

FAIR Data Access Expedites Global Research

The collage illustrates the global reach and FAIR data access across various bioinformatics databases and research platforms:

- VEuPathDB**: Eukaryotic Pathogen, Vector & Host Informatics Resources.
- FungiDB**: Fungal & Oomycete Informatics Resources.
- OrthoMCL DB**: Ortholog Groups of Protein Sequences.
- PlasmoDB**: Plasmodium Informatics Resources.
- HostDB**: Pathogen Host Informatics Resources.
- VectorBase**: Bioinformatics Resources for Invertebrate Vectors of Human Pathogens.
- MicrobiomeDB**: A Microbiome Resource.
- ClinEpiDB**: Clinical Epidemiology Resources.
- EuPathDB**: Pathogen Infection and Disease.
- BRC (NIH Biostatistics Resource Centers)**: Various search and analysis tools for genomics and proteomics.
- MicrobiomeDB Examples**: CAMP study details and participant selection interface.
- MicrobiomeDB Participant Results**: 534 Participants table and distribution chart.



Production Resources, Professional Staff

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VEuPathDB.org: The Eukaryotic Pathogen, Host & Vector Bioinformatics Resource Center ... and affiliated projects

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Production Resources, Professional Staff

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Alternative Career Paths in Biology & Bioinformatics:

- Indep't faculty (*tenure track*)
- Collab faculty (*tenure track*)
- Research track faculty
- Bioinformatics/Data wrangling
- Software development
- Data visualization
- Data management
- Biocuration & annotation
- Ontology development
- Scientific outreach/education
- Scientific management

Trying to swim (not drown) in a sea of data: 25+ years integrating wet & dry lab research



Science 16 February 2001:
Vol. 291, no. 5507, pp. 1260 - 1261
DOI: 10.1126/science.291.5507.1260

VIEWPOINT

COMPUTATIONAL BIOLOGY: Bioinformatics – Trying to Swim in a Sea of Data

David S. Roos*

Advances in many areas of genomics research are heavily rooted in engineering technology, from the capillary electrophoresis units used in large-scale DNA sequencing projects, to the photolithography and robotics technology used in chip manufacture, to the confocal imaging systems used to read those chips, to the beam and detector technology driving high-throughput mass spectroscopy. Further advances in (for example) materials science and nanotechnology promise to improve the sensitivity and cost of these technologies greatly in the near future. Genomic research makes it possible to look at biological phenomena on a scale not previously possible: all genes in a genome, all transcripts in a cell, all metabolic processes in a tissue.

One feature that all of these approaches share is the production of massive quantities of data. GenBank, for example, now accommodates $>10^{10}$ nucleotides of nucleic acid sequence data and continues to more than double in size every year. New technologies for assaying gene expression patterns, protein structure, protein-protein interactions, etc., will provide even more data. How to handle these data, make sense of them, and render them accessible to biologists working on a wide variety of problems is the challenge facing bioinformatics – an emerging field that seeks to integrate computer science with applications derived from molecular biology. We are swimming in a rapidly rising sea of data ...



Plasmodium genomics

Genomics and proteomics pave the way for controlling malaria

Cold antihydrogen CERN delivers
Antarctic ice Flow reversals
Antigen presentation A 'customizing' protease



THE MOSQUITO GENOME *Anopheles gambiae*



ANTIMALARIAL ARSENAL

Thousands of compounds active against blood-stage parasites

OCEAN WARMING
It's really happening
NUCLEAR WEAPONS
The science of disarmament



Published online 7 November 2011

Nucleic Acids Research, 2012, Vol. 40, Database issue D675-D681
doi:10.1093/nar/gkr918

FungiDB: an integrated functional genomics database for fungi

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Received August 16, 2011; Revised October 6, 2011; Accepted October 8, 2011

ABSTRACT

FungiDB (<http://FungiDB.org>) is a functional genomic resource for pan-fungal genomes that was developed in partnership with the Eukaryotic Pathogen Bioinformatic resource center (<http://EuPathDB.org>). FungiDB uses the same infrastructure and user interface as EuPathDB, which allows for sophisticated and integrated searches to be performed using an intuitive graphical system. The current release of FungiDB contains genome sequence and annotation from 18 species spanning

through the milieu of data. Importantly, it has become essential to be able to interrogate data sets from multiple genomes in an integrated fashion. To this end, FungiDB (<http://fungidb.org>) was developed as a resource for genomic and functional genomic data across the fungal kingdom.

FungiDB was developed in partnership with the NIAID-funded Eukaryotic Pathogen Bioinformatic Resource Center (<http://europathdb.org>) (1). As such this resource uses the same database structural framework and employs the graphical strategies Web Development Kit (WDK) search interface (2). Current genomes in FungiDB are primarily obtained via the Broad

Netscape: PlasmoDB: The Plasmodium Genome Resource

Location: http://plasmodb.

PlasmoDB

The Plasmodium Genome Resource

PlasmoDB is the official database of the *Plasmodium falciparum* Genome Project. It contains finished and draft sequence for *P. falciparum* (3D7) generated at the Sanger Center, Stanford, and TIGR/IMRC, as well as additional data from various sources (see Acknowledgements). Data is available for browsing, querying, and determining subject to the Data Release Policy. You must register to take full advantage of the site.

Release 3.1
Data Release: 7/11/01

To register

- 1 Read Data
- 2 Release Policy
- 3 Check Browser
- 4 Settings
- 5 Register

Quick Links >

- Microsatellite/Optical Maps: for chromosome: 1 GO!
- View/Download Contig: contig ID: chr1_P205867 GO! new view contig
- Specific Locus: gene name: PFC0025c GO!
- Organellar Genome: Mitochondrial GO!
- Gene Queries: new -- Select a Query! -- GO!
- Bulk Sequence Download: new select a species: GO!

Download Data >

- Sequence Naming Convention
- Select a Species
- BLAST
- ePCR
- Find a Protein Motif
- All Tools

Malaria CDs & Links >

- P. falciparum* GenePlot Online
- WHO/TDR *P. falciparum* Genome
- Malaria Links
- Related Publications

Browse the Data >

- P.f.* Sequence Statistics
- Sources of Data in PlasmoDB
- Blast Result viewer
- Gene prediction viewer
- Blast of Genome against itself
- Medline Malaria Updates
- Codon Usage

Queries >

- Text Search
- Search Sequence Features
 - Gene Structure
 - Gene Location (chr 2 and 3)
 - GO Function
- Query Gene Expression Data new
 - EST
 - Microarrays: Oligos or cDNAs
 - View Query History
 - All Queries

Help >

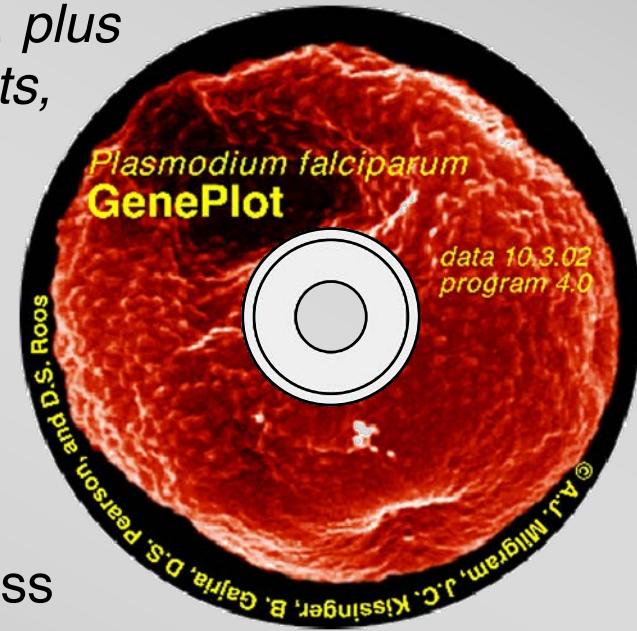
- Tutorial on PlasmoDB new
- Frequently Asked Questions
- What's New at PlasmoDB new
- Known Bugs at PlasmoDB

<http://PlasmoDB.org>

The philosophy behind PlasmoDB

first public release in October 2002

- **Rapid access to both finished and draft datasets.**
Unfinished data is of growing importance, especially for large eukaryotic genomes
- **Curated annotation, integrated with automated analyses.** Predicted genes, proteins, motifs, structures, functions, pathways
- **Integration of diverse data types**
Genome & EST sequences for *Plasmodium* species and related taxa, genetic maps ... plus expression analysis, proteomic hits, publications, clinical data, etc
- **Enable laboratory researchers to ask their own questions**
An Encyclopedia of Malaria is not the goal: correct answers are a lower priority than defining hypotheses that can be tested in the lab
- **Worldwide distribution, universal access**
3,000+ hits/day, around the clock, from more than 50 countries!
CD-ROM distribution for investigators without reliable high-speed net access





Search for...

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

Filter the searches below... ?

▶ Genes

▶ Organisms

▶ Popset Isolate Sequences

▶ Genomic Sequences

▶ Genomic Segments

▶ ESTs

 National Institute of Allergy and Infectious Diseases
Leading research to understand, treat, and prevent infectious, immunologic, and allergic diseases. genome.gov
National Human Genome Research Institute
National Institutes of Health

BILL & MELINDA GATES foundation

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BURROUGHS WELLCOME FUND
 USDA
 CIENCIA SEM FRONTEIRAS TDR
For research on diseases of poverty
UNICEF • UNDP • World Bank • WHO BRC
NIAID Bioinformatics Resource Centers

GLOBAL CORE BIODATA RESOURCE

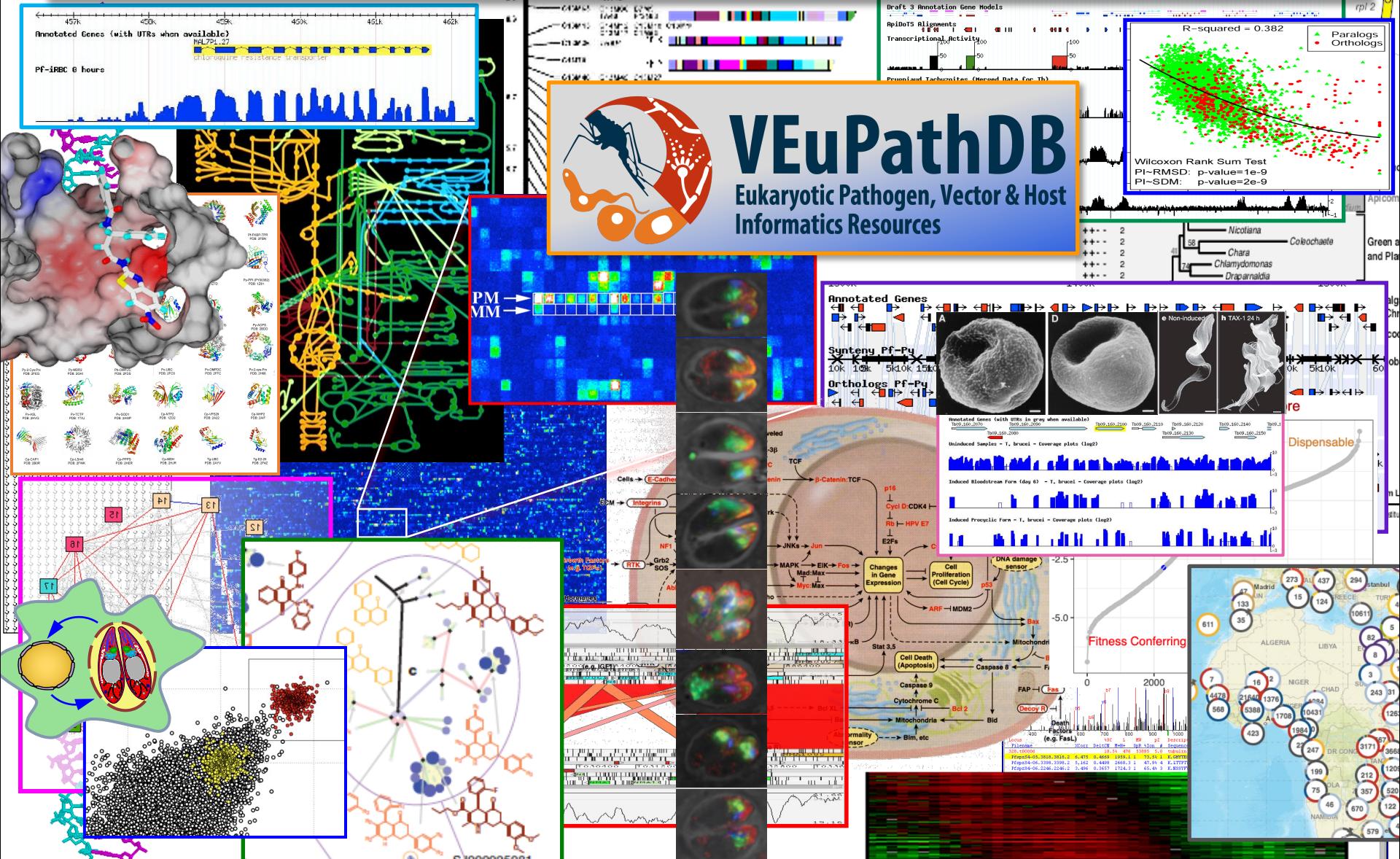
The philosophy behind VEuPathDB databases ... 20+ years on!

- ❖ ***Curated annotation, integrated with automated analyses, in a semantically-defined context to facilitate cross-study analysis.*** Predicted genes, proteins, motifs, structures, functions, locations, pathways, etc ... for diverse microbes and their host/vector species.
- ❖ ***Incorporation & integration of diverse data types:*** genome sequences, variation data, field & clinical isolates (with relevant metadata), chromatin marks, transcriptomic & proteomic profiling (multiple platforms), localization data, interactomes, pathways, phenotypes, structural genomics, metabolomics, comparative genomics & orthology-based inference etc.
- ❖ ***Rapid, FAIR access to both finished & draft datasets.*** Unfinished (and unpublished) data is increasingly important, as genomic-scale datasets are typically incomplete or incompletely analyzed; most VEuPathDB datasets are now deposited and/or released *prior to publication ... but depositors always control release schedules.*
- ❖ ***Robust, sustainable production resources, free universal ,access.*** >28K citations to date; 12M hits/month from >40K unique users in ~200 countries (the average user returns ~weekly); >4 Tb/yr downloads; extensive scientific outreach & education activities
- ❖ ***Provide researchers with the data and tools to ask their own questions!***



COMMUNITY CHAT

BIG DATA: Getting the most out of 'Omics Resources



We're here for you, as a free community service, enhancing FAIR (Findable, Accessible, Interoperable, Reusable) access to genomic-scale datasets, to support & expedite research

- Available since 2000 (PlasmoDB); reengineered as a production resource in 2004 (NIH, WT, BWF, others), cost-effective infrastructure progressively expanded as the VEuPathDB Bioinformatics Resource Center (FungiDB for fungi/oomycetes released in 2012)
- The VEuPathDB BRC is widely used: ~48K unique users/mo (~6K for FungiDB), returning 2-3x monthly, accessing 100+ pages/visit (11M pages/month); 28K citations to date (*2022 statistics*).

Contact Us, tutorials & videos, workshops (in person & remote), virtual lab meetings, social media, **Help Desk** (in person & virtual)

Lots of useful functionality that you & your lab may not be fully familiar with

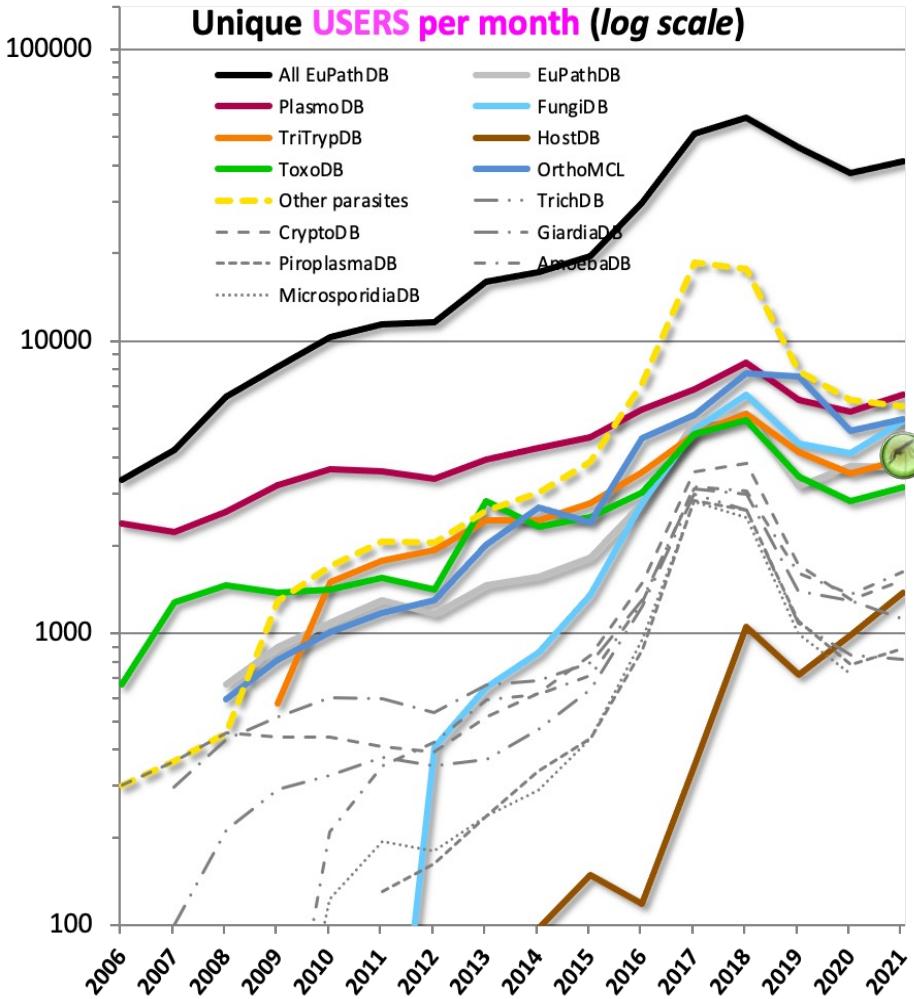
FungiDB is **not an annotation shop** (cost ineffective for 100s-1000s of species) ... but users (*i.e. you*) can evaluate gene model accuracy (Jbrowse), correct (Apollo), add expert knowledge (User Comments), and call on curatorial staff for help, ultimately updating archival repositories



Usage Statistics (2021)

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Guest

 My Organism Preferences (719 of 719) enabled


42K unique users/mo
ave user returns weekly

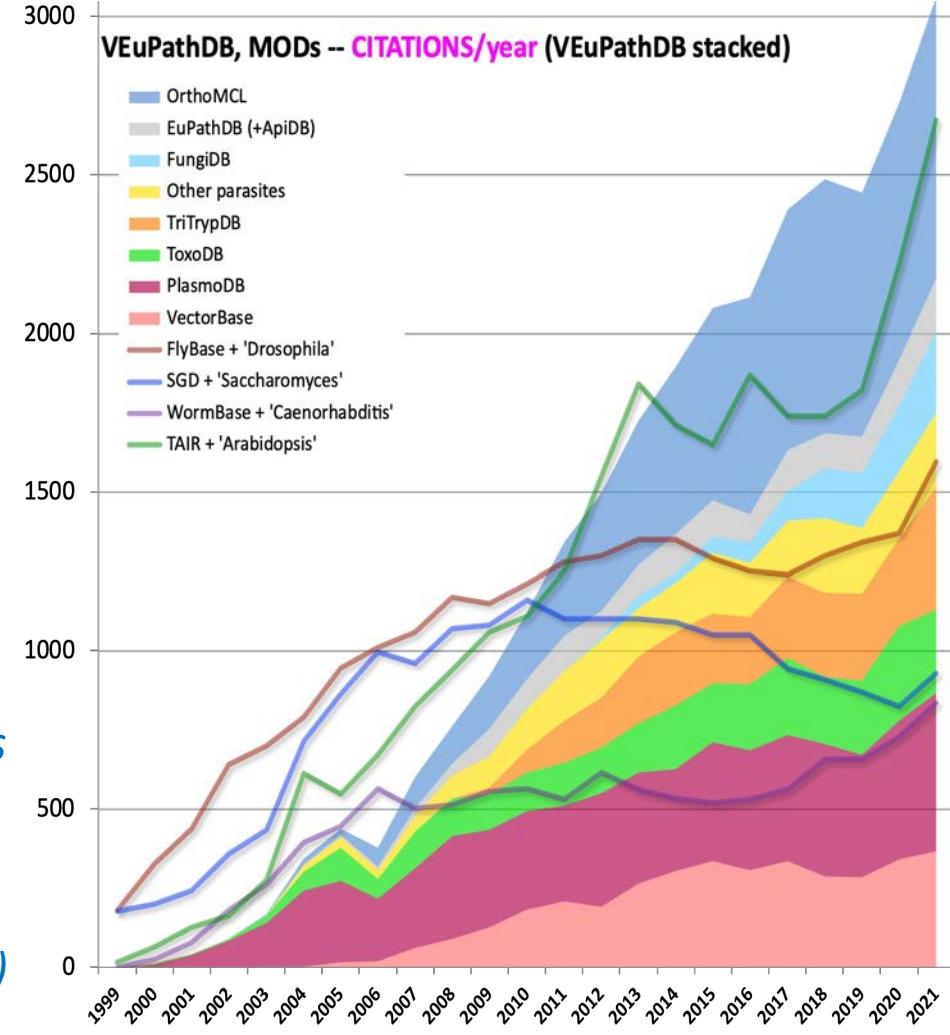
6.5K PlasmoDB
3.9K TriTrypDB
1.5K CryptoDB

25K registered
(from >200 countries)

3.1K Citations/yr

>38K User Comments
>3.3K Galaxy workspaces
>385 Apollo users

4.7Gb/mo





Global Engagement

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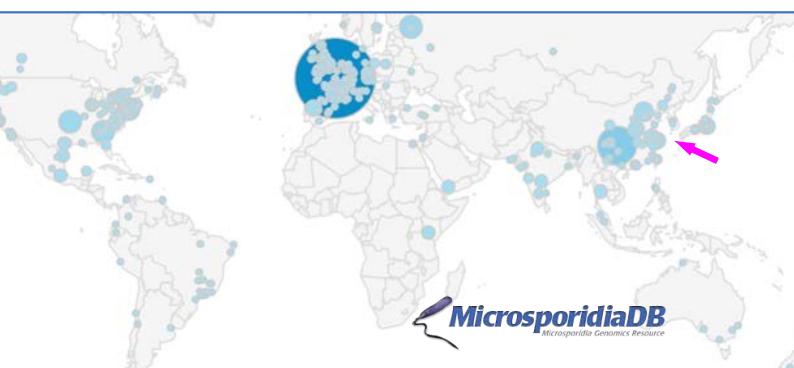
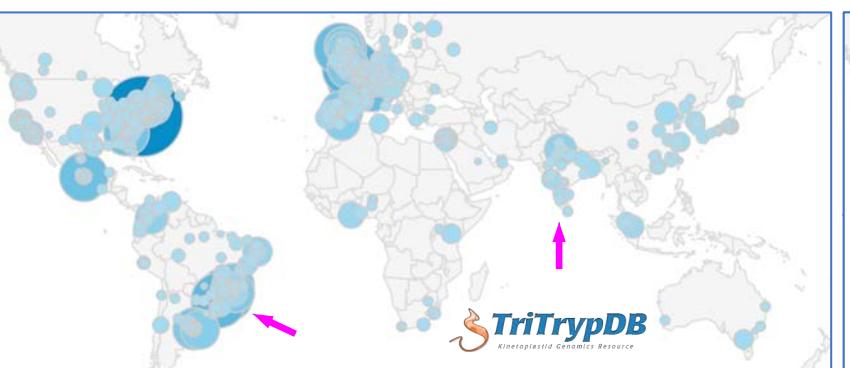
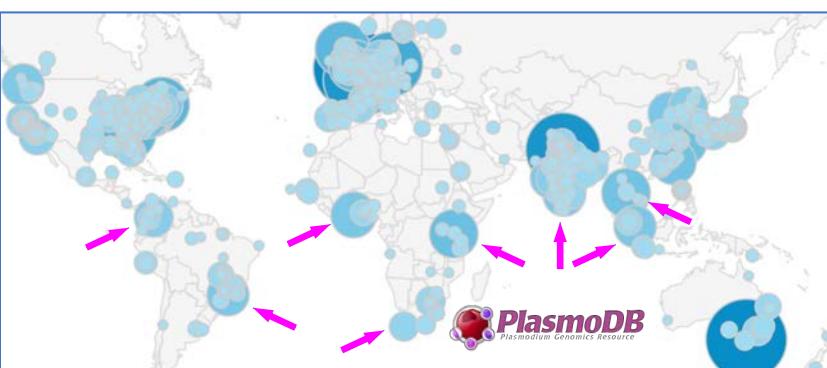
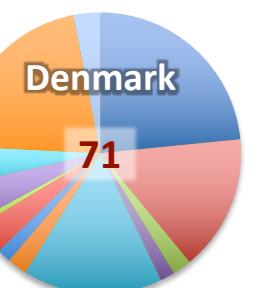
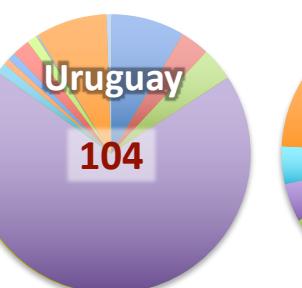
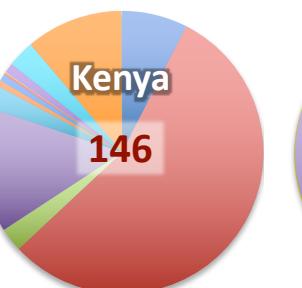
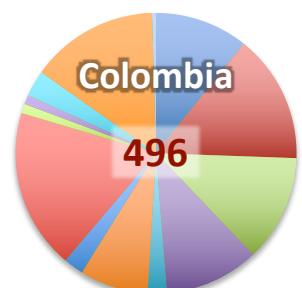
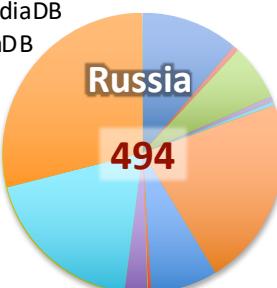
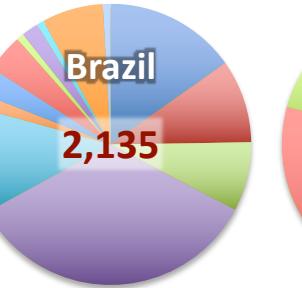
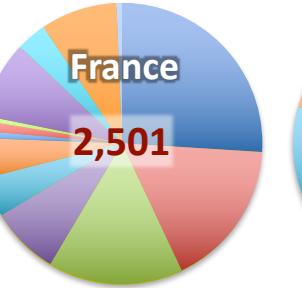
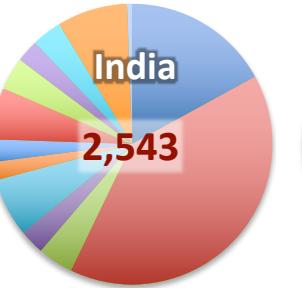
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My Organism Preferences (719 of 719)

enabled

- OrthoMCL
- PlasmoDB
- ToxoDB
- TriTrypDB
- FungiDB
- CryptoDB
- TrichDB
- GiardiaDB
- AmoebaDB
- MicrosporidiaDB
- PiroplasmaDB
- EuPathDB
- HostDB



... did you know that you can

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
 - ▶ Proteomics
 - ▶ Sequence analysis
 - ▶ Structure analysis
 - ▶ Taxonomy
 - ▶ Text

▶ Organisms

▶ Ponset Isolate Sequences

- ❖ **Assess gene annotation accuracy**, revise (if warranted) using the Apollo annotation platform, and/or add expert knowledge (references, functions, etc) as User Comments
 - ❖ **Visualize & interrogate expression profiles** ... based on multiple transcriptomic and proteomic datasets (now including single-cell RNAseq data!)
 - ❖ **Integrate diverse datatypes**, identifying genes of interest based on signatures of selection, species distribution, expression patterns, subcellular localization, phenotypic impact, etc
 - ❖ **Leverage orthology** ... to infer structure & function based on data in related species
 - ❖ **Assess GO-term & metabolic pathway enrichment** ... associated with your gene lists
 - ❖ **Share the results of your *in silico* analyses** ... with friends, colleagues, reviewers, etc
 - ❖ **Analyze your own 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
 - ❖ **Download** query results and datasets for further analysis off-line
 - ❖ **Propose key datasets** (or your own or others) for incorporation into VEuPathDB
 - ❖ **Obtain further help:** on-line resources, email support, Virtual Lab Meeting with your group

... ask us during the workshop, or click the ‘Contact Us’ link at any time!

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

Afu1g09250 Ortholog of *A. nidulans* FGSC A4 : AN1362, *A. niger* CBS 513.88 : An08g00770, *A. oryzae* RIB...

Type: protein coding gene

Chromosome: 1

Location:

Chr1_A_fumigatus_Af293:2,398,651..2,401,196(+)

Species: *Aspergillus fumigatus*
Strain: Af293

Status: Curated Reference Strain

[Add the first user comment](#) 
[View and update community annotations in Apollo](#)
Model Organism Orthologs
[PomBase](#): SPBC16E9.02c

Shortcuts

 Also see Afu1g09250 in the [Genome Browser](#) or [Protein Browser](#)
 Collapse all sections for better performance

1 Gene models

Afu1g09250

expand all | collapse all

Search section names... 

- ▶ 1 Gene models 
- ▶ 2 Annotation, curation and identifiers 
- ▶ 3 Link outs 
- ▶ 4 Genomic Location 

Exons in Gene  5

Transcripts  1

Gene Models

NEW This gene is available in **Apollo** for community annotation. To find out more about Apollo, please visit [this help page](#)  [COMMUNITY CHAT](#)

Afu1g09250



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

[Search section names...](#)

- ▶ 1 Gene models
- ▶ 2 Annotation, curation and identifiers
- ▶ 3 Link outs
- ▶ 4 Genomic Location
- ▶ 5 Literature
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- RNA-Seq Transcription Summary
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- User Dataset Transcriptomics Graphs
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- ▶ 13 Structure analysis
- ▶ 14 Protein features and properties
- ▶ 15 Function prediction
- ▶ 16 Pathways and interactions
- ▶ 17 Proteomics
- ▶ 18 Immunology

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

▼ RNA-Seq Transcription Summary NEW

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

Gene: Afu1g09250

0

2

4

6

8

10

Adaptation to different growth environments (blood), Irmer et al. 2015

Adaptation to oxygen limitation, Hillmann et al. 2014

Comparative transcriptomics of dormant and germinating conidia, Hagiwara et al. 2016

Determining *Aspergillus fumigatus* transcription factor expression and function during invasion of the mammalian lung, Liu et al. 2021

Gene expression in WT, hrmA deletion, hrmA OE, hrmA_REV, EVOL under hypoxia and normoxia conditions, Kowalski et al. 2019

Gene expression under oxidative and iron stresses, Kurucz et al. 2018

Mycelial gene expression in response to treatment with 5,8-diHODE, Niu et al. 2020

Response to caspofungin, Valero et al. 2020

Transcriptome of wild-type vs veA and mtfA deletion mutants - mtfA, Lind et al. 2015

Transcriptome of wild-type vs veA and mtfA deletion mutants - veA, Lind et al. 2015

Transcriptome under normoxia and hypoxia conditions, Losada et al. 2014

Transcriptomes of itraconazole-resistant strains, Bowyer 2016

Transcriptomes of WT, nctA, and nctB mutants in response to itraconazole., Furukawa et al. 2020

Scale: $\log_2(\text{TPM} + 1)$ TPM



COMMUNITY CHAT

sample

My Organism Preferences (238 of 238)

enabled

Genome	Track	View	Help	Aspergillus fumigatus Af293		Share
0	500,000	1,000,000	1,500,000	2,000,000	2,500,000	3,000,000

Select Tracks

[Select tracks](#)

[Genome](#)

[Annotations](#) [Afu1g09220](#) [\(s\) have role i](#)

[RNA-Seq](#) [Matches Ann](#) [Novel \(Stron](#)

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[Respons](#) [H](#)

[Respons](#) [H](#)

[Syntetic](#) [AfumAf293](#)

My Tracks

Currently Active

Recently Used

Category

- 1 Comparative Genomics
- 9 Epigenomics
- 3 Gene Models
- 495 Genetic Variation
- 4 Proteomics
- 8 Sequence Analysis
- 203 Transcriptomics

Subcategory

- 2 (no data)
- 3 BLAT and Blast Alignments
- 9 ChIP-Seq
- 1 DNA polymorphism
- 494 DNA-Seq
- 1 Orthology and Synteny
- 4 Protein Expression
- 202 RNA-Seq
- 1 Sequence assembly
- 3 Sequence composition, complexity and repeats
- 1 Sequence sites, features and motifs
- 2 Transcripts

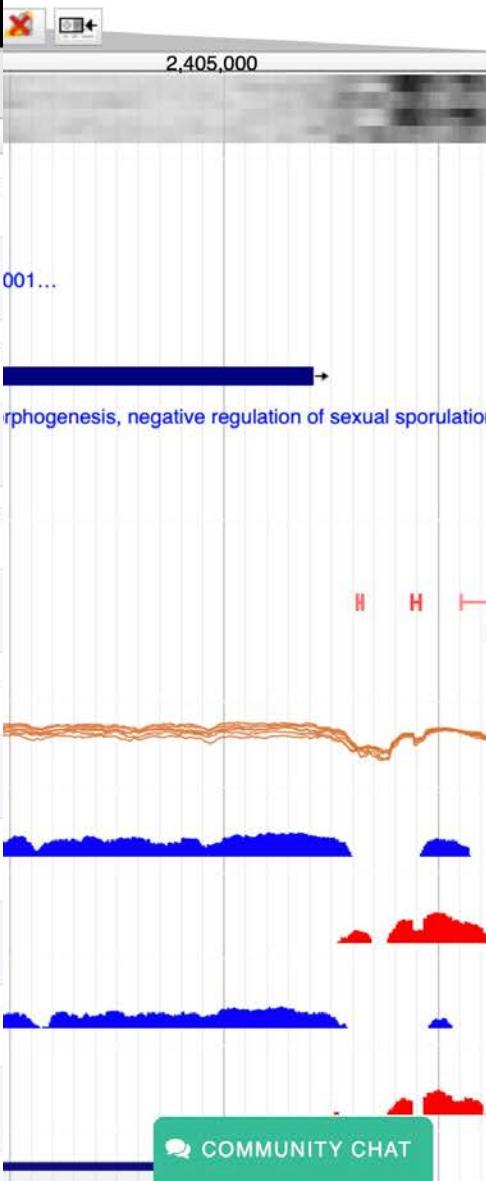
Dataset

- 16 (no data)
- 14 Adaptation to different growth environments (blood)
- 12 Adaptation to oxygen limitation
- 1 Adaptive mechanisms of conidia to nutrient restriction
- 2 Aligned SNPs - Aspergillus fumigatus Af1163 strain
- 1 Combined all RNA-Seq data for AfumigatusAf293
- 14 Comparative transcriptomics of dormant and germinating conidia
- 8 Determining Aspergillus fumigatus transcription factor expression and functional analysis in various

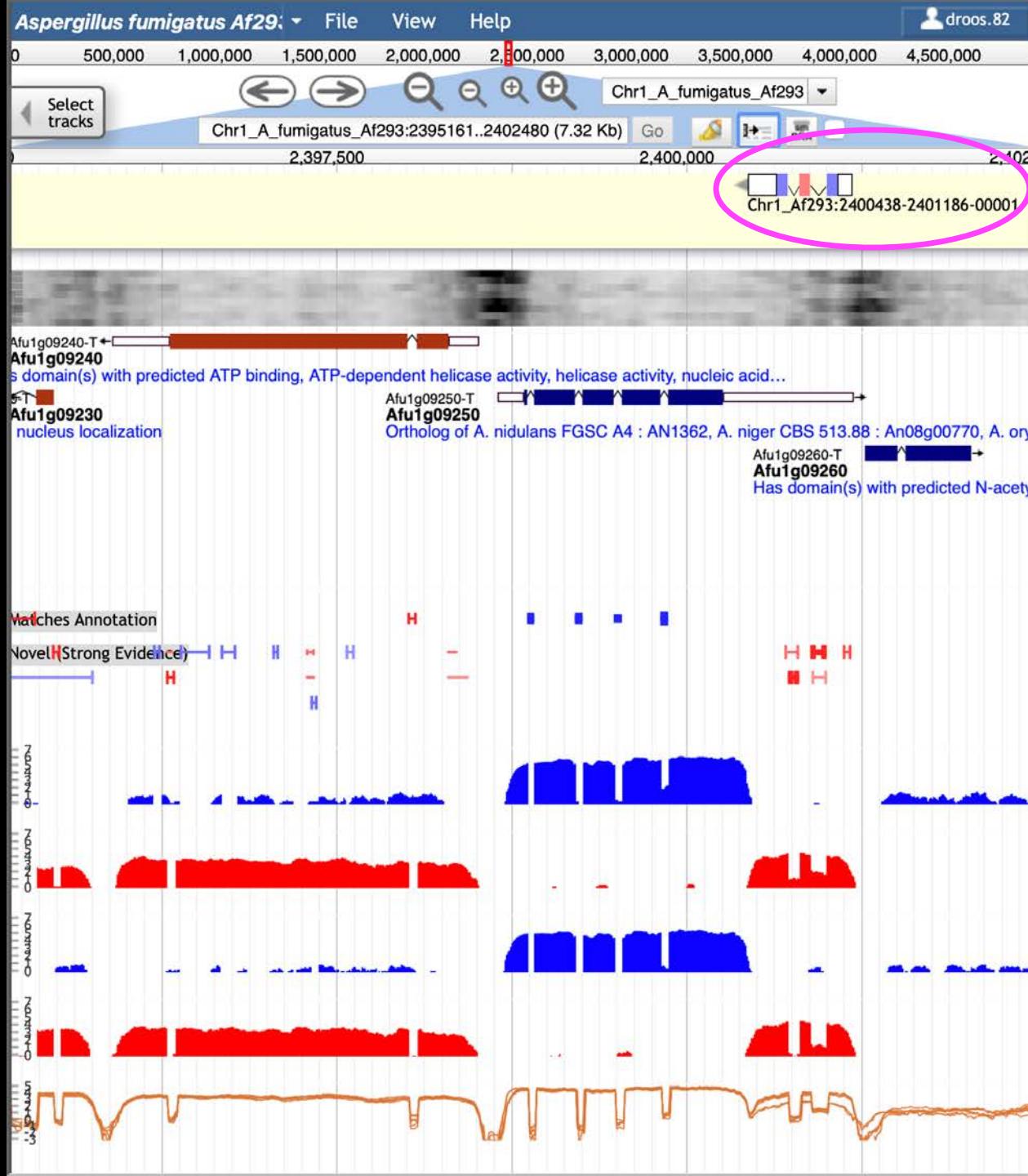
[Back to browser](#) [Clear All Filters](#) [Contains text](#)

723 tracks

<input type="checkbox"/>	Name	Category	Subcategory	Dataset	Track Type
<input type="checkbox"/>	08-12-12-13 Coverage and Alignments	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (Read Alignments zoomed)
<input type="checkbox"/>	08-12-12-13 Coverage normalised to chromosome copy number (ploidy)	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (ploidy Normalized)
<input type="checkbox"/>	08-19-02-10 Coverage and Alignments	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (Read Alignments zoomed)
<input type="checkbox"/>	08-19-02-10 Coverage normalised to chromosome copy number (ploidy)	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (ploidy Normalized)
<input type="checkbox"/>	08-19-02-30 Coverage and Alignments	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (Read Alignments zoomed)
<input type="checkbox"/>	08-19-02-30 Coverage normalised to chromosome copy number (ploidy)	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (ploidy Normalized)
<input type="checkbox"/>	08-19-02-46 Coverage and Alignments	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (Read Alignments zoomed)
<input type="checkbox"/>	08-19-02-46 Coverage normalised to chromosome copy number (ploidy)	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (ploidy Normalized)
<input type="checkbox"/>	08-19-02-61 Coverage and Alignments	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (Read Alignments zoomed)
<input type="checkbox"/>	08-19-02-61 Coverage normalised to chromosome copy number (ploidy)	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (ploidy Normalized)
<input type="checkbox"/>	08-31-08-91 Coverage and Alignments	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (Read Alignments zoomed)
<input type="checkbox"/>	08-31-08-91 Coverage normalised to chromosome copy number (ploidy)	Genetic Variation	DNA-Seq	Genomic Context of Azole-Resistance Mutations in Aspergillus fumigatus	Coverage (ploidy Normalized)
<input type="checkbox"/>	08-36-02-25 Coverage and Alignments	Genetic Variation	DNA-Seq	Genomic Context of Azole-	Coverage (Read Alignments zoomed)



COMMUNITY CHAT



Annotations Tracks Ref Sequence Search

Show All Show Visible Only

Annotation Name	ID	All Types	GO	GP	Prov
Chr1_Af293:2306357-2307367	Chr1_A_fumigatus_Af293	gene	1,011	Mar 07, 2022	
Chr2_Af293:57960-58449	Chr2_A_fumigatus_Af293	gene	490	Mar 07, 2022	
Chr2_Af293:1419529-1420432	Chr2_A_fumigatus_Af293	gene	904	Mar 07, 2022	
Chr1_Af293:2294139-2294897	Chr1_A_fumigatus_Af293	gene	759	Mar 07, 2022	
Afu4g04160-T	Chr4_A_fumigatus_Af293	gene	2,846	Mar 05, 2022	
Afu3g08020-Ta	Chr3_A_fumigatus_Af293	gene	1,282	Mar 02, 2022	
Afu3g08020-T	Chr3_A_fumigatus_Af293	gene	3,538	Mar 02, 2022	
Chr2_Af293:3832898-3833984	Chr2_A_fumigatus_Af293	gene	1,087	Mar 02, 2022	
Afu2g13960-T	Chr2_A_fumigatus_Af293	gene	1,583	Mar 02, 2022	
Chr2_Af293:3646965-3647860	Chr2_A_fumigatus_Af293	gene	896	Mar 02, 2022	
Chr2_Af293:2958153-2959166	Chr2_A_fumigatus_Af293	gene	1,014	Mar 02, 2022	
Chr2_Af293:2447767-2448430	Chr2_A_fumigatus_Af293	gene	664	Mar 02, 2022	
Afu1g08860-T	Chr1_A_fumigatus_Af293	gene	1,564	Mar 02, 2022	
Afu1g08870-T	Chr1_A_fumigatus_Af293	gene	3,788	Mar 02, 2022	
Chr1_Af293:4561546-4563026	Chr1_A_fumigatus_Af293	gene	1,481	Feb 19, 2022	
Chr2_Af293:1411035-1412904	Chr2_A_fumigatus_Af293	gene	1,870	Feb 18, 2022	



My Organism Preferences (238 of 238)

enabled



MGG_04778



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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 Sequence analysis
- ▶ 12 Sequences

nature
chemical biology

ARTICLE

PUBLISHED ONLINE: 10 AUGUST 2015 | DOI: 10.1038/NCHEMBIO.1885

A fungal monooxygenase-derived jasmonate attenuates host innate immunity

Rajesh N Patkar^{1*}, Peter I Benke^{2–4}, Ziwei Qu^{1,2}, Yuan Yi Constance Chen^{1,6}, Fan Yang¹, Sanjay Swarup^{2–4} & Naweed I Naqvi^{1,2,5*}

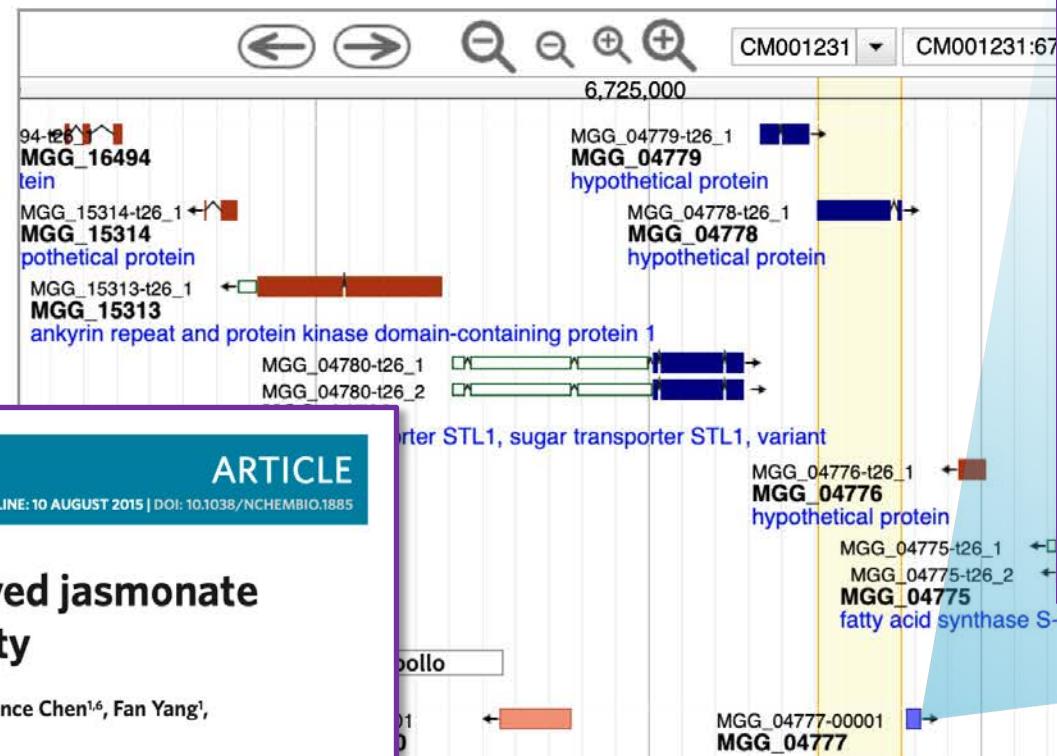
Distinct modifications fine-tune the activity of jasmonic acid (JA) in regulating plant growth and immunity. Hydroxylated JA (12OH-JA) promotes flower and tuber development but prevents induction of JA signaling, plant defense or both. However, biosynthesis of 12OH-JA has remained elusive. We report here an antibiotic biosynthesis monooxygenase (Abm) that converts endogenous free JA into 12OH-JA in the model rice blast fungus *Magnaporthe oryzae*. Such fungal 12OH-JA is secreted during host penetration and helps evade the defense response. Loss of Abm in *M. oryzae* led to accumulation of methyl JA (MeJA), which induces host defense and blocks invasive growth. Exogenously added 12OH-JA markedly attenuated abm Δ -induced immunity in rice. Notably, Abm itself is secreted after invasion and most likely converts plant JA into 12OH-JA to facilitate host colonization. This study sheds light on the chemical arms race during plant-pathogen interaction, reveals Abm as an antifungal target and outlines a synthetic strategy for transformation of a versatile small-molecule phytohormone.

Gene Models

NEW This gene is available in **Apollo** for community annotation. To find out more about Apollo, please visit [this help page](#).

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features Click to open GFF in a new tab

MGG_04777 details

Gene Details

Gene	MGG_04777
Position	CM001231:6729856..6730134 (+ strand)
Links	Apollo
Apollo Gene Product	Jasmonate monooxygenase ABM
Apollo Evidence Code	ECO:0000314
Apollo DBxref	PMID:26258762

Transcript Details

MGG_04777-00001

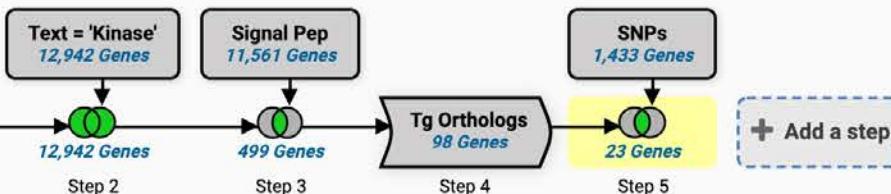
Exon 6729856..6730134

fatty acid synthase S-acetyltransferase, fatty acid synthase S-acetyltransferase, variant



Opened (1) All (3) Public (10) Help

Secretory Kinases (Peixoto) *

**Kinases (Text, Interpro)****Secreted (SP+)****Orthologs in *T.gondii* ME49****Under diversifying selection (dN/dS)****optional: up/down-regulated during differentiation**<https://tinyurl.com/SecretoryKinases>**23 Genes (6 ortholog groups)**Gene Results [Genome View](#) [Analyze Results](#)Cell Host & Microbe
Resource

Rows per page: 100

Gene ID	Transcript ID	Genomic Location (Gene)
TGME49_215775	TGME49_215775-t26_1	TGME49_chrX:7,152,523..7,155,157(+)
TGME49_295110	TGME49_295110-t26_1	TGME49_chrla:1,408,407..1,410,953(-)
TGME49_308090	TGME49_308090-t26_1	TGME49_chrXII:566,721..568,370(-)
TGME49_295125	TGME49_295125-t26_1	TGME49_chrla:1,413,184..1,414,491(-)
TGME49_215785	TGME49_215785-t26_1	TGME49_chrX:7,156,315..7,158,043(+)
TGME49_205250	TGME49_205250-t26_1	TGME49_chrvIIa:1,513,497..1,516,22(+)
TGME49_258580	TGME49_258580-t26_1	TGME49_chrvIIb:3,321,442..3,324,43(+)
TGME49_262730	TGME49_262730-t26_1	TGME49_chrvIIb:1,053,320..1,056,33(+)
TGME49_242110	TGME49_242110-t26_1	TGME49_chrvI:1,905,949..1,908,520(+)
TGME49_258800	TGME49_258800-t26_1	TGME49_chrvIIb:3,177,133..3,178,72(+)
TGME49_242230	TGME49_242230-t26_1	TGME49_chrvI:1,913,970..1,915,439(+)
TGME49_252360	TGME49_252360-t26_1	TGME49_chrIII:512,377..515,416(+)

Integrative Genomic Approaches Highlight a Family of Parasite-Specific Kinases that Regulate Host ResponsesLucia Peixoto,¹ Feng Chen,¹ Omar S. Harb,¹ Paul H. Davis,² Daniel P. Belting,¹ Catie Small Brownback,¹ Dinkoma Ouloguem,¹ and David S. Roos^{1,*}¹Department of Biology and Penn Genome Frontiers Institute, University of Pennsylvania, Philadelphia, PA 19104, USA²Department of Biology, University of Nebraska at Omaha, Omaha, NE 68182, USA

*Correspondence: dros@sas.upenn.edu

DOI 10.1016/j.chom.2010.07.004

SUMMARY

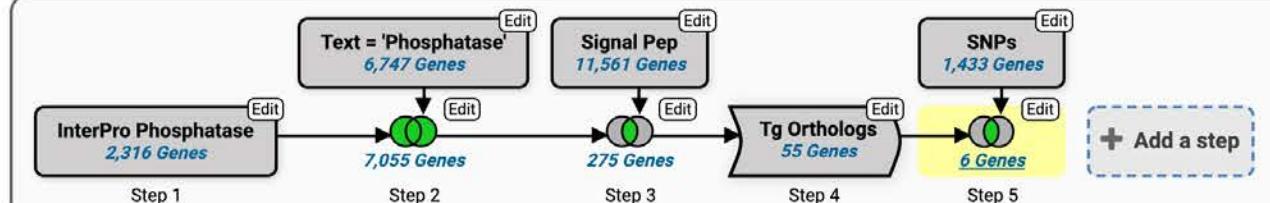
Apicomplexan parasites release factors via specialized secretory organelles (rhoptries, micronemes) that are thought to control host cell responses. In order to explore parasite-mediated modulation of

is associated with establishment of an intracellular "parasitophorous vacuole" (Carruthers and Sibley, 1997; Bradley and Sibley, 2007). Several rhoptry (ROP) proteins contain kinase-like domains, although many lack an obvious catalytic triad (El Hajj et al., 2006). Recent work on the active rhoptry kinases ROP16 and ROP18 (El Hajj et al., 2007a) shows that the former is secreted into the infected cell and alters STAT3 phosphorylation (Roos



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Secretory Kinases (Peixoto) *



Phosphatases (Text, Interpro)

Secreted (SP+)

Orthologs in *T.gondii* ME49

Under diversifying selection (dN/dS)

optional: up/down-regulated during differentiation

<https://tinyurl.com/SecretoryKinases>

6 Genes (6 ortholog groups)

Gene Results Genome View Analyze Results

Rows per page: 100

Download

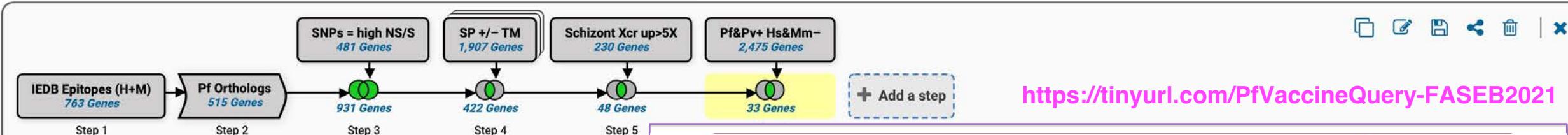
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Add Columns

Gene ID	Transcript ID	Genomic Location (Gene)	Ortholog Group	Product Description
TGME49_244450	TGME49_244450-t26_1	TGME49_chrVI:3,266,125..3,275,088(+)	OG6_489581	protein phosphatase 2C domain-containing protein
TGME49_201630	TGME49_201630-t26_1	TGME49_chrVIIa:3,885,849..3,891,351(+)	OG6_126697	protein phosphatase 2C domain-containing protein
TGME49_277240	TGME49_277240-t26_1	TGME49_chrXII:6,698,797..6,699,642(-)	OG6_224222	NTPase I
TGME49_215990	TGME49_215990-t26_1	TGME49_chrXI:6,478,171..6,494,251(+)	OG6_102316	helicase, putative
TGME49_278878	TGME49_278878-t26_1	TGME49_chrXII:5,790,682..5,793,202(-)	OG6_491601	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_254660	TGME49_254660-t26_1	TGME49_chrIII:1,877,394..1,879,835(-)	OG6_107449	ankyrin repeat-containing protein

Rows per page: 100

My Search Strategies

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Plasmodium vaccine antigens? 

33 Genes (24 ortholog groups)

[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	?	X	Graph
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

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

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 Rüitho,¹ Kevin Marsh,¹ and David J. Conway^{*2}

¹Kenya Medical Research Institute, Centre for Geographic Medicine Research Coast, Kilifi, Kenya²Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, United Kingdom

*Corresponding author: E-mail: dconway@mrcgm, 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

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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
- ▶ Proteomics
- ▶ Sequence analysis
- ▶ Structure analysis
- ▶ Taxonomy
- ▶ Text
- ▶ Transcriptomics

Organisms

Popset Isolate Sequences

- ❖ **Assess gene annotation accuracy**, revise (if warranted) using the Apollo annotation platform, and/or add expert knowledge (references, functions, etc) as User Comments
- ❖ **Visualize & interrogate expression profiles** ... based on multiple transcriptomic and proteomic datasets (now including single-cell RNAseq data!)
- ❖ **Integrate diverse datatypes**, identifying genes of interest based on signatures of selection, species distribution, expression patterns, subcellular localization, phenotypic impact, etc
- ❖ **Leverage orthology** ... to infer structure & function based on data in related species
- ❖ **Assess GO-term & metabolic pathway enrichment** ... associated with your gene lists
- ❖ **Share the results of your *in silico* analyses** ... with friends, colleagues, reviewers, etc
- ❖ **Analyze your own 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
- ❖ **Download query results and datasets for further analysis off-line**
- ❖ **Propose key datasets** (or your own or others) for incorporation into VEuPathDB
- ❖ **Obtain further help:** on-line resources, email support, Virtual Lab Meeting with your group

... ask us during the workshop, or click the 'Contact Us' link at any time!

Time (BST)	Tuesday 9 May 2023	Wednesday 10 May 2023	Thursday 11 May 2023	Friday 12 May 2023	Time (BST)	Saturday 13 May 2023
09:00		Breakfast	Breakfast	Breakfast	09:00	Breakfast
09:30	Arrival & Registration	SNPs & Variants	Enrichment analysis	Pathways & Metabolites	09:30	Group projects (continued)
10:00					10:00	
10:30	Welcome, Instructor Introductions			Tea break	10:30	Tea break
11:00	Database Introductions	Tea break	Tea break	Pathways & Metabolites (continued)	11:00	Group presentations - 12 min/team
11:30		Comparative Genomics & Orthology	Enrichment analysis (continued)		11:30	
12:00				Group projects	12:00	
12:30			Introduction to Group Projects		12:30	
13:00	Lunch	Lunch	Lunch	Lunch	13:00	Lunch & Departure
13:30					13:30	
14:00	Introduction to Database Queries	Comp Gx & Orthology (continued)	Sanger Tour (optional)		14:00	
14:30				Group projects (continued)	14:30	
15:00					15:00	
15:30			Tea break		15:30	
16:00	Tea break	Tea break	NGS data analysis II	Tea break	16:00	
16:30	Transcriptomics & Proteomics	NGS data analysis (Intro & setup) Background, Intro to VEuPathDB Galaxy	RNAseq analysis Variant calling (parallel sessions)		16:30	
17:00				Group projects (continued)	17:00	
17:30		RNAseq analysis Variant calling (parallel sessions)			17:30	
18:00					18:00	
18:30					18:30	
19:00	Welcome reception & Dinner	Dinner	Dinner	Dinner	19:00	
19:30					19:30	
20:00	Participant presentations: flash presentations - 2 min each	Research Seminar: <i>Michel Bromley, MRC</i>	Research Seminar: <i>Ester Gaya, Kew</i>	Free time (or time for project prep)	20:00	
20:30					20:30	
21:00	Adjourn (bar open)	Adjourn (bar open)	Adjourn (bar open)	Adjourn (bar open)	21:00	
onwards						onwards