The scientific resource for fission yeast

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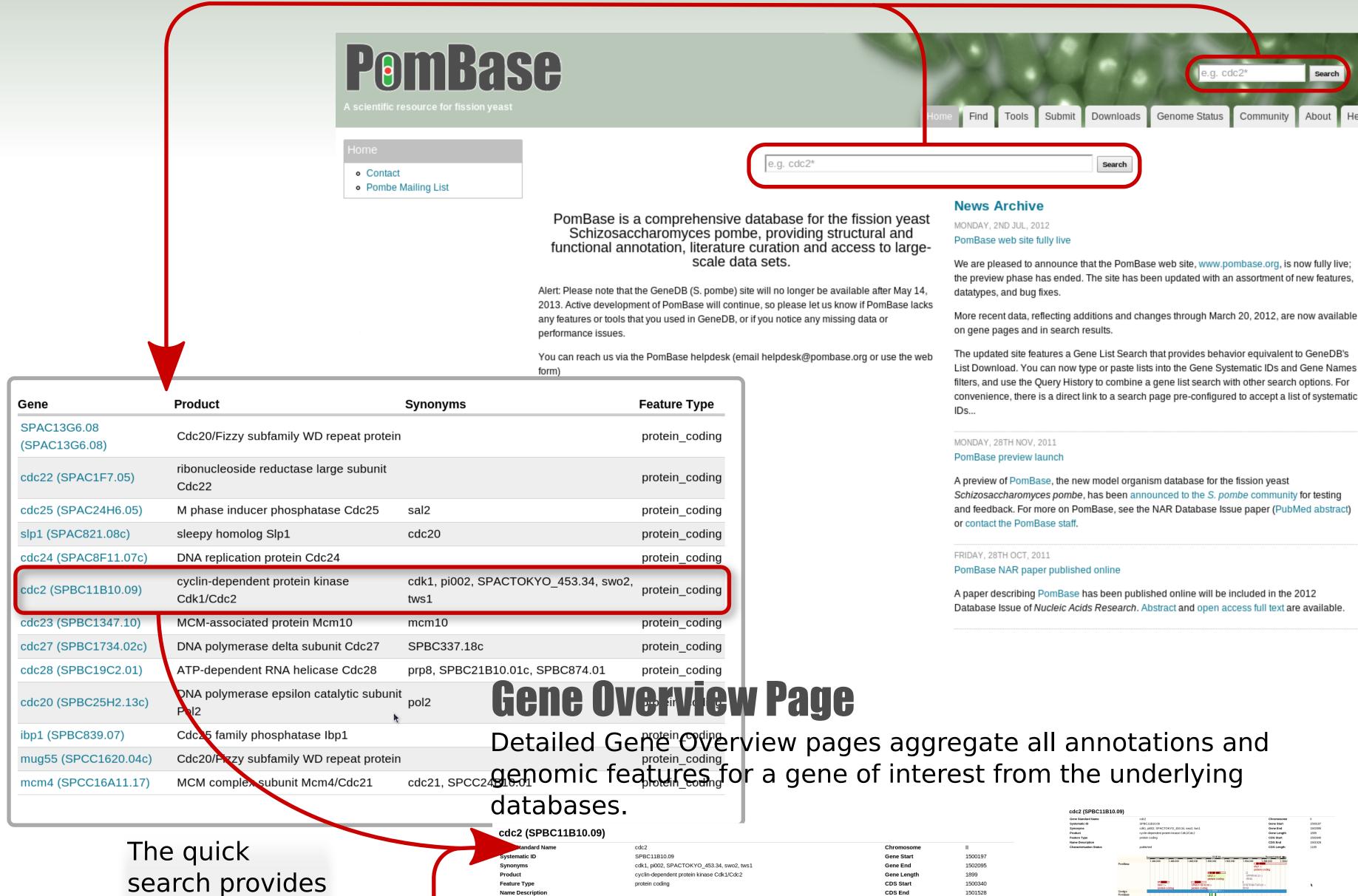
ABSTRACT

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

The PomBase interface is built on a Drupal server with the data housed within an Ensembl genome database (http://www.ensemblgenomes.org). Gene summary 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. A query builder has been, on top of a BioMart server, to allow 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 summary pages.

The Ensembl platform (http://www.ensembl.org) also has a genome browser that can be used to visualise the data. Every gene summary page has direct links to the relevant pages of a customised Ensembl genome browser providing the functionality to store, analyse and visualise a wide variety of datasets mapped to the genome either from sources located on the server or via externally loaded URLs or data files. Examples of supported datasets include whole genome resequencing data, ChIP-chip and ChIP-seq assay, mapping to microarray probes and other highthroughput data types. The Ensembl-style browser also provides views of orthologous regions by comparative analysis of related genomes.

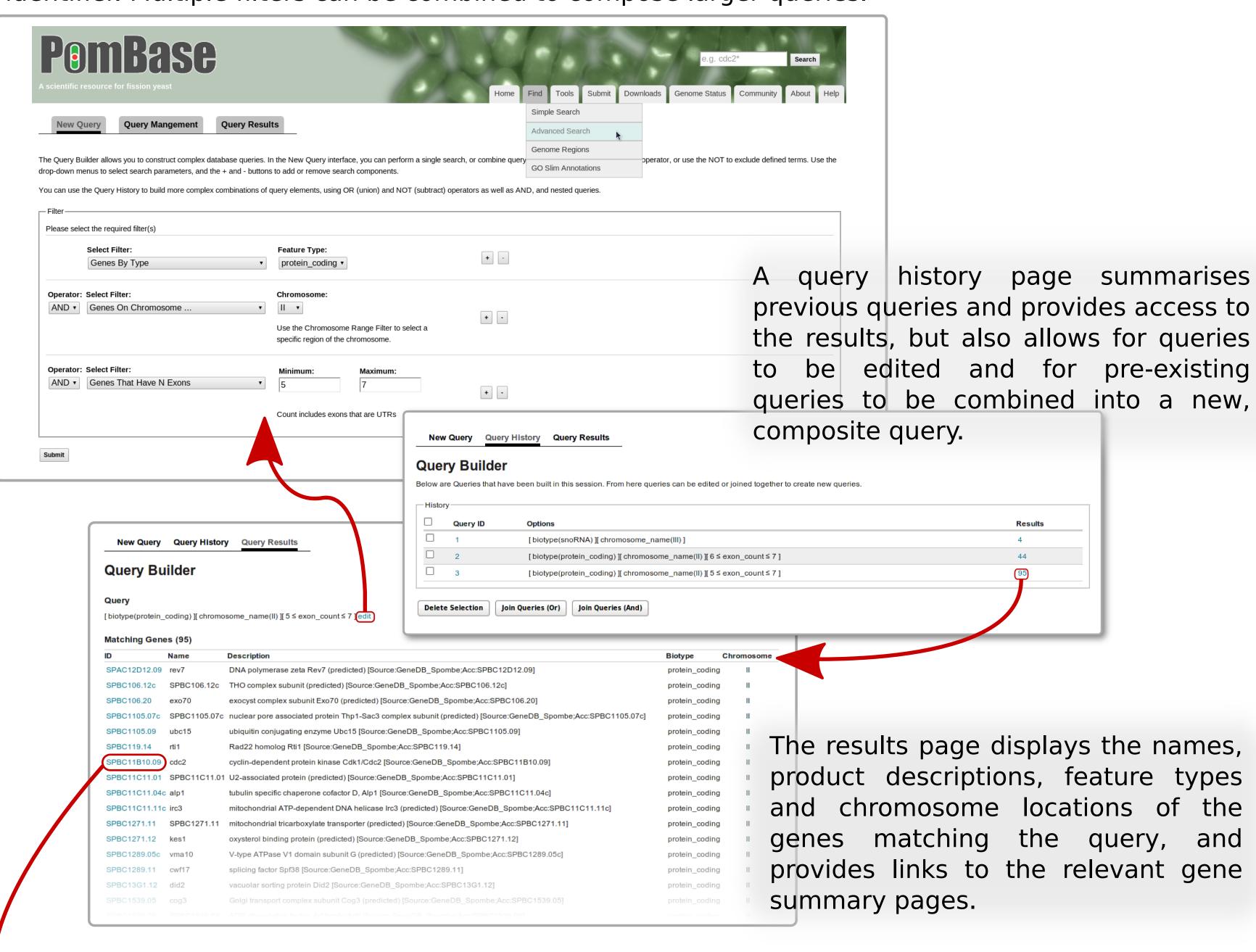
PomBase also provides a community hub for researchers, providing genome statistics, a community curation interface, news, events, documentation FAQs and mailing lists.



a simple way to query the database.

Advanced Search

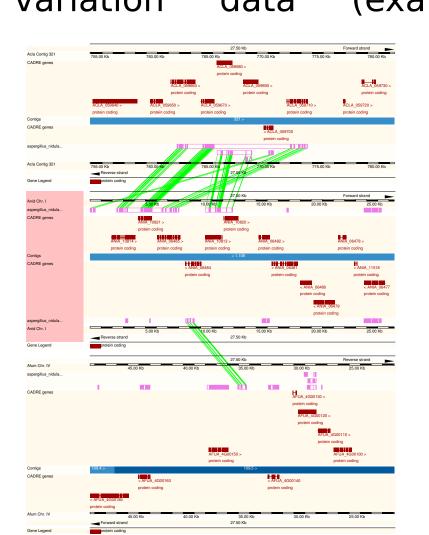
The Advanced Search allows users to search by gene ID or name, feature type (e.g. protein coding, tRNA or rRNA), chromosome, Gene Ontology annotations, exon count or protein domain identifier. Multiple filters can be combined to compose larger queries.



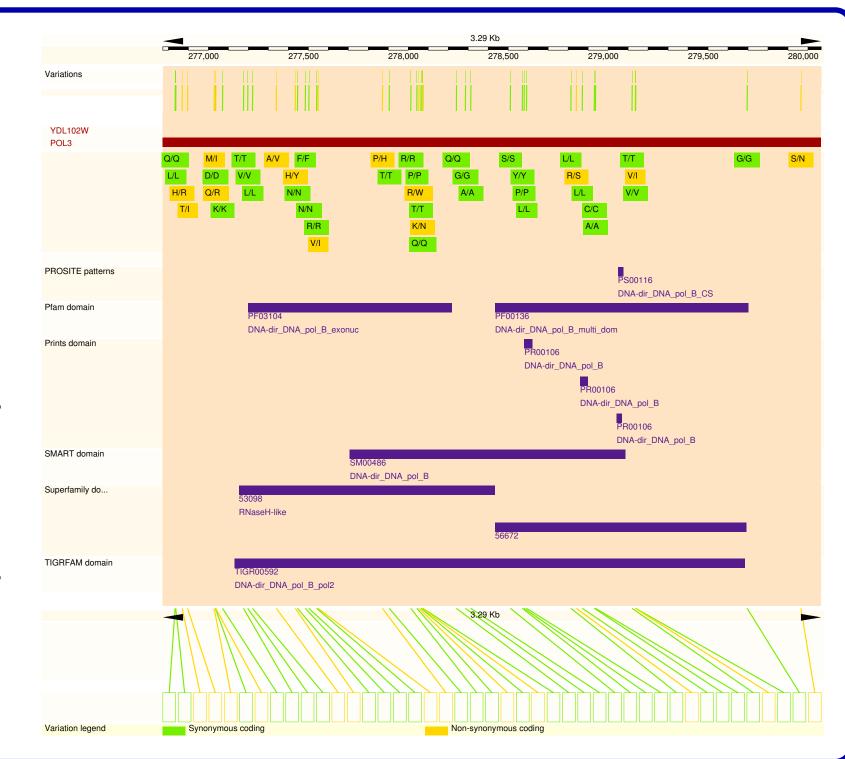
The query builder is constructed on top of a BioMart data warehouse, a flexible queryoriented database able to support a wide variety of gene-centric queries.

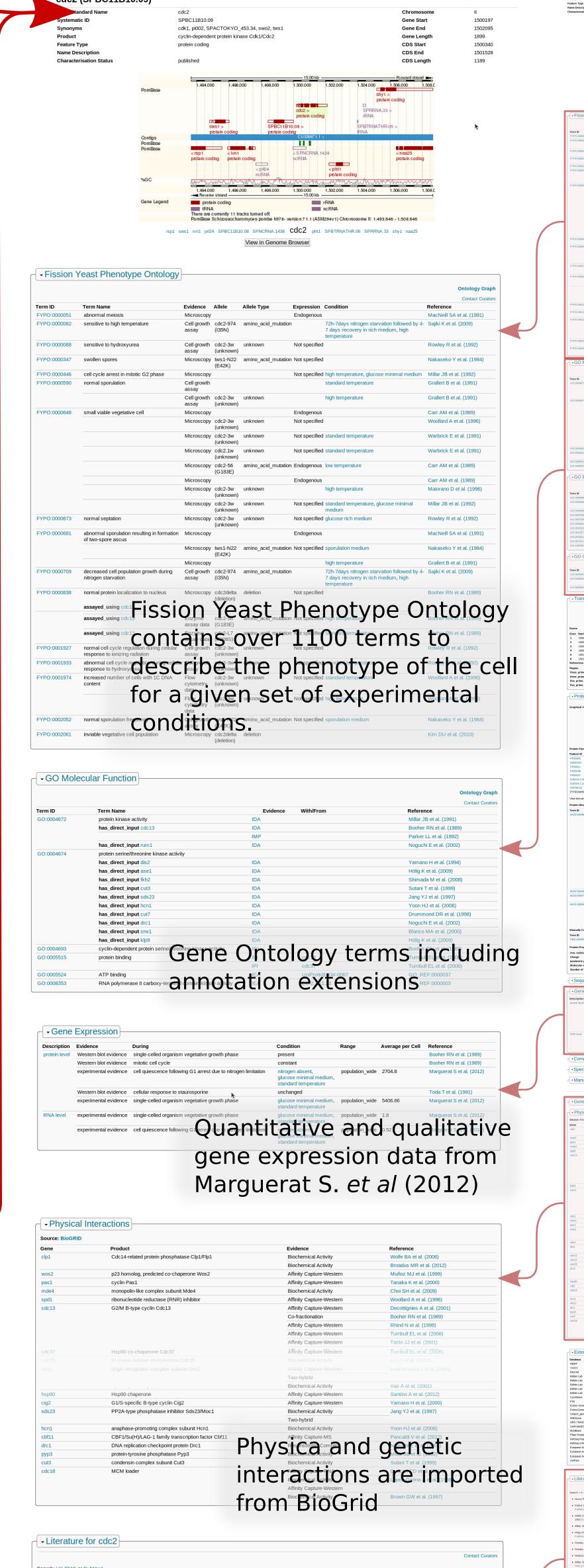
Ensembl

The Ensembl-based genome browser provides the capability to visualise mapped datasets, such as variation shown right (example



Saccharomyces) or views orthologous syntenic regions closely related genomes (example shown left for Aspergillus). Data can imported be other sources, such as externally loaded URLs or files that gets data aligned on the genome viewer.





Full reference list for articles

depend in Legulator of miliosis in Schizosacch Tron voes nombe." FM80 J 10:4291-4299 196
CITED ON THE BASE

f.C., Miadokova E., Gregan J., "A Knockout screen for protein kinases required for the proper m