Using the PomBase Genome Browser

McDowall MD (1), Staines DM (1), Rutherford K (2), Harris MA (2), Lock A (2), Wood V (2) Bähler J (3), Oliver SG (2), Kersey PJ (1)
[1] European Molecular Biology Laboratory, European Bioinformatics Insitute, Wellcome Trust Genome Campus, Cambridge CB10 1SD, UK
[2] Department of Biochemistry and Cambridge Systems Biology Centre, University of Cambridge, Cambridge CB2 1GA, UK
[3] Department of Genetics, Evolution & Environment & UCL Cancer Institute, London WC1E 6BT

Abstract

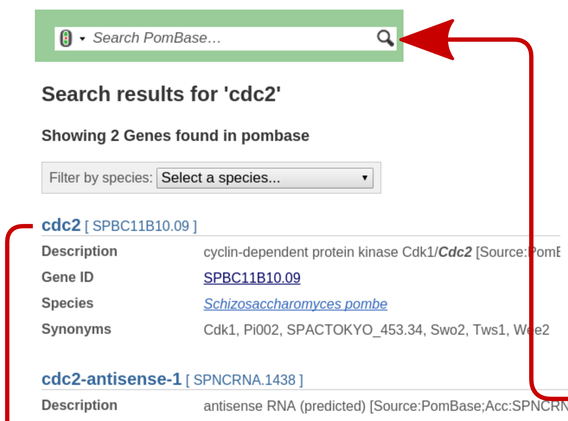
The PomBase Genome Browser (http://genomebrowser.pombase.org) provides access to genome-scale data for the four sequenced *Schizosaccharomyces* species. The browser uses a customised version of the current Ensembl software platform (www.ensembl.org).

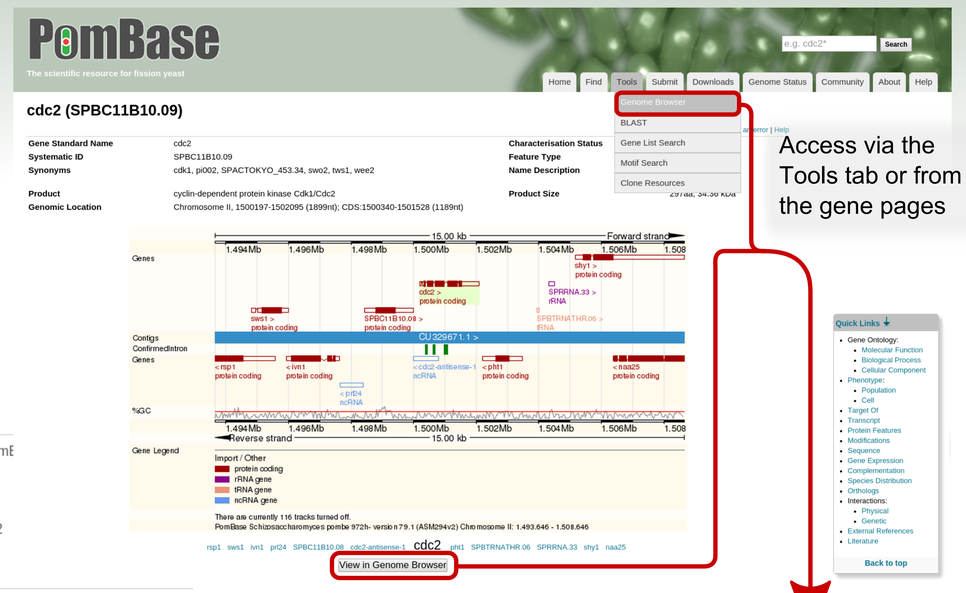
Using the browser it is possible to visualise gene models, comparative alignments, and other annotated sequence features. Variation data will be made available in the near future. For each gene, a summary of gene annotations and cross-references to external resources is available, in addition to sequence-based information such as gene structure and protein domain architecture. In addition, gene trees are generated by peptide alignment with 49 other fungal species, representing the inferred evolutionary history of each gene family. A second set of gene trees are also available to present the history of widely-conserved genes, based on a wider taxonomic range of species that includes human and other model organisms.

Moreover, PomBase works with the research community to incorporate published experimental into the genome browser tracks, where it can be visualised in a user-configurable display. Data types already integrated include expression, polymerase usage and intron branch points. By attaching WIG, BED, GFF, VCF or indexed BAM files researchers can also directly visualise their own data as tracks aligned to the genome.

Search

Search is provided via a box at the top of all pages in the genome browser.

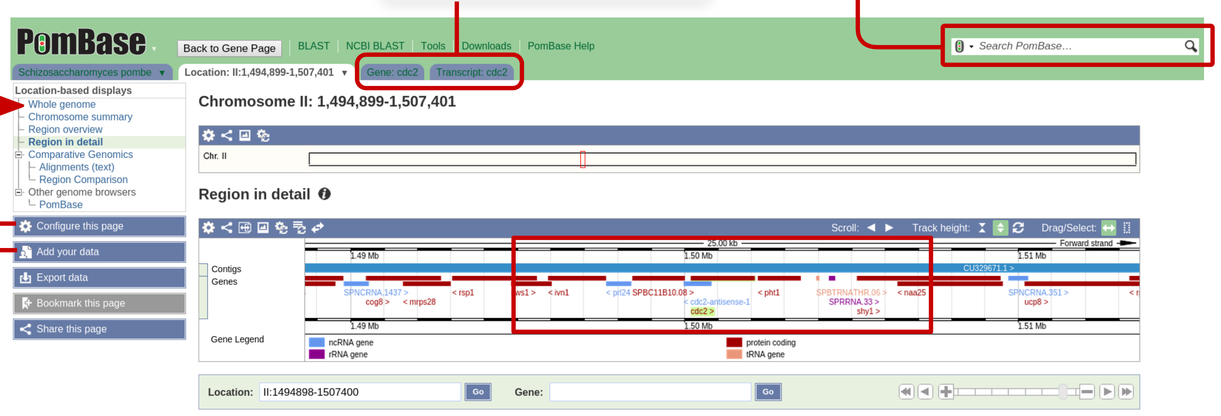




Access via the Tools tab or from the gene pages

Gene and Transcript Tabs

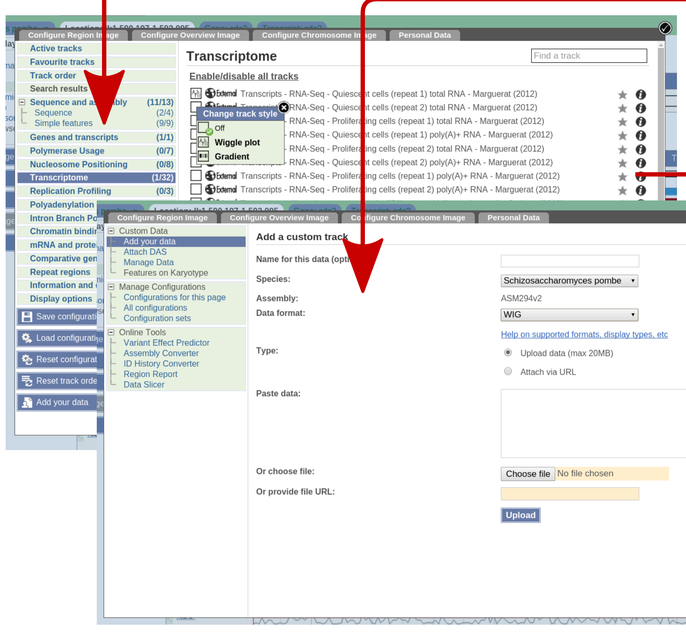
Location Tab

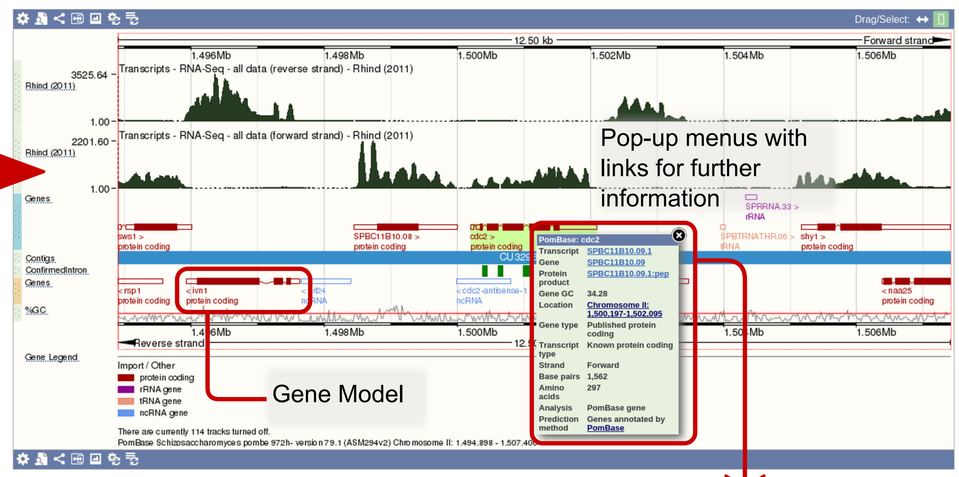


Data Tracks

A wide range of experiements can be visualised within the genome browser. By clicking on the "Configure this page" button tracks can be selected or removed.

Users are able to upload their own data by clicking on the "Add your data" button. Files can be uploaded (<20MB) or attached by hosting the data on a local web server or FTP. These tracks are only available to the user, but can be shared with collaborators by clicking the share button in the top left of the image.

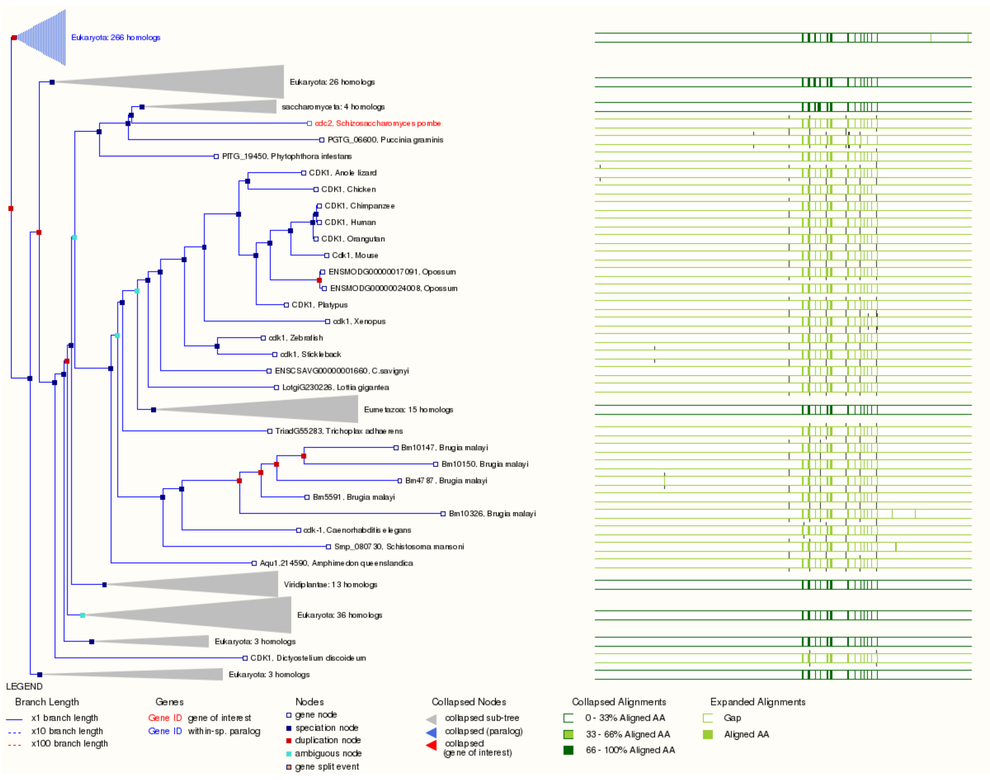




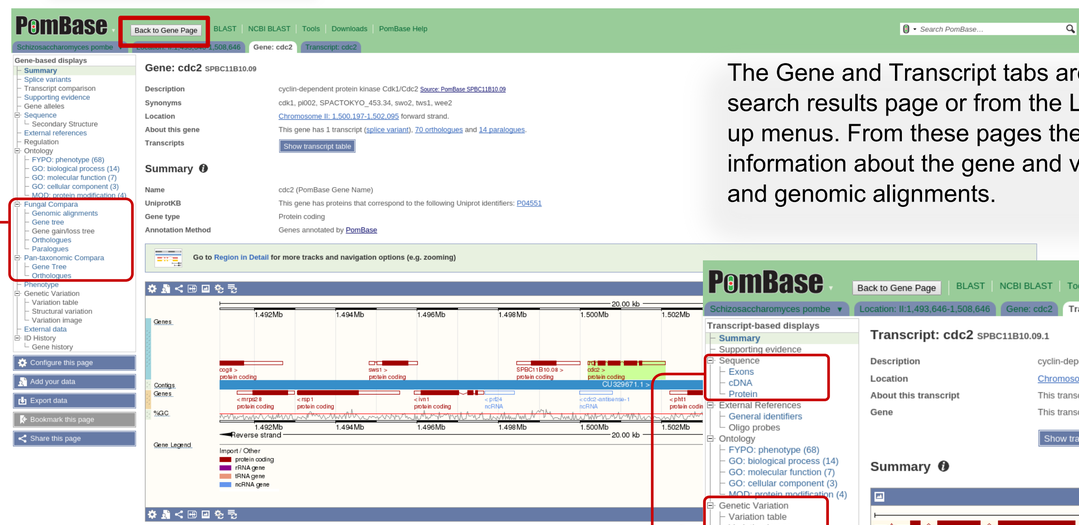
Pop-up menus with links for further information

Comparative Genomics

Comparative alignments have been calculated between all fungal proteins within Ensembl Genomes Fungi. There are also a second set of alignments with species across the full taxonomic range. Access to the gene trees is from the Gene and Transcript tabs for each gene. Clicking on a gene in the tree takes you to the relevant gene tab. The trees can also be expanded and collapsed by clicking on the nodes. From the Location tab whole genome alignments have been calculated between the 4 *Schizosaccaromyces* species

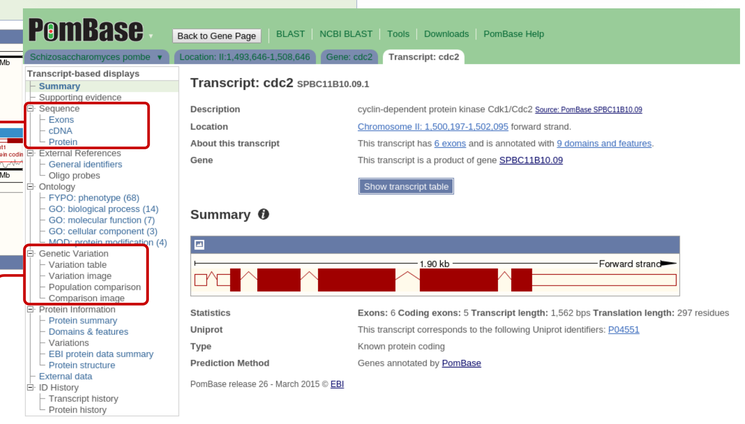


Go to the Gene Page for the current gene

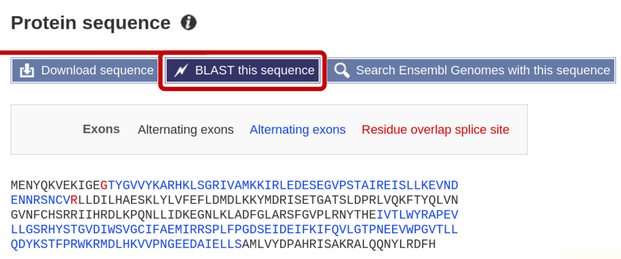


Gene and Transcript Tabs

The Gene and Transcript tabs are accessed either from the search results page or from the Location tab by using the pop-up menus. From these pages the user can review annotated information about the gene and view comparative proteomic and genomic alignments.

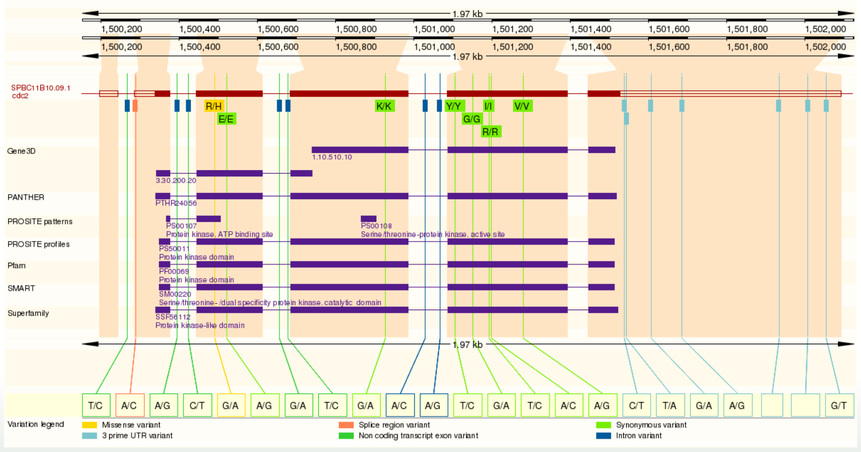


Sequence

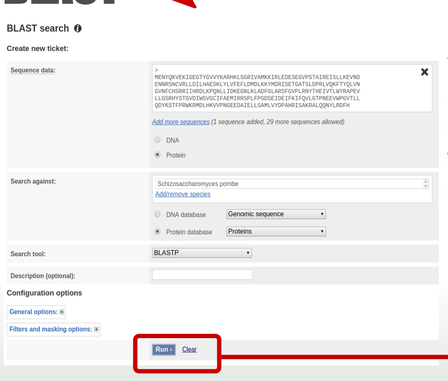


Variation

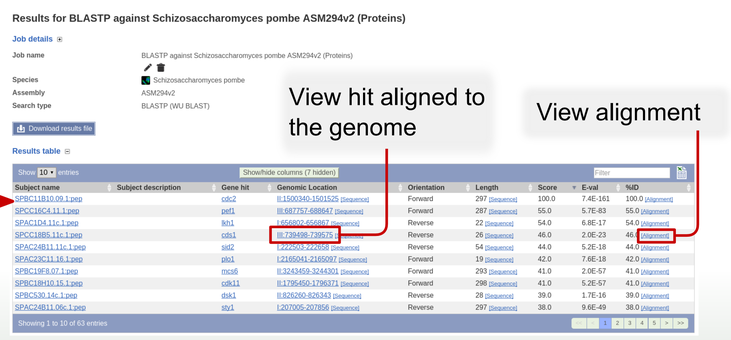
We are currently working on importing variation datasets provided by Jeffares *et al*. (2015). When available the data can be accessed from the gene and transcript tabs.



BLAST



The BLAST interface can either be accessed directly from PomBase.org to search using your sequences, or via the Sequence section on all gene pages.



View hit aligned to the genome

View alignment

@PomBase
EMBL-EBI
UNIVERSITY OF CAMBRIDGE
UCL
Supported by wellcome trust
empowered
/PomBase