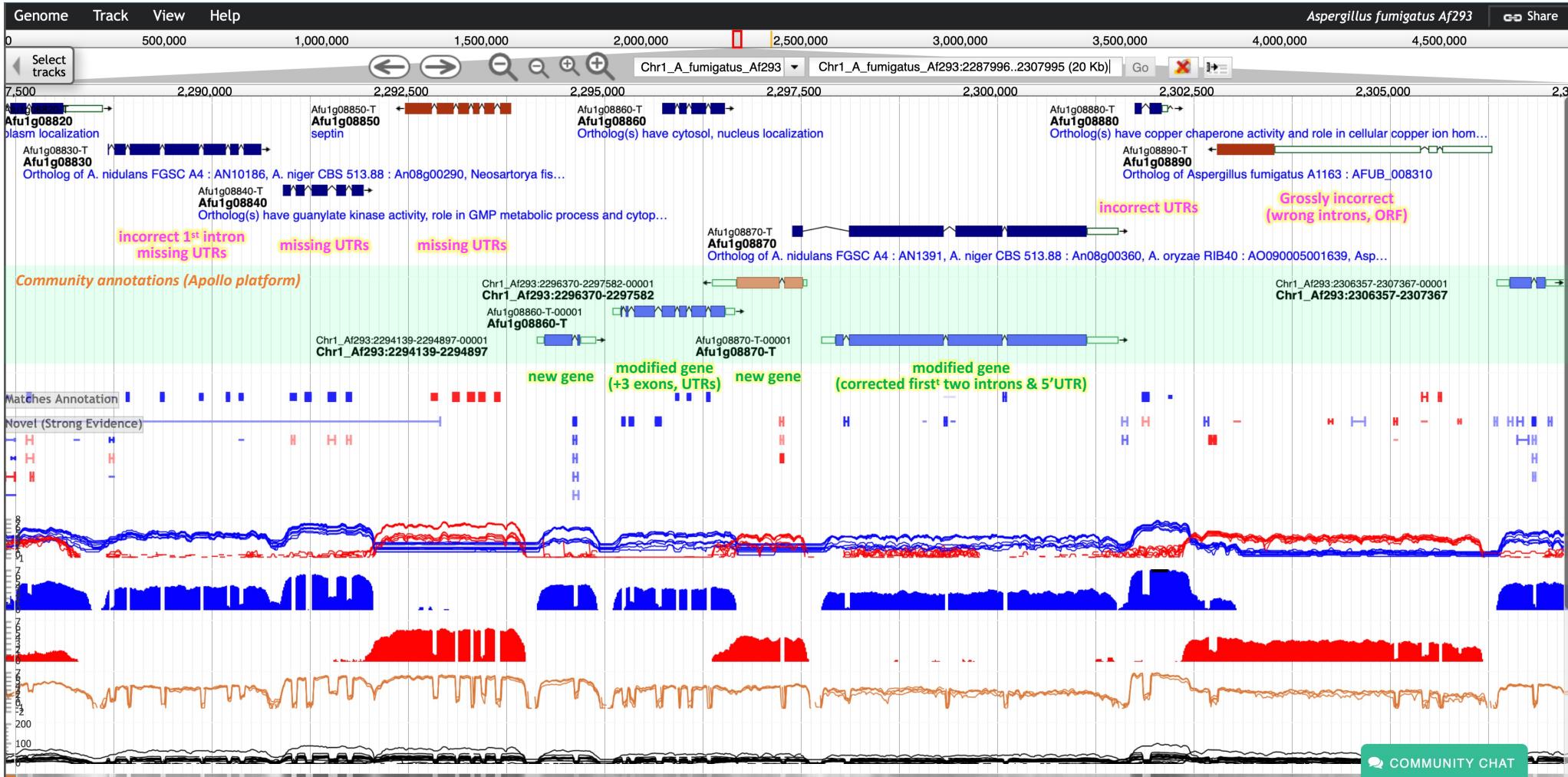
- ❖ **FungiDB is your resource:** tutorials & other on-line materials, webinars & workshops, 'Contact Us' link, virtual meetings w/ your lab, **Visit the help desk during poster sessions**
- ❖ **Help us to identify & prioritize key datasets (and features):** genomes, population diversity data, transcriptomes (incl long-read & single cell cell data), proteomes, metabolomics datasets, interactomes, functional genomics data, phenotypic data, epidemiology
- ❖ **Contribute to the database:** User Comments, Apollo annotation interface
- ❖ **Did you know that you can:**
 - **Define your own questions *in silico*, to ID genes of interest based on** genome loc'n, taxonomic distrib'n, synteny, orthology, signatures of selection, RNA & protein expression, protein domains / motifs / structures, subcellular location, experimental metadata, etc ... and share with others
 - **Visualize & interrogate expression profiles ... based on multiple transcriptomic and proteomic datasets** (now including support for long-read & single-cell RNAseq data)
 - **Assess gene annotation accuracy**, and revise (if warranted) using the Apollo annotation platform, and/or add expert knowledge (references, functions, etc) as User Comments
 - **Leverage orthology ... to infer structure & function based on data in related species**
 - **Determine GO-term & metabolic pathway enrichment ... for your searches or favorite gene lists**
 - **Analyze your own – or any publicly-available – data (privately) ... map RNAseq reads, or identify SNPs in mutant strains or field isolates, via a user-friendly interface to a cloud-based Galaxy platform**



COMMUNITY CHAT

My Organism Preferences (238 of 238)

enabled



Globus Genomics

Analyze Data Workflow Visualize Shared Data Help User GG-v5.4 Using 0 bytes

Tools VEuPathDB Eukaryotic Pathogen, Vector & Host Interactions Resources

DESeq2 Workflow for paired-end unstranded reads (v.7)

Define datasets

quality control

trimming alignment read counts

differential expression & normalization

94: DESeq2 plots on data 88, data 86, and others

93: DESeq2 result file on data 88, data 86, and others

90: BAM to BigWig on collection 72

a list with 2 items

75: BAM to BigWig on collection 69

a list with 2 items

39: FastQC on collection 18: Webpage

a list of pairs with 2 items

24: FastQC on collection 13: Webpage

a list of pairs with 2 items

18: biofilm

a list of pairs with 2 items

Genome Track View Help Aspergillus fumigatus Af293 Share

Select tracks 1,782,500 1,785,000 Chr4_A_fumigatus_Af293 1,787,500 1,790,000 1,792,500 1,795,000 1,797,500 1,799,000

Chr4_A_fumigatus_Af293.1780293..1799063 (18.77 Kb) Go

Alu4g06890-T 14-alpha sterol demethylase

Alu4g06890-T Ortholog(s) have asparagine synthetase (glutamine-hydrolyzing) activity, role in asparagine ...

Alu4g06891D-T Putative outer mitochondrial membrane protein porin

Alu4g06920-T Ortholog of A. nidulans FGSC A4 : AN4403, Aspergillus wentii : Aspwet1_0167198...

Alu4g06930-T Ortholog(s) have cytosol localization

B180 (unique) Coverage

export to JBrowse

All results matching "transcription factor"

 Export as a Search Strategy
 to download or mine your results 

1 - 20 of 342,714

    ...  

Filter results

 Hide zero counts

 Genome
Genes

338,629

 Population biology
Popset isolate sequences

4,048

 Metabolism
Compounds

3

 Data access
Data sets
Searches

18

15

 About
News

1

Filter fields

Select a result filter above

Filter organisms

[select all](#) | [clear all](#) | [expand all](#) | [collapse all](#)

 Type a taxonomic name   Reference only

 Fungi 311,166
 Oomycota 27,481

Data set - Aspergillus fumigatus transcription factor KO collection

Summary: Part of COFUN the Aspergillus fumigatus gene-wide knock out collection.

 Fields matched: Name

Data set - Aspergillus fumigatus transcription factor KO collection

Summary: Part of COFUN the Aspergillus fumigatus gene-wide knock out collection.

 Fields matched: Name

Data set - Comparative transcriptome of Candida parapsilosis wild type and transcription factor mutants

Summary: Transcriptomes collected from WT in planktonic growth conditions and WT and seven transcription factor mutants grown in biofilm conditions.

 Fields matched: Name; Summary

Data set - Sensitivity of transcription factor mutants of Aspergillus fumigatus to Congo Red

Summary: Examination of mRNA patterns of 4 transcription factor mutants of Aspergillus fumigatus and its parental strains in presence of 2 concentrations of Congo Red

 Fields matched

Description: More specifically, mRNA patterns of 4 transcription factor mutants of Aspergillus fumigatus and its parental strains in presence of 2 concentrations of Congo Red (0 and 50 or 300ug/mL).

Name: Sensitivity of transcription factor mutants of Aspergillus fumigatus to Congo Red

Summary: Examination of mRNA patterns of 4 transcription factor mutants of Aspergillus fumigatus and its parental strains in presence of 2 concentrations of Congo Red

Data set - The transcription factor Pdr802 regulates Titan cell production and Cryptococcus neoformans pathogenicity

Summary: The study of the role of Pdr802, whose expression is highly induced under host-like conditions in vitro and is critical for C. neoformans dissemination and virulence in a mouse model of infection.

 Fields matched: Associated publications; Name

Data set - Determining Aspergillus fumigatus transcription factor expression and function during invasion of the mammalian lung

Summary: Determining Aspergillus fumigatus transcription factor expression and function during invasion of the mammalian lung

 COMMUNITY CHAT

Genes matching "transcription factor" (filtered by fields and organisms)

[Export as a Search Strategy](#)
to download or mine your results 

1 - 20 of 296

    ...  

Filter results

Genome
Genes

Hide zero counts

[Clear filter](#)
296

Filter Gene fields

[select all](#) | [clear all](#)

<input type="checkbox"/> GO terms	401
<input type="checkbox"/> InterPro domains	331
<input type="checkbox"/> Notes from annotators	15
<input type="checkbox"/> Orthologs	1,047
<input type="checkbox"/> PDB chains	52
<input checked="" type="checkbox"/> Product description	294
<input checked="" type="checkbox"/> Product descriptions (all)	296
<input type="checkbox"/> PubMed	55
<input type="checkbox"/> User comments	4

Filter organisms

[Clear filter](#)

[select only these](#) | [add these](#) | [clear these](#)

<input type="checkbox"/> fum	  <input type="checkbox"/> Reference only
<input type="checkbox"/> Fungi	19,241
<input type="checkbox"/> Ascomycota	15,739
<input type="checkbox"/> Eurotiomycetes	9,947
<input type="checkbox"/> Eurotiales	6,705
<input type="checkbox"/> Aspergillaceae	6,029
<input type="checkbox"/> Aspergillus	5,834
<input type="checkbox"/> Aspergillus fumigatus	575
<input type="checkbox"/> Aspergillus fumigatus A1163	279
<input checked="" type="checkbox"/> Aspergillus fumigatus Af293	296
[Ref]	

[Gene - Afu1g02860](#) putative transcription factor

Gene type: protein coding gene

Organism: Aspergillus fumigatus Af293

► Fields matched: Orthologs; Product description; Product descriptions (all)

[Gene - Afu1g13750](#) C2H2 transcription factor

Gene type: protein coding gene

Organism: Aspergillus fumigatus Af293

► Fields matched: GO terms; Orthologs; Product description; Product descriptions (all)

[Gene - Afu2g05250](#) putative transcription factor

Gene name or symbol: rfeD

Gene type: protein coding gene

Organism: Aspergillus fumigatus Af293

► Fields matched: Orthologs; Product description; Product descriptions (all)

[Gene - Afu2g10770](#) putative transcription factor

Gene type: protein coding gene

Organism: Aspergillus fumigatus Af293

► Fields matched: InterPro domains; Orthologs; Product description; Product descriptions (all)

[Gene - Afu3g05760](#) C6 transcription factor

Gene type: protein coding gene

Organism: Aspergillus fumigatus Af293

► Fields matched: GO terms; Orthologs; Product description; Product descriptions (all)

[Gene - Afu3g08010](#) C2H2 transcription factor

Gene name or symbol: ace1

Gene type: protein coding gene

Organism: Aspergillus fumigatus Af293

► Fields matched: Orthologs; Product description; Product descriptions (all)

 COMMUNITY CHAT

My Search Strategies

Opened (1) All (374) Public (47) Help

Unnamed Search Strategy * 

Step 1

Afum XcrF 296 Genes

30 Genes (30)

Gene Results  

Rows per page: 100

Gen	Gene
	Afu6g05
	Afu6g09
	Afu3g12
	Afu5g06
	Afu2g14
	Afu7g00

Add a step to your strategy

1,118 Set of Samples Total  

212 of 1,118 Set of Samples

Data Set

Keep checked values at top

SNP calls on WGS of *Aspergillus fumigatus* isolates from a CDC surveillance of triazole resistance in the United States

SNP calls on WGS of *Aspergillus fumigatus* isolates from the UK and Ireland

SNP calls on WGS of *Aspergillus fumigatus* strains collected in Spain

SNP calls on WGS of *Aspergillus fumigatus* strains serially isolated from patients with aspergillosis

expand all | collapse all

Filter the searches below... 

Genes

- ▶ Annotation, curation and identifiers
- ▶ Epigenomics
- ▶ Function prediction
- ▶ Gene models
- Genetic variation**

 - ▶ Copy Number (CNV)
 - ▶ Copy Number Comparison (CNV)
 - ▶ SNP Characteristics

- ▶ Genomic Location
- ▶ Immunology
- ▶ Orthology and synteny
- ▶ Pathways and interactions
- ▶ Phenotype
- ▶ Protein features and properties
- ▶ Protein targeting and localization
- ▶ Proteomics
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- ▶ Structure analysis
- ▶ Taxonomy
- ▶ Text
- ▶ Transcriptomics

Organisms

- ▶ Popset Isolate Sequences
- ▶ Genomic Sequences
- ▶ Genomic Segments
- ▶ SNPs
- ▶ ESTs
- ▶ Metabolic Pathways
- ▶ Compounds

My Organism Preferences (327 of 327) 

Send to... 

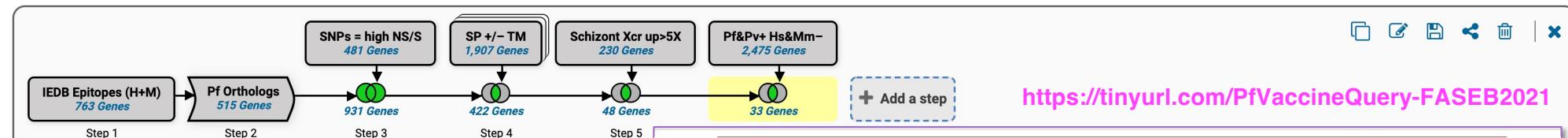
COMMUNITY CHAT

My Search Strategies

[Opened \(2\)](#) All (378) Public (51) Help

Plasmodium vaccine antigens? ↗

Immunoreactive (manual curation, from Immune Epitope DB)
P. falciparum Orthologs (of any *Plasmodium* antigen)
 Under diversifying selection (dN/dS)
 Surface expression (SP ± TM)
 Expressed at the desired stage (schizonts)
 Orthologs in *P. falciparum* & *P. vivax*; not in humans/mice



```

graph LR
    A[IEBD Epitopes (H+M)  
763 Genes] --> B[Pf Orthologs  
515 Genes]
    B --> C(( ))
    C --> D[SNPs = high NS/S  
481 Genes]
    C --> E[SP +/- TM  
1,907 Genes]
    C --> F[Schizont Xcr up>5X  
230 Genes]
    C --> G[Pf&Pvv Hs&Mm-  
2,475 Genes]
    D --> H[931 Genes]
    E --> I[422 Genes]
    F --> J[48 Genes]
    G --> K[33 Genes]
    H --> L[active targets (positive controls)]
    I --> M[other targets of interest]
    J --> N[novel candidates?]
    K --> O[https://tinyurl.com/PfVaccineQuery-FASEB2021]
    
```

33 Genes (24 ortholog groups)

active targets (positive controls)
 other targets of interest
 novel candidates?

Gene Results | Genome View | Analyze Results

Genes: 33 Transcripts: 34 (hiding 1) Show Only One Transcript Per Gene

Rows per page: 50

Gene ID	Transcript ID	Product Description
PF3D7_1133400	PF3D7_1133400.1	apical membrane antigen 1
PF3D7_1352900	PF3D7_1352900.1	Plasmodium exported protein, unknown function
PF3D7_0202100	PF3D7_0202100.1	liver stage associated protein 2
PF3D7_0930300	PF3D7_0930300.1	merozoite surface protein 1
PF3D7_0508000	PF3D7_0508000.1	6-cysteine protein
PF3D7_1335100	PF3D7_1335100.1	merozoite surface protein 7
PF3D7_0207500	PF3D7_0207500.1	serine repeat antigen 6
PF3D7_0831600	PF3D7_0831600.1	cytoadherence linked asexual protein 8

Research a

2344 Mol. Biol. Evol. 27(10):2344–2351. 2010 doi:10.1093/molbev/msq119 Advance Access publication May 9, 2010

Allele Frequency-Based and Polymorphism-Versus-Divergence Indices of Balancing Selection in a New Filtered Set of Polymorphic Genes in *Plasmodium falciparum*

Lynette Isabella Ochola,¹ Kevin K. A. Tetteh,² Lindsay B. Stewart,² Victor Riitho,¹ Kevin Marsh,¹ and David J. Conway^{*2}

¹Kenya Medical Research Institute, Centre for Geographic Medicine Research Coast, Kilifi, Kenya
²Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, United Kingdom

*Corresponding author: E-mail: dconway@mrc.gm, david.conway@lshtm.ac.uk.
 Associate editor: John H. McDonald

Abstract

Signatures of balancing selection operating on specific gene loci in endemic pathogens can identify candidate targets of naturally acquired immunity. In malaria parasites, several leading vaccine candidates convincingly show such signatures when subjected to several tests of neutrality, but the discovery of new targets affected by selection to a similar extent has been slow. A small minority of all genes are under such selection, as indicated by a recent study of 26 *Plasmodium falciparum* merozoite-stage genes that were not previously prioritized as vaccine candidates, of which only one (locus PF10_0348) showed a strong signature. Therefore, to focus discovery efforts on genes that are polymorphic, we scanned all available shotgun genome

Site search, e.g. NCU06658 or *reductase or "binding protein"

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David

[My Organism Preferences \(327 of 327\)](#)

enabled

[Add to basket](#) [Add to favorites](#) [Download Gene](#)

Afu6g05160 Putative zinc-finger C2H2-type transcription factor

Name: azf1**Gene Type:** protein coding gene**Biotype Classification:** protein_coding**Chromosome:** 6**Location:**

Chr6_A_fumigatus_Af293:1,240,613..1,242,708(+)

Species: Aspergillus fumigatus**Strain:** Af293**Status:** Reference Strain[View 1 user comment, or add a comment](#)[View and update community annotations in Apollo](#)**Model Organism Database(s)****SGD:** YOR113W**Shortcuts**[Also see Afu6g05160 in the Genome Browser or Protein Browser](#) [Collapse all sections for better performance](#)

1 Gene models

Afu6g05160[expand all](#) | [collapse all](#) Search section names...
 1 Gene models

Exons in Gene 4

Transcripts 1

COMMUNITY CHAT

Afu6g05160



[expand all](#) | [collapse all](#)

- ▼ Search section names...
- ▶ 1 Gene models
 - ▶ 2 Annotation, curation and identifiers
 - ▶ 3 Link outs
 - ▶ 4 Genomic Location
 - ▶ 5 Literature
 - ▶ 6 Taxonomy
 - ▶ 7 Orthology and synteny
 - ▶ 8 Phenotype
 - ▶ 9 Genetic variation
 - ▶ 10 Transcriptomics
 - ▶ 11 Sequences
 - ▶ 12 Sequence analysis
 - ▶ 13 Structure analysis
 - ▶ 14 Protein features and properties
 - ▶ 15 Function prediction
 - ▶ 16 Pathways and interactions
 - ▶ 17 Proteomics
 - ▶ 18 Immunology

7 Orthology and synteny

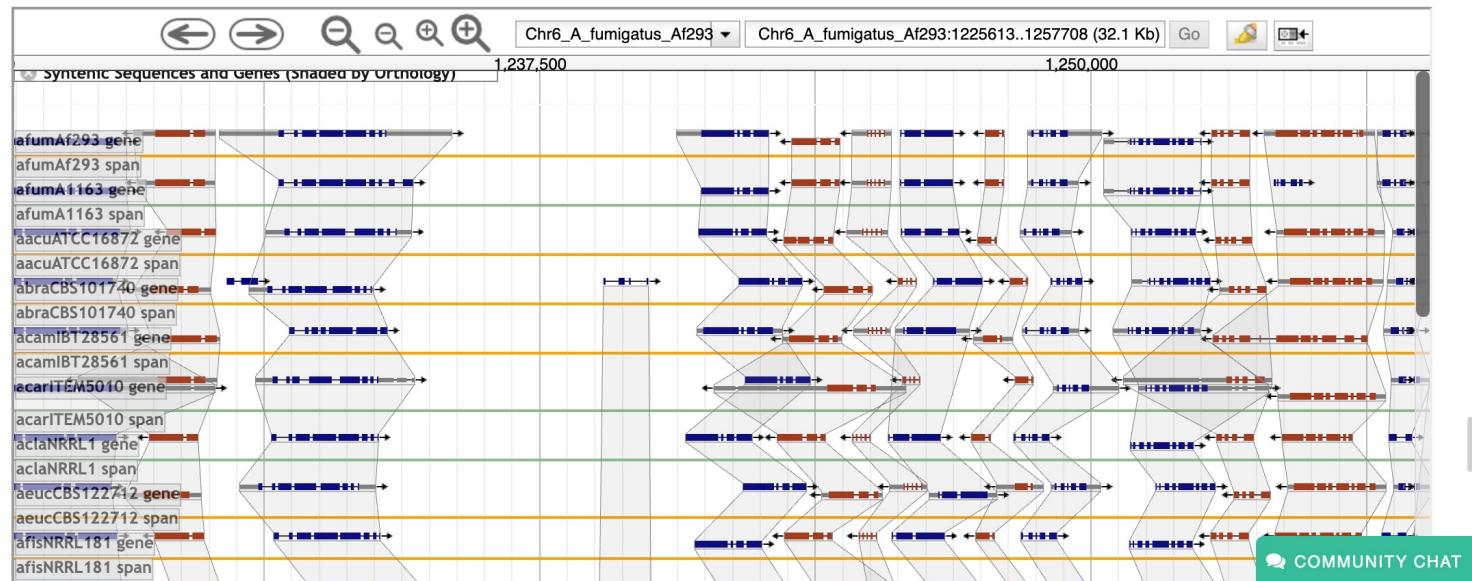
Ortholog Group ⓘ OG6_115680

▶ Orthologs and Paralogs within FungiDB

▼ Synteny ⓘ

[View in JBrowse genome browser](#)

[Reset view](#)



Afu6g05160

«

[expand all](#) | [collapse all](#)

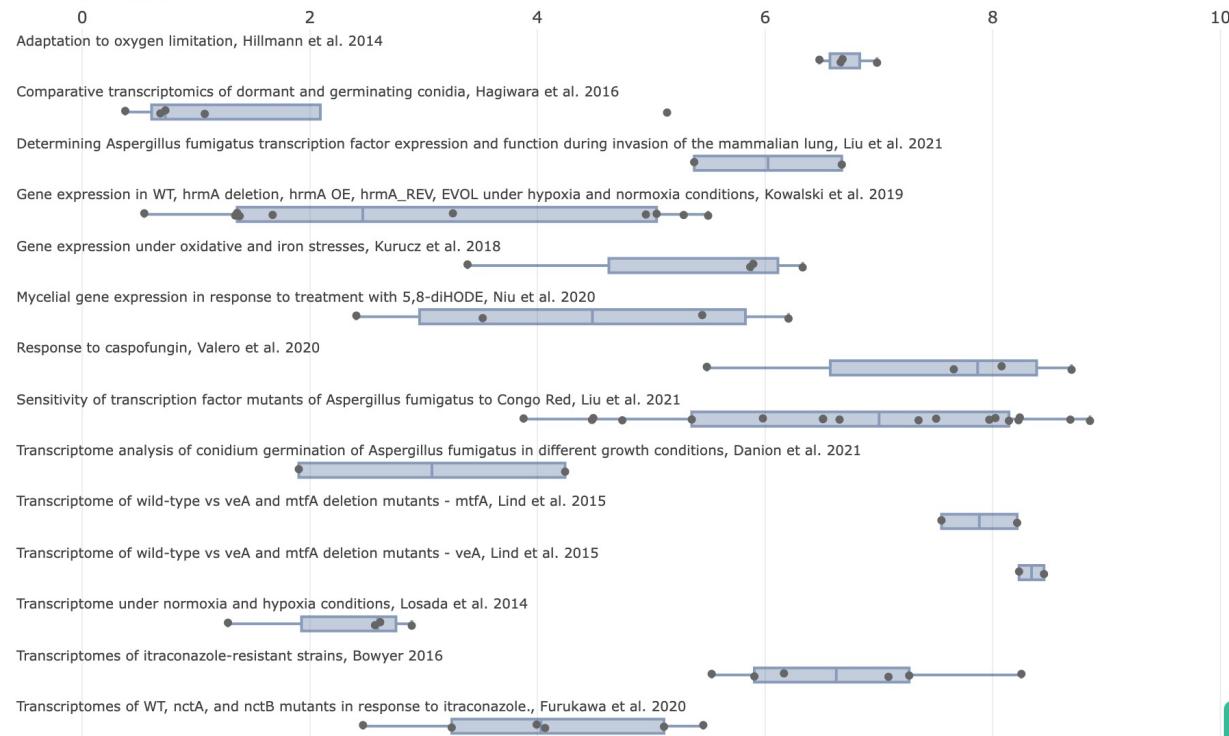
- ▼ Search section names...
- ▶ 1 Gene models
 - ▶ 2 Annotation, curation and identifiers
 - ▶ 3 Link outs
 - ▶ 4 Genomic Location
 - ▶ 5 Literature
 - ▶ 6 Taxonomy
 - ▶ 7 Orthology and synteny
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 - ▶ 13 Structure analysis
 - ▶ 14 Protein features and properties
 - ▶ 15 Function prediction
 - ▶ 16 Pathways and interactions
 - ▶ 17 Proteomics
 - ▶ 18 Immunology

10 Transcriptomics

▼ RNA-Seq Transcription Summary

► Summary of expression values. Each row represents a distinct RNA-Seq experiment. [Click to read more...](#)

Gene: Afu6g05160



COMMUNITY CHAT 

Afu6g05160



[expand all](#) | [collapse all](#)

- ▼ Search section names...
- 1 Gene models
 - 2 Annotation, curation and identifiers
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 - 17 Proteomics
 - 18 Immunology

▼ AlphaFold Structure Prediction Visualization ?

VEuPathDB uses UniProt IDs to associate AlphaFold predictions with genes.

In some cases where specific organisms or genes are not in UniProt, associations between genes and UniProt entries have been made by sequence similarity. This may result in multiple UniProt IDs mapping to a gene.

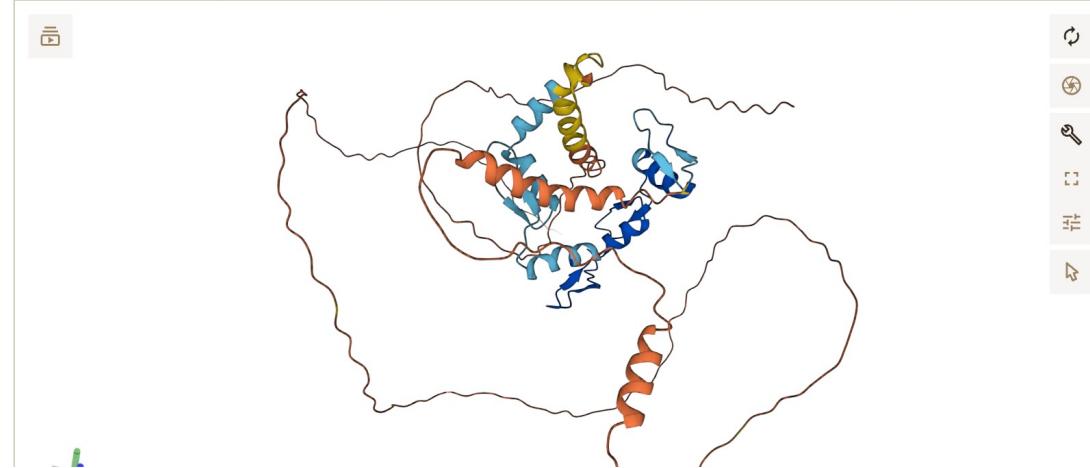
In these cases, we have selected a representative structure to show on this page. Where possible, this is a direct UniProt entry. Where only associations using sequence similarity are available, we have shown the longest prediction. A full list of AlphaFold predictions putatively associated with this gene is available in the AlphaFold table above.

Key:

AlphaFold structures are colored using a per-residue confidence metric called pLDDT, which is scaled from 1 - 100.

Very high (pLDDT > 90) | Confident (90 > pLDDT > 70) | Low (70 > pLDDT > 50) | Very low (pLDDT < 50)

Sequence of	AF-Q4WDL5-F1	Chain	1: C2H2 trans...	A	②
1	METAEPVSYEFTGHAMGSMAPRLLLHAGLGSNFYYNNPATSFPLPYHPSSSTPYGFSHLTINQHPHQHQLPGYQHFYLTNHPSLNSQPVRLSSEPTVQQIPDIRPAKN	21	51	61	71
111	AISRIVGKPLAKSEQSASSQPIAAQPPATGVTKQEGPGSTEIEFSTEVDILMKTIQAKAVPQQSALQCLPPLQQLTGGGENGSQAYAMASSTLRCNVAVEELASR	121	141	151	161
221	PGKKRKYICRLPNCGKSFAQKTHLDIHMRAHTGDKPFVCKEPSCGQRFSQLGNLKTHQRRTGEKPFSCDICQKRFAQRGNVRAHKITHQHAKPFTCLLDDCGKQFT	231	241	251	261



COMMUNITY CHAT

Site search, e.g. ENSMUSG00000021403 or *reductase or "binding protein"



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X f G Y Guest

My Organism Preferences (10 of 10) enabled

Search for...

[expand all](#) | [collapse all](#)

?

▼ Genes

- ▶ Annotation, curation and identifiers
- ▶ Function prediction
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▶ Organisms

▶ Genomic Sequences

▶ Genomic Segments

▶ Metabolic Pathways

Overview of Resources and Tools

Take a Tour



Getting Started



Search Strategies



Genome Browser



Transcriptomic Resources



Analyze My Data



Downloads



How to Submit Data

Getting Started

VEuPathDB is packed with data, tools and visualizations that can help answer your research questions. We gather data from many sources, analyze according to standard workflows, and present the results for you to mine in a point and click interface. Here's how to get started:

SITE SEARCH: Explore the site; find what you need

Enter a term or ID in the site search box at the top of any page. The site search finds documents and records that contain your term and returns a summary of categorized matches. It's easy to find genes, pathways, searches, data sets and more with the site search.



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COMMUNITY CHAT

Explore the Studies

[Study summaries table](#)

Namibia rfMDA RAVC Cluster Randomized Trial - EDA data for QA

[Study Details](#)

Namibia QA, 2017

- Cluster randomized controlled open-label, two-by-two factorial design trial
- 1365 index cases triggered 342 interventions covering 8948 individuals
- Impact of reactive focal mass drug administration (rfMDA) and reactive focal vector control (RAVC) were evaluated in a low endemic setting

[EXPLORE THE DATA](#)


PERCH Case Control

[Study Details](#)

9 Sites in S. Asia and Africa, 2011-2014

- Case-control study with 24 hour, 48 hour, and 30 day follow-up
- 4232 cases with 5325 frequency-matched controls
- The Pneumonia Etiology Research for Child Health (PERCH) study investigated the etiology and risk factors for pneumonia
- See the study page to learn how to request access to the data

[EXPLORE THE DATA](#)


VIDA Case Control

[Study Details](#)

Kenya, Mali, The Gambia, 2015-2018

- Case-control study with 60-day follow-up visit
- 11,053 participants
- The Vaccine Impact on Diarrhea in Africa (VIDA) study determined the effectiveness of rotavirus vaccine at 3 sites in sub-Saharan Africa in children under 5

[EXPLORE THE DATA](#)


VIDA HUCS Gambia Mali Survey

[Study Details](#)

The Gambia, Mali, 2015-2018

- Cross-sectional community survey
- 20,813 participants
- The Health care Utilization and Coverage Survey (HUCS) was conducted semiannually as part of the Demographic Surveillance System at each Vaccine Impact on Diarrhea in Africa (VIDA) study site.

[EXPLORE THE DATA](#)


VIDA HUCS Kenya Survey

[Study Details](#)

Kenya, 2015-2018

- Cross-sectional community survey
- 56,087 participants
- The Health care Utilization and Coverage Survey (HUCS) was conducted semiannually as part of the Demographic Surveillance System at each Vaccine Impact on Diarrhea in Africa (VIDA) study site.

[EXPLORE THE DATA](#)

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News

ClinEpiDB 32 Released

WED FEB 21 2024

We are pleased to announce the release of ClinEpiDB 32! New Data NECTAR (4 studies): The NECTAR datasets represent data from four malaria control trials in Mali. The NECTAR1 tr... [read more](#)

ClinEpiDB 31 Released

TUE NOV 28 2023

We are pleased to announce the release of ClinEpiDB 31! New Data The Southern Africa ICEMR Cross-sectional study was a serial cross-sectional study of malaria in different tran... [read more](#)

ClinEpiDB 29 Released

WED JUL 12 2023

We are pleased to announce the release of ... See all news

Tweets from @ClinEpiDB

 **ClinEpiDB** @ClinEpi... · Mar 22, 2023

We are pleased to announce our latest release! ClinEpiDB 27 is now live with 3 new datasets plus new features in our Mosaic plot 2x2 tool. Read our newsletter here: clinepidb.org/ce/app/static-...

 * * **ClinEpiDB.org** Clinical Epidemiology Resources
Release 32 IS NOW LIVE!
WITH 3 NEW DATASETS + NEW FEATURES

Explore Example Analyses

ClinEpiDB can be used to explore and visualize study data. Use the example analyses below to see some examples.

[VIEW ALL >](#)


Effect of PPF vs PBO ILLNs on malaria

ClinEpiDB Release 32 · 21 Feb 2024



LINEUP demo I LINEUP Cluster Randomized



Plasmodium species in severe malaria patients



Malaria prevalence in different areas of India



Pathogens associated with diarrhea

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