PomBase.org

A scientific resource for fission yeast

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Abstract

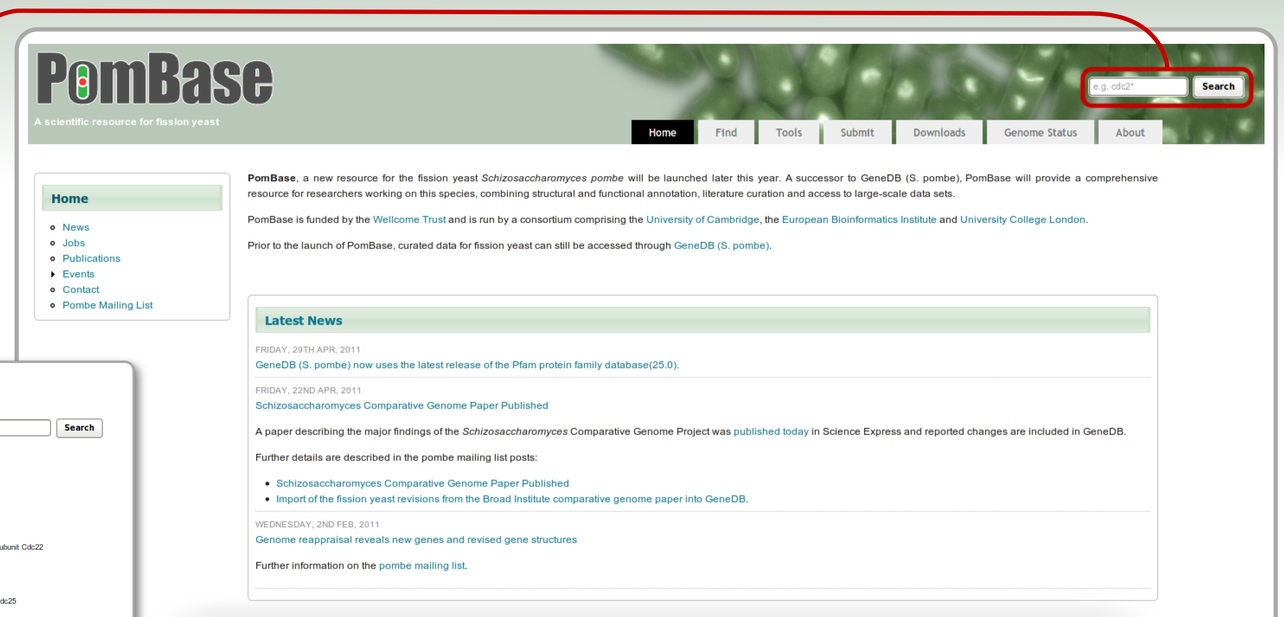
PomBase (http://www.pombase.org) is a new model organism database to support the organization of and access to scientific data for the fission yeast *Schizosaccharomyces pombe*. PomBase will support genomic sequence and features, genome-wide datasets and manual literature curation.

Gene overview pages present the data related to a gene, including the gene type, product, sequence features, phenotypes, Gene Ontology annotation, modifications and physical and genetic interactions. The data is housed within an Ensembl genome database, and the gene overview pages link through to an interactive, Ensembl-style, genome browser.

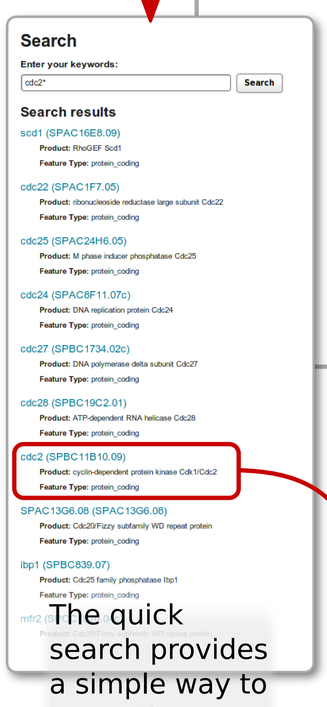
A query builder has been implemented to allows users to search by multiple feature types. A query history summarises queries and allows queries to be combined and edited. Results pages provide access to gene overview pages.

The Ensembl-style genome browser, which is accessible from the gene overview pages, provides the functionality to store, analyse and visualise a wide variety of datasets mapped to the genome either from internal sources or via externally loaded URLs or data files. Examples of supported datasets that can be imported include whole genome resequencing data, ChIP-chip and ChIP-seq assay, mapping to microarray probes and other high-throughput data types. The Ensembl-style browser also provides views of orthologous and syntenic regions by comparative analysis of closely related genomes (*S. japonicus* and *S. octosporus*).

PomBase will also provide a community hub for researchers, providing genome statistics, a community curation interface, news, events, documentation FAQs and mailing lists.



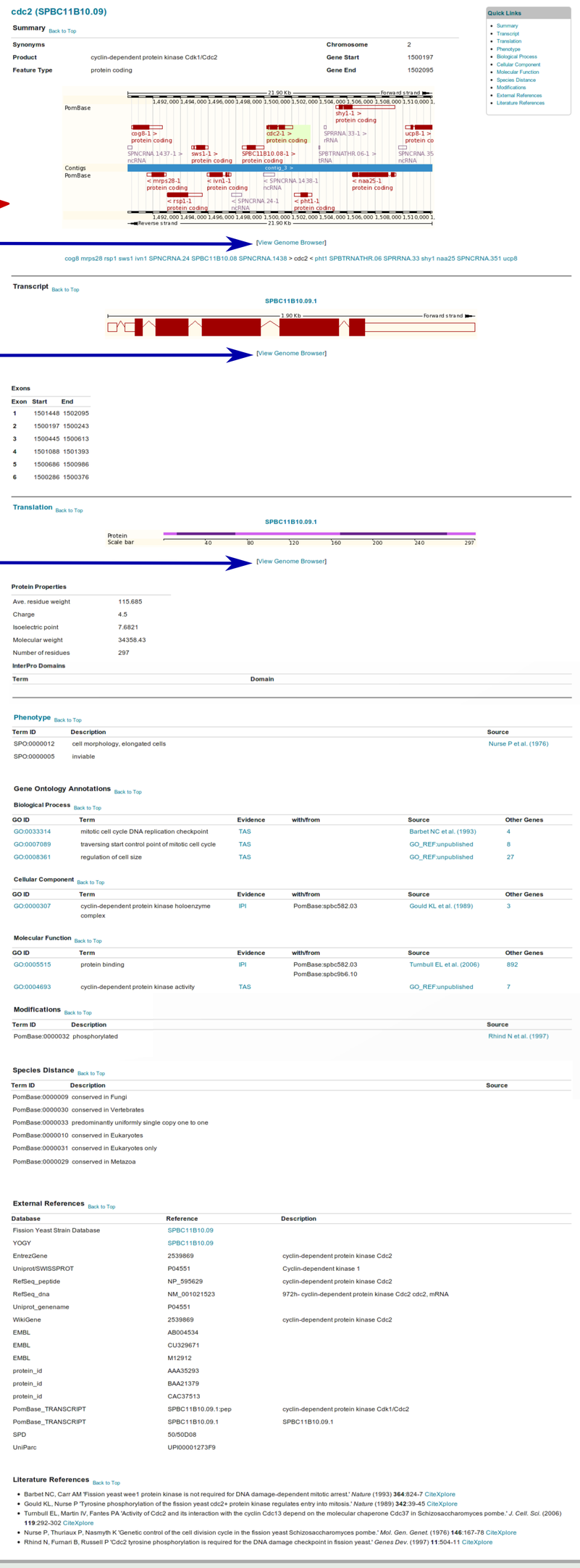
The home page provides access to search and browse options, genome statistics, tools, resources and community news.



The quick search provides a simple way to query the database.

Gene Overview Page

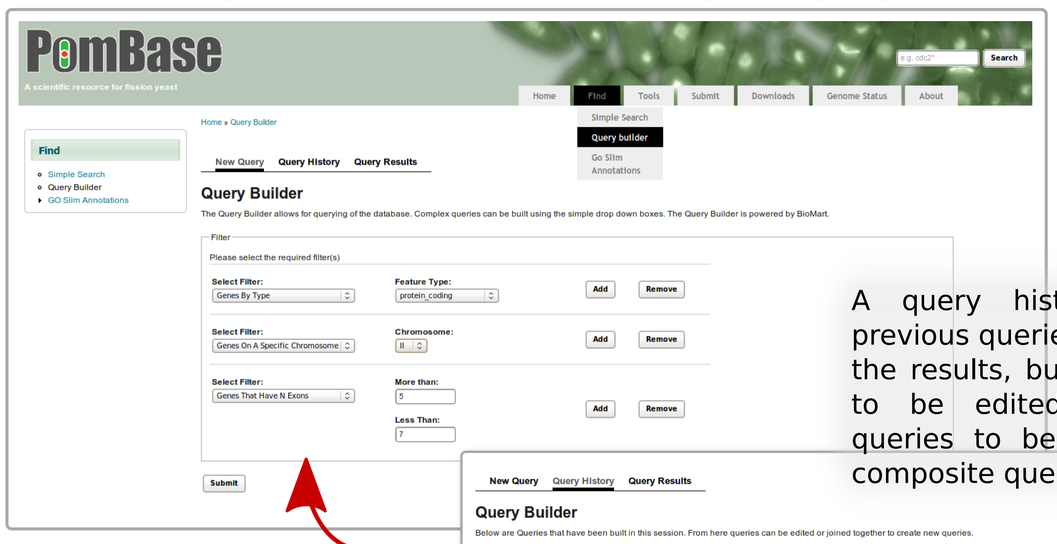
Detailed Gene Overview pages aggregate all annotations and genomic features for a gene of interest from underlying databases.



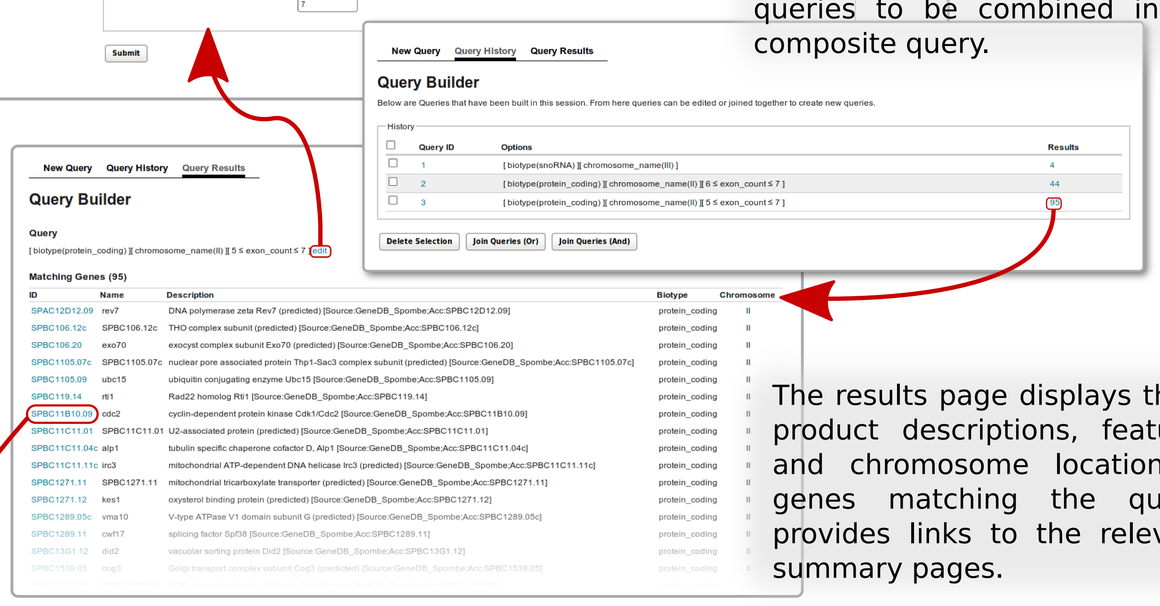
Links out to an Ensembl style interface provide access to further analysis tools.

Query Builder

The query builder allows users to search by gene ID or name, feature type (*e.g.* protein coding, tRNA or rRNA), chromosome, Gene Ontology annotations, exon count or protein domain identifier. Multiple filters can be combined to compose larger queries.



A query history page summarises previous queries and provides access to the results, but also allows for queries to be edited and for pre-existing queries to be combined into a new, composite query.

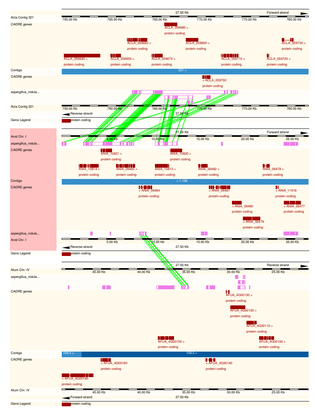


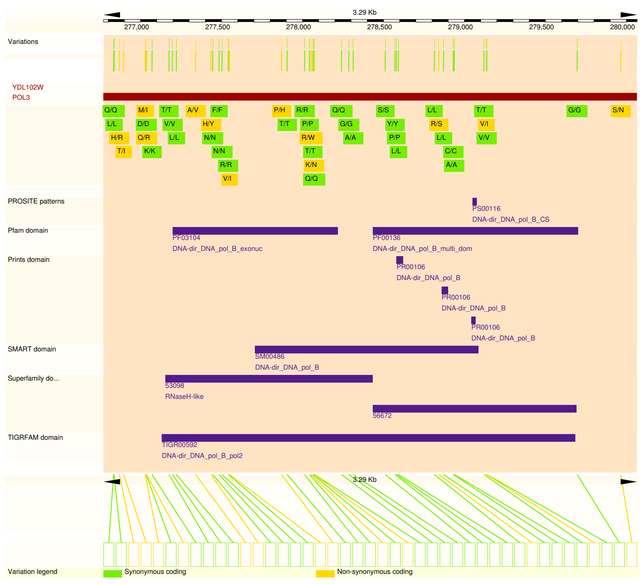
The results page displays the names, product descriptions, feature types and chromosome locations of the genes matching the query, and provides links to the relevant gene summary pages.

The query builder is constructed on top of a BioMart data warehouse, a flexible query-oriented database able to support a wide variety of gene-centric queries.

Ensembl

The Ensembl-based genome browser provides the capability to visualise mapped datasets, such as variation data (example shown right for *Saccharomyces*) or views of orthologous and syntenic regions with closely related genomes (example shown left for *Aspergillus*). Data can also be imported from other sources, such as externally loaded URLs or data files that gets aligned on the genome viewer.





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