

# PomBase

## The scientific resource for fission yeast

## 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 high-throughput 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.

## 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.

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Search: e.g. cdc2<sup>+</sup>

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New Query Query Management Query Results

The Query Builder allows you to construct complex database queries. In the New Query interface, you can perform a single search, or combine query drop-down menus to select search parameters, and the + and - buttons to add or remove search components.

You can use the Query History to build more complex combinations of query elements, using OR (union) and NOT (subset) operators as well as AND, and nested queries.

Filter: Please select the required filter(s)

Select Filter: Genes By Type Feature Type: protein\_coding

Operator: Select Filter: AND Genes On Chromosome ... Chromosome: 8

Operator: Select Filter: AND Genes That Have N Exons Minimum: 5 Maximum: 7

Count includes exons that are UTRs

**Query Builder**

Below are Queries that have been built in this session. From here queries can be edited or joined together to create new queries.

History	Query ID	Options	Results
<input type="checkbox"/>	1	[biotype(protein_coding)] [chromosome_name(8)]	4
<input type="checkbox"/>	2	[biotype(protein_coding)] [chromosome_name(8)] [5 < exon_count < 7]	44
<input type="checkbox"/>	3	[biotype(protein_coding)] [chromosome_name(8)] [5 < exon_count < 7]	44

Delete Selection Join Queries (Or) Join Queries (And)

**Matching Genes (95)**

ID	Name	Description	Biotype	Chromosome
SPBC12012.09	rev7	DNA polymerase zeta Rev7 (predicted) [Source:GeneDB, Spombe:Acc:SPBC12012.09]	protein_coding	8
SPBC106.12c	SPBC106.12c	THO complex subunit (predicted) [Source:GeneDB, Spombe:Acc:SPBC106.12c]	protein_coding	8
SPBC106.20	exo70	exonuclease complex subunit Exo70 (predicted) [Source:GeneDB, Spombe:Acc:SPBC106.20]	protein_coding	8
SPBC1105.07c	SPBC1105.07c	nuclear pore associated protein Nup133 (predicted) [Source:GeneDB, Spombe:Acc:SPBC1105.07c]	protein_coding	8
SPBC1105.09	ubc15	ubiquitin conjugating enzyme Ubc15 [Source:GeneDB, Spombe:Acc:SPBC1105.09]	protein_coding	8
SPBC119.14	rfl1	Rfa22 homolog Rfl1 [Source:GeneDB, Spombe:Acc:SPBC119.14]	protein_coding	8
SPBC119.14	cdc2	cyclin-dependent protein kinase Cdk1/Cdc2 [Source:GeneDB, Spombe:Acc:SPBC119.14]	protein_coding	8
SPBC1111.01	cdc2	U2 associated protein (predicted) [Source:GeneDB, Spombe:Acc:SPBC1111.01]	protein_coding	8
SPBC1111.04c	ap1	ubiquitin specific protease subunit 1 Ap1 [Source:GeneDB, Spombe:Acc:SPBC1111.04c]	protein_coding	8
SPBC1111.11c	inc3	mitochondrial ATP-dependent DNA helicase Inc3 (predicted) [Source:GeneDB, Spombe:Acc:SPBC1111.11c]	protein_coding	8
SPBC1271.11	SPBC1271.11	mitochondrial bicarbonate transporter (predicted) [Source:GeneDB, Spombe:Acc:SPBC1271.11]	protein_coding	8
SPBC1271.12	kes1	oxysterol binding protein (predicted) [Source:GeneDB, Spombe:Acc:SPBC1271.12]	protein_coding	8
SPBC1289.05c	vma10	V-type ATPase V1 domain subunit G (predicted) [Source:GeneDB, Spombe:Acc:SPBC1289.05c]	protein_coding	8
SPBC1289.11	cwi17	splicing factor Spf17 [Source:GeneDB, Spombe:Acc:SPBC1289.11]	protein_coding	8
SPBC1301.12	dks2	vesicular sorting protein Dks2 [Source:GeneDB, Spombe:Acc:SPBC1301.12]	protein_coding	8
SPBC1309.05	cap5	Glnp transport complex subunit Cap5 (predicted) [Source:GeneDB, Spombe:Acc:SPBC1309.05]	protein_coding	8

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.

