

# Using the Genome Browser

Mark McDowall



# Introduction



- Powered by ensembl
- Ensembl project has been running for over 10 years
- Ability visualise a variety of data types, such as gene models annotations, comparative genomics, variations and common data tracks
- Images from the genome browser are used on the gene pages



# Getting to the genome browser

**PomBase**

The scientific resource for fission yeast

e.g. *cdc2*\*

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Genome Browser

BLAST

Gene List Search

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## *cdc2* (SPBC11B10.09)

Gene Standard Name

*cdc2*

Systematic ID

SPBC11B10.09

Synonyms

*cdk1*, *pi002*, SPACTOKYO\_453.34, *swo2*, *tw1*, *wee2*

Product

cyclin-dependent protein kinase Cdk1/Cdc2

Genomic Location

Chromosome II, 1500197-1502095 (1899nt); CDS:1500340-1501528 (1189nt)

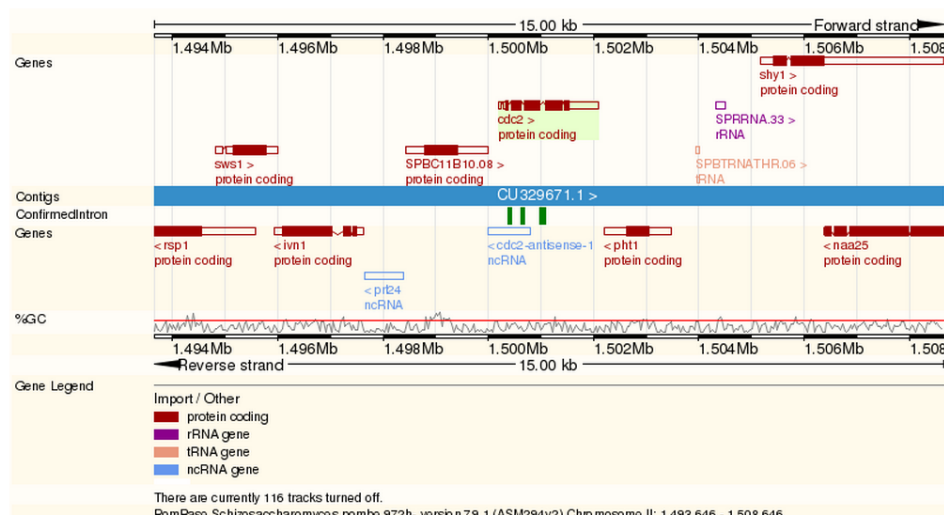
Characterisation Status

Feature Type

Name Description

Product Size

297 aa, 34.36 kDa



[rsp1](#) [sws1](#) [ivn1](#) [pti24](#) [SPBC11B10.08](#) [cdc2-antisense-1](#) ***cdc2*** [pti1](#) [SPBTRNATHR.06](#) [SPRRNA.33](#) [shy1](#) [naa25](#)

[View in Genome Browser](#)

### Quick Links

- Gene Ontology:
  - Molecular Function
  - Biological Process
  - Cellular Component
- Phenotype:
  - Population
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- Target Of
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- Modifications
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[GO Molecular Function](#)

[genomebrowser.pombase.org/Schizosaccharomyces\\_pombe/Info/Index](http://genomebrowser.pombase.org/Schizosaccharomyces_pombe/Info/Index)

# Location tab

**PomBase** [Back to Gene Page](#) [BLAST](#) [NCBI BLAST](#) [Tools](#) [Downloads](#) [PomBase Help](#)

Schizosaccharomyces pombe [Location: II:1,493,646-1,508,646](#) [Gene: cdc2](#) [Transcript: cdc2](#)

**Location-based displays**

- Whole genome
- Chromosome summary
- Region overview
- Region in detail**
- Comparative Genomics
- Alignments (text)
- Region Comparison
- Other genome browsers
- PomBase

**Configure this page**

**Add your data**

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**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

Contigs  
Genes

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646 [Go](#) Gene:  [Go](#)

Genes

Contigs

Confirmed Intron

Genes

%GC

Gene Legend

- Import / Other
- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

# Location tab

**PomBase** [Back to Gene Page](#) [BLAST](#) [NCBI BLAST](#) [Tools](#) [Downloads](#) [PomBase Help](#) 0

Schizosaccharomyces pombe [Location: II:1,493,646-1,508,646](#) [Gene: cdc2](#) [Transcript: cdc2](#)

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**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

25.00 kb

1.49 Mb 1.50 Mb 1.51 Mb

Contigs Genes

SPNCRNA.1437 > < mps28 < rsp1 sws1 < lvn1 < prt24 SPBC11810.08 > < cdc2-antisense-1 < cdc2 > < phl1 SPBTRNATHR.06 > SPRRNA.33 > shy1 > < naa25 SPNCRNA.351 > ucp8 > < prp

1.49 Mb 1.50 Mb 1.51 Mb

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646  Gene:

15.00 kb

1.494Mb 1.496Mb 1.498Mb 1.500Mb 1.502Mb 1.504Mb 1.506Mb 1.508Mb

Forward strand

Genes

sws1 > protein coding

SPBC11810.08 > protein coding

cdc2 > protein coding

CU329671.1 >

SPRRNA.33 > rRNA

SPBTRNATHR.06 > rRNA

shy1 > protein coding

< rsp1 protein coding

< lvn1 protein coding

< prt24 ncRNA

< cdc2-antisense-1 ncRNA

< phl1 protein coding

< naa25 protein coding

1.494Mb 1.496Mb 1.498Mb 1.500Mb 1.502Mb 1.504Mb 1.506Mb 1.508Mb

Reverse strand

Gene Legend

- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene

Import / Other

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

[PomBase release 26 - March 2015](#) © [EBI](#)

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# Location tab

**PomBase** [Back to Gene Page](#) [BLAST](#) [NCBI BLAST](#) [Tools](#) [Downloads](#) [PomBase Help](#)

Location: II:1,493,646-1,508,646 Gene: *cdc2* Transcript: *cdc2*

**Location-based displays**

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**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

Contigs  
Genes

Gene Legend

Location: II:1493646-1508646 Go Gene: Go

15.00 kb

Forward strand

Reverse strand

Gene Legend

Import / Other

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

# Location tab

**PomBase** Schizosaccharomyces pombe BLAST NCBI BLAST Tools Downloads PomBase Help

Search PomBase...

Schizosaccharomyces pombe Location-based display

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- Region Comparison
- Other genome browsers
- PomBase

Configure this page Add your data Export data Bookmark this page Share this page

Location: II:1,493,646-1,508,646 Gene: cdc2 Transcript: cdc2

**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

25.00 kb

Contigs Genes

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646 Go Gene: Go

15.00 kb

Forward strand

Reverse strand

Gene Legend

- Import / Other
- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene

There are currently 116 tracks turned off.  
PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

# Location tab

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Schizosaccharomyces pombe [Location: II:1,493,646-1,508,646](#) [Gene: cdc2](#) [Transcript: cdc2](#)

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**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

Contigs  
Genes

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646 [Go](#) Gene: [Go](#)

Genes

Contigs

Confirmed Intron

Genes

%GC

Gene Legend

- Import / Other
- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

# Search box

 Search PomBase...



## Search results for 'cdc2'

Showing 2 Genes found in pombase

Filter by species:

### [cdc2](#) [ [SPBC11B10.09](#) ]

Description	cyclin-dependent protein kinase Cdk1/ <b>Cdc2</b> [Source:PomBase;Acc:SPBC11B10.09]
Gene ID	<a href="#">SPBC11B10.09</a>
Species	<a href="#">Schizosaccharomyces pombe</a>
Synonyms	Cdk1, Pi002, SPACTOKYO_453.34, Swo2, Tws1, Wee2

### [cdc2-antisense-1](#) [ [SPNCRNA.1438](#) ]

Description	antisense RNA (predicted) [Source:PomBase;Acc:SPNCRNA.1438]
Gene ID	<a href="#">SPNCRNA.1438</a>
Species	<a href="#">Schizosaccharomyces pombe</a>



# Location tab

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Schizosaccharomyces pombe [Location: II:1,493,646-1,508,646](#) [Gene: cdc2](#) [Transcript: cdc2](#)

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**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

Contigs  
Genes

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646 [Go](#) Gene:  [Go](#)

Genes

Contigs

Confirmed Intron

Genes

%GC

Gene Legend

- Import / Other
- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene

There are currently 116 tracks turned off.  
PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646



# Location tab

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Schizosaccharomyces pombe [Location: II:1,493,646-1,508,646](#) [Gene: cdc2](#) [Transcript: cdc2](#)

**Location-based displays**

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**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

Contigs  
Genes

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646 [Go](#) Gene:  [Go](#)

**Region in detail**

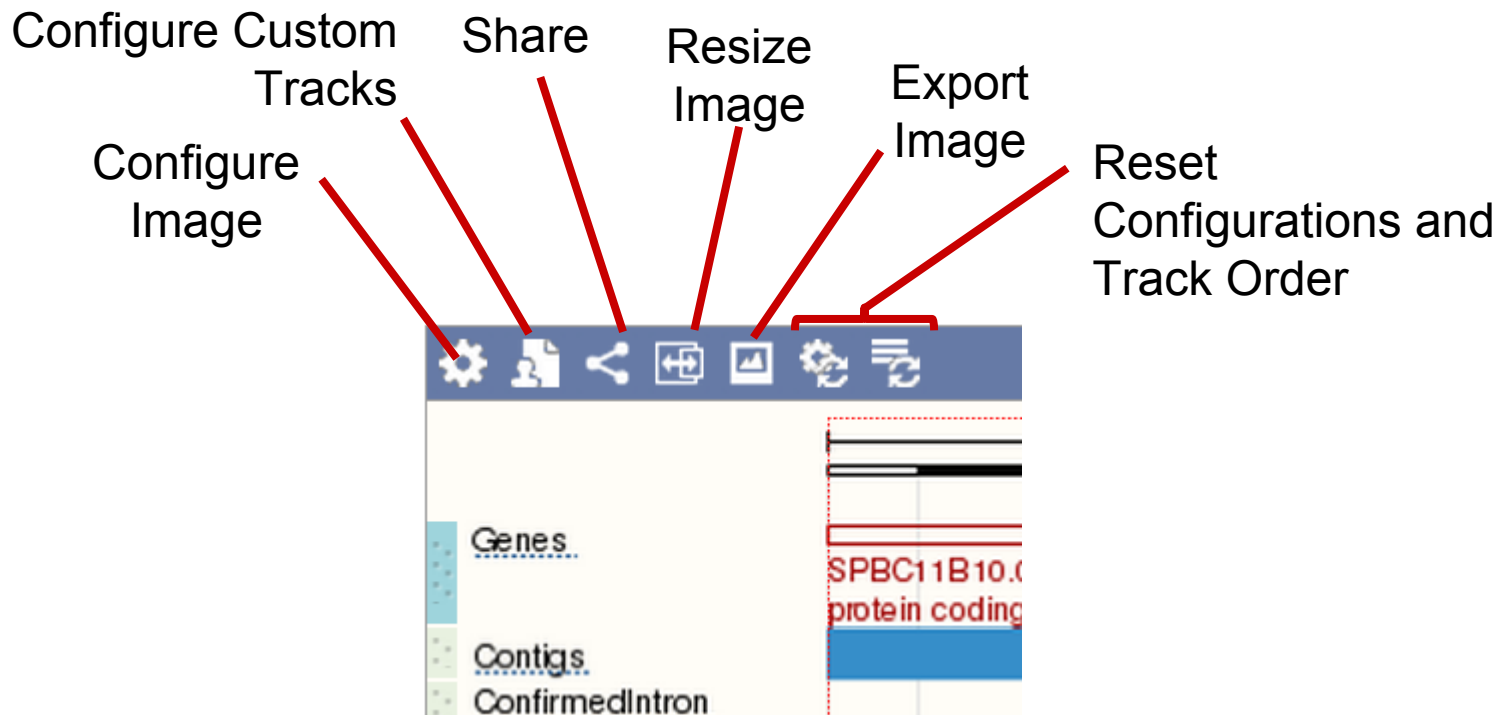
Contigs  
Confirmed Intron  
Genes  
%GC

Gene Legend

- Import / Other
- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene

There are currently 116 tracks turned off.  
PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

# Image buttons



# Displaying tracks

**PomBase** [Back to Gene Page](#) [BLAST](#) [NCBI BLAST](#) [Tools](#) [Downloads](#) [PomBase Help](#)

Location: II:1,493,646-1,508,646 Gene: *cdc2* Transcript: *cdc2*

**Location-based displays**

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**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

25.00 kb

1.49 Mb 1.50 Mb 1.51 Mb

Contigs

Genes

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646 Go Gene: Go

15.00 kb

1.494Mb 1.496Mb 1.498Mb 1.500Mb 1.502Mb 1.504Mb 1.506Mb 1.508Mb

Forward strand

Reverse strand

Genes

Contigs

Confirmed Intron

Genes

%GC

Gene Legend

- Import / Other
- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene


There are currently 116 tracks turned off.


PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646


# Add your own data


**Location-based displays**


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 Configure this page

 Add your data

 Export data

 Bookmark this page

 Share this page

# Adding tracks

The screenshot displays a genome browser interface with a sidebar on the left and a main panel on the right. The sidebar contains a list of tracks with checkboxes and counts, and a 'Display options' section with buttons for saving, loading, and resetting configurations. The main panel shows the 'Transcriptome' track configuration, including a search bar, a list of tracks with checkboxes, and a 'Change track style' dropdown menu.

**Transcriptome**

Find a track

Enable/disable all tracks

Change track style

- Off
- Wiggle plot
- Gradient

Active tracks

Favourite tracks

Track order

Search results

Sequence and assembly (11/13)

- Sequence (2/4)
- Simple features (9/9)

Genes and transcripts (1/1)

Polymerase Usage (0/7)

Nucleosome Positioning (0/8)

Transcriptome (1/32)

Replication Profiling (0/3)

Polyadenylation sites (0/14)

Intron Branch Point (0/1)

Chromatin binding (0/29)

mRNA and protein alignments (0/1)

Comparative genomics (0/3)

Repeat regions (0/16)

Information and decorations (8/9)

Display options

Save configuration as...

Load configuration

Reset configuration

Reset track order

Add your data

External Transcripts - RNA-Seq - Quiescent cells (repeat 1) total RNA - Marguerat (2012)

External Transcripts - RNA-Seq - Quiescent cells (repeat 2) total RNA - Marguerat (2012)

External Transcripts - RNA-Seq - Proliferating cells (repeat 1) total RNA - Marguerat (2012)

External Transcripts - RNA-Seq - Quiescent cells (repeat 1) poly(A)+ RNA - Marguerat (2012)

External Transcripts - RNA-Seq - Proliferating cells (repeat 2) total RNA - Marguerat (2012)

External Transcripts - RNA-Seq - Quiescent cells (repeat 2) poly(A)+ RNA - Marguerat (2012)

External Transcripts - RNA-Seq - Proliferating cells (repeat 1) poly(A)+ RNA - Marguerat (2012)

External Transcripts - RNA-Seq - Proliferating cells (repeat 2) poly(A)+ RNA - Marguerat (2012)

External Transcripts - tiling microarray - mitosis, 972h-, haploid (forward strand) - Soriano (2013)

External Transcripts - tiling microarray - mitosis, 972h-, haploid (reverse strand) - Soriano (2013)

External Transcripts - tiling microarray - mitosis, pat1.114, diploid (forward strand) - Soriano (2013)

External Transcripts - tiling microarray - mitosis, pat1.114, diploid (reverse strand) - Soriano (2013)

External Transcripts - tiling microarray - meiosis 0h, pat1.114, diploid (forward strand) - Soriano (2013)

External Transcripts - tiling microarray - meiosis 0h, pat1.114, diploid (reverse strand) - Soriano (2013)

External Transcripts - tiling microarray - meiosis 3h, pat1.114, diploid (forward strand) - Soriano (2013)

External Transcripts - tiling microarray - meiosis 3h, pat1.114, diploid (reverse strand) - Soriano (2013)

External Transcripts - tiling microarray - meiosis 5h, pat1.114, diploid (forward strand) - Soriano (2013)

External Transcripts - tiling microarray - meiosis 5h, pat1.114, diploid (reverse strand) - Soriano (2013)

External Transcripts - tiling microarray - mitosis, atf1(delta), haploid (forward strand) - Soriano (2013)

External Transcripts - tiling microarray - mitosis, atf1(delta), haploid (reverse strand) - Soriano (2013)

External Transcripts - tiling microarray - mitosis, pcr1(delta), haploid (forward strand) - Soriano (2013)

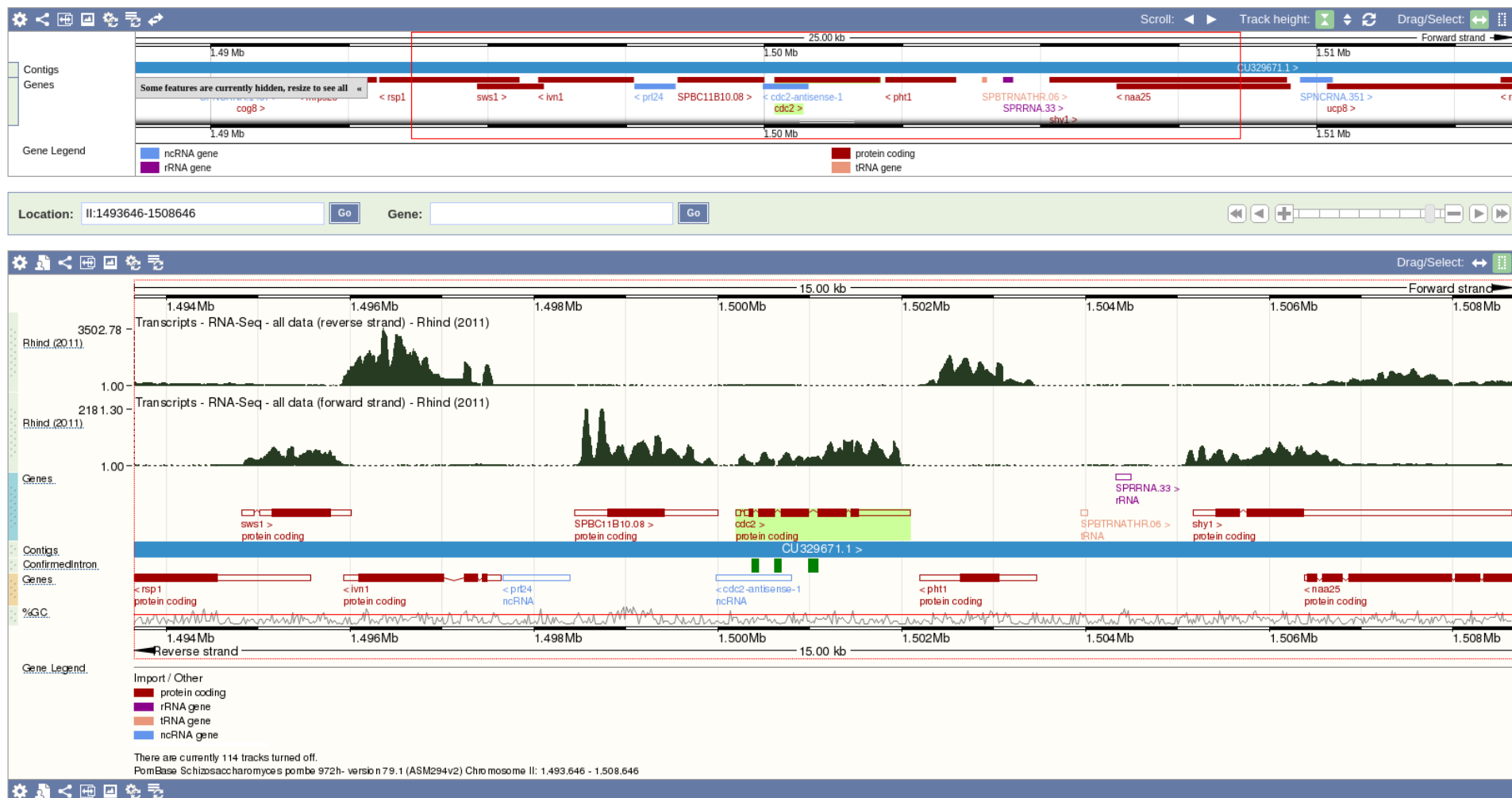
External Transcripts - tiling microarray - mitosis, pcr1(delta), haploid (reverse strand) - Soriano (2013)

External Transcripts - RNA-Seq - all data (forward strand) - Rhind (2011)

External Transcripts - RNA-Seq - all data (reverse strand) - Rhind (2011)

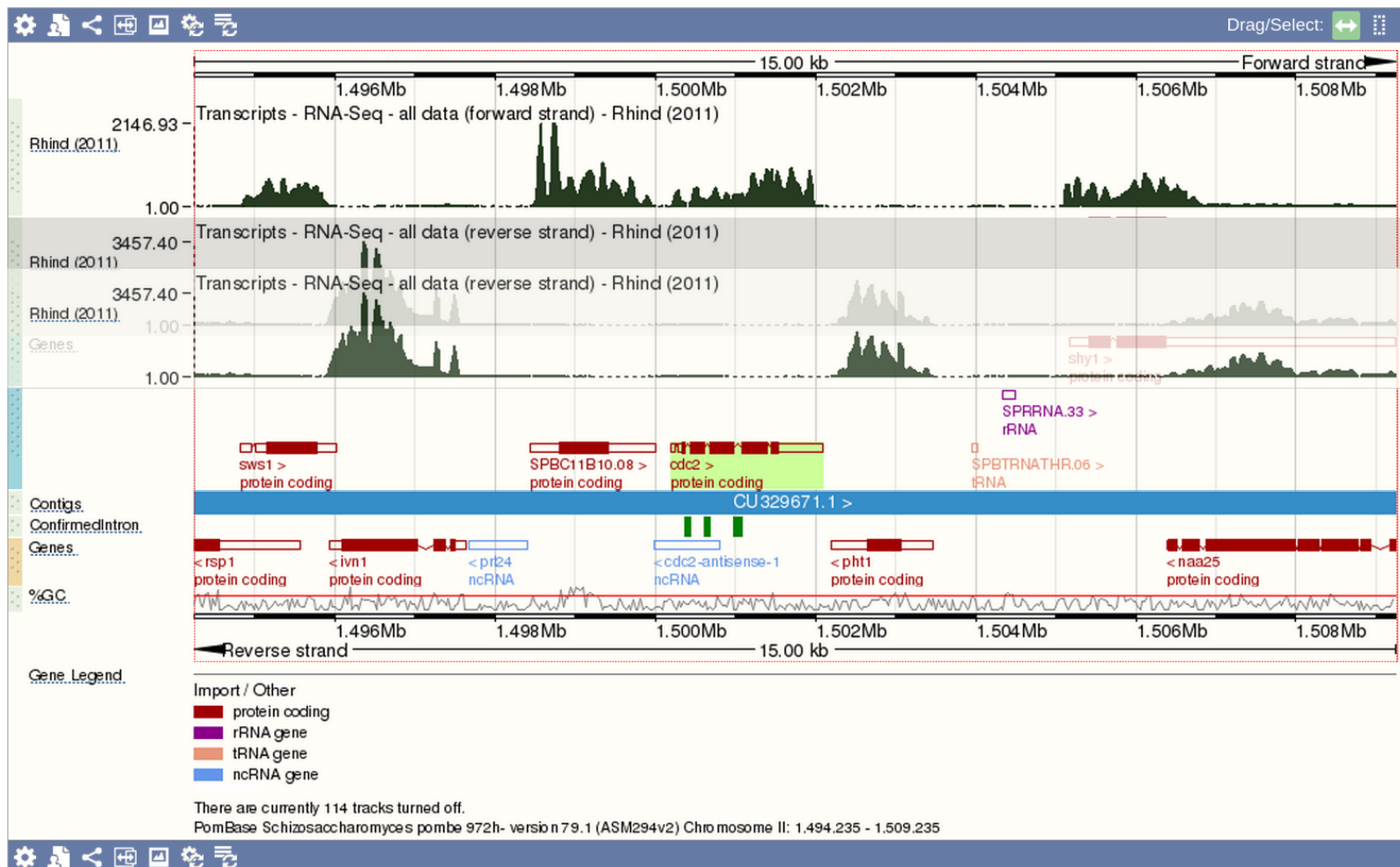
External Transcripts - RNA-Seq - glucose depletion (forward strand) - Rhind (2011)

# Displaying tracks






# Dragging tracks





# Add your own data


**Location-based displays**


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- Chromosome summary
- Region overview
- Region in detail**
- Comparative Genomics
  - Alignments (text)
  - Region Comparison
- Other genome browsers
  - PomBase

 Configure this page

 **Add your data**

 Export data

 Bookmark this page

 Share this page



# View your own data

**Configure Region Image** **Configure Overview Image** **Configure Chromosome Image** **Personal Data**

**Add a custom track**

Name for this data (optional):

Species:

Assembly:

Data format:

[Help on supported formats, display types, etc](#)

Type:

☒ Upload data (max 20MB)

☐ Attach via URL

Paste data:

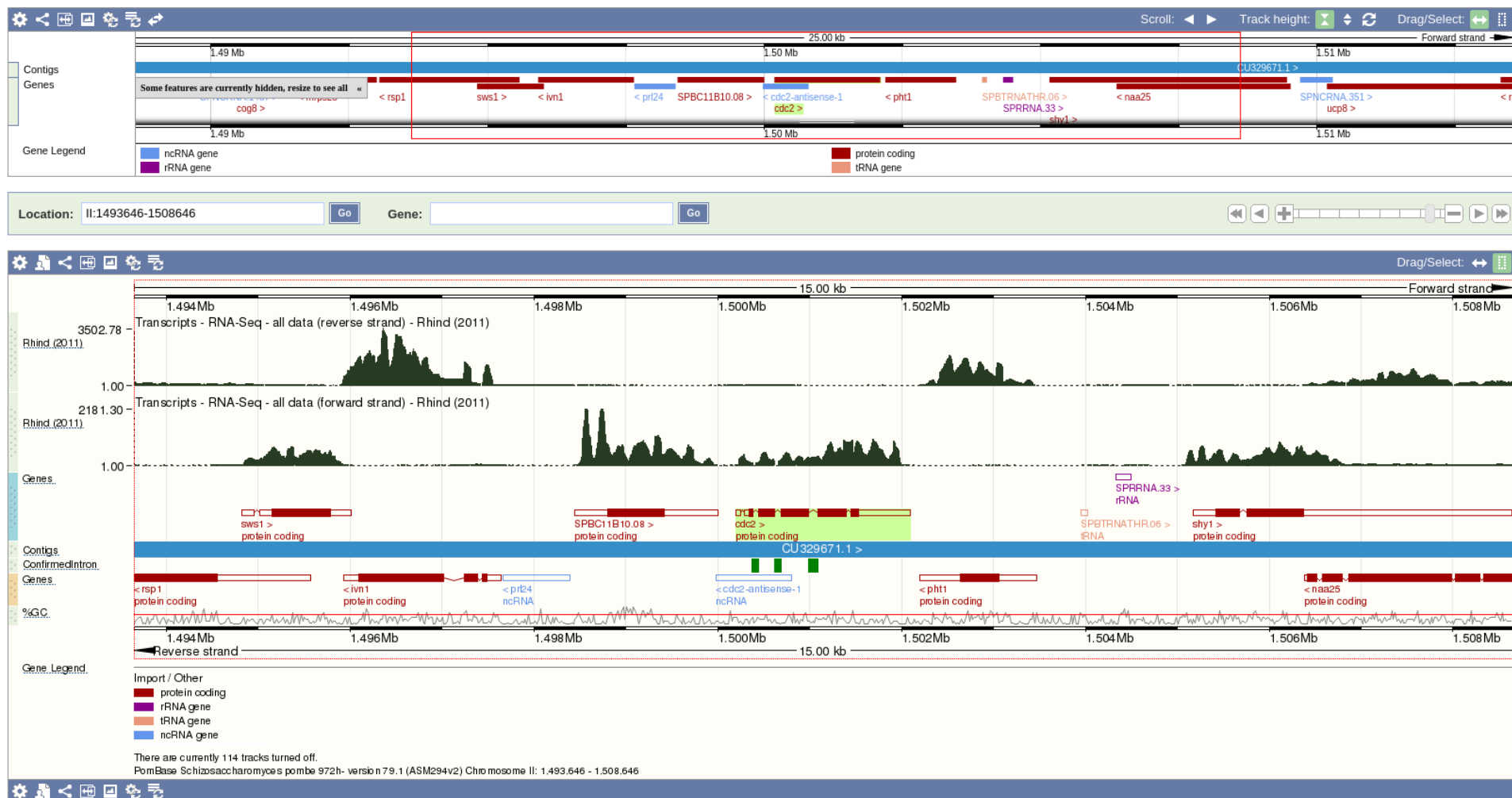
Or choose file:  No file chosen

Or provide file URL:

## Data Formats:

- bam
- bedGraph
- (big)Bed
- GFF
- TrackHub
- VCF
- (big)Wig

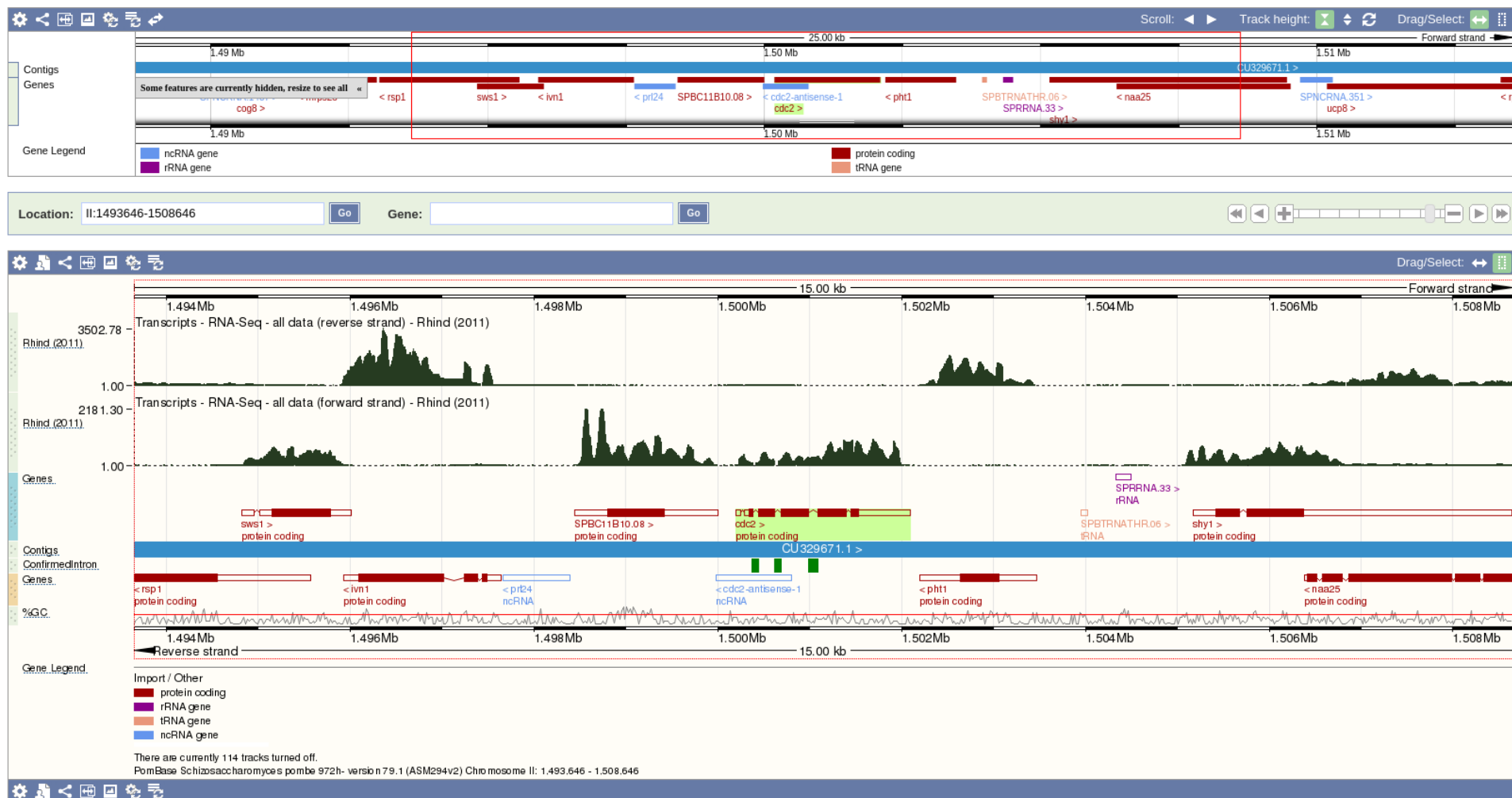
# Displaying tracks



# Making your data accessible to others

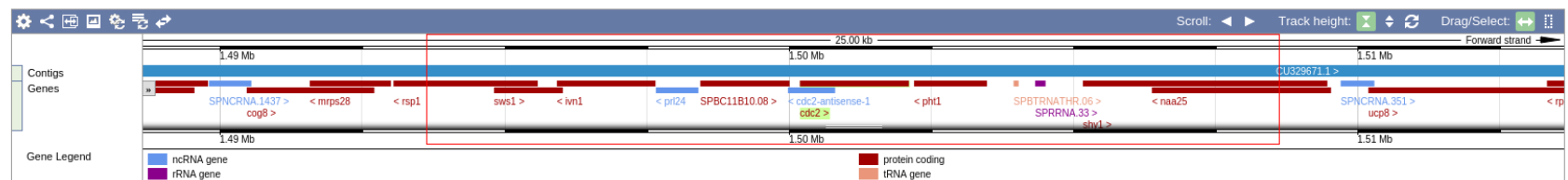
- If you are able to view your data, but want to make it publically accessible please fill in the form at:
  - <http://www.pombase.org/submit-data/data-submission-form>
- This can be found under the Submit tab from the PomBase.org home page

# Pop-up menus

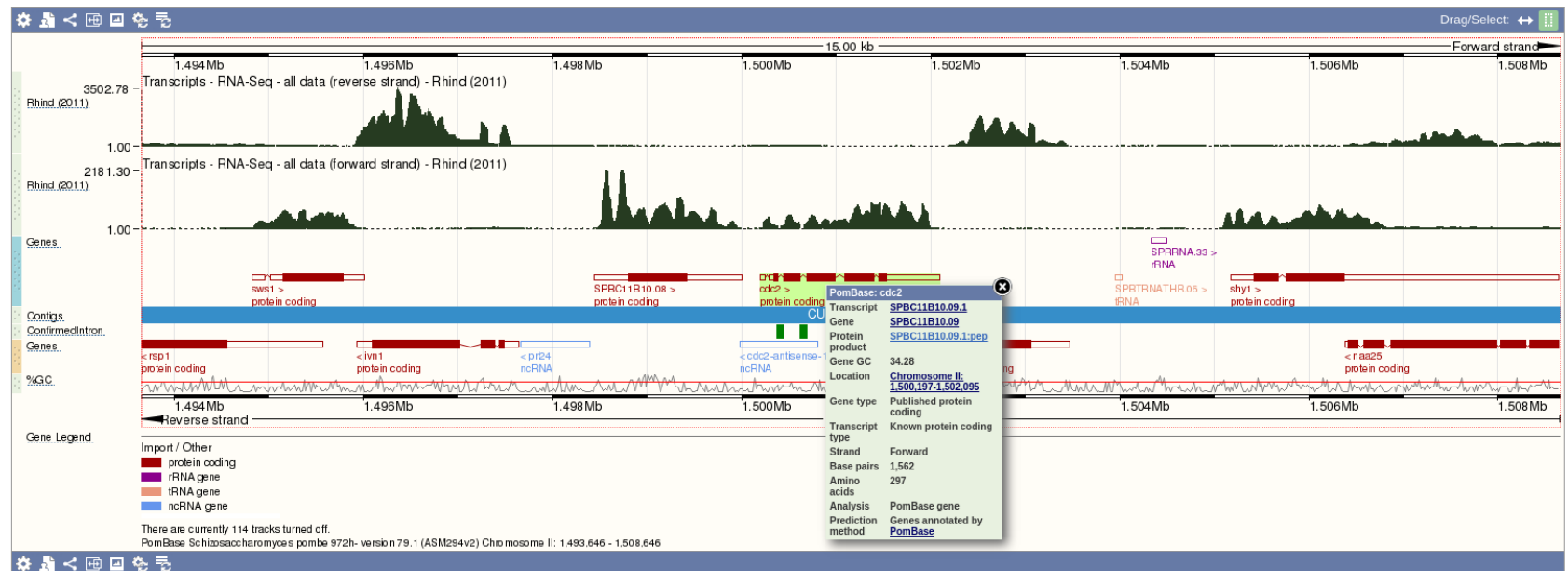


# Pop-up menus

## Region in detail ⓘ

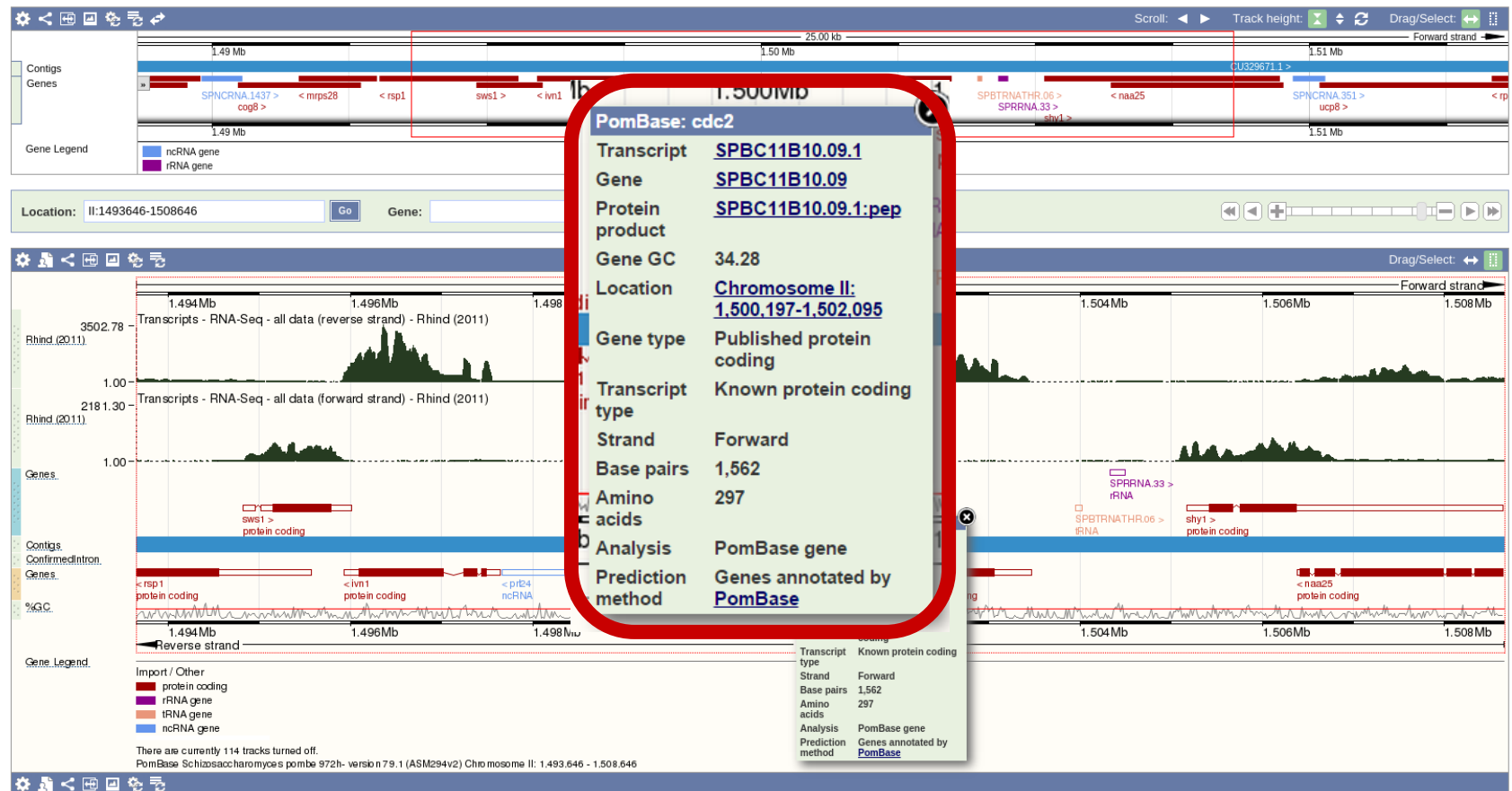


Location: IL:1493646-1508646 Go Gene: Go



# Pop-up menus

## Region in detail ⓘ



# Exporting data

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Schizosaccharomyces pombe

**Location-based displays**

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**Chromosome II: 1,493,646-1,508,646**

Chr. II

**Region in detail**

Contigs  
Genes

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646  Gene:

Genes

Contigs

Confirmed Intron

Genes

%GC

Gene Legend

- Import / Other
- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene

There are currently 116 tracks turned off.


PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646




# Exporting data


**Location-based displays**


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# Exporting data

**PomBase** [Back to Gene Page](#) [BLAST](#) [Search PomBase...](#)

## Export data

### Export Configuration - Feature List

**Location to export:** chromosome:ASM294v2:II:1499820:1502096:1

**Output:** FASTA sequence \*

**Select location:** II \* 1499820 \* 1502096 \* 1 ▾

**5' Flanking sequence (upstream):** 0 \* (Maximum of 1000000)

**3' Flanking sequence (downstream):** 0 \* (Maximum of 1000000)

[Next >](#)

Fields marked \* are required

### Options for FASTA sequence

**Genomic:** Unmasked \*

Fields marked \* are required

# Exporting data

**PomBase** | [Back to Gene Page](#) | [BLAST](#) | [Search PomBase...](#)

## Export data

### Export Configuration - Feature List

Location to export: chromosome:ASM294v2:II:1499820:1502096:1

Output: **FASTA sequence** \*

Select location:

5' Flanking sequence (upstream):

3' Flanking sequence (downstream):

Fields marked \* are required

### Options for FASTA sequence

Genomic:

Fields marked \* are required

- Bed Format**
  - BED Format
- FASTA sequence**
  - FASTA sequence
- Feature File**
  - CSV (Comma separated values)
  - Tab separated values
  - GTF (Gene Transfer Format)
  - GFF (Generic Feature Format)
  - GFF3 (Generic Feature Format Version 3)
- Flat File**
  - EMBL
  - GenBank
- PIP (%age identity plot)**
  - Pipmaker / zPicture format
  - Vista Format

# Exporting data

The screenshot shows a web browser window with the PomBase logo in the top left. The browser's address bar contains 'Search PomBase...'. The page has a dark header bar with the text 'Export data' and a checkmark icon. Below this, the main content area is titled 'Export Configuration - Output Format'. It contains the instruction 'Please choose the output format for your export' followed by three radio button options: 'HTML', 'Text', and 'Compressed text (.gz)'. A '< Back' button is located at the bottom center of the form area. The left sidebar of the browser shows a navigation menu with various categories like 'hiz', 'cati', 'Wh', 'Chr', 'Reg', 'Reg', 'Cor', 'A', 'F', 'Oth', 'F', 'C', 'A', 'E', 'B', 'S'. The right sidebar shows a vertical list of items including 'd', 'Mb', 'RN', 'v', 'Mb'.

PomBase

Back to Gene Page | BLAST | Search PomBase...

Export data

### Export Configuration - Output Format

Please choose the output format for your export

- ☐ [HTML](#)
- ☐ [Text](#)
- ☐ [Compressed text \(.gz\)](#)

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# Gene tab

PomBase

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Schizosaccharomyces pombe

Location: II:1,493,646-1,508,646

Gene: cdc2

Transcript: cdc2

## Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Supporting evidence
- Gene alleles
- Sequence
  - Secondary Structure
- External references
- Regulation
- Ontology
  - FYPO: phenotype (68)
  - GO: biological process (14)
  - GO: molecular function (7)
  - GO: cellular component (3)
  - MOD: protein modification (4)
- Fungal Compara
  - Genomic alignments
  - Gene tree
  - Gene gain/loss tree
  - Orthologues
  - Paralogues
- Pan-taxonomic Compara
  - Gene Tree
  - Orthologues
- Phenotype
- Genetic Variation
  - Variation table
  - Structural variation
  - Variation image
- External data
- ID History
  - Gene history

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## Gene: cdc2 SPBC11B10.09

### Description

cyclin-dependent protein kinase Cdk1/Cdc2 [Source: PomBase SPBC11B10.09](#)

### Synonyms

cdk1, pi002, SPACTOKYO\_453.34, swo2, tws1, wee2

### Location

[Chromosome II: 1,500,197-1,502,095](#) forward strand.

### About this gene

This gene has 1 transcript ([splice variant](#)), [70 orthologues](#) and [14 paralogues](#).

### Transcripts

[Show transcript table](#)

## Summary ⓘ

### Name

cdc2 (PomBase Gene Name)

### UniprotKB

This gene has proteins that correspond to the following Uniprot identifiers: [P04551](#)

### Gene type

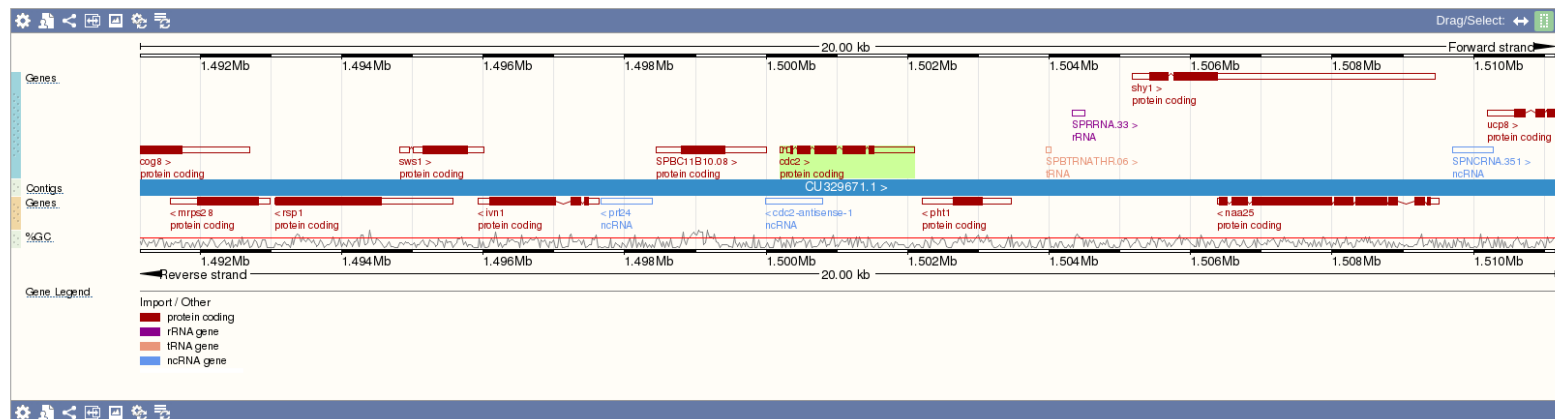
Protein coding

### Annotation Method

Genes annotated by [PomBase](#)



Go to [Region in Detail](#) for more tracks and navigation options (e.g. zooming)



## Configuring the display ⓘ

Tip: use the ["Configure this page"](#) link on the left to show additional data in this region.

 Search PomBase...

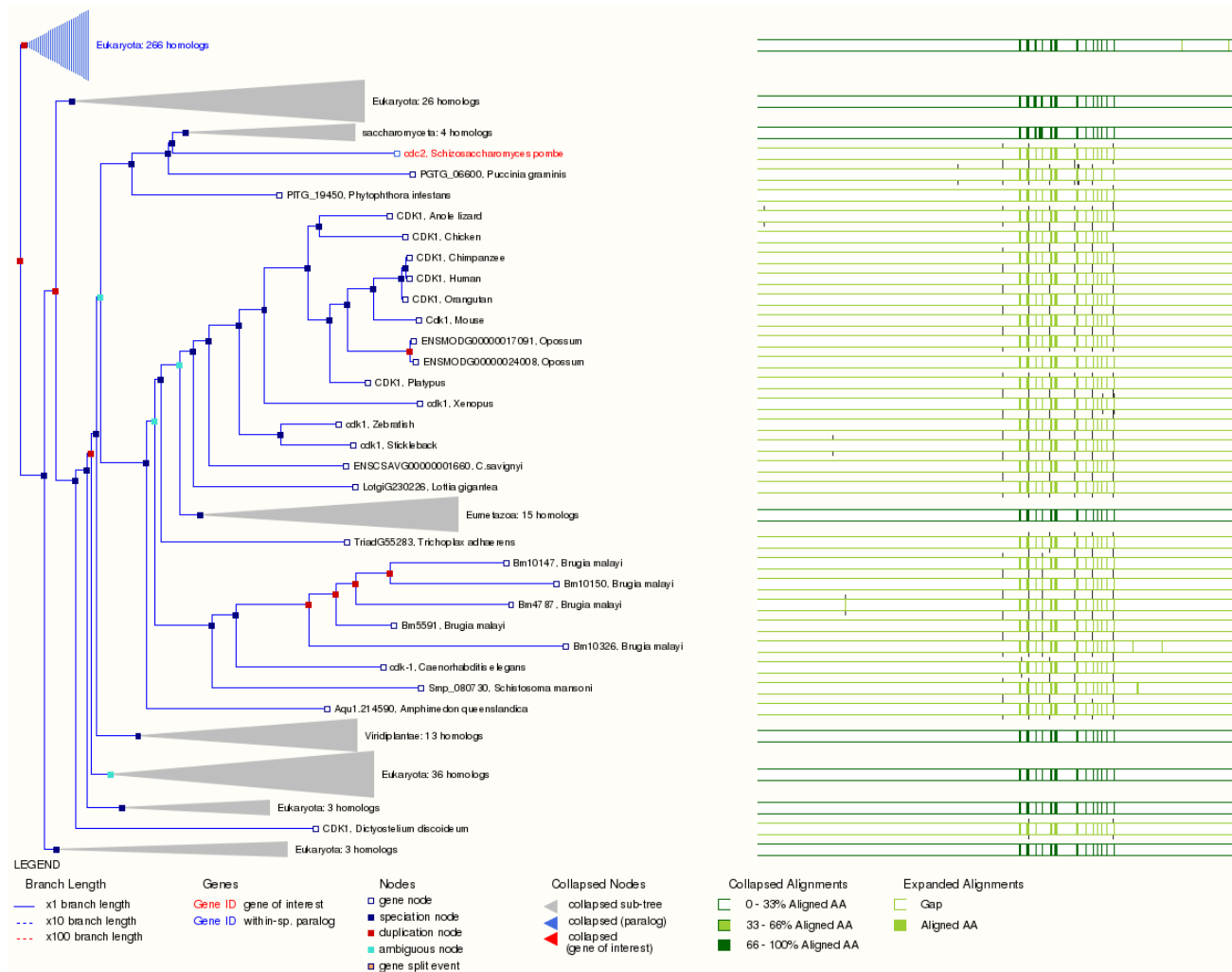
Transcript: *cdc2*

## Orthologues

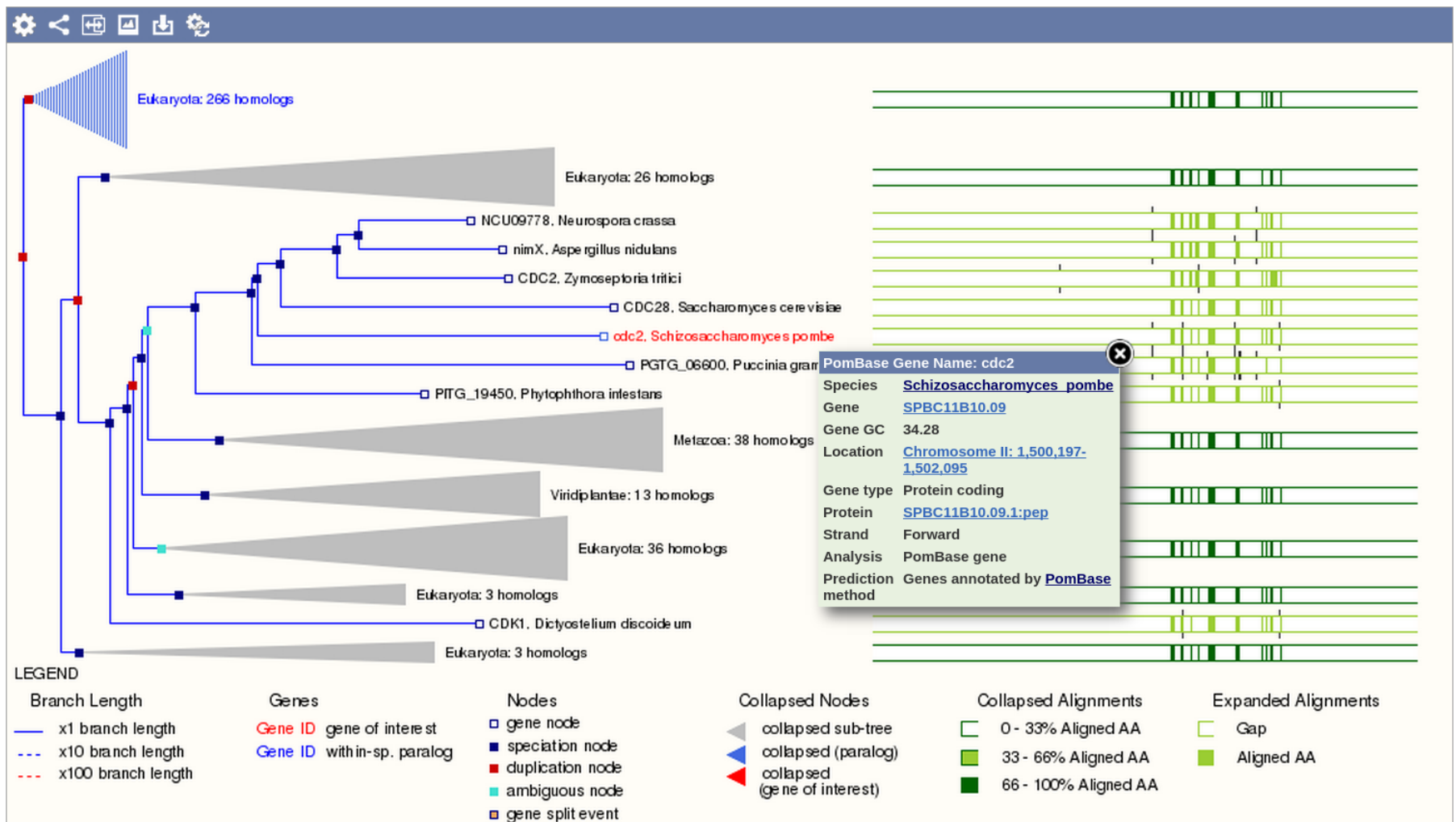


Tip: use the "Configure this page" link on the left to show additional data in this region.

# Comparative genomics



# More pop-up menu





# Location tab - Synteny

**PomBase** [Back to Gene Page](#) [BLAST](#) [NCBI BLAST](#) [Tools](#) [Downloads](#) [PomBase Help](#) [Search PomBase...](#)

Schizosaccharomyces pombe [Location: II:1,493,646-1,508,646](#) [Gene: cdc2](#) [Transcript: cdc2](#)

**Location-based displays**

- Whole genome
- Chromosome summary
- Region overview
- Region in detail**
- Comparative Genomics
  - Alignments (text)
  - Region Comparison
- Other genome browsers
  - PomBase

**Configure this page**

**Add your data**

**Export data**

**Bookmark this page**

**Share this page**

**Chromosome II: 1,493,646-1,508,646**

**Region in detail**

Chr. II

Contigs  
Genes

Gene Legend

- ncRNA gene
- rRNA gene
- protein coding
- tRNA gene

Location: II:1493646-1508646 [Go](#) Gene: [Go](#)

Genes

Contigs

Confirmed Intron

Genes

%GC

Gene Legend

- Import / Other
- protein coding
- rRNA gene
- tRNA gene
- ncRNA gene

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h - version n79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646





# Location tab


## - Synteny


**Location-based displays**


- Whole genome
- Chromosome summary
- Region overview
- Region in detail
- Comparative Genomics**
  - Alignments (text)
  - Region Comparison**
- Other genome browsers
  - PomBase


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 Share this page


 Select species or regions


# Location tab


## - Synteny


**Location-based displays**


- Whole genome
- Chromosome summary
- Region overview
- Region in detail
- Comparative Genomics
  - Alignments (text)
  - Region Comparison**
- Other genome browsers
  - PomBase


 Configure this page

 Add your data

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 Share this page

 Select species or regions

# Location - Synten

- Alignments (text)
- Region Comparison**
- Other genome browsers
  - PomBase

Configure this page

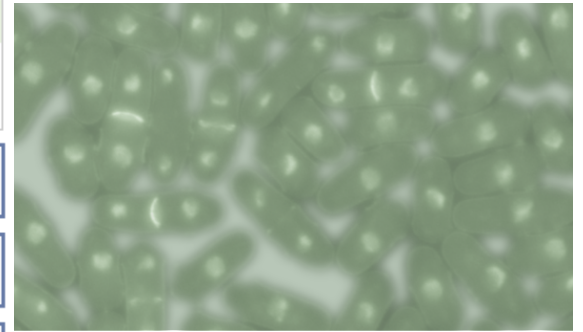
Add your data

Export data

Bookmark this page

Share this page

Select species or regions



# Location tab

## - Synteny

on-based displays

Configure Comparison Image   Configure Comparison Overview   Configure Chromosome Image   **Select species or regions**   Personal Data

**Tip**

Click on the plus and minus buttons to select or deselect options.

Selected options can be reordered by dragging them to a different position in the list

**Selected species or regions**

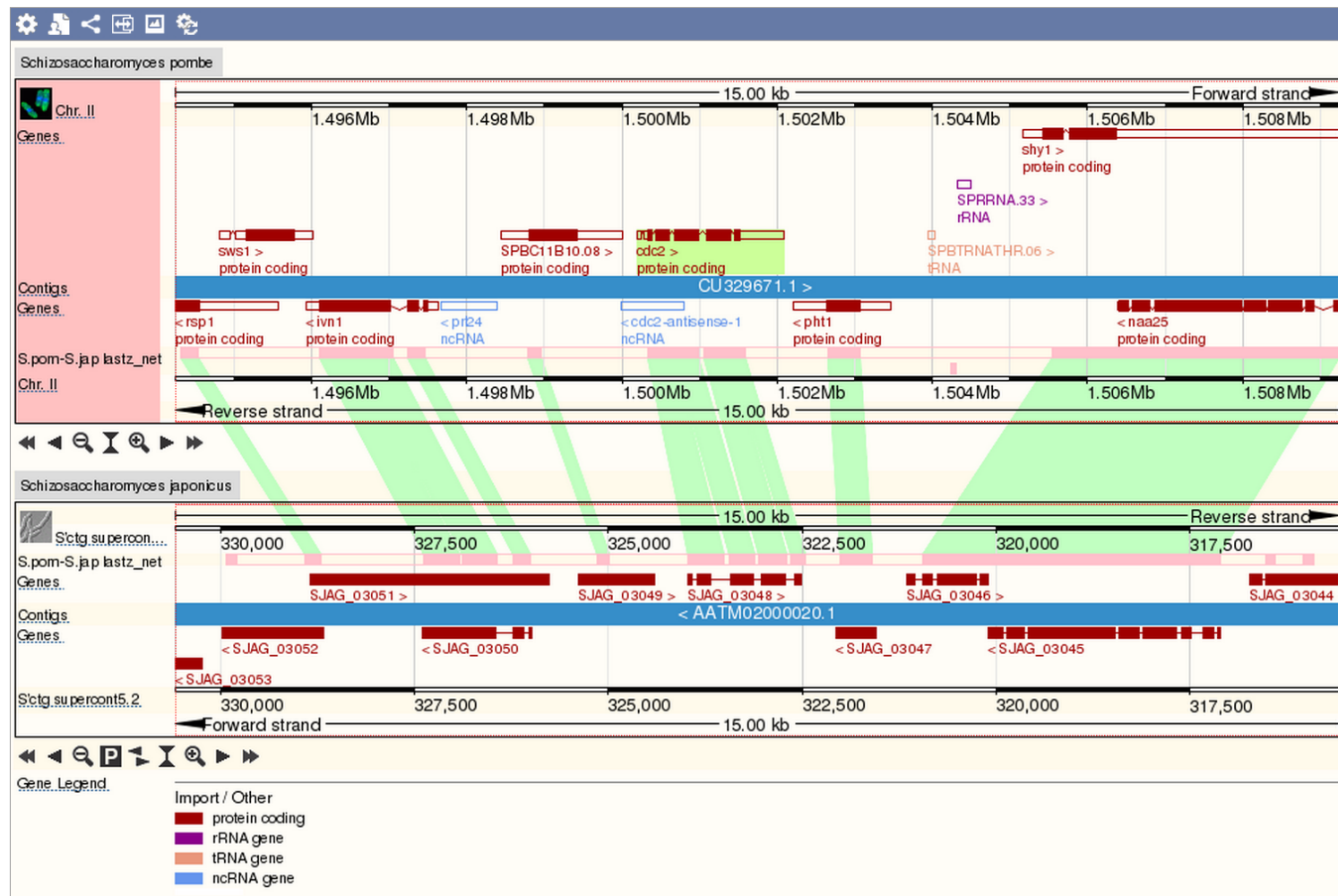
- − Schizosaccharomyces japonicus - lastz

**Unselected species or regions**

- + Schizosaccharomyces cryophilus - lastz
- + Schizosaccharomyces octosporus - lastz

# Location tab

## - Synteny



# Gene tab - Preview

PomBase

[Back to Gene Page](#)

[BLAST](#)

[NCBI BLAST](#)

[Tools](#)

[Downloads](#)

[PomBase Help](#)

[Search PomBase...](#)

Schizosaccharomyces pombe

Location: II:1,493,646-1,508,646

Gene: cdc2

Transcript: cdc2

## Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Supporting evidence
- Gene alleles
- Sequence
  - Secondary Structure
- External references
- Regulation
- Ontology
  - FYPO: phenotype (68)
  - GO: biological process (14)
  - GO: molecular function (7)
  - GO: cellular component (3)
  - MOD: protein modification (4)
- Fungal Compara
  - Genomic alignments
  - Gene tree
  - Gene gain/loss tree
  - Orthologues
  - Paralogues
- Pan-taxonomic Compara
  - Gene Tree
  - Orthologues
- Phenotype
- Genetic variation
  - Variation table
  - Structural variation
  - Variation image
- External data
- ID History
- Gene history

[Configure this page](#)

[Add your data](#)

[Export data](#)

[Bookmark this page](#)

[Share this page](#)

## Gene: cdc2 SPBC11B10.09

### Description

cyclin-dependent protein kinase Cdk1/Cdc2 [Source: PomBase SPBC11B10.09](#)

### Synonyms

cdk1, pi002, SPACTOKYO\_453.34, swo2, tws1, wee2

### Location

[Chromosome II: 1,500,197-1,502,095](#) forward strand.

### About this gene

This gene has 1 transcript ([splice variant](#)), [70 orthologues](#) and [14 paralogues](#).

### Transcripts

[Show transcript table](#)

## Summary ⓘ

### Name

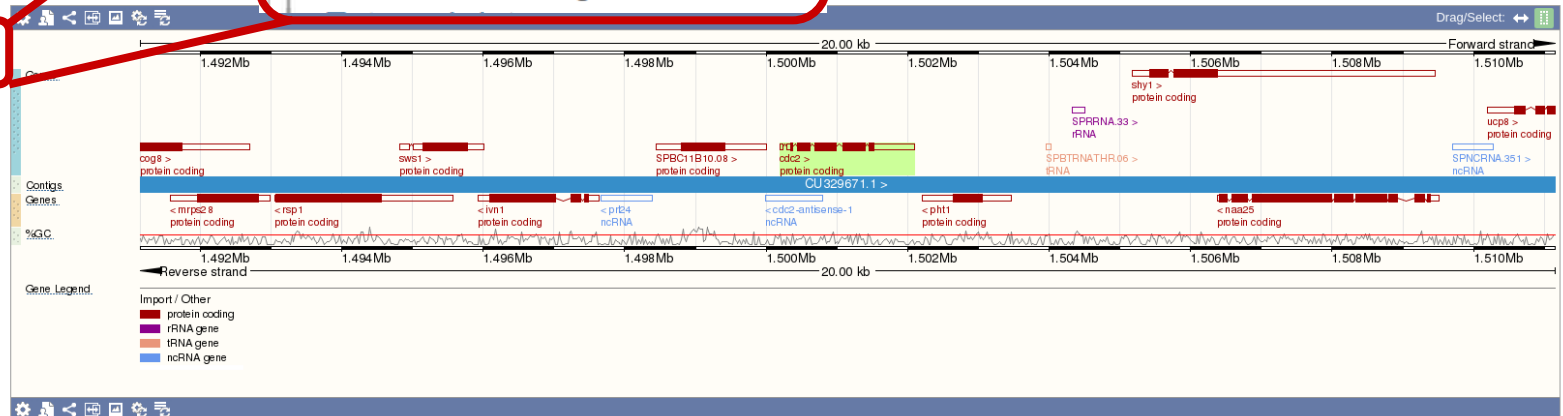
UniprotKB

Gene type

Annotation Method

[Go to Region in Detail for more](#)

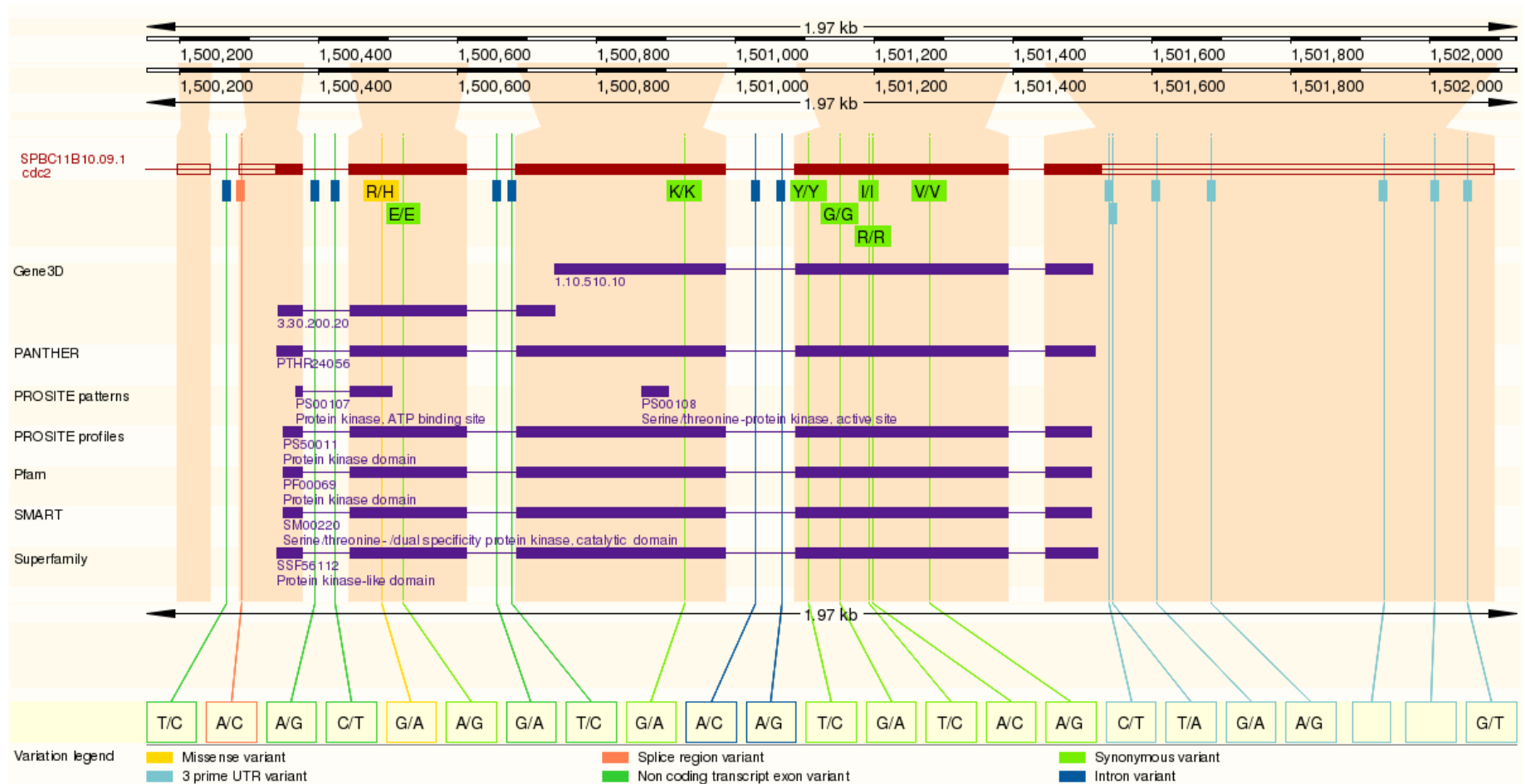
- Genetic Variation
  - Variation table
  - Structural variation
  - Variation image



## Configuring the display ⓘ

Tip: use the ["Configure this page"](#) link on the left to show additional data in this region.

# Variation - Preview







# Acknowledgements

- **European Bioinformatics Institute:**

- Paul Kersey
- Mark McDowall
- Dan Staines
- Ensembl Genomes Team

- **University of Cambridge:**

- Steve Oliver
- Valerie Wood
- Midori Harris
- Kim Rutherford

- **University College London:**


- Jürg Bähler
- Antonia Lock


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**wellcome**trust


# Left Hand Menus


**Location-based displays**


- Whole genome
- Chromosome summary
- Region overview
- Region in detail**
- Comparative Genomics
  - Alignments (text)
  - Region Comparison
- Other genome browsers
  - PomBase

 Configure this page

 Add your data


 Export data


 Bookmark this page


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**Gene-based displays**


- Summary**
- Splice variants
- Transcript comparison
- Supporting evidence
- Gene alleles
- Sequence
  - Secondary Structure
- External references
- Regulation
- Ontology
  - FYPO: phenotype (68)
  - GO: biological process (14)
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  - MOD: protein modification (4)
- Fungal Compara
  - Genomic alignments
  - Gene tree
  - Gene gain/loss tree
  - Orthologues
  - Paralogues
- Pan-taxonomic Compara
  - Gene Tree
  - Orthologues
- Phenotype
- Genetic Variation
  - Variation table
  - Structural variation
  - Variation image
- External data
- ID History
  - Gene history

 Configure this page

 Add your data


 Export data


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**Transcript-based displays**


- Summary**
- Supporting evidence
- Sequence
  - Exons
  - cDNA
  - Protein
- External References
  - General identifiers
  - Oligo probes
- Ontology
  - FYPO: phenotype (68)
  - GO: biological process (14)
  - GO: molecular function (7)
  - GO: cellular component (3)
  - MOD: protein modification (4)
- Genetic Variation
  - Variation table
  - Variation image
  - Population comparison
  - Comparison image
- Protein Information
  - Protein summary
  - Domains & features
  - Variations
  - EBI protein data summary
  - Protein structure
- External data
- ID History
  - Transcript history
  - Protein history

 Configure this page

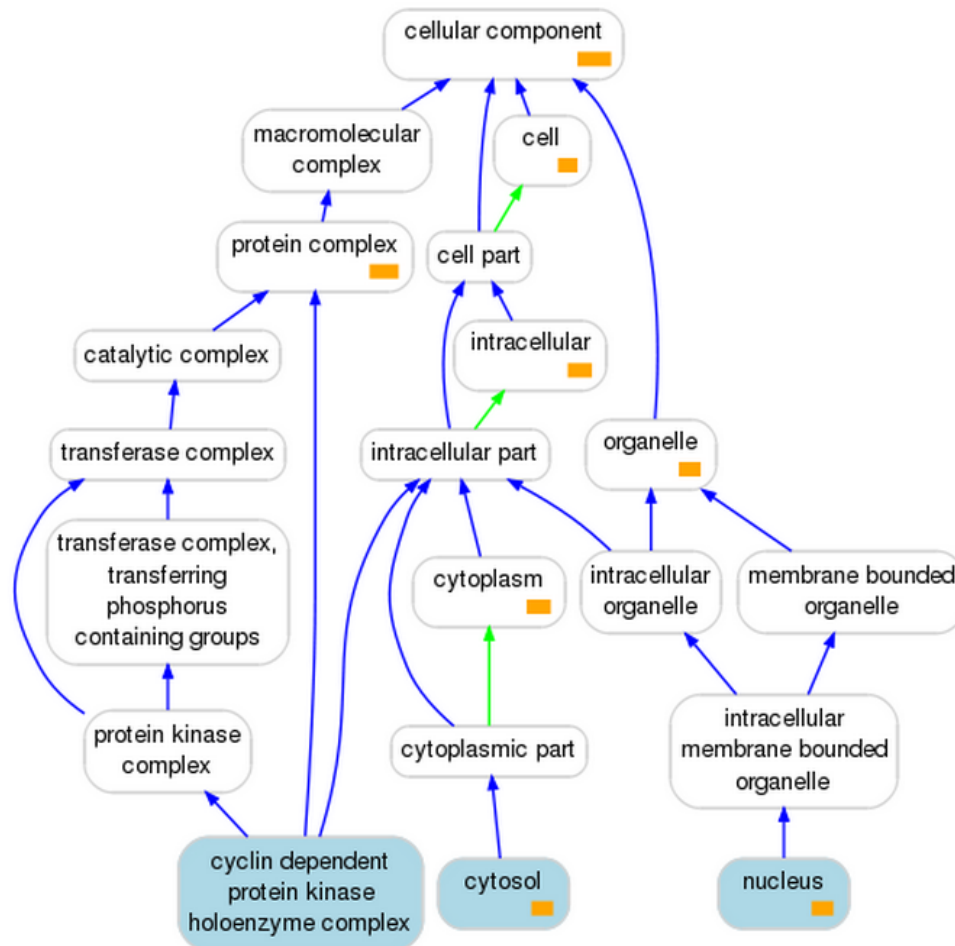
 Add your data

 Export data

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# Ontology Annotations



# Transcript

## Transcript-based displays

- Summary
- Supporting evidence
- Sequence
  - Exons
  - cDNA
  - Protein
- External References
  - General identifiers
  - Oligo probes
- Ontology
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- Protein Information
  - Protein summary
  - Domains & features
  - Variations
  - EBI protein data summary
  - Protein structure
- External data
- ID History
  - Transcript history
  - Protein history

## Transcript: cdc2 SPBC11B10.09.1

**Description** cyclin-dependent protein kinase Cdk1/Cdc2 [Source: PomBase SPBC11B10.09](#)

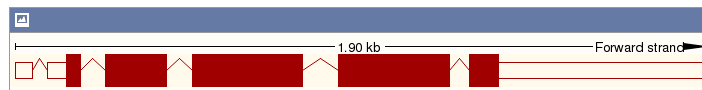
**Location** [Chromosome II: 1,500,197-1,502,095](#) forward strand.

**About this transcript** This transcript has [6 exons](#) and is annotated with [9 domains and features](#).

**Gene** This transcript is a product of gene [SPBC11B10.09](#)

[Show transcript table](#)

## Summary



**Statistics** Exons: 6 Coding exons: 5 Transcript length: 1,562 bps Translation length: 297 residues

**Uniprot** This transcript corresponds to the following Uniprot identifiers: [P04551](#)

**Type** Known protein coding

**Prediction Method** Genes annotated by [PomBase](#)

PomBase release 26 - March 2015 © [EBI](#)

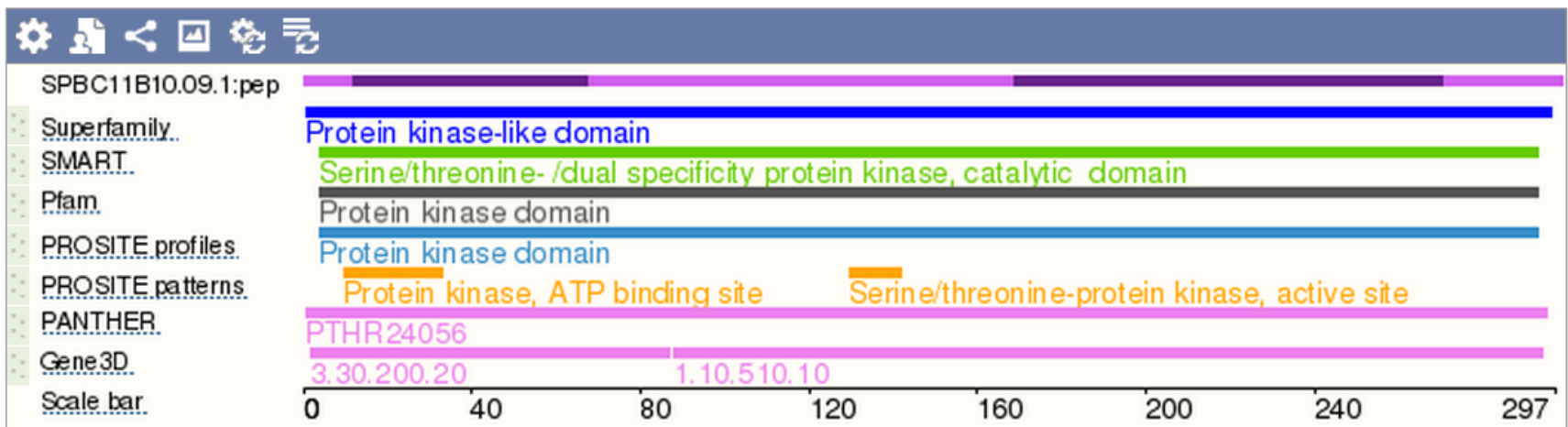
[About EnsemblGenomes](#) | [Contact PomBase](#) | [Contact Ensembl](#) | [Ensembl Help](#)

- Configure this page
- Add your data
- Export data
- Bookmark this page
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# Translation

## Protein summary ⓘ

Protein domains for SPBC11B10.09.1:pep.1



## Statistics

Ave. residue weight: 115.685 g/mol

Charge: 4.5

Isoelectric point: 7.6821

Molecular weight: 34,358.53 g/mol

Number of residues: 297 aa

# Sequence

Gene-based displays	
Summary	
Splice variants	
Transcript comparison	
Supporting evidence	
Gene alleles	
Sequence	
Secondary Structure	
External references	
Regulation	
Ontology	
FYPO: phenotype (68)	
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Fungal Compara	
Genomic alignments	
Gene tree	
Gene gain/loss tree	
Orthologues	
Paralogues	
Pan-taxonomic Compara	
Gene Tree	
Orthologues	
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Genetic Variation	
Variation table	
Structural variation	
Variation image	
External data	
ID History	
Gene history	

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Transcript-based displays	
Summary	
Supporting evidence	
Sequence	
Exons	
cDNA	
Protein	
External References	
General identifiers	
Oligo probes	
Ontology	
FYPO: phenotype (68)	
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Comparison image	
Protein Information	
Protein summary	
Domains & features	
Variations	
EBI protein data summary	
Protein structure	
External data	
ID History	
Transcript history	
Protein history	

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# Sequences

## Protein sequence ⓘ

[Download sequence](#)[BLAST this sequence](#)[Search Ensembl Genomes with this sequence](#)[Exons](#)[Alternating exons](#)[Alternating exons](#)[Residue overlap splice site](#)

MENYQKVEKIGE**GT**YGVVYKARHKLSGRIVAMKKIRLEDESEGV PSTAIREISLLKEVND  
EN**NR**SNCV**R**LLDILHAESKLYLVFEFLDMDLK KYMDRISETGATSLDPRLVQKFTYQLVN  
GVNFCHSRRIIHRDLKPQNLLIDKEGNLKLADFG LARSFGVPLRNYTHE**IVTLWYRAPEV**  
**LLGSRHYSTGVDIWSVGCIFAEMIRRSPLFP**GDSEID**E**IFK**IFQVLGTPNEEVWPGVTLL**  
**QDYKSTFPRWKRMDLHKVVPNGEEDAIELLS**AMLVYDPAHRISAKRALQQNYLRDFH

# Sequence - BLAST

## Protein sequence ⓘ

[Download sequence](#)[BLAST this sequence](#)[Search Ensembl Genomes with this sequence](#)[Exons](#)[Alternating exons](#)[Alternating exons](#)[Residue overlap splice site](#)

MENYQKVEKIGE**GT**YGVVYKARHKLSGRIVAMKKIRLEDESEGV PSTAIREISLLKEVND  
EN**NR**SNCV**R**LLDILHAESKLYLVFEFLDMDLKKYMDRISETGATSLDPRLVQKFTYQLVN  
GVNFCHSRRIIHRDLKPQNLLIDKEGNLKLADFGLARSGVPLRNYTHE**IVTLWYRAPEV**  
**LLGSRHYSTGVDIWSVGCIFAEMIRRSPLFP**GDSEID**E**IFK**IFQVLGTPNEEVWPGVTLL**  
**QDYKSTFPRWKRMDLHKVVPNGEEDAIELLS**AMLVYDPAHRISAKRALQQNYLRDFH

# From the gene page

## ▼ Sequence

[Report an error](#) | [Help](#)

### Sequence Download

- ☒ Coding Sequence (CDS)
- ☐ CDS + UTRs
- ☐ CDS + UTRs + Introns
- ☐ Translation
- ☐ Custom Sequence

### Display Options

- ☒ Highlight Sequence Regions
- ☐ Plain

Retrieve ...

### BLAST Sequence

BLAST Gene Sequence | BLAST Coding Sequence | BLAST Protein Sequence

- [NCBI BLAST Gene Coding Sequence](#)
- [NCBI BLAST Protein Sequence](#)

# From the genome browser

**PomBase** | Back to Gene Page | **BLAST** | NCBI BLAST | Tools | Downloads | PomBase Help

Schizosaccharomyces pombe | Location: II:1,493,646-1,508,646 | Gene: cdc2 | Transcript: cdc2

Search PomBase...

### Transcript-based displays

- Summary
- Supporting evidence
- Sequence
  - Exons
  - cDNA
  - Protein
- External References
  - General identifiers
  - Oligo probes
- Ontology
  - FYPO: phenotype (68)
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  - Protein summary
  - Domains & features
  - Variations
  - EBI protein data summary
  - Protein structure
- External data
- ID History
  - Transcript history
  - Protein history

Configure this page | Add your data | Export data | Bookmark this page | Share this page

### Transcript: cdc2 SPBC11B10.09.1

**Description** cyclin-dependent protein kinase Cdk1/Cdc2 [Source: PomBase SPBC11B10.09](#)


**Location** [Chromosome II: 1,500,197-1,502,095](#) forward strand.

**About this transcript** This transcript has [6 exons](#) and is annotated with [9 domains and features](#).

**Gene** This transcript is a product of gene [SPBC11B10.09](#)

[Show transcript table](#)

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**Statistics** Exons: 6 Coding exons: 5 Transcript length: 1,562 bps Translation length: 297 residues

**Uniprot** This transcript corresponds to the following Uniprot identifiers: [P04551](#)

**Type** Known protein coding

**Prediction Method** Genes annotated by [PomBase](#)

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# BLAST - Submitting a job

## BLAST search ⓘ

Create new ticket:

### Sequence data:

```
>
MENYQKVEKIGEGTYGVVYKARHKLSGRIVAMKKIRLEDESEGVSTAIRESILLKEVND
ENNRSNCVRLDILHAESKLYLVFEFLDMDLKKYMDRISETGATSLDPLRVQKFTYQLVN
GVNFCHSRRIIHRDLKPQNLIDKEGNLKLADFGLARSGVPLRNYTHEIVTLWYRAPEV
LLGSRHYSTGVDIWSVGCIFAEMIRRSPLFPGDSEIDEIFKIFQVLGTPNEEVWPGVTLL
QDYKSTFPRWKRMDLHKVVPNGEEDAIELLSAMLVYDPAHRISAKRALQQNYLRDFH
```

[Add more sequences](#) (1 sequence added, 29 more sequences allowed)

- ☐ DNA
- ☒ Protein

### Search against:

Schizosaccharomyces pombe

[Add/remove species](#)

- ☐ DNA database    Genomic sequence ▾
- ☒ Protein database    Proteins ▾

### Search tool:

BLASTP ▾

### Description (optional):

## Configuration options

[General options:](#) ⓘ

[Filters and masking options:](#) ⓘ

[Run >](#) [Clear](#)

# BLAST - Results

## BLAST search ⓘ

New Search

Recent Blast tickets: ⓘ

Refresh




Show/hide columns (1 hidden)

Filter

Analysis ⓘ Jobs




Submitted at ⓘ

BLASTP  BLASTP against Schizosaccharomyces pombe ASM294v2 (Proteins) **Done: 63 hits found** [View results](#)

08/06/2015, 14:11    

## Results for BLASTP against Schizosaccharomyces pombe ASM294v2 (Proteins)

### Job details ⓘ

Job name BLASTP against Schizosaccharomyces pombe ASM294v2 (Proteins)  
   
Species  Schizosaccharomyces pombe  
Assembly ASM294v2  
Search type BLASTP (WU BLAST)

 Download results file

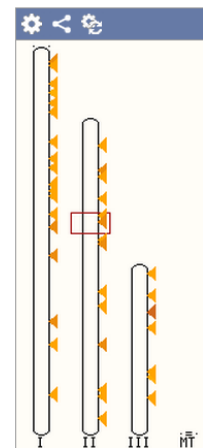
### Results table ⓘ

Show 10 entries		Show/hide columns (7 hidden)							Filter	
Subject name	Subject description	Gene hit	Genomic Location	Orientation	Length	Score	E-val	%ID		
<a href="#">SPBC11B10.09.1.pep</a>		<a href="#">cdc2</a>	<a href="#">II:1500340-1501525 [Sequence]</a>	Forward	297 <a href="#">[Sequence]</a>	100.0	7.4E-161	100.0 <a href="#">[Alignment]</a>		
<a href="#">SPCC16C4.11.1.pep</a>		<a href="#">pef1</a>	<a href="#">III:687757-688647 [Sequence]</a>	Forward	287 <a href="#">[Sequence]</a>	55.0	5.7E-83	55.0 <a href="#">[Alignment]</a>		
<a href="#">SPAC1D4.11c.1.pep</a>		<a href="#">lkb1</a>	<a href="#">I:656802-656867 [Sequence]</a>	Reverse	22 <a href="#">[Sequence]</a>	54.0	6.8E-17	54.0 <a href="#">[Alignment]</a>		
<a href="#">SPCC18B5.11c.1.pep</a>		<a href="#">cds1</a>	<a href="#">III:739498-739575 [Sequence]</a>	Reverse	26 <a href="#">[Sequence]</a>	46.0	2.0E-23	46.0 <a href="#">[Alignment]</a>		
<a href="#">SPAC24B11.11c.1.pep</a>		<a href="#">sid2</a>	<a href="#">I:222503-222658 [Sequence]</a>	Reverse	54 <a href="#">[Sequence]</a>	44.0	5.2E-18	44.0 <a href="#">[Alignment]</a>		
<a href="#">SPAC23C11.16.1.pep</a>		<a href="#">plo1</a>	<a href="#">I:2165041-2165097 [Sequence]</a>	Forward	19 <a href="#">[Sequence]</a>	42.0	7.6E-18	42.0 <a href="#">[Alignment]</a>		
<a href="#">SPBC19F8.07.1.pep</a>		<a href="#">mcs6</a>	<a href="#">II:3243459-3244301 [Sequence]</a>	Forward	293 <a href="#">[Sequence]</a>	41.0	2.0E-57	41.0 <a href="#">[Alignment]</a>		
<a href="#">SPBC18H10.15.1.pep</a>		<a href="#">cdk11</a>	<a href="#">II:1795450-1796371 [Sequence]</a>	Forward	298 <a href="#">[Sequence]</a>	41.0	5.2E-57	41.0 <a href="#">[Alignment]</a>		
<a href="#">SPBC530.14c.1.pep</a>		<a href="#">dsk1</a>	<a href="#">II:826260-826343 [Sequence]</a>	Reverse	28 <a href="#">[Sequence]</a>	39.0	1.7E-16	39.0 <a href="#">[Alignment]</a>		
<a href="#">SPAC24B11.06c.1.pep</a>		<a href="#">sty1</a>	<a href="#">I:207005-207856 [Sequence]</a>	Reverse	297 <a href="#">[Sequence]</a>	38.0	9.6E-49	38.0 <a href="#">[Alignment]</a>		

Showing 1 to 10 of 63 entries

<< < 1 2 3 4 5 > >>

## HSP distribution on genome: ⓘ



Click on the image above to jump to a chromosome, or click and drag to select a region