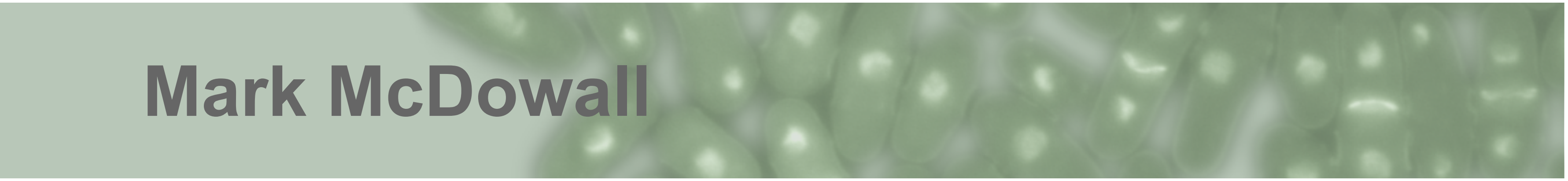
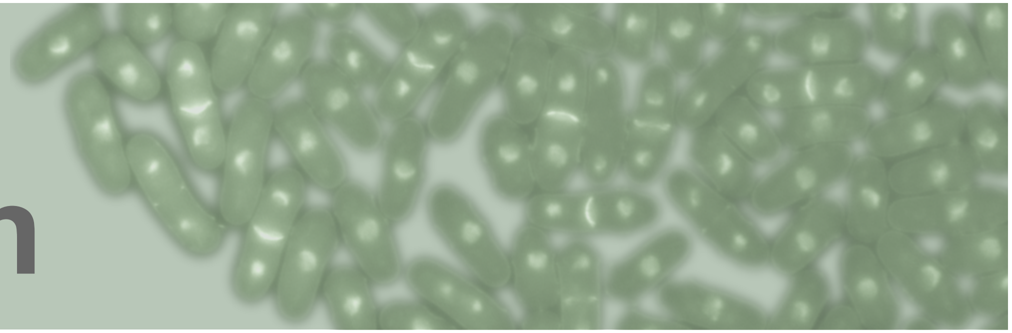
Using the Genome Browser



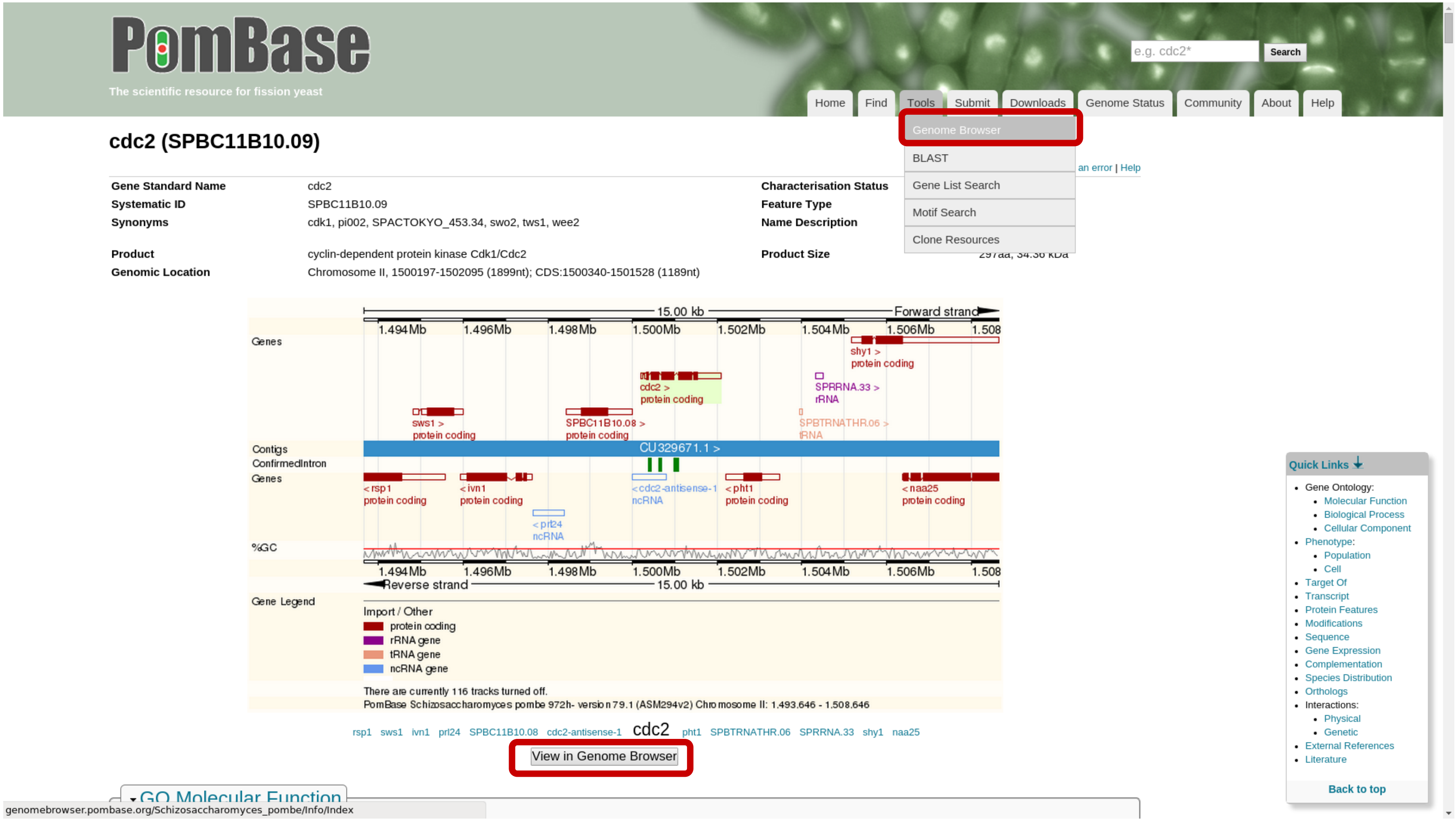
Mark McDowall

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



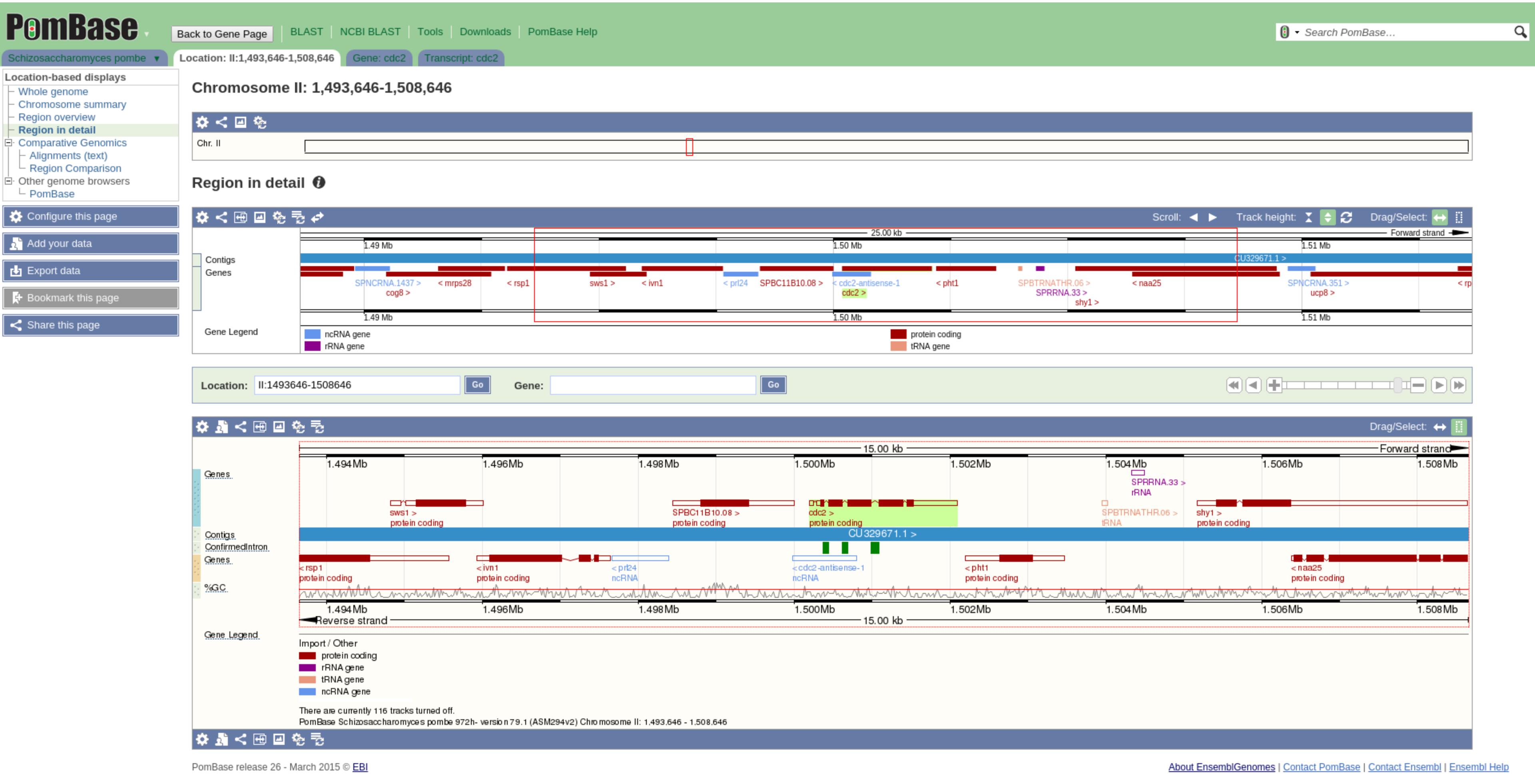
cdc2 (SPBC11B10.09)

Gene Standard Name	cdc2	**Characterisation Status**	
Systematic ID	SPBC11B10.09	**Feature Type**	
Synonyms	cdk1, pi002, SPACTOKYO_453.34, swo2, tws1, wee2	**Name Description**	
Product	cyclin-dependent protein kinase Cdk1/Cdc2	**Product Size**	297aa, 34.36 kDa
Genomic Location	Chromosome II, 1500197-1502095 (1899nt); CDS:1500340-1501528 (1189nt)		

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1.493.646 - 1.508.646

Location tab



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

Region in detail

Location: II:1493646-1508646 Go

Gene: Go

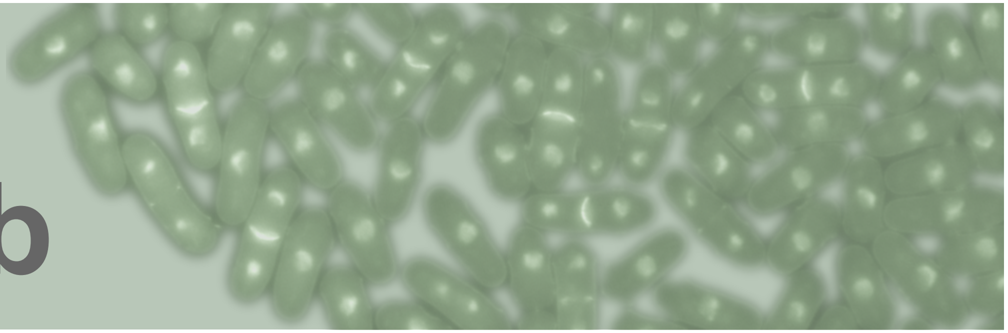
There are currently 116 tracks turned off.

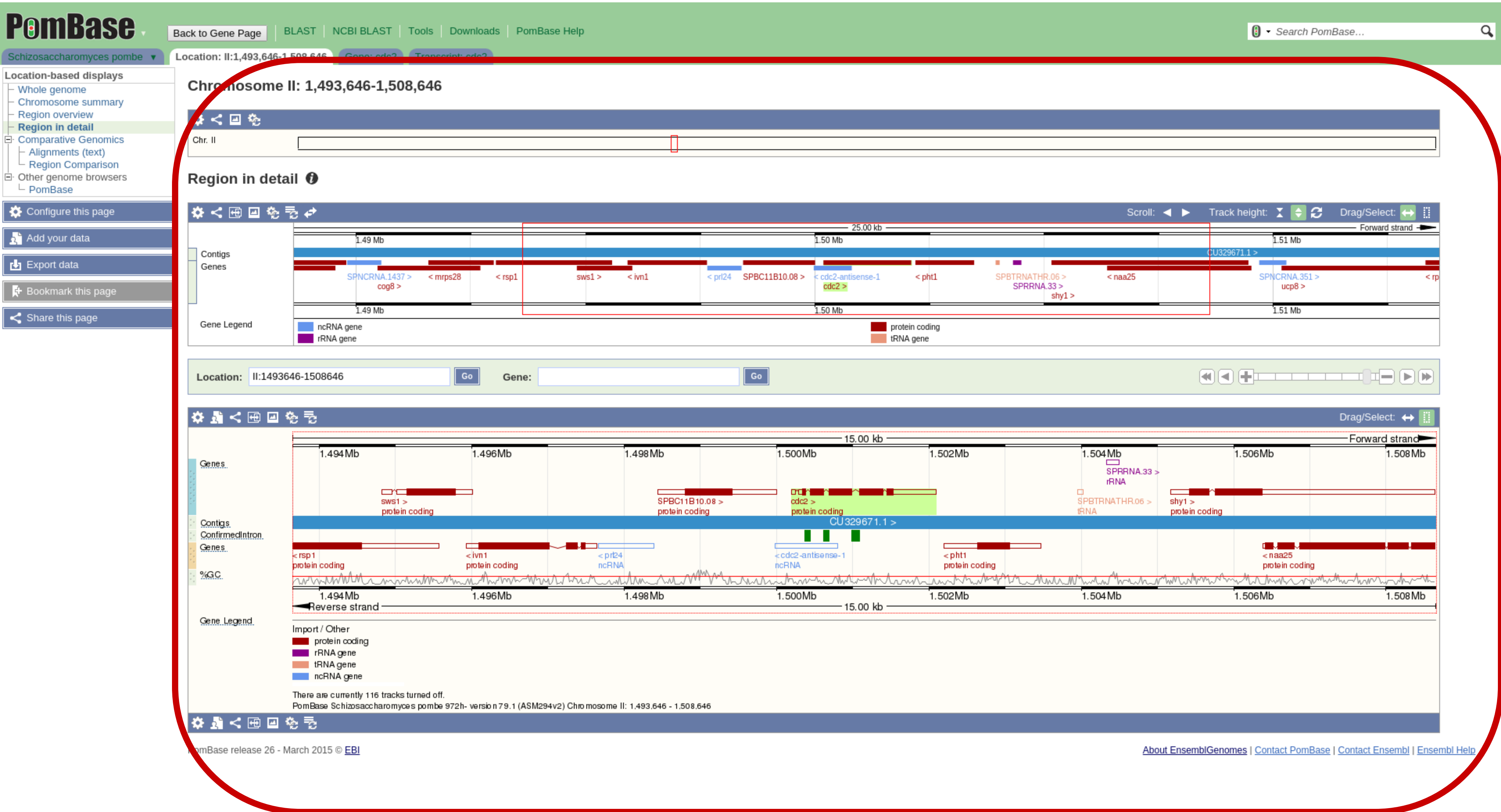
PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

PomBase release 26 - March 2015 © EBI

About EnsemblGenomes | Contact PomBase | Contact Ensembl | Ensembl Help

Location tab





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

Region in detail

Location: II:1493646-1508646

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

PomBase release 26 - March 2015 © EBI

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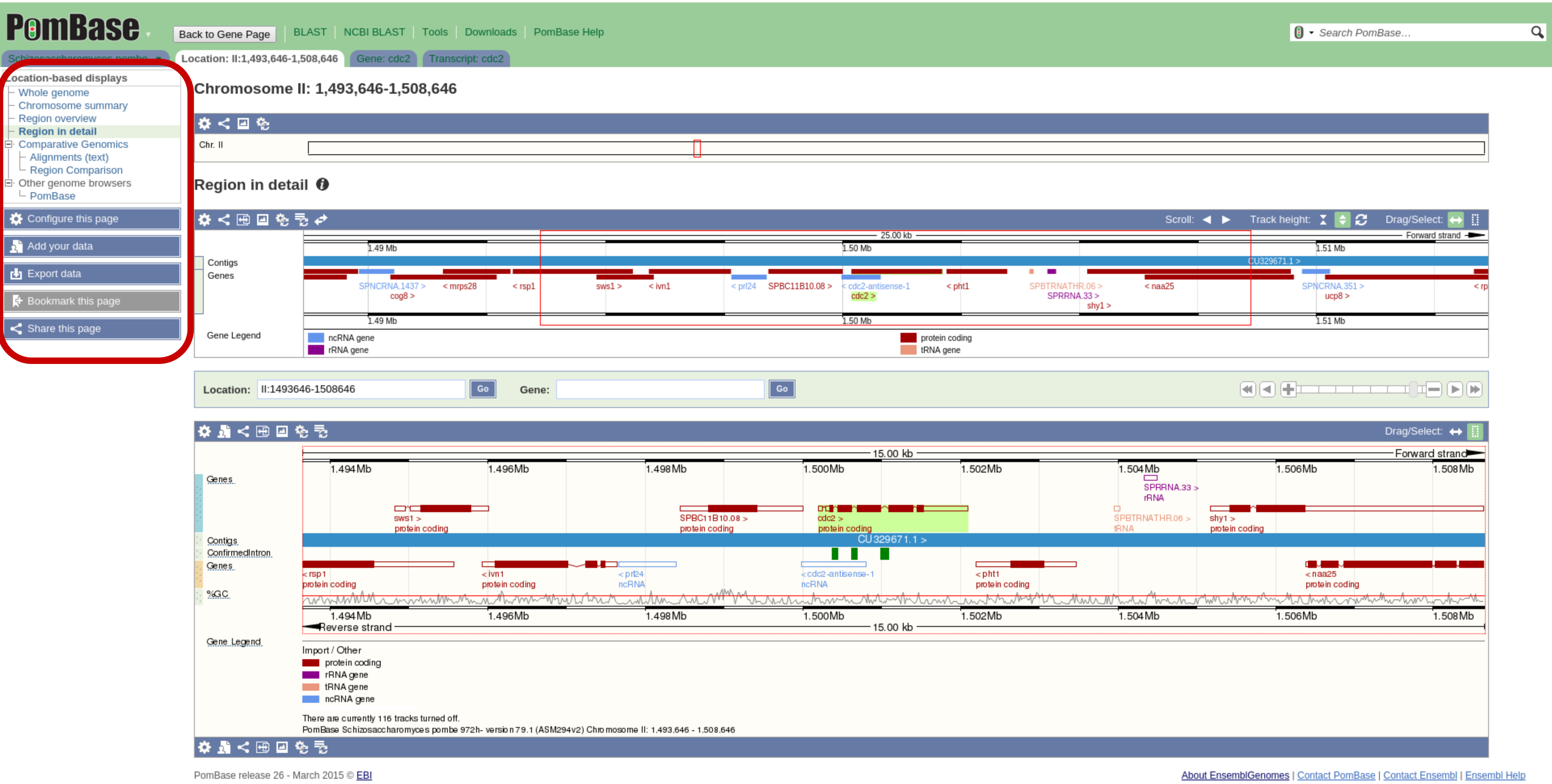
Location tab



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

Region in detail

Location: II:1493646-1508646

Gene:

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

PomBase release 26 - March 2015 © EBI

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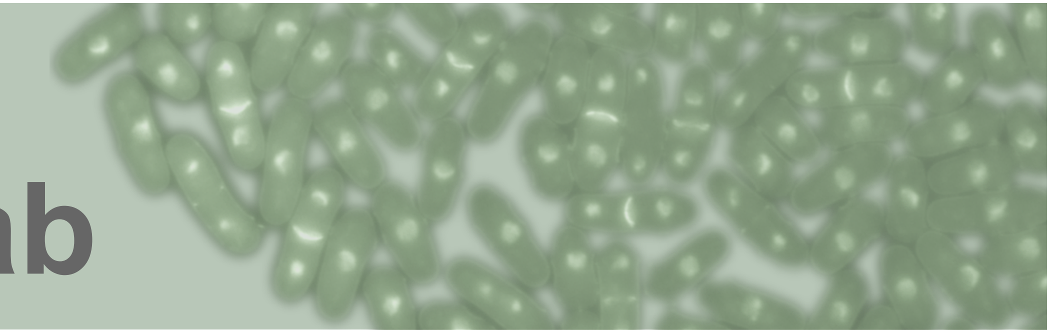
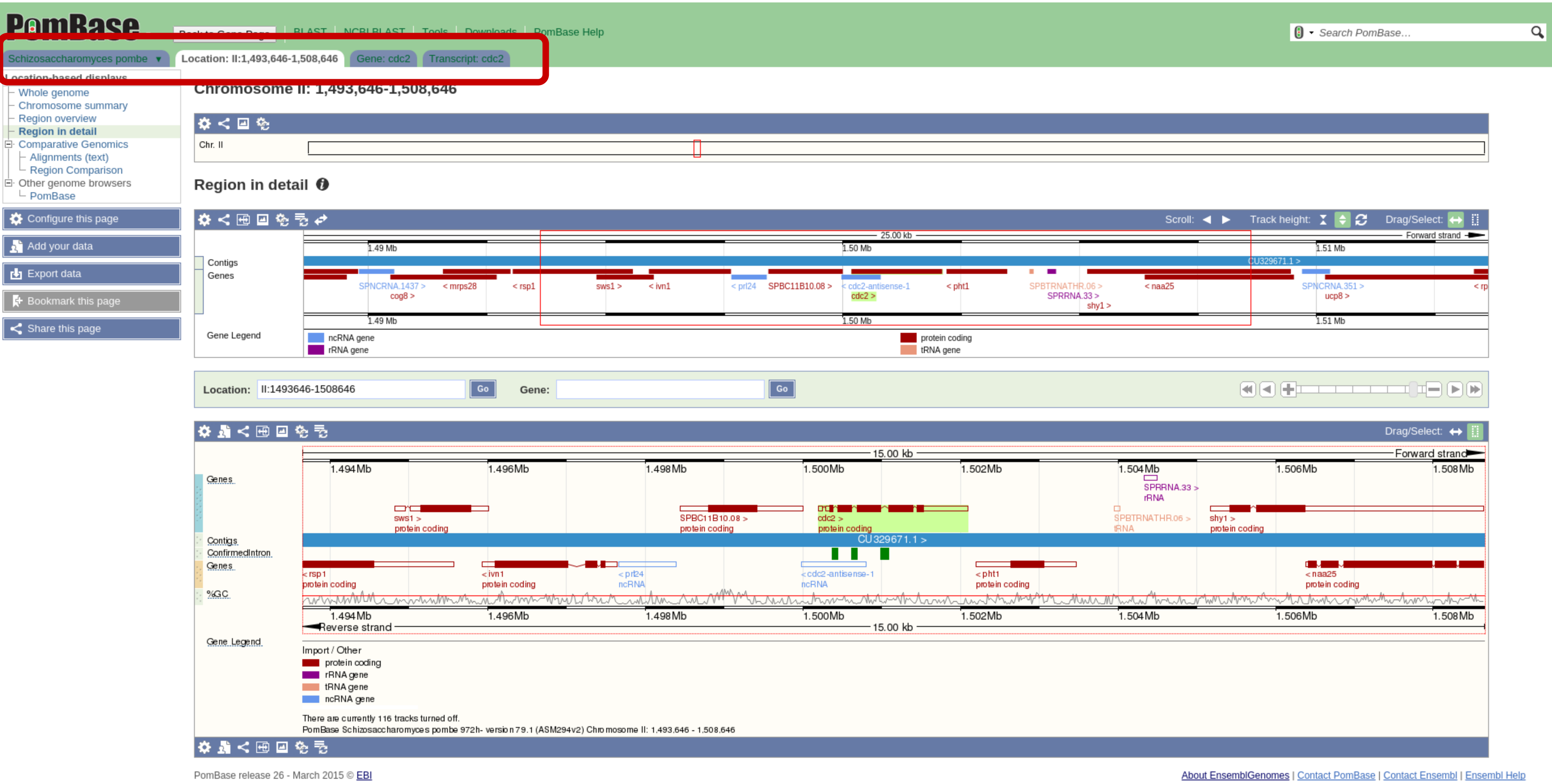
Location tab





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

Region in detail

Location: II:1493646-1508646

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

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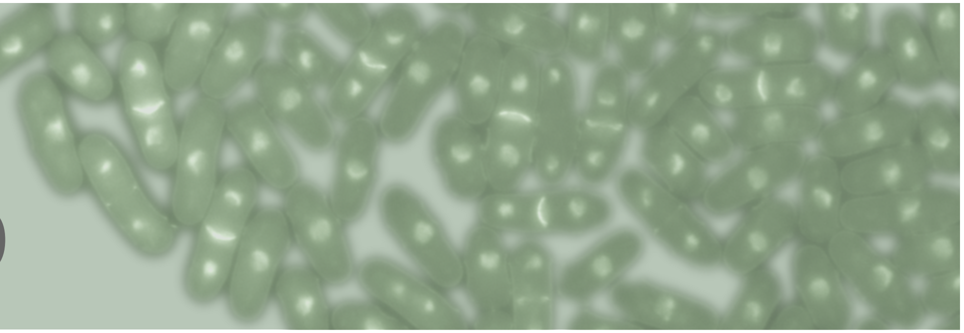
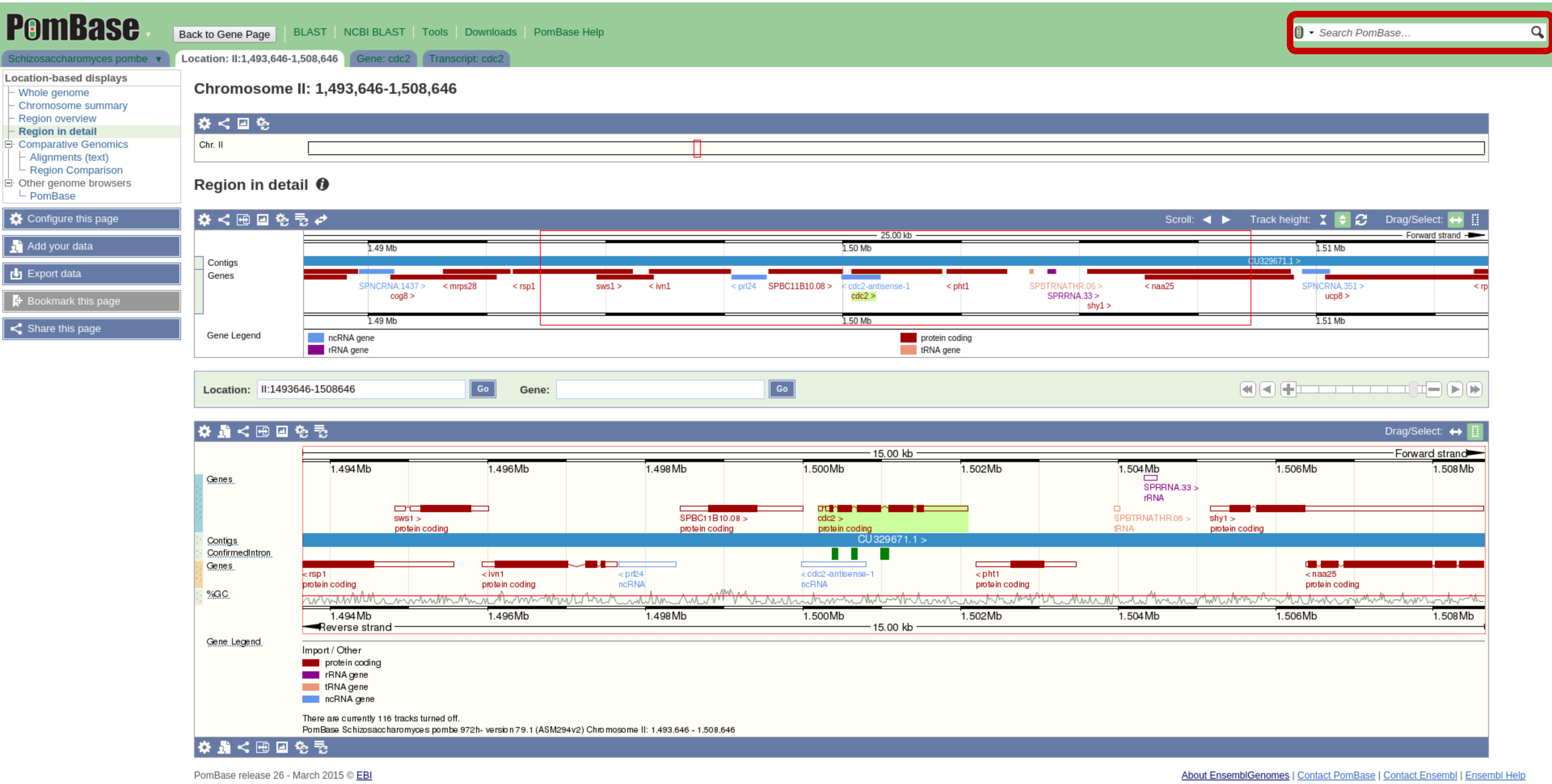
Location tab





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

Region in detail

Location: II:1493646-1508646 Go **Gene:** Go

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

PomBase release 26 - March 2015 © EBI

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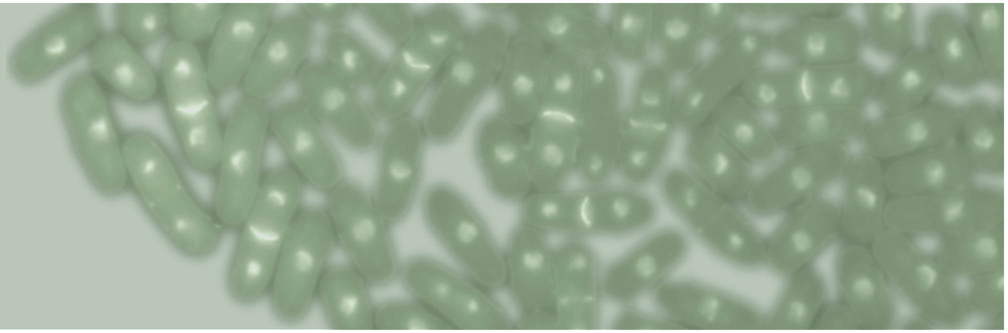
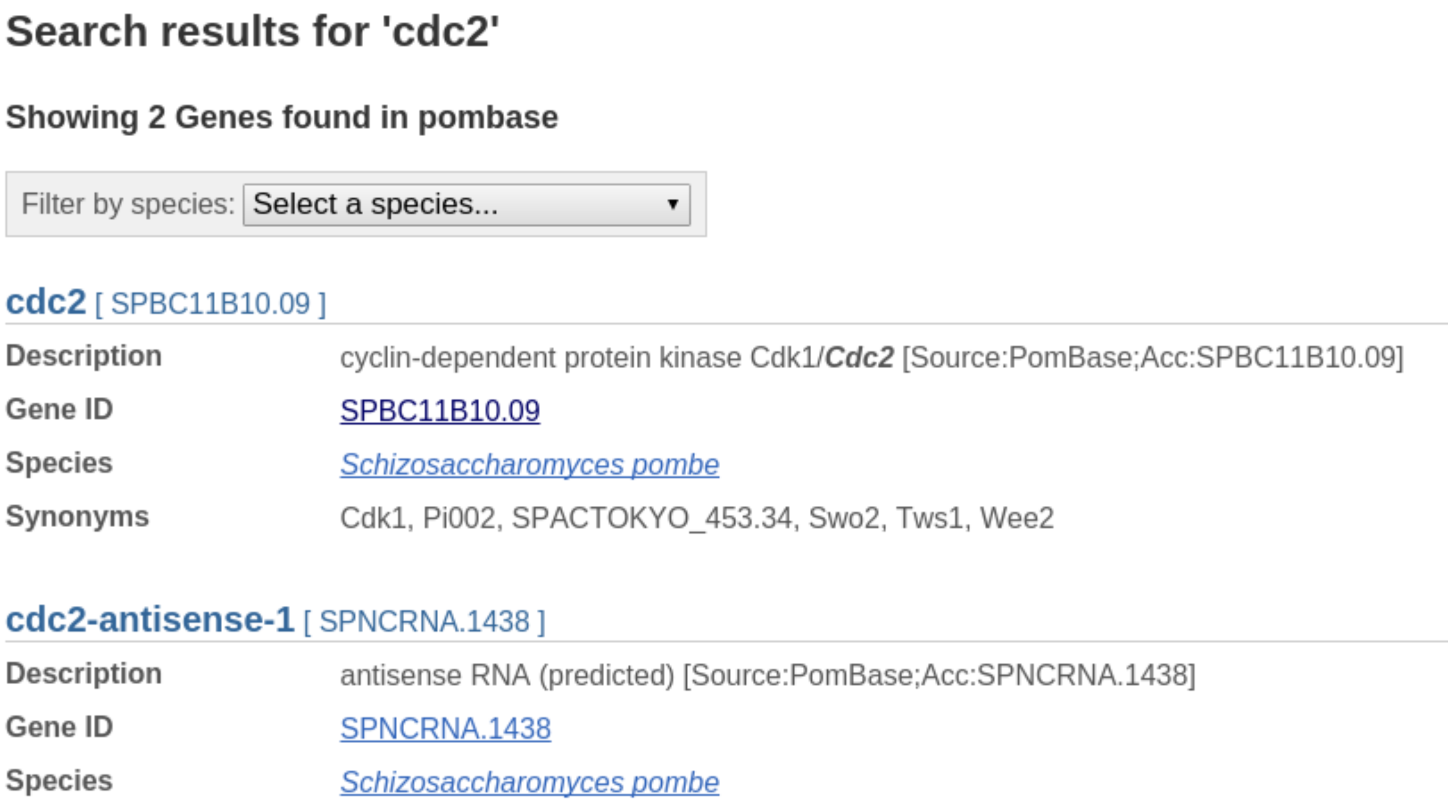
Search box





Search results for 'cdc2'

Showing 2 Genes found in pombase

Filter by species: Select a species...

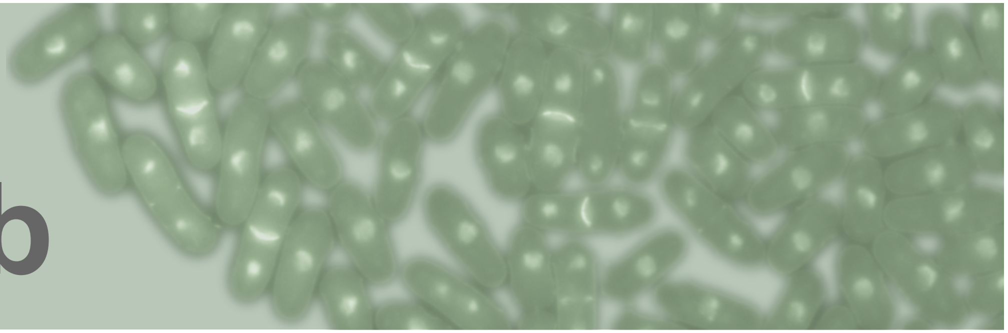
cdc2 [SPBC11B10.09]

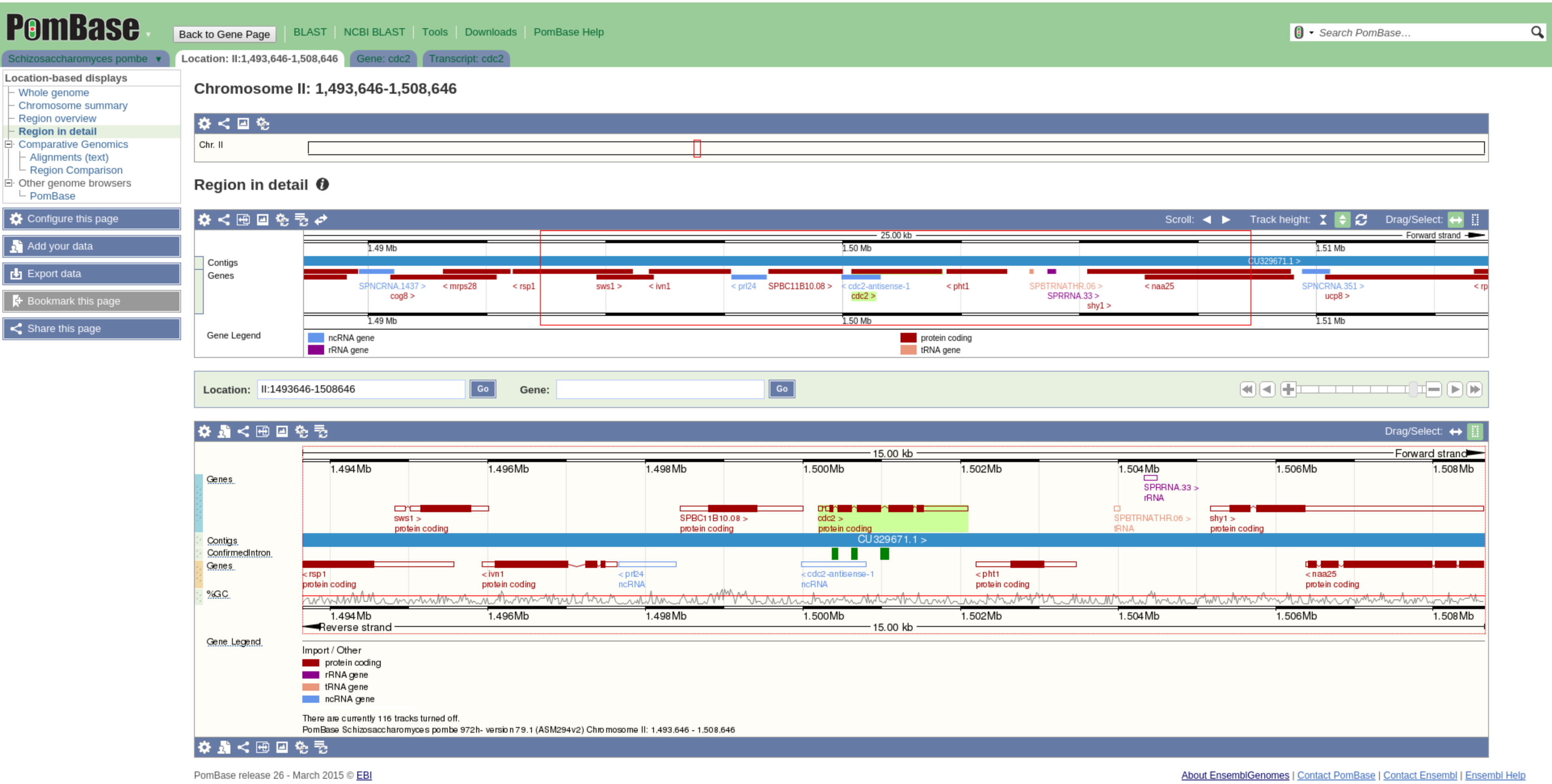
Description	cyclin-dependent protein kinase Cdk1/***Cdc2*** [Source:PomBase;Acc:SPBC11B10.09]
Gene ID	SPBC11B10.09
Species	*Schizosaccharomyces pombe*
Synonyms	Cdk1, Pi002, SPACTOKYO_453.34, Swo2, Tws1, Wee2

cdc2-antisense-1 [SPNCRNA.1438]

Description	antisense RNA (predicted) [Source:PomBase;Acc:SPNCRNA.1438]
Gene ID	SPNCRNA.1438
Species	*Schizosaccharomyces pombe*

Location tab





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

Region in detail

Location: II:1493646-1508646

Gene:

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

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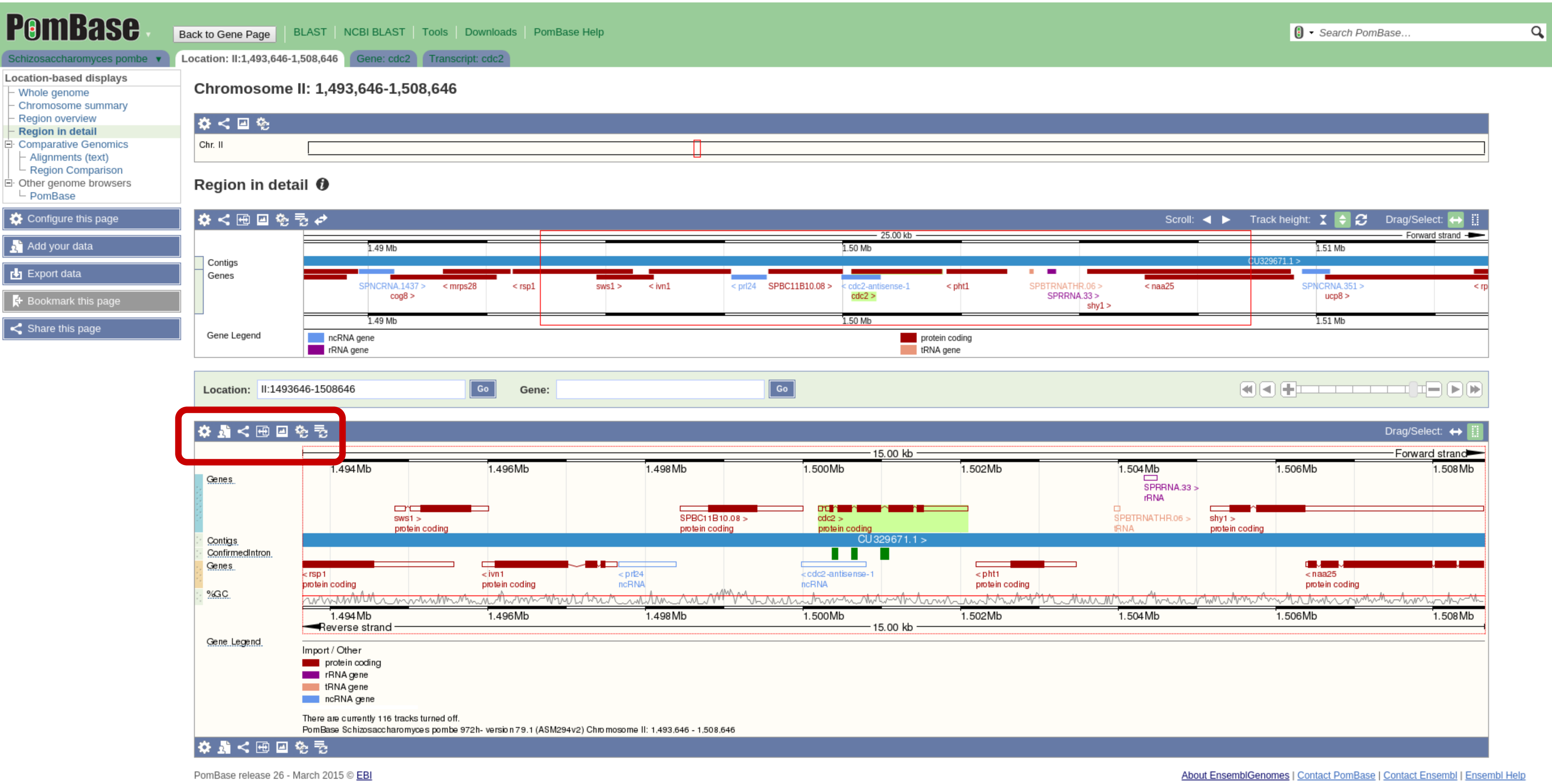
Location tab



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

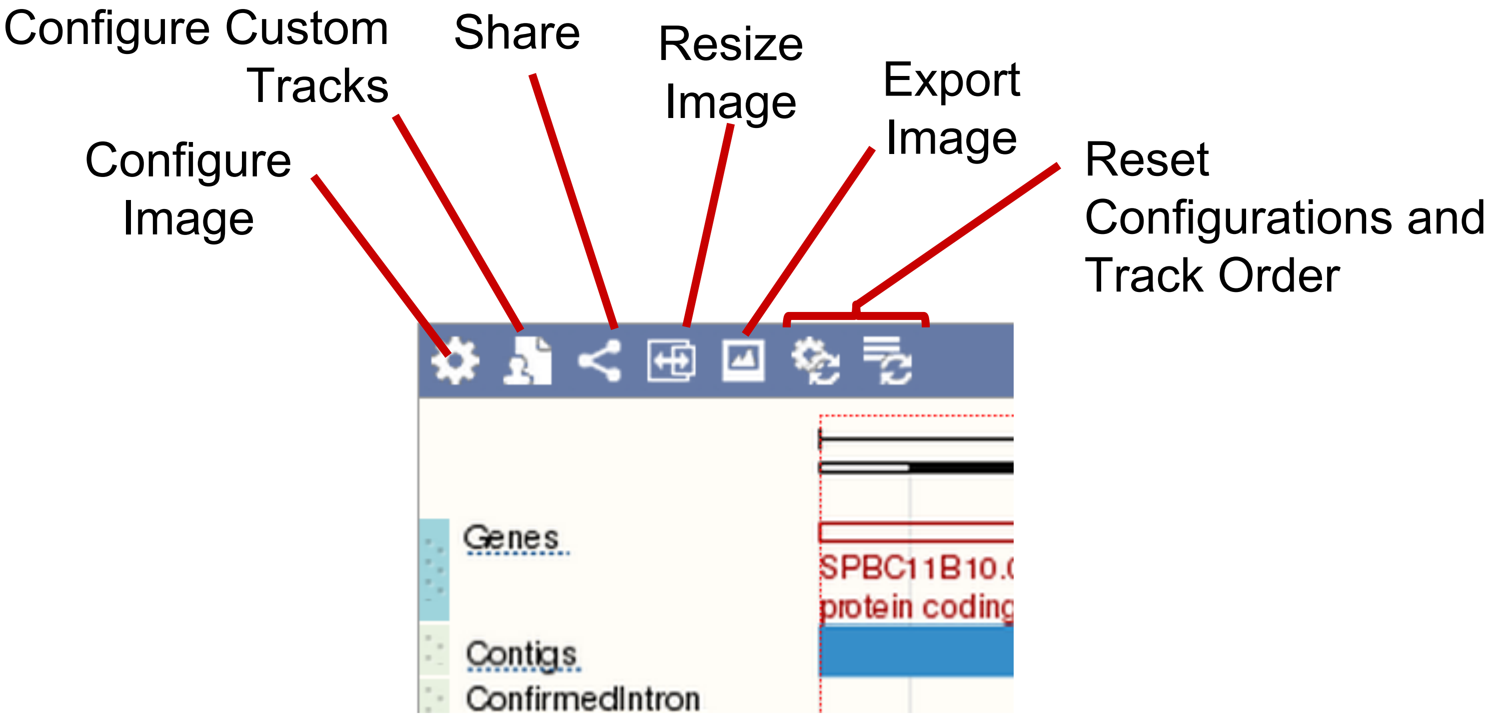
Region in detail

There are currently 116 tracks turned off.

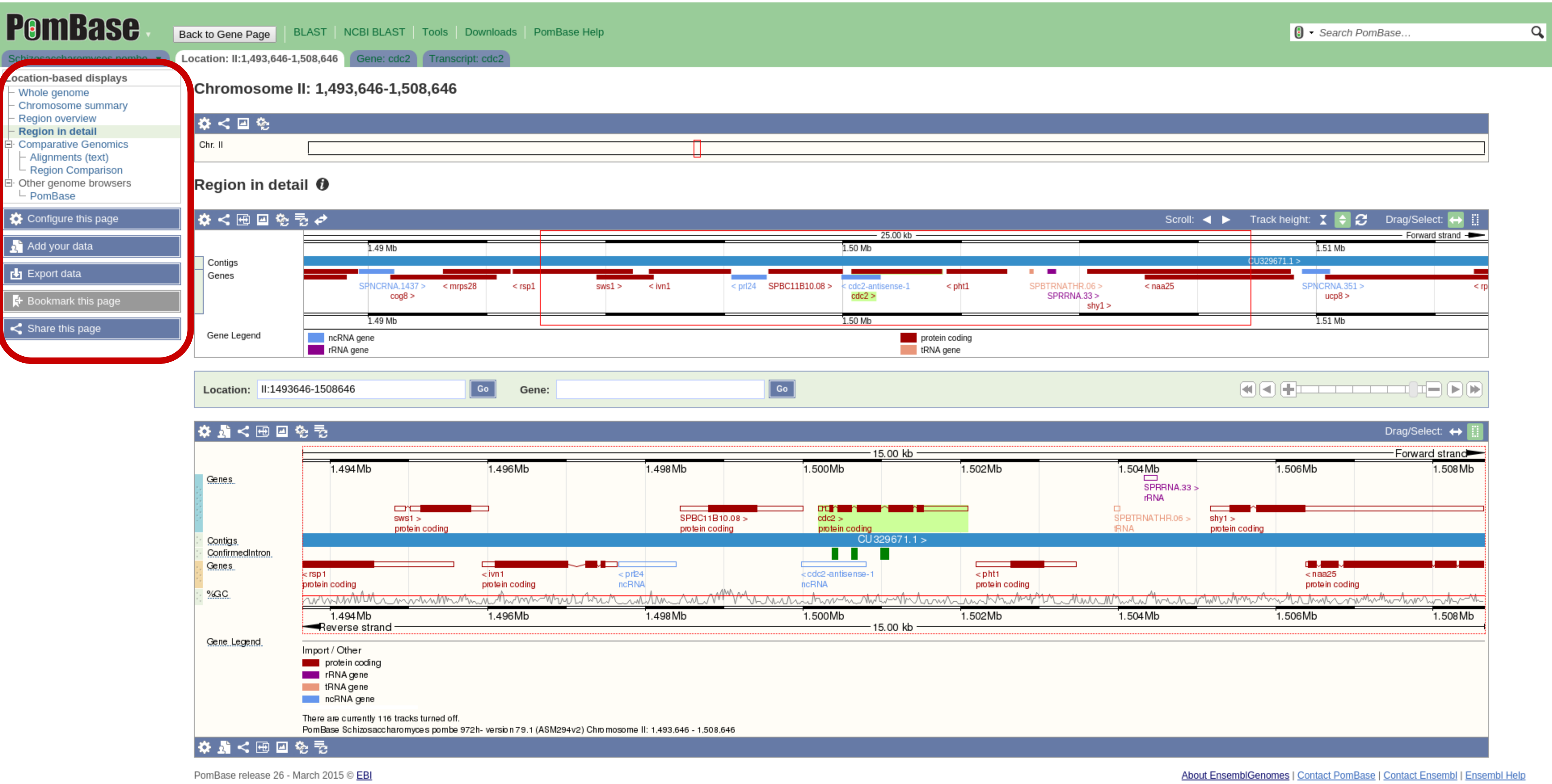
PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

PomBase release 26 - March 2015 © EBI

Image buttons



Displaying tracks



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

Region in detail

Location: II:1493646-1508646

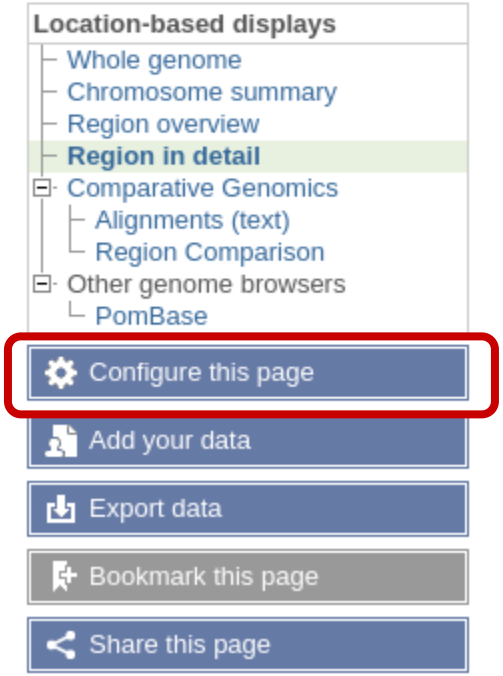
Gene:

There are currently 116 tracks turned off.

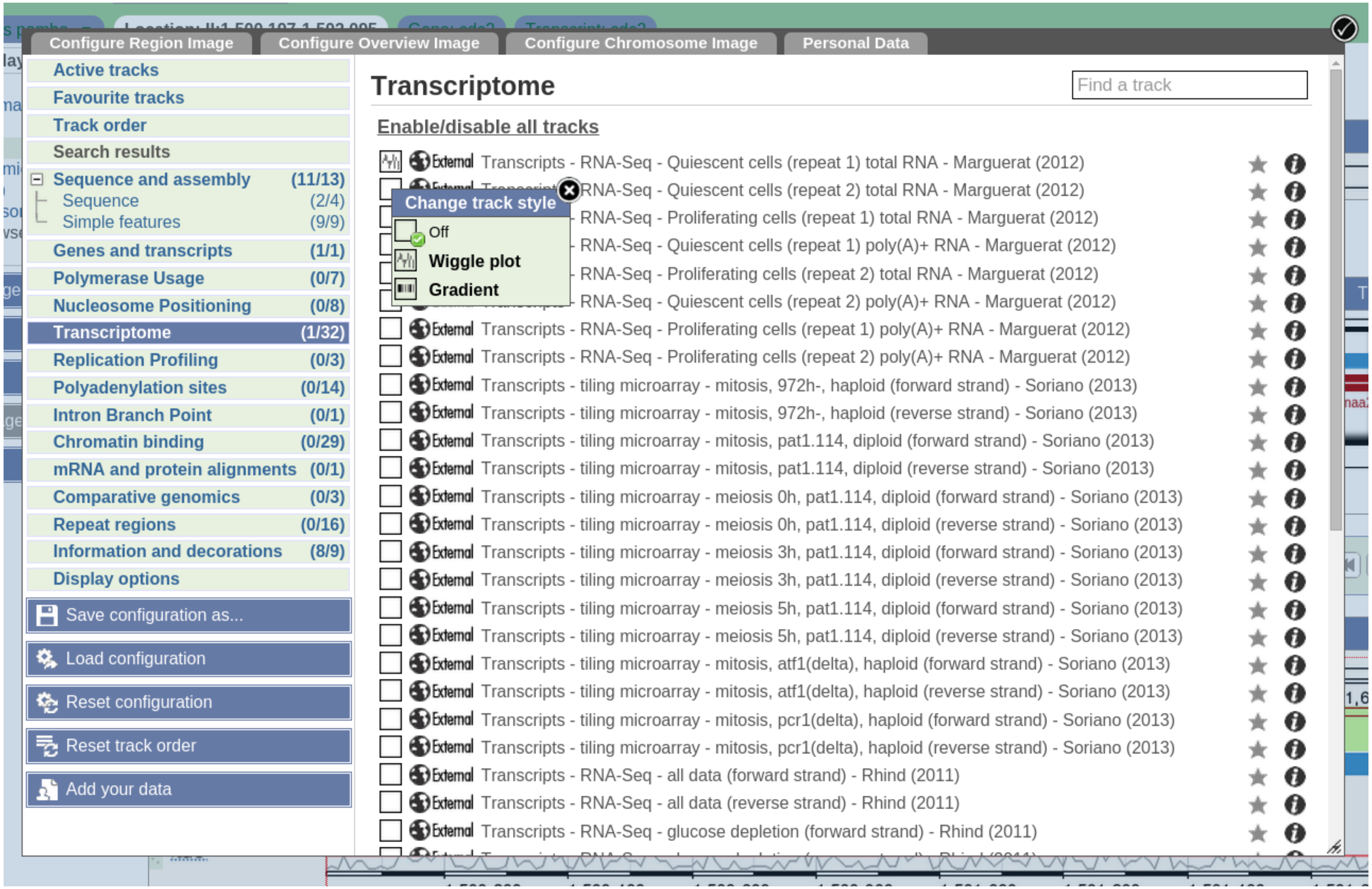
PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

PomBase release 26 - March 2015 © EBI

Add your own data



Adding tracks



Configure Region Image | Configure Overview Image | Configure Chromosome Image | Personal Data

- 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

Transcriptome

Find a track

Enable/disable all tracks

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

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

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

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

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

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

Change track style

- ☑ Off
- **Wiggle plot**
- **Gradient**

☐ 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)

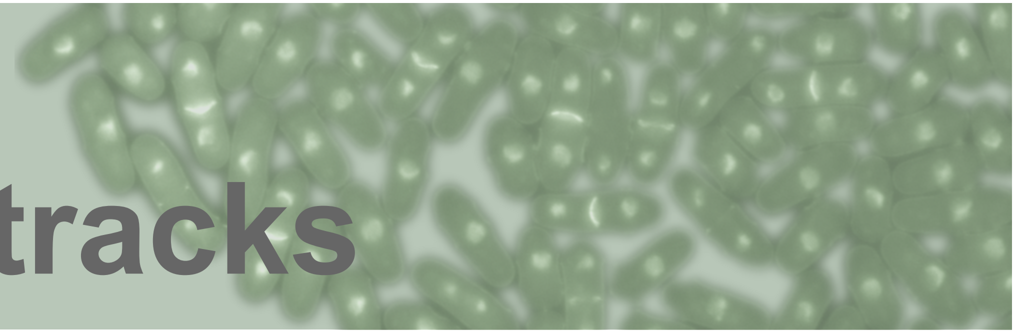
☐ External Transcripts - tiling microarray - mitosis, pcr1(delta), haploid (reverse strand) - Soriano (2013)

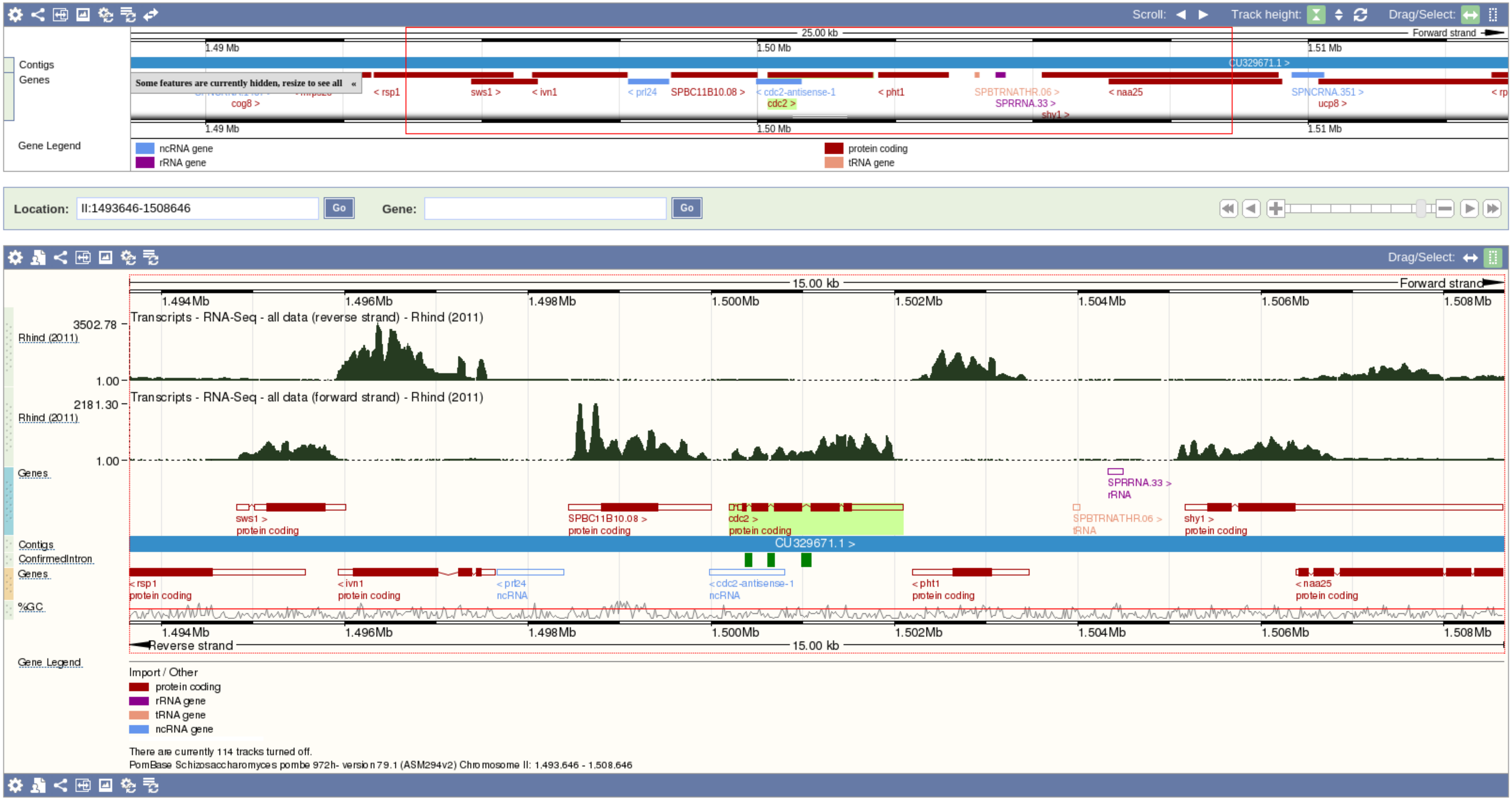
☐ External Transcripts - RNA-Seq - all data (forward strand) - Rhind (2011)

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

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

Displaying tracks





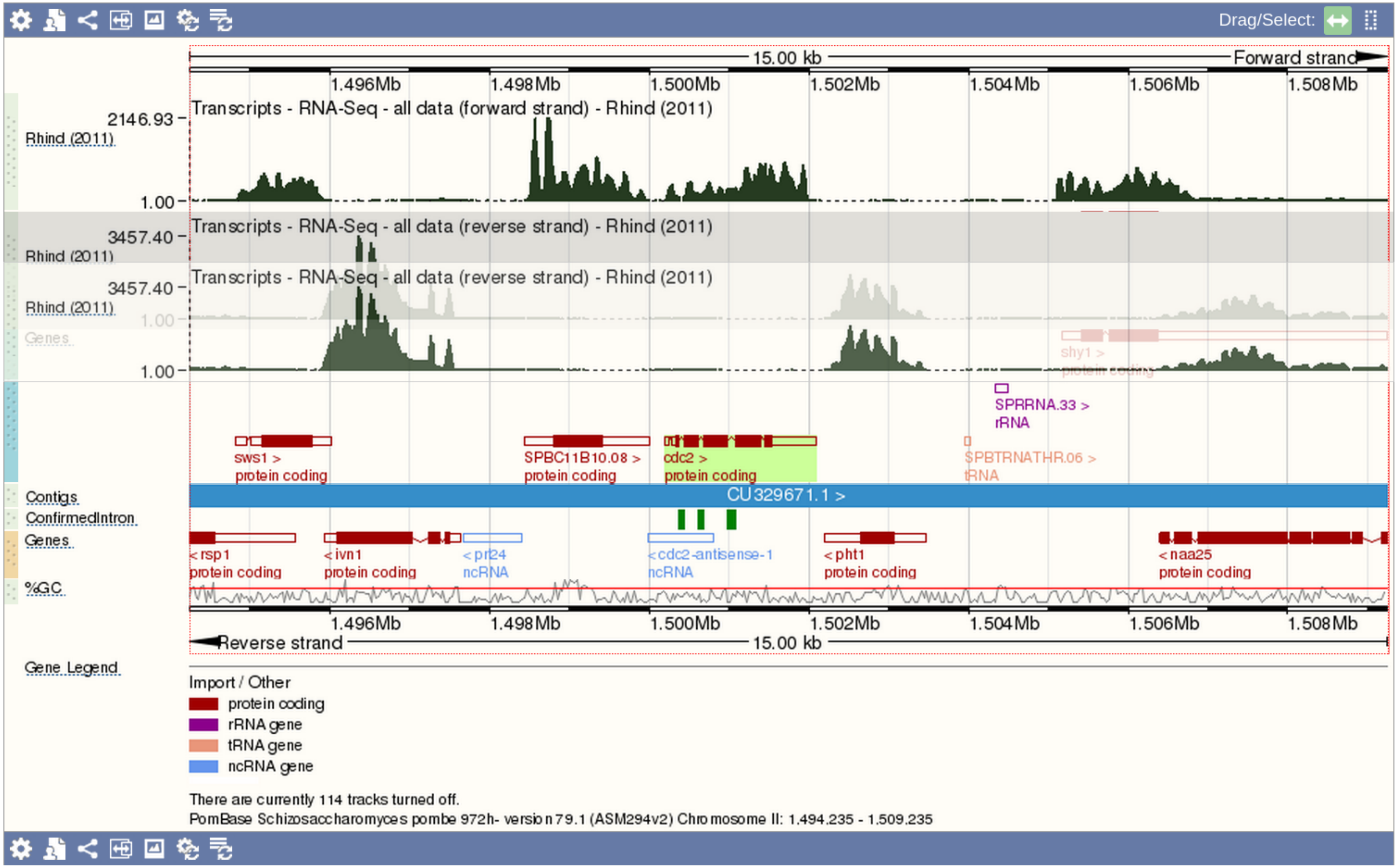
Some features are currently hidden, resize to see all

Location: II:1493646-1508646 Go **Gene:** Go

There are currently 114 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1.493.646 - 1.508.646

Dragging tracks



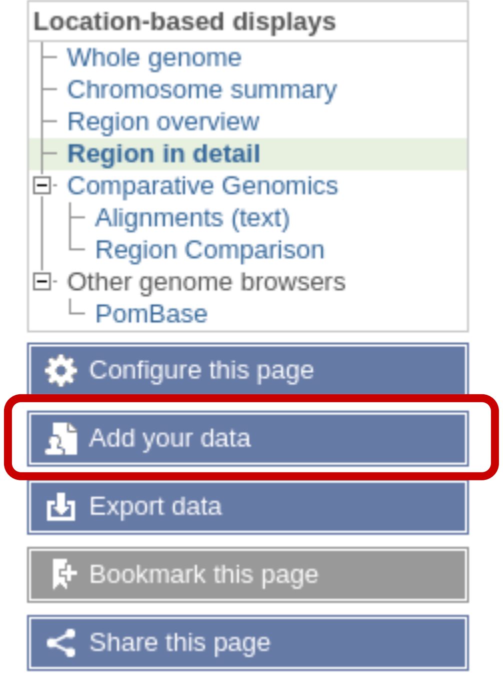
Import / Other

- 🟥 protein coding
- 🟪 rRNA gene
- 🟧 tRNA gene
- 🟦 ncRNA gene

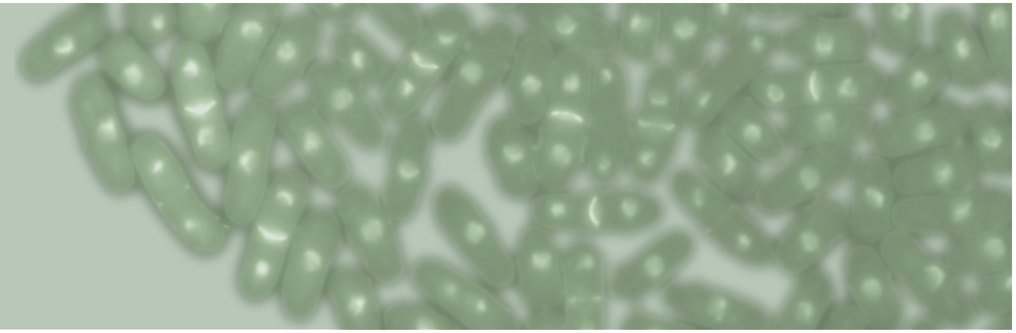
There are currently 114 tracks turned off.

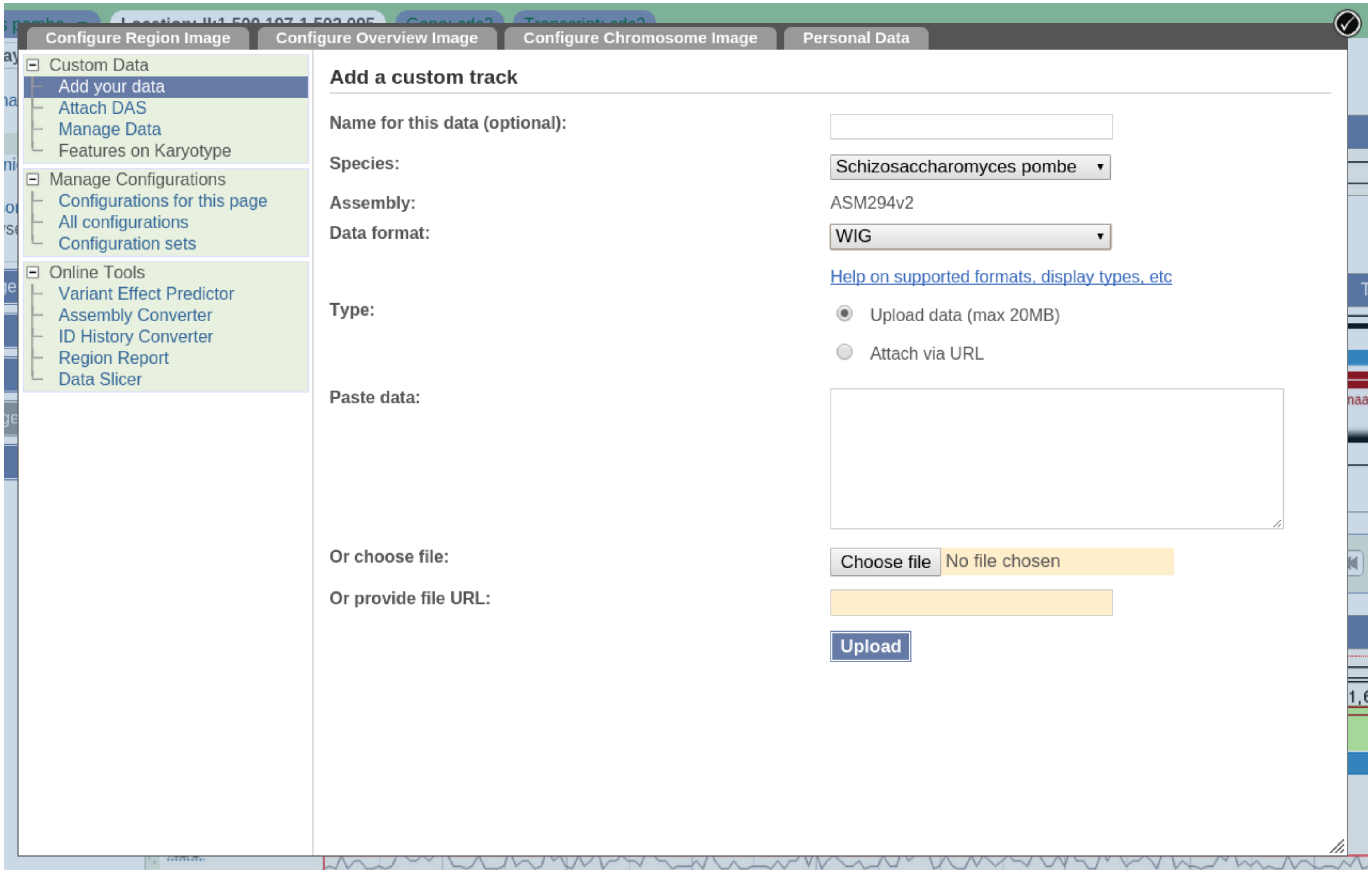
PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,494,235 - 1,509,235

Add your own data



View your own data





Add a custom track

Name for this data (optional):

Species: Schizosaccharomyces pombe

Assembly: ASM294v2

Data format: WIG

Type:
● Upload data (max 20MB)
○ Attach via URL

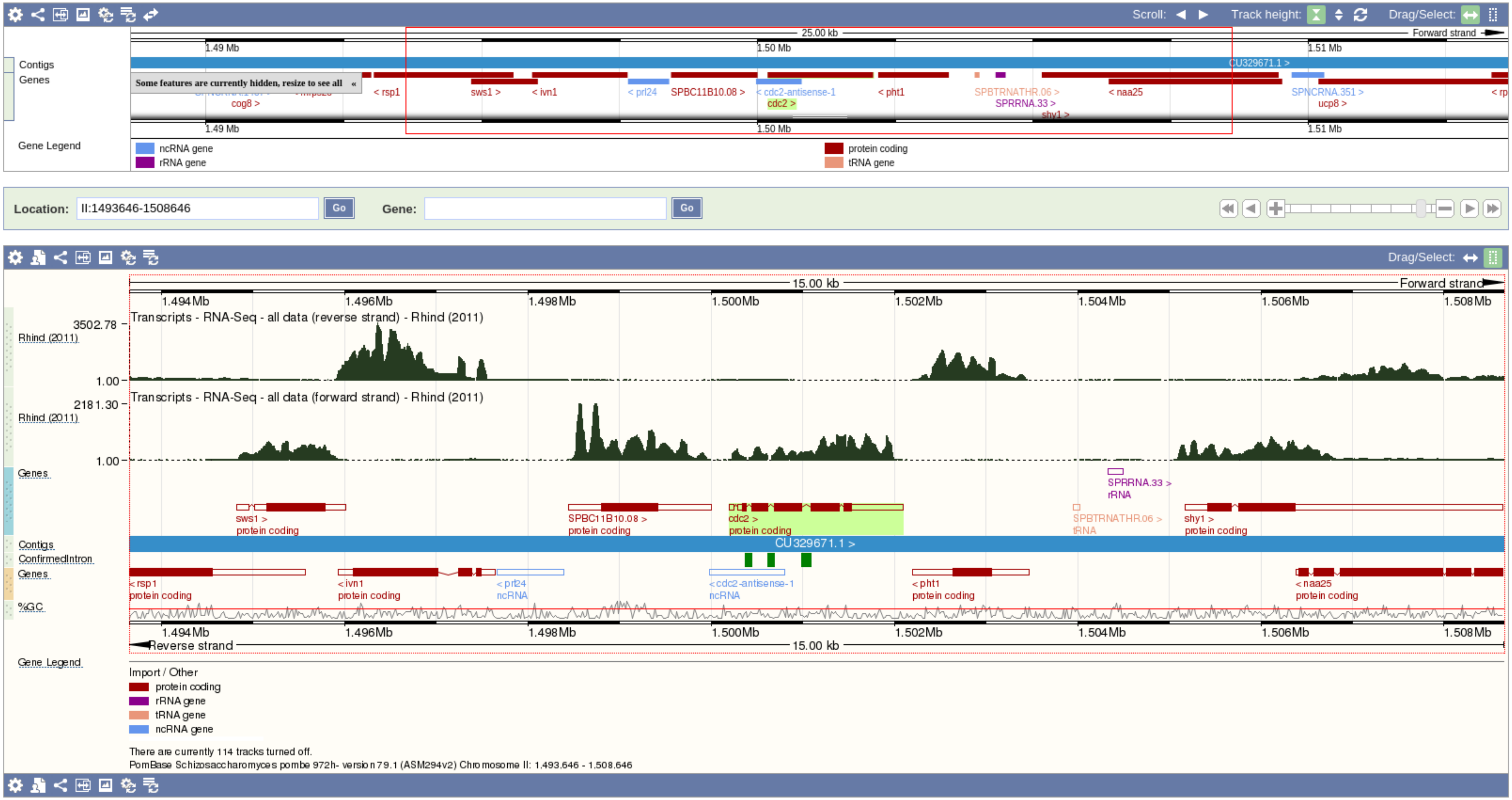
Paste data:

Or choose file: No file chosen

Or provide file URL:

Data Formats:
- bam
- bedGraph
- (big)Bed
- GFF
- TrackHub
- VCF
- (big)Wig

Displaying tracks



Location: II:1493646-1508646 Go

Gene: Go

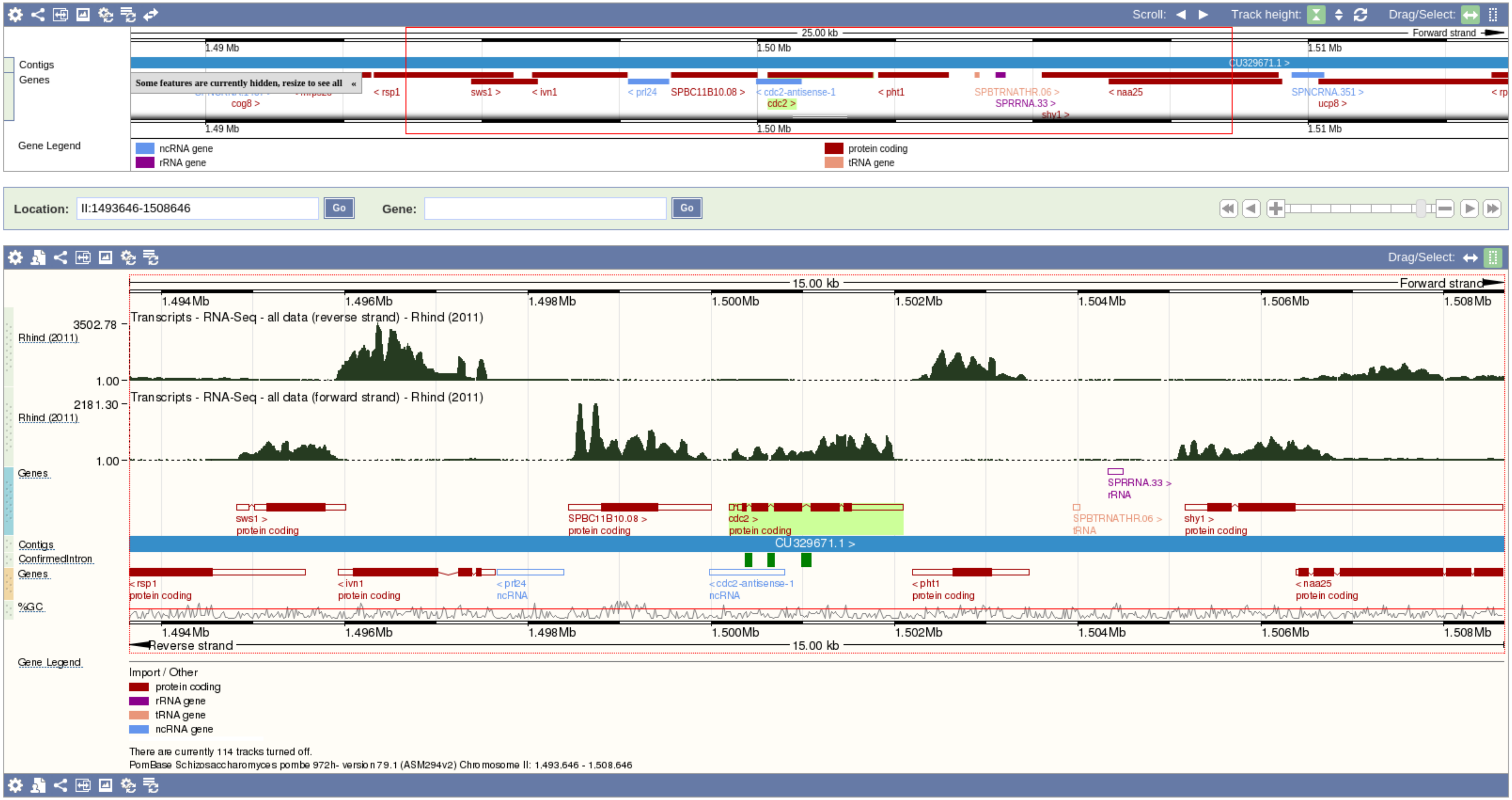
There are currently 114 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

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



Location: II:1493646-1508646

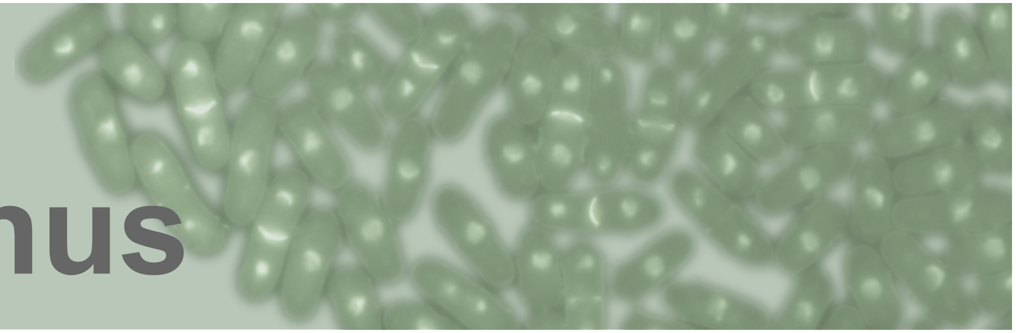
Gene:

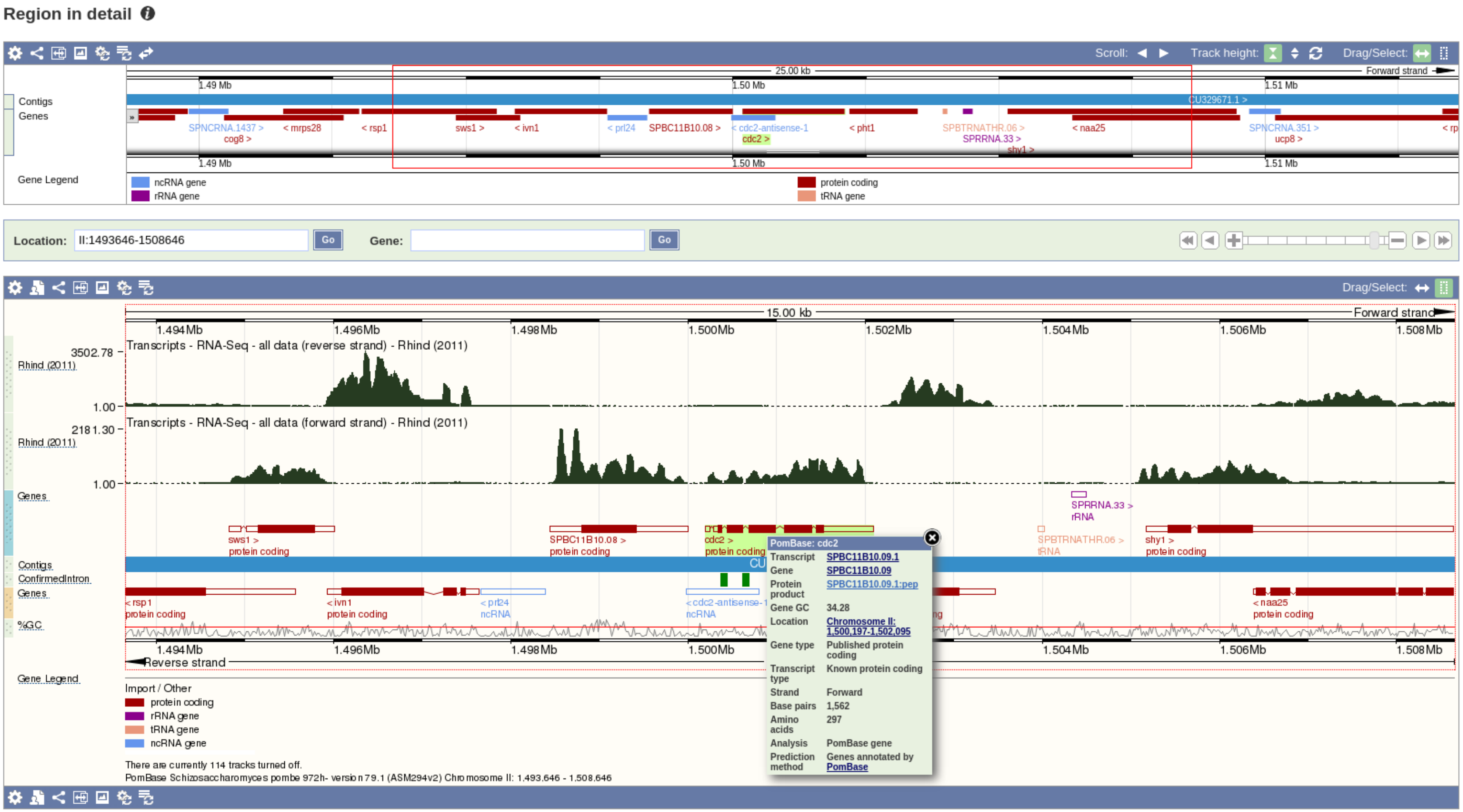
Some features are currently hidden, resize to see all

There are currently 114 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1.493.646 - 1.508.646

Pop-up menus





Location: II:1493646-1508646

Gene:

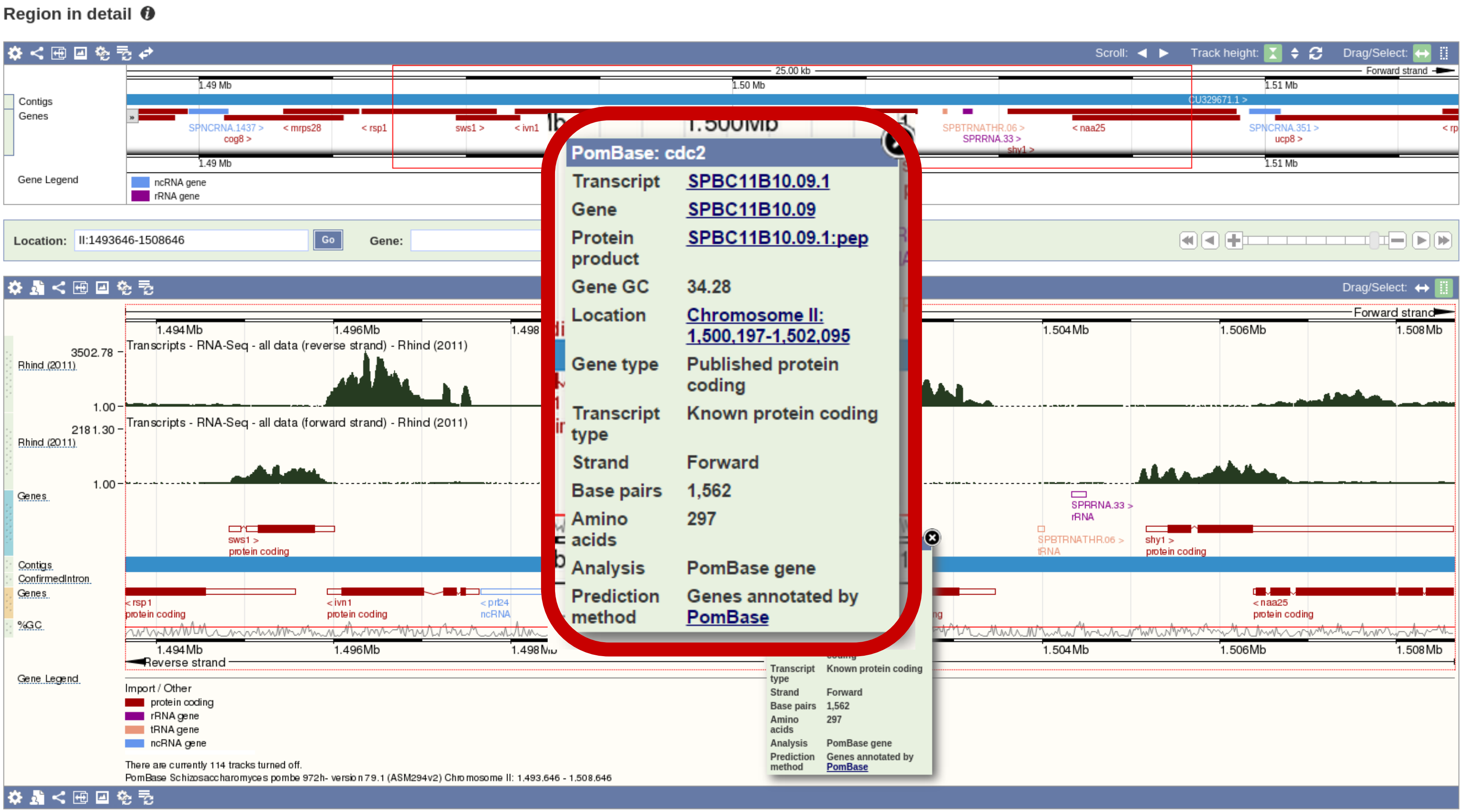
PomBase: cdc2

Transcript	SPBC11B10.09.1
Gene	SPBC11B10.09
Protein product	SPBC11B10.09.1:pep
Gene GC	34.28
Location	Chromosome II: 1,500,197-1,502,095
Gene type	Published protein coding
Transcript type	Known protein coding
Strand	Forward
Base pairs	1,562
Amino acids	297
Analysis	PomBase gene
Prediction method	Genes annotated by PomBase

There are currently 114 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

Pop-up menus



PomBase: cdc2

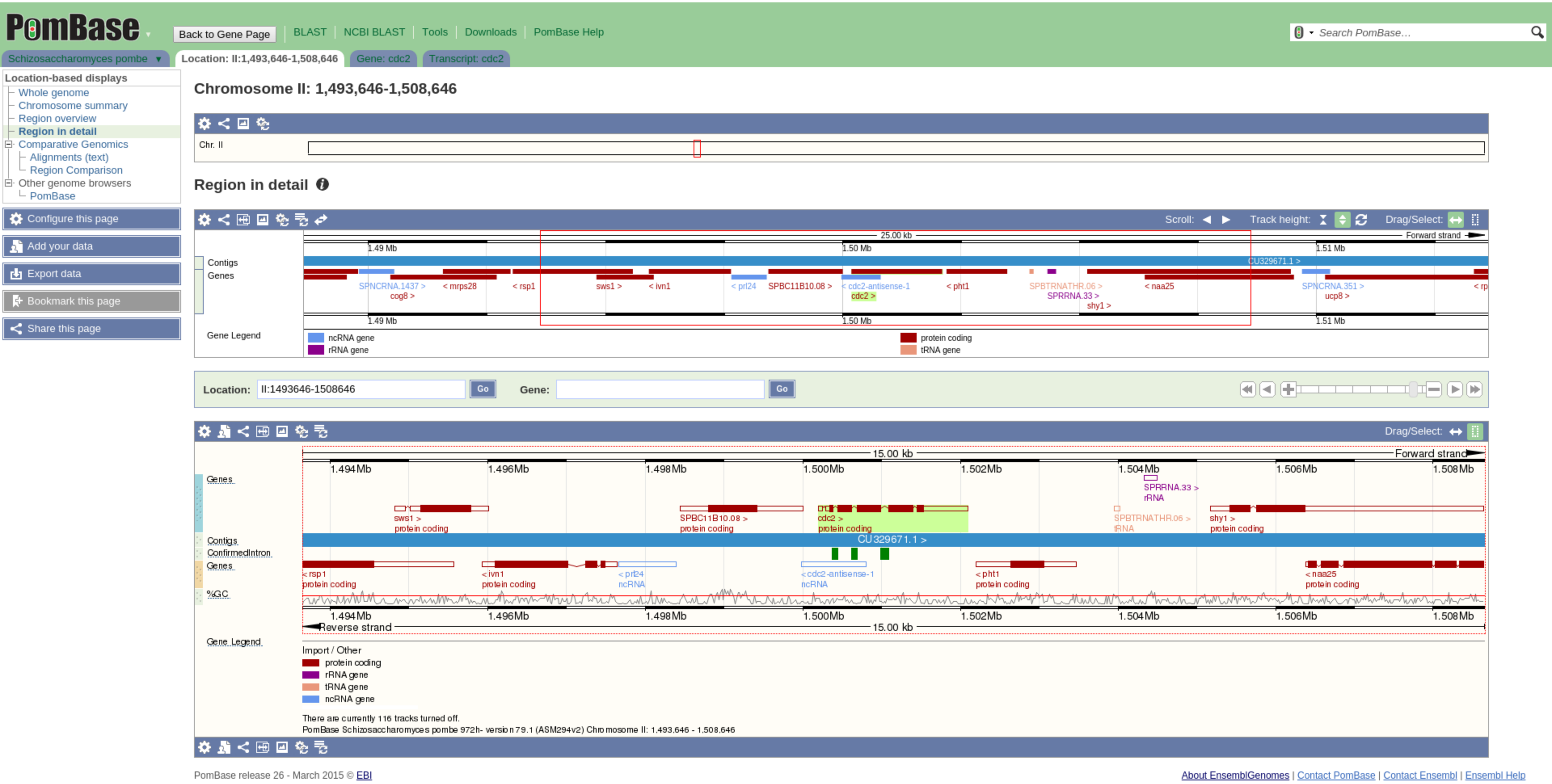
Transcript	SPBC11B10.09.1
Gene	SPBC11B10.09
Protein product	SPBC11B10.09.1:pep
Gene GC	34.28
Location	Chromosome II: 1,500,197-1,502,095
Gene type	Published protein coding
Transcript type	Known protein coding
Strand	Forward
Base pairs	1,562
Amino acids	297
Analysis	PomBase gene
Prediction method	Genes annotated by PomBase

Transcript type	Known protein coding
Strand	Forward
Base pairs	1,562
Amino acids	297
Analysis	PomBase gene
Prediction method	Genes annotated by PomBase

There are currently 114 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

Exporting data



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

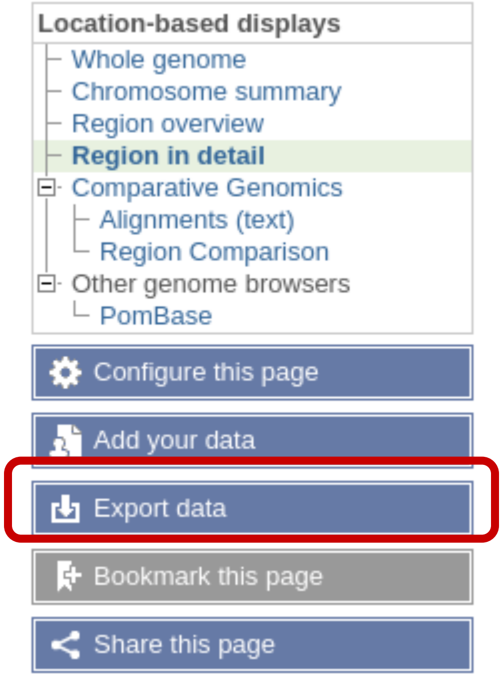
Location: II:1493646-1508646

There are currently 116 tracks turned off.

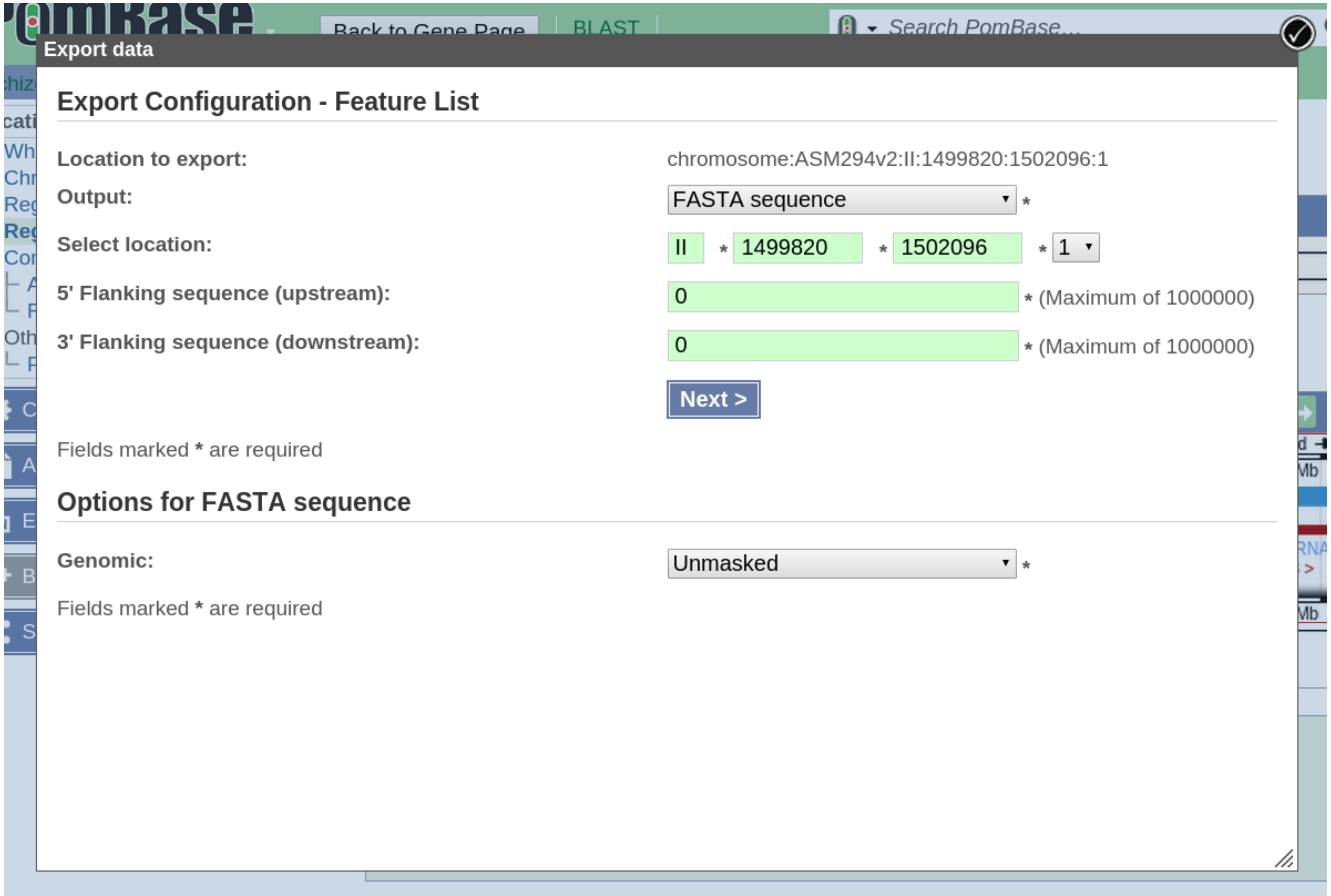
PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

PomBase release 26 - March 2015 © EBI

Exporting data



Exporting data



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)

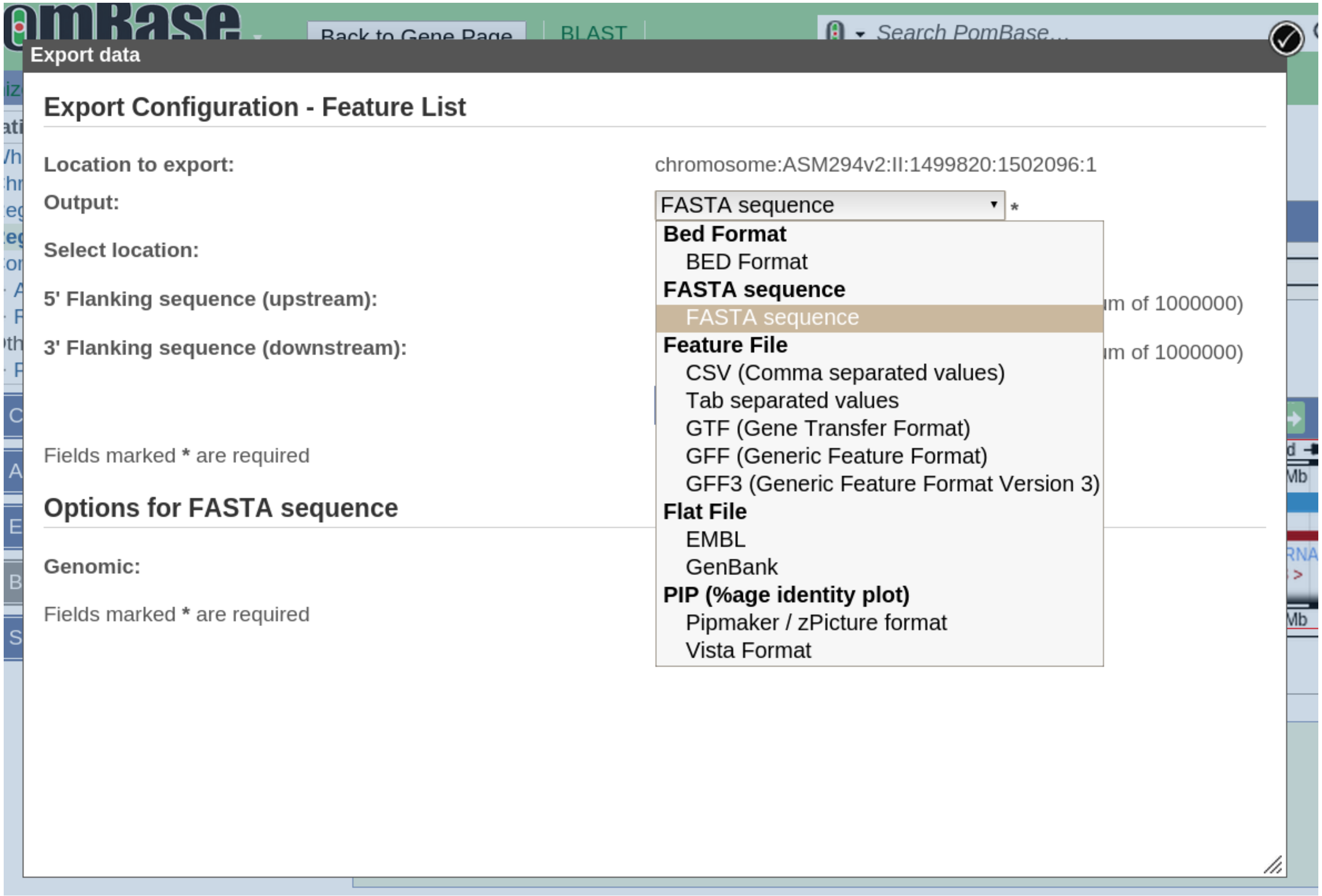
Fields marked * are required

Options for FASTA sequence

Genomic: Unmasked *

Fields marked * are required

Exporting data



Export data

Export Configuration - Feature List

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

Output: FASTA sequence *

Select location:

5' Flanking sequence (upstream): um of 1000000)

3' Flanking sequence (downstream): um of 1000000)

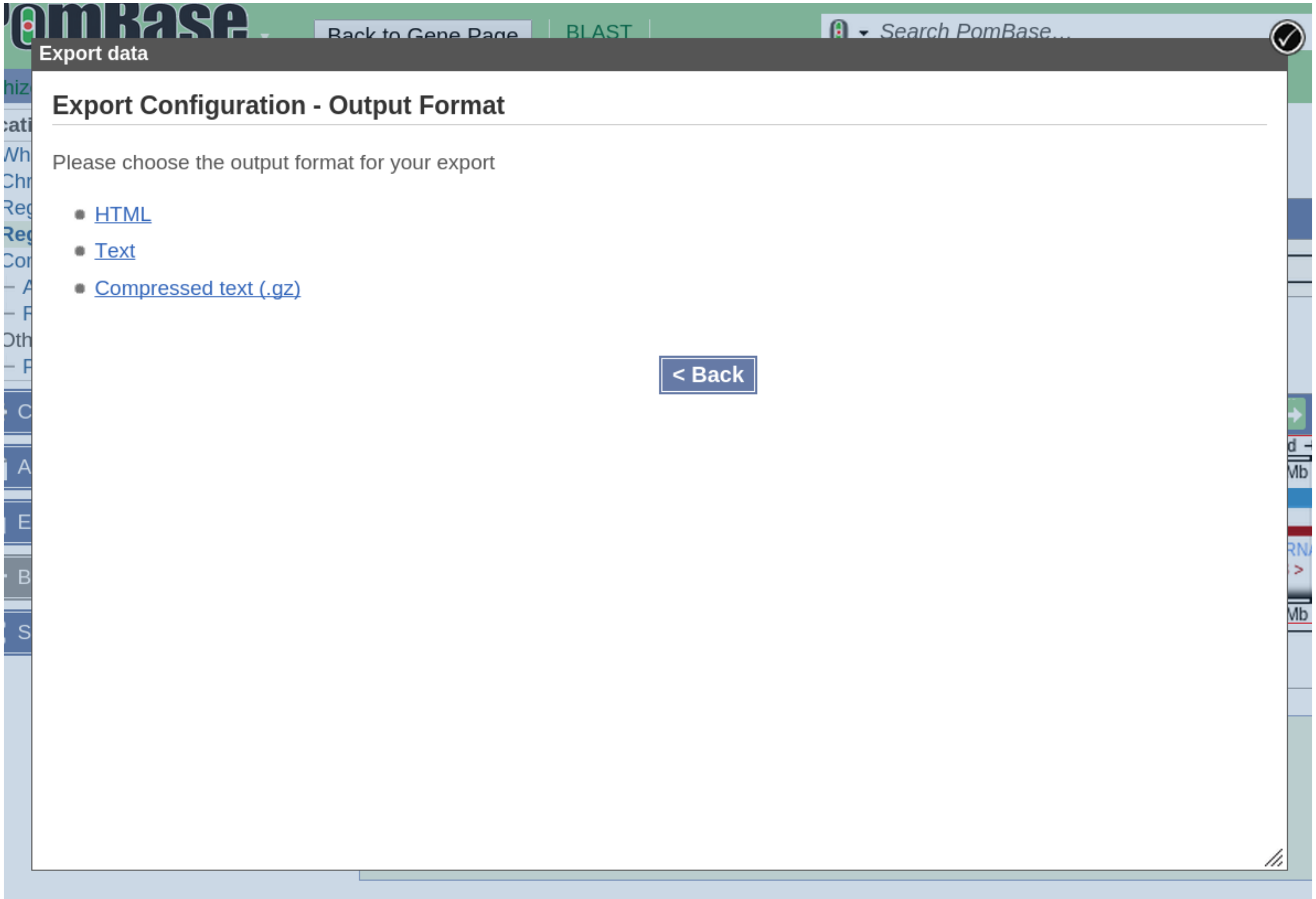
Fields marked * are required

Options for FASTA sequence

Genomic:

Fields marked * are required

Exporting data

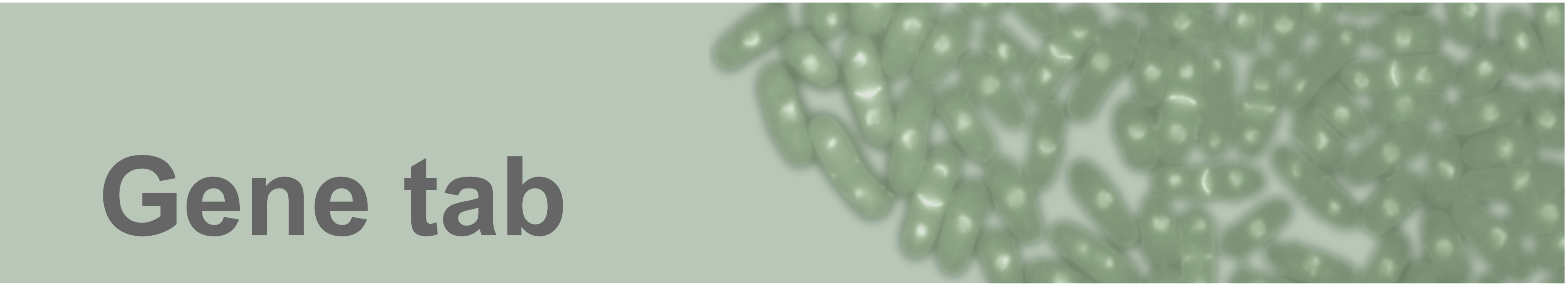


Export data

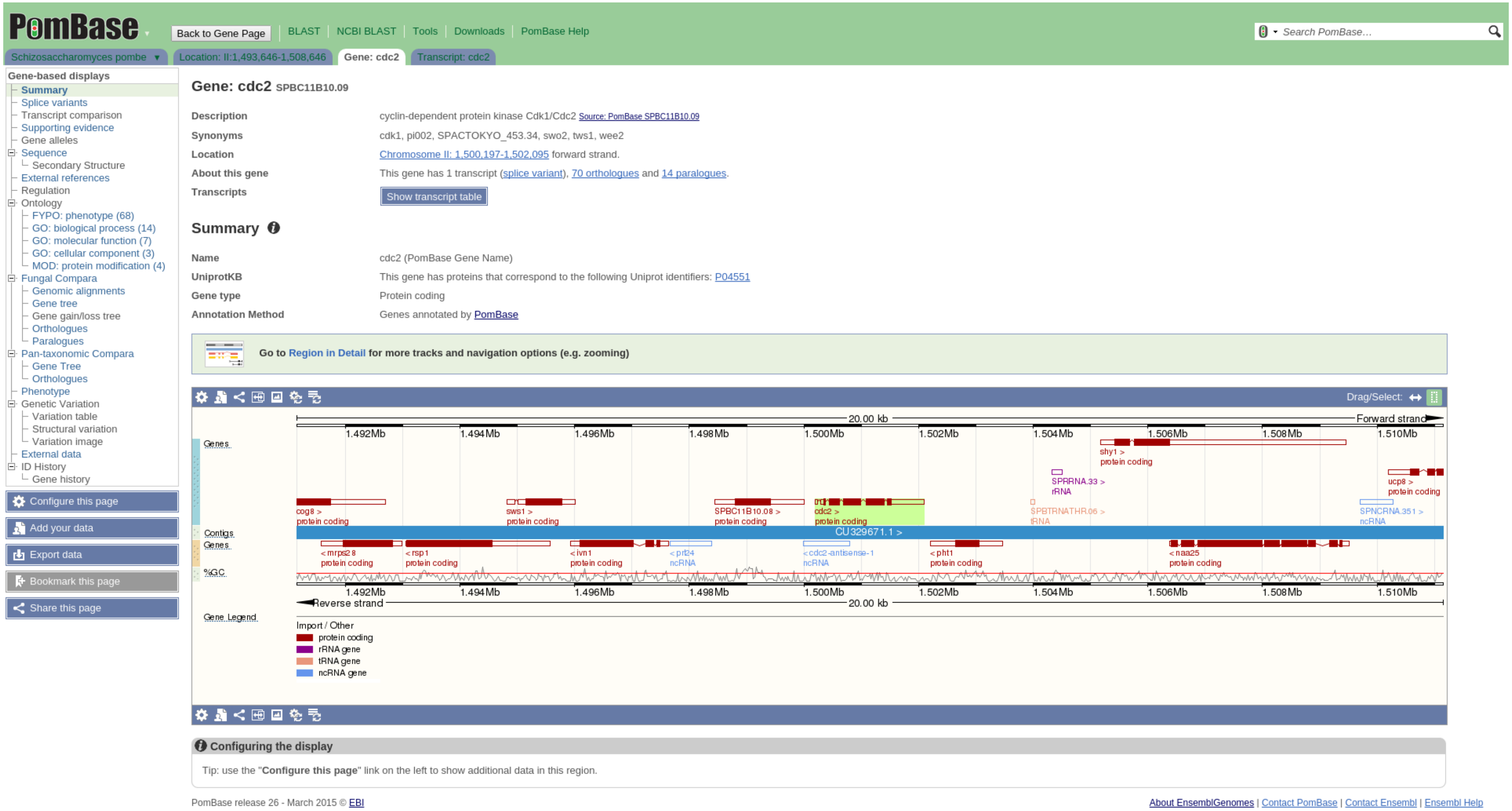
Export Configuration - Output Format

Please choose the output format for your export

- HTML
- Text
- Compressed text (.gz)



Gene tab



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

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.

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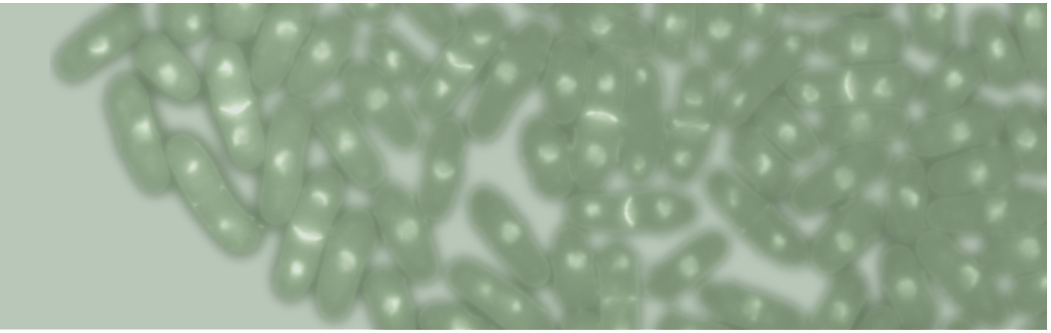
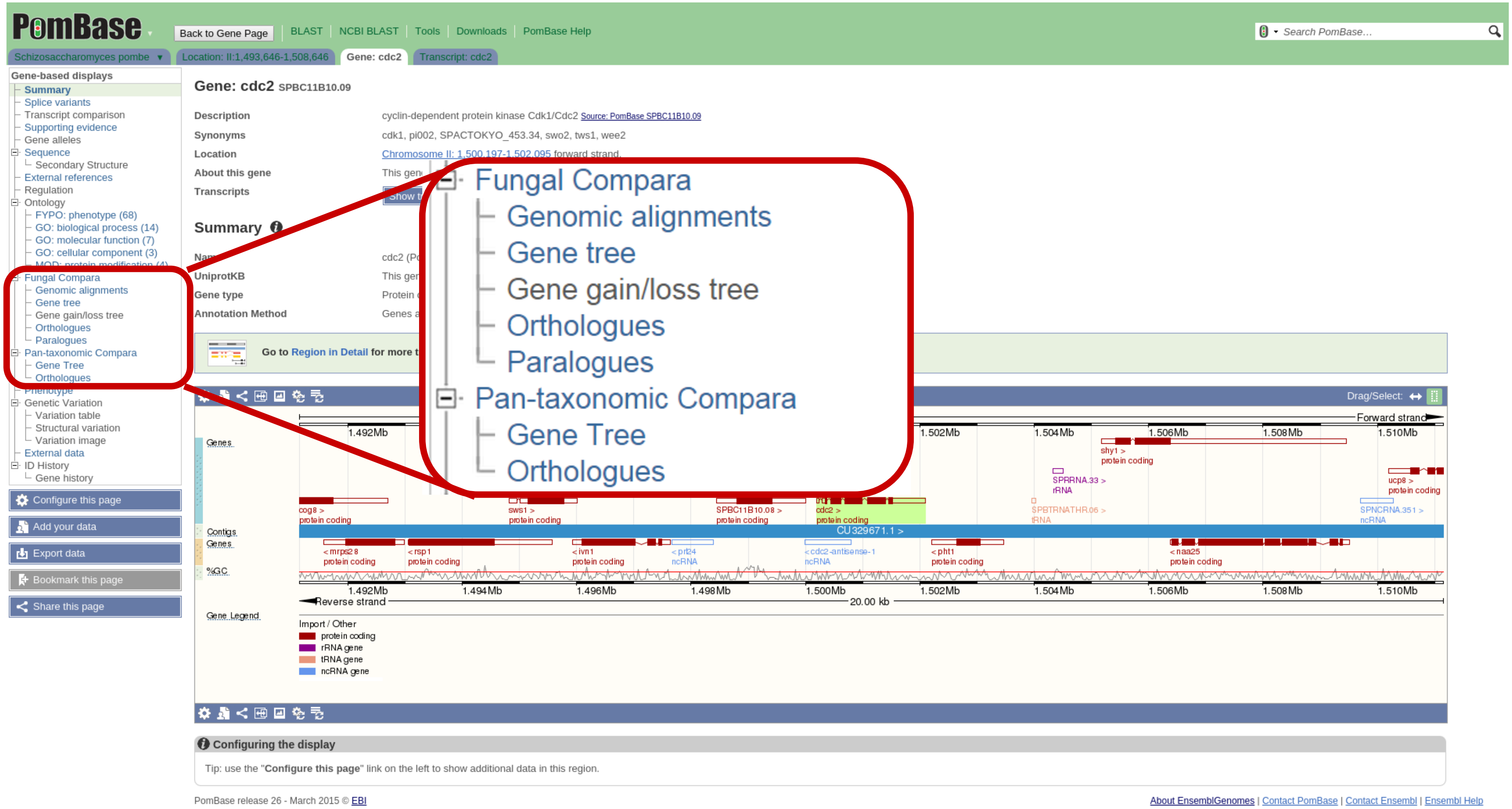
Gene tab





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

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 gen
Transcripts	Show t

Summary

Nam	cdc2 (P
UniprotKB	This ge
Gene type	Protein
Annotation Method	Genes a

Go to Region in Detail for more t

Fungal Compara
- Genomic alignments
- Gene tree
- Gene gain/loss tree
- Orthologues
- Paralogues

Pan-taxonomic Compara
- Gene Tree
- Orthologues

Configuring the display

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

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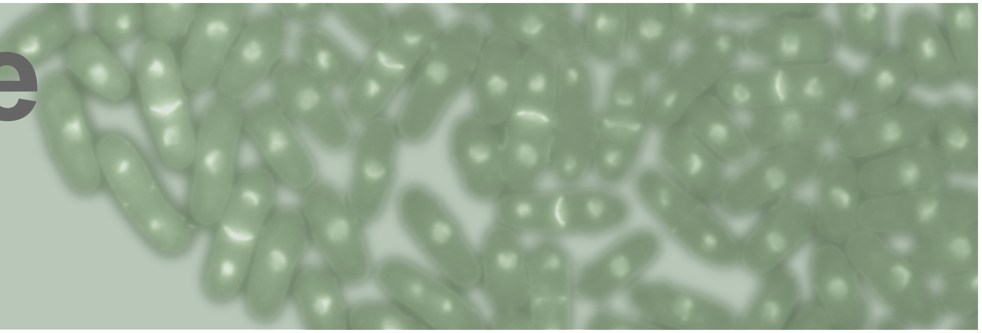
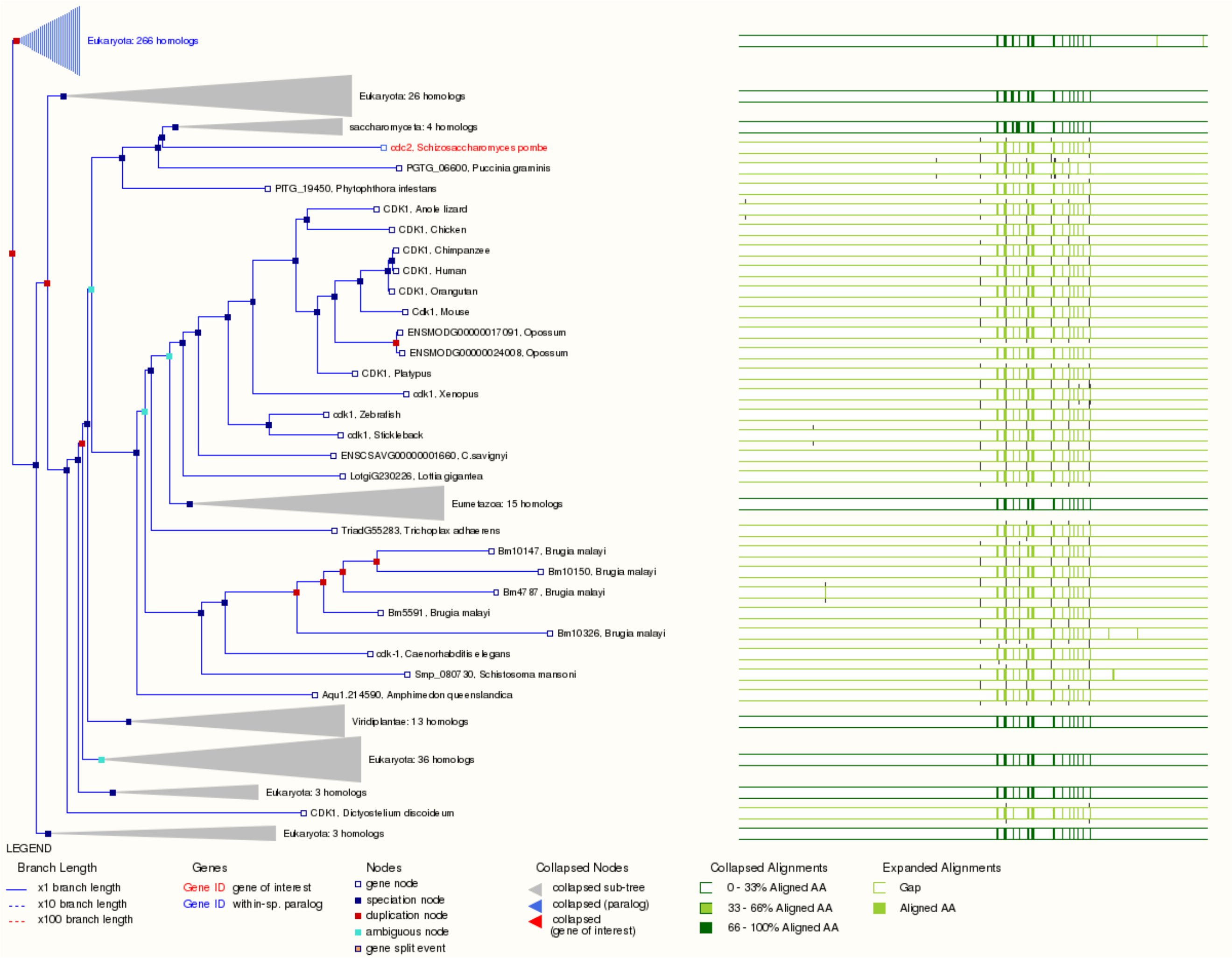
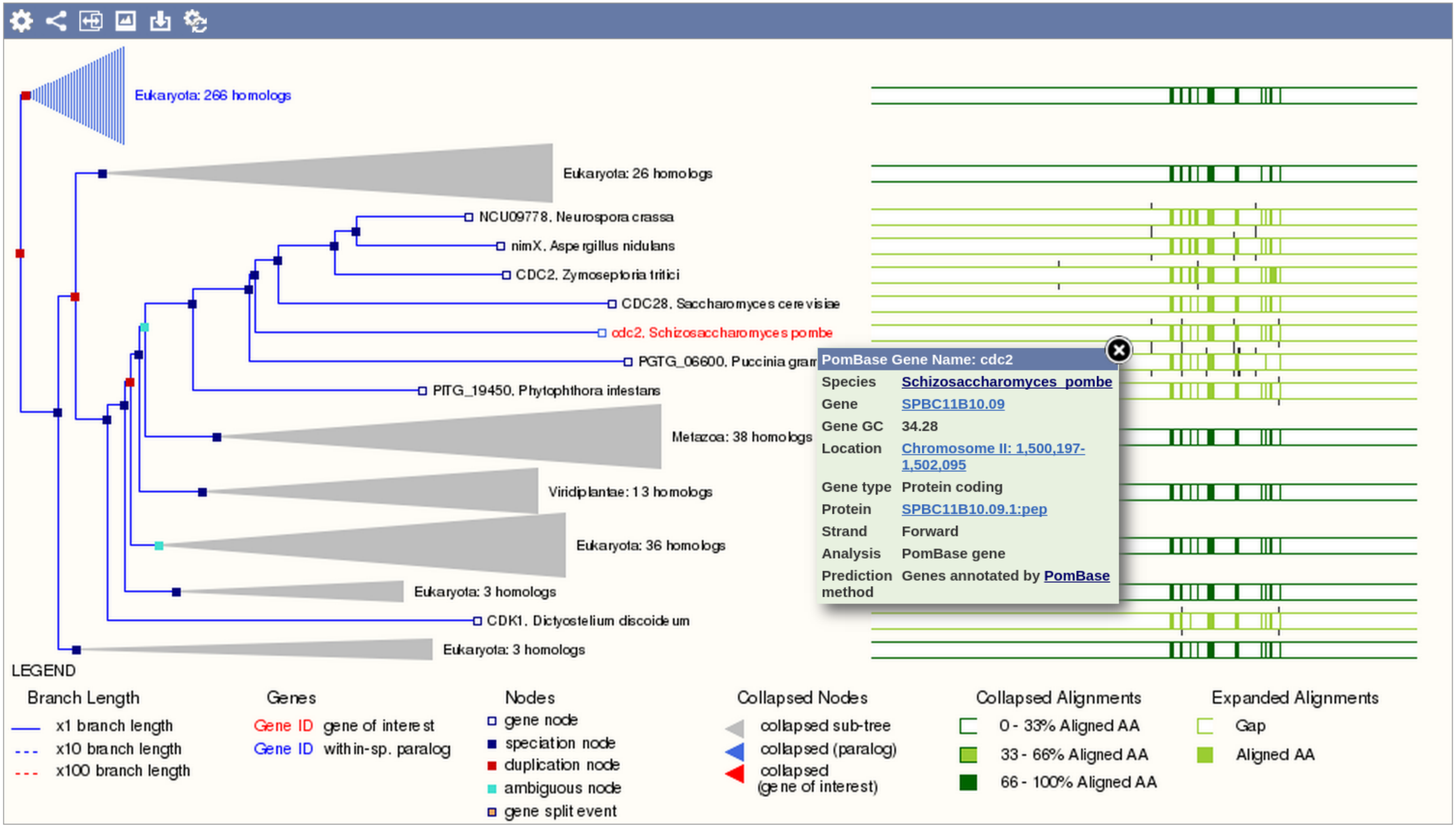
Comparative genomics





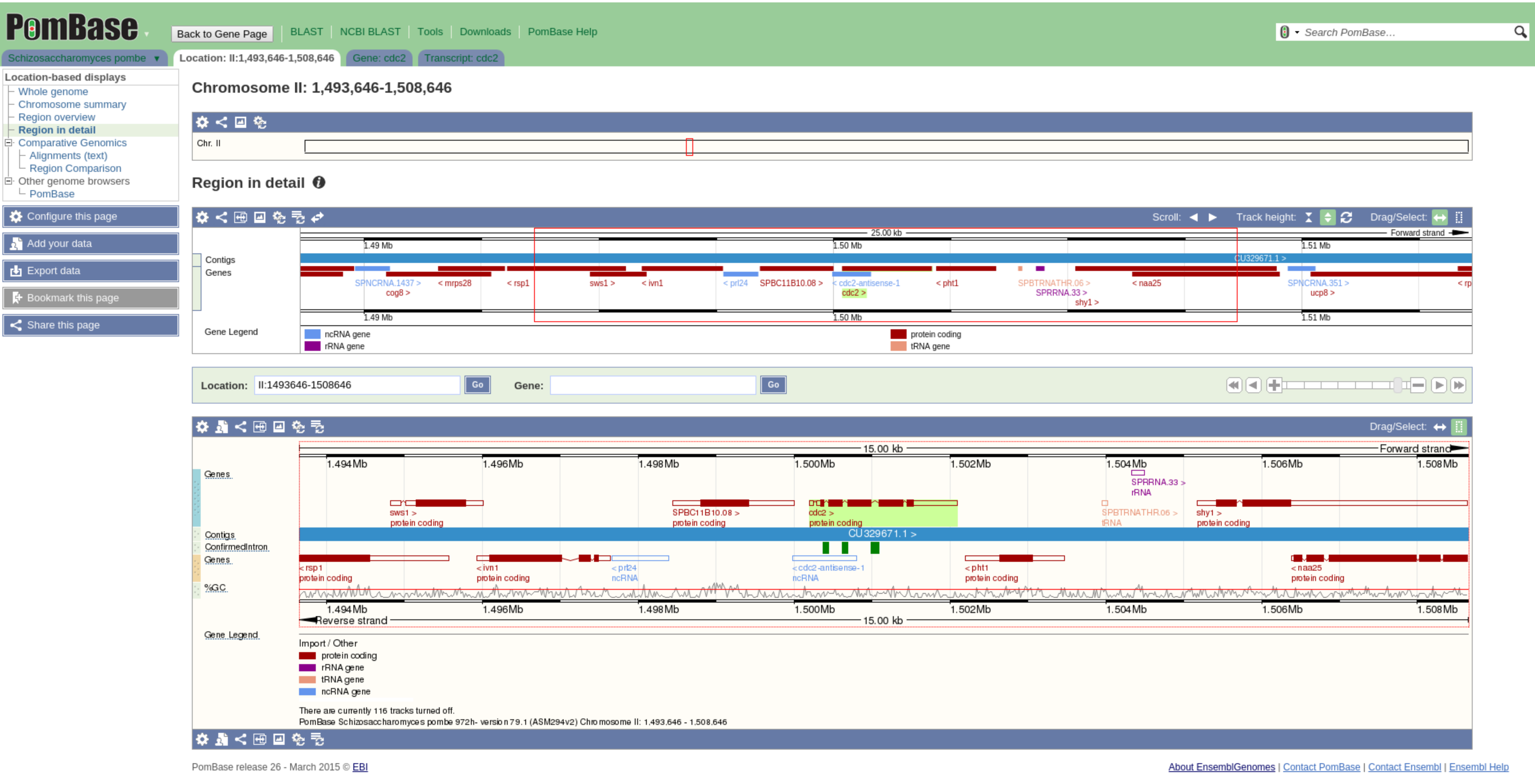
More pop-up menu



PomBase Gene Name: cdc2

Species	Schizosaccharomyces_pombe
Gene	SPBC11B10.09
Gene GC	34.28
Location	Chromosome II: 1,500,197-1,502,095
Gene type	Protein coding
Protein	SPBC11B10.09.1:pep
Strand	Forward
Analysis	PomBase gene
Prediction method	Genes annotated by PomBase

Location tab - Synteny



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

Region in detail

Location: II:1493646-1508646

Gene:

There are currently 116 tracks turned off.

PomBase Schizosaccharomyces pombe 972h- version 79.1 (ASM294v2) Chromosome II: 1,493,646 - 1,508,646

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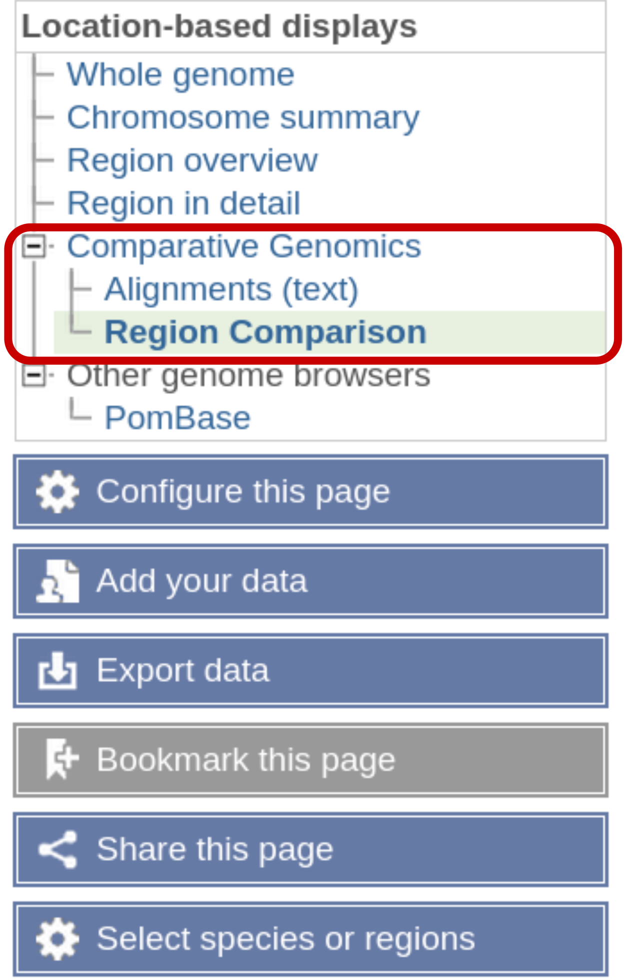
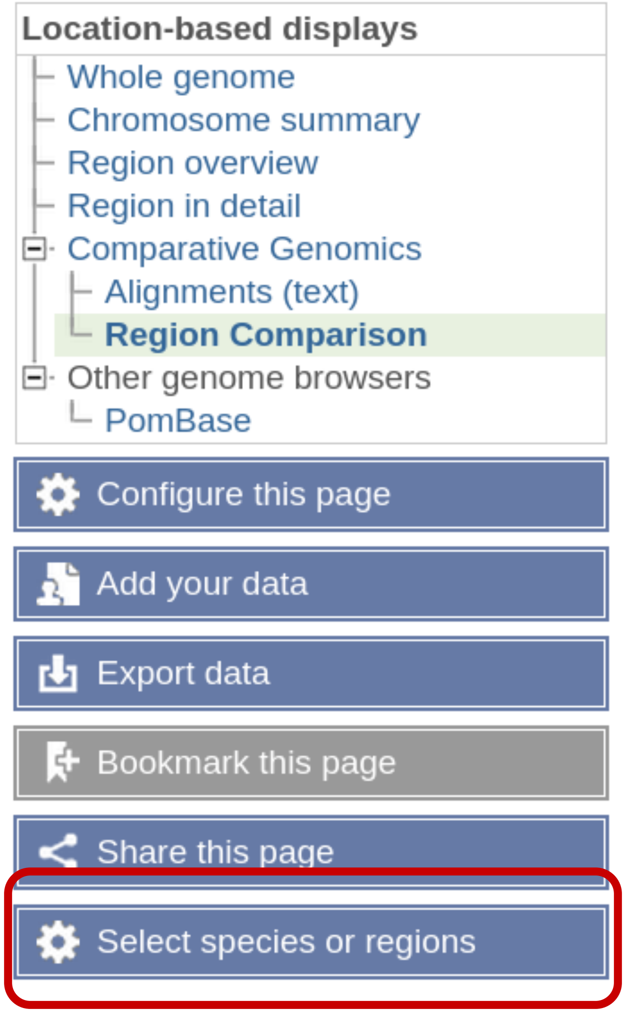
Location tab
- Synteny



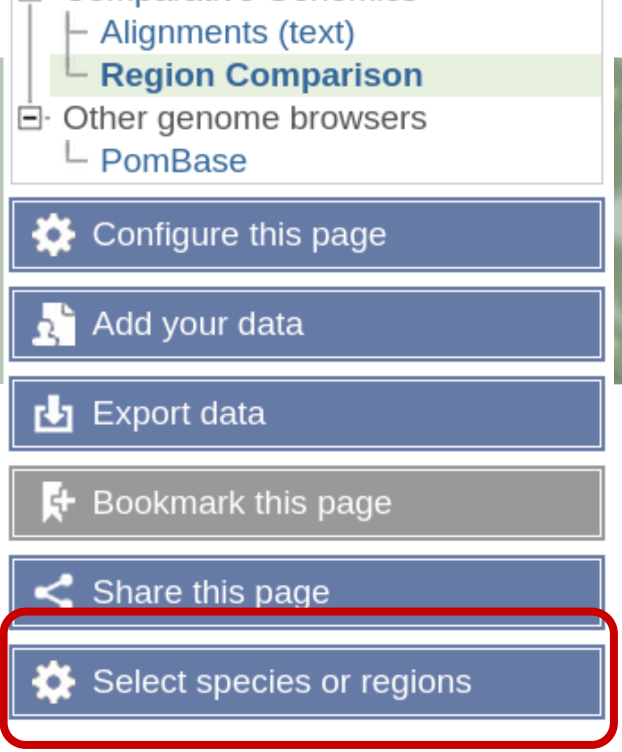
Location-based displays

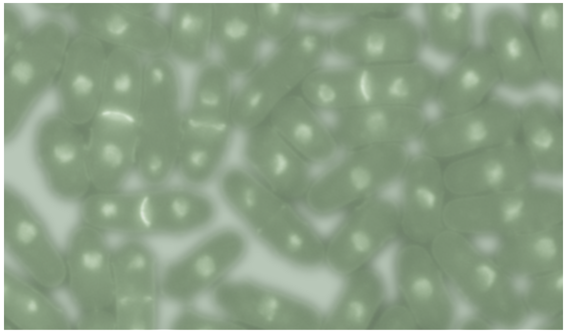
- Whole genome
- Chromosome summary
- Region overview
- Region in detail
- Comparative Genomics
  - Alignments (text)
  - **Region Comparison**
- Other genome browsers
  - PomBase

Location tab
- Synteny

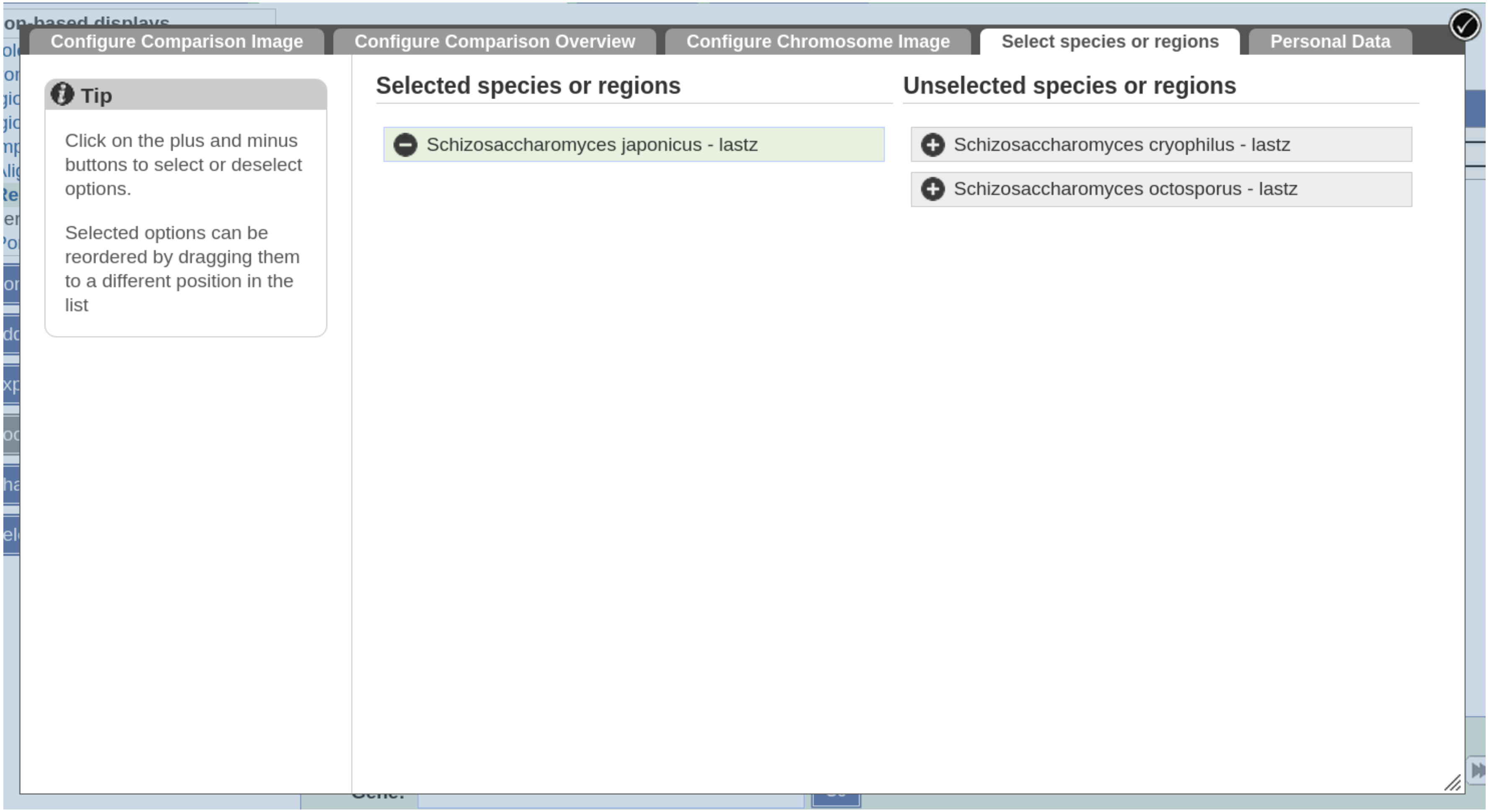


Location - Synten





Location tab
- Synteny



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

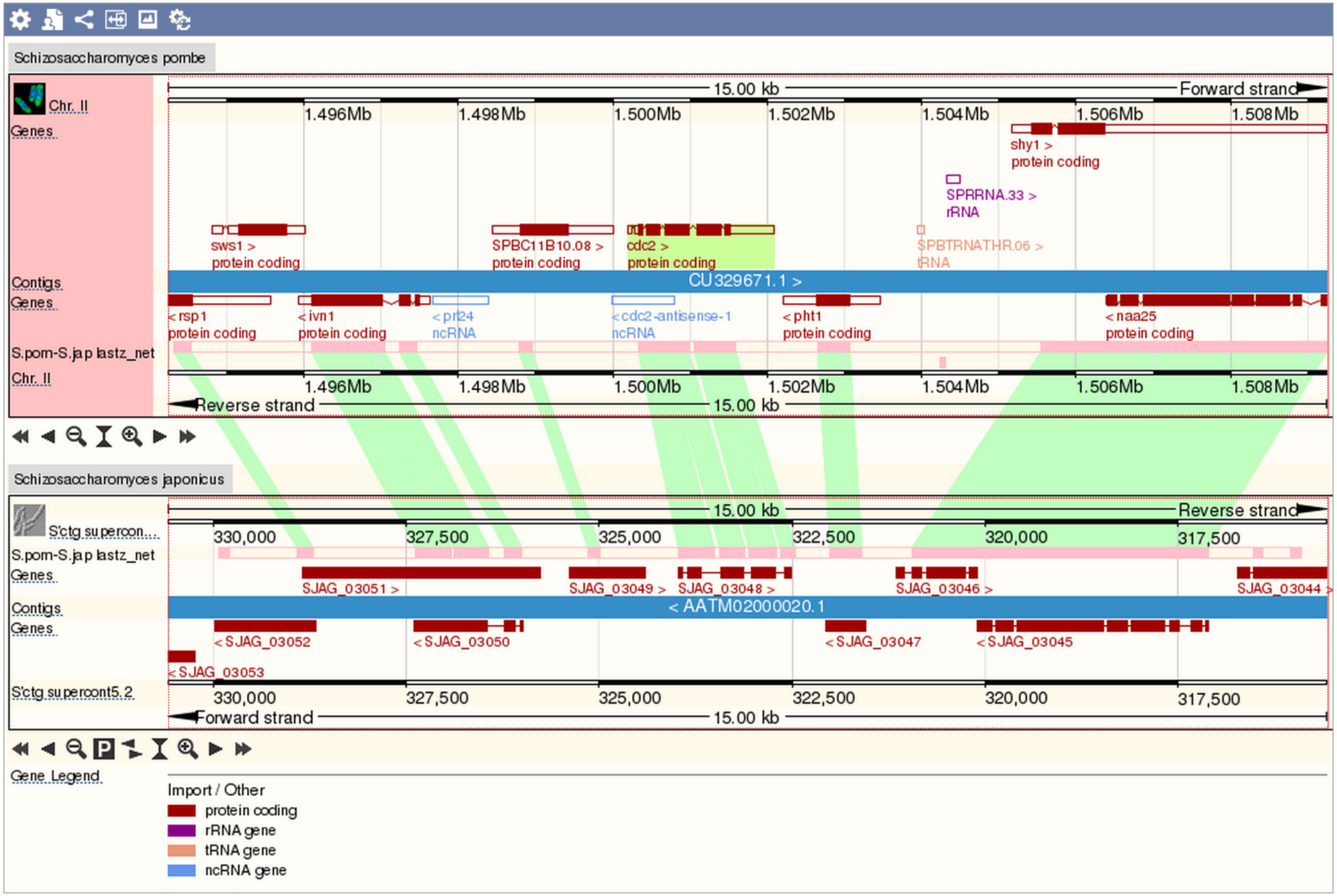
⊖ Schizosaccharomyces japonicus - lastz

Unselected species or regions

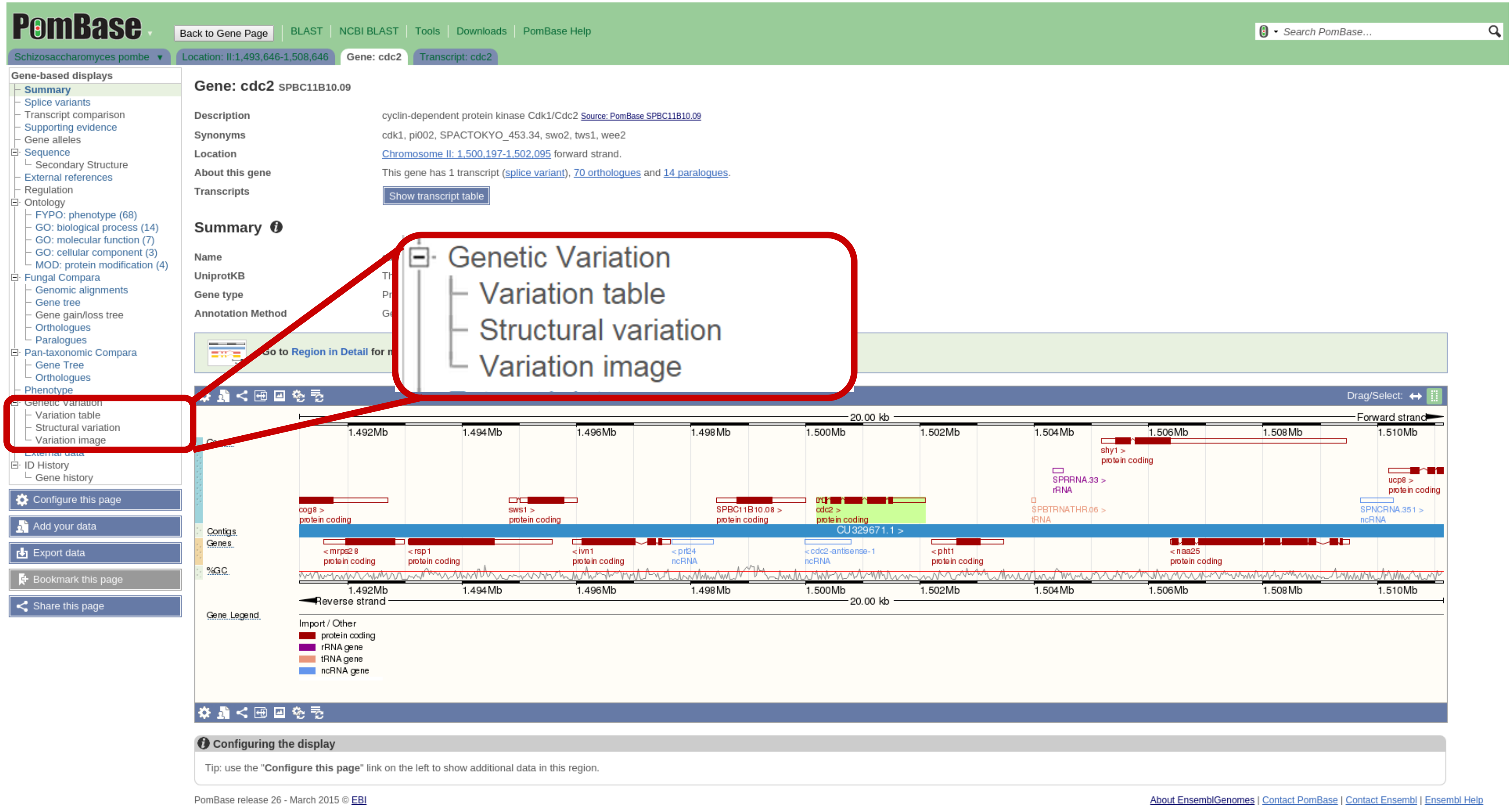
⊕ Schizosaccharomyces cryophilus - lastz

⊕ Schizosaccharomyces octosporus - lastz

Location tab - Synteny



Gene tab - Preview



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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  - Variation table
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Gene: cdc2 SPBC11B10.09

Description	cyclin-dependent protein kinase Cdk1/Cdc2 Source: PomBase SPBC11B10.09
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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	Th
Gene type	Pr
Annotation Method	Ge

Go to Region in Detail for m

Genetic Variation
- Variation table
- Structural variation
- Variation image

Configuring the display

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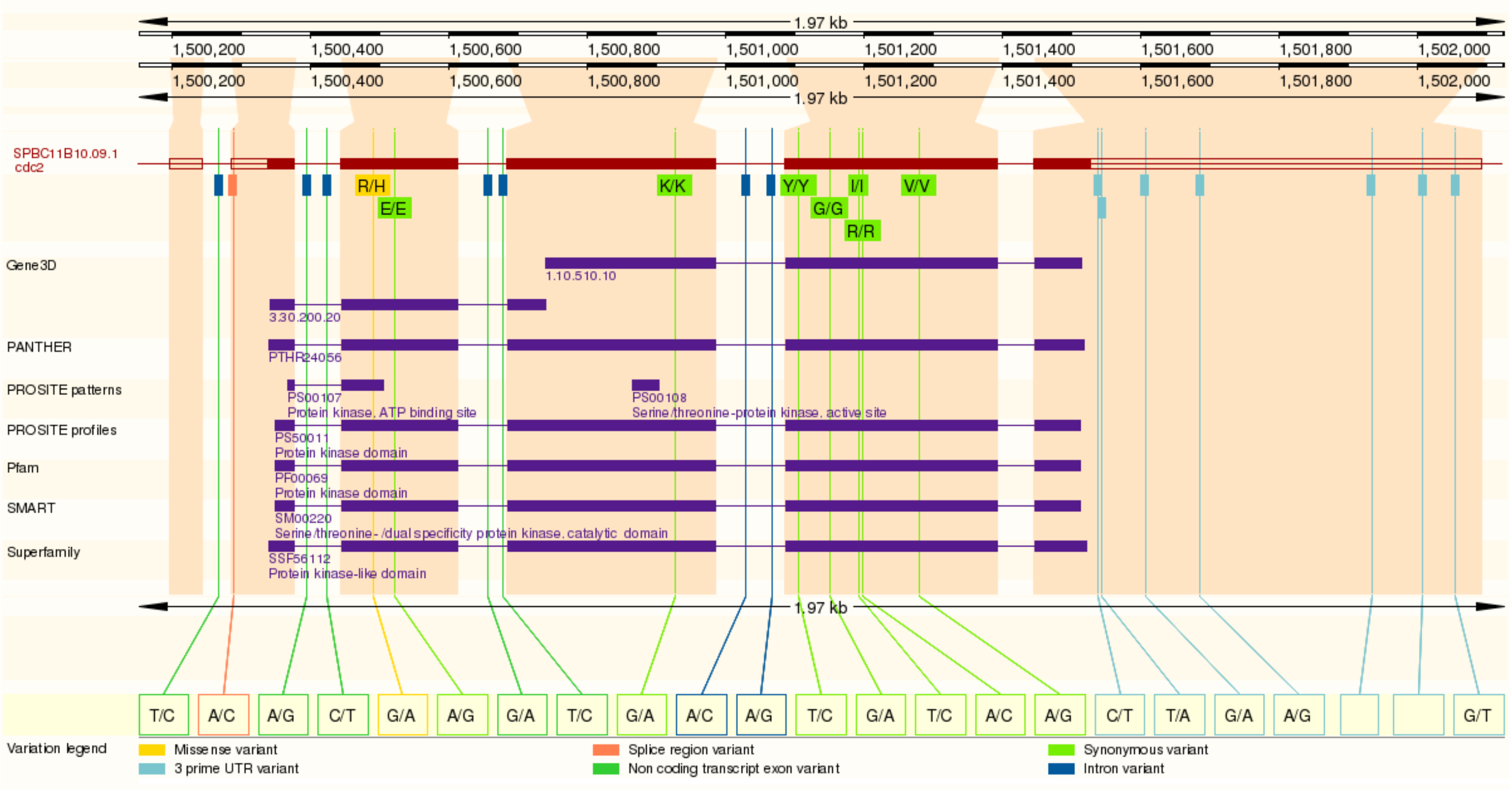
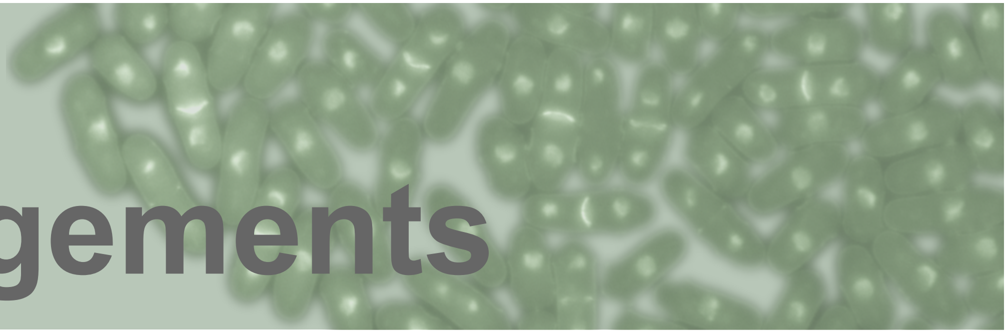
Variation - Preview



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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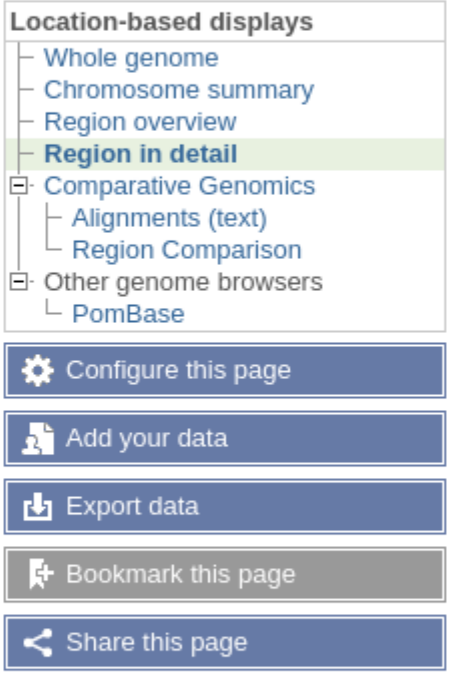
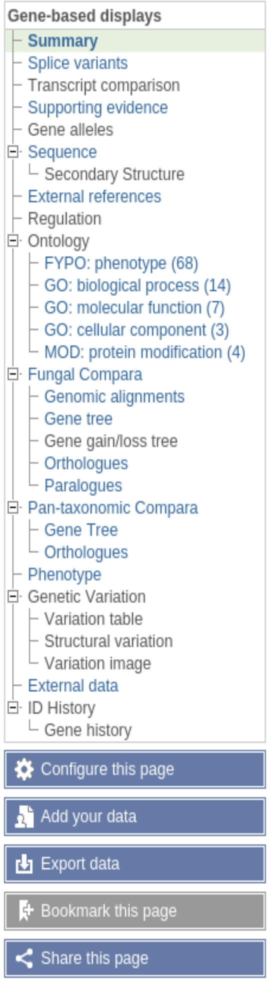
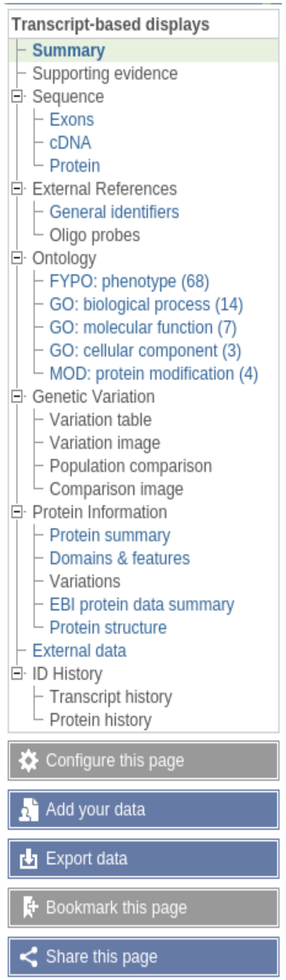
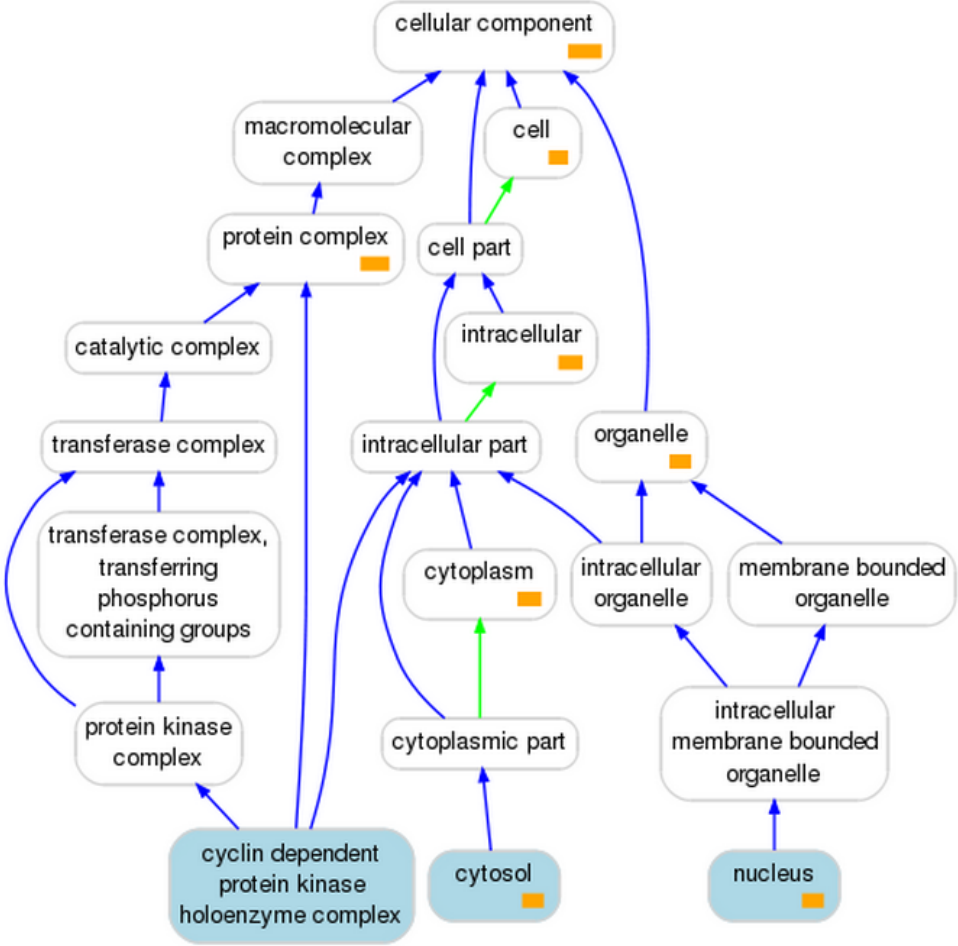
Left Hand Menus



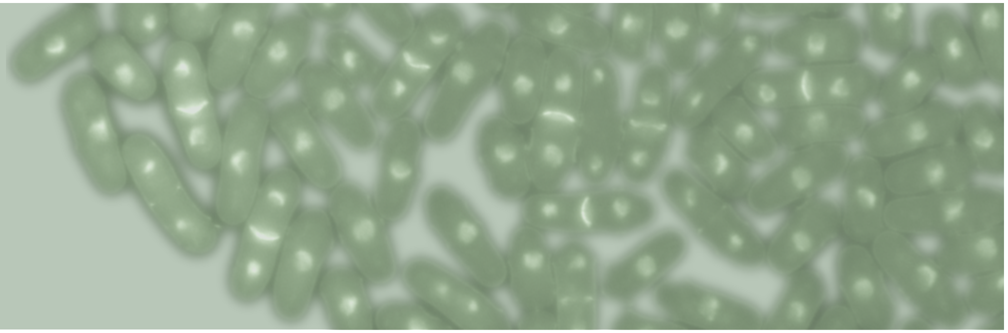


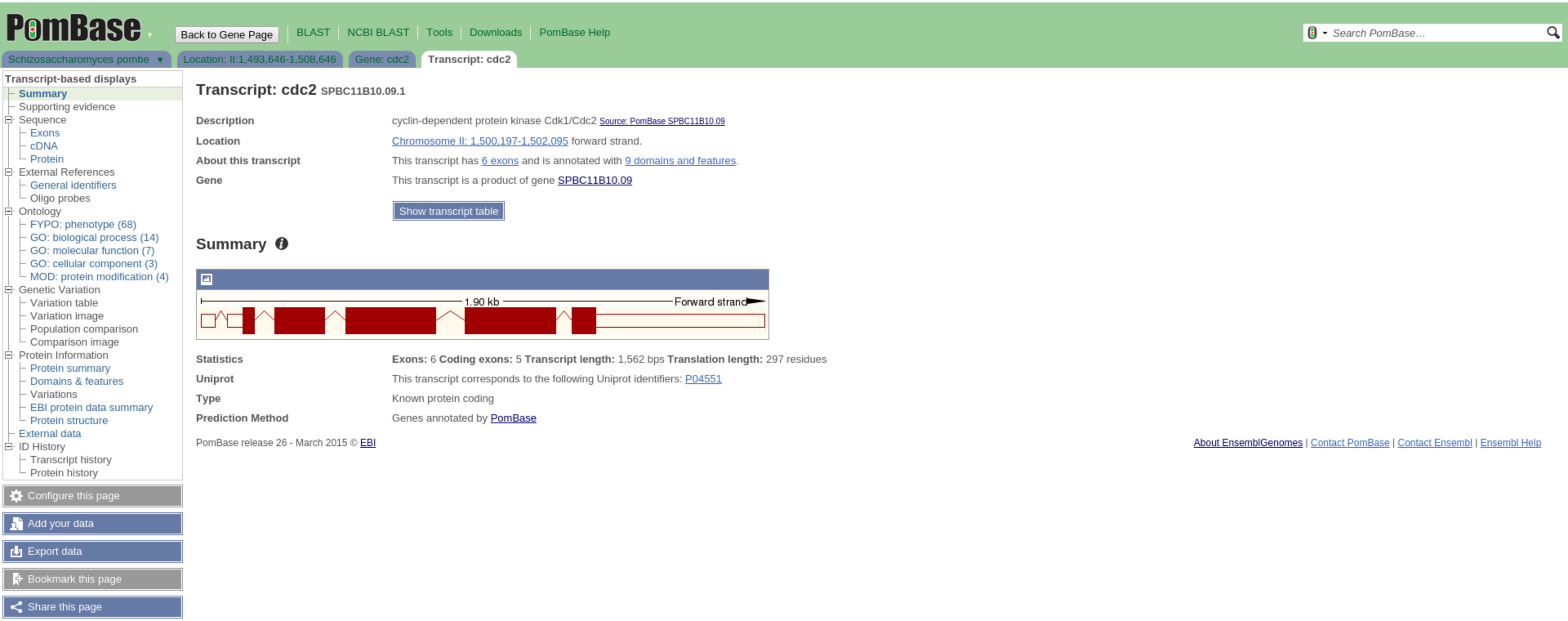


Ontology Annotations



Transcript





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

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

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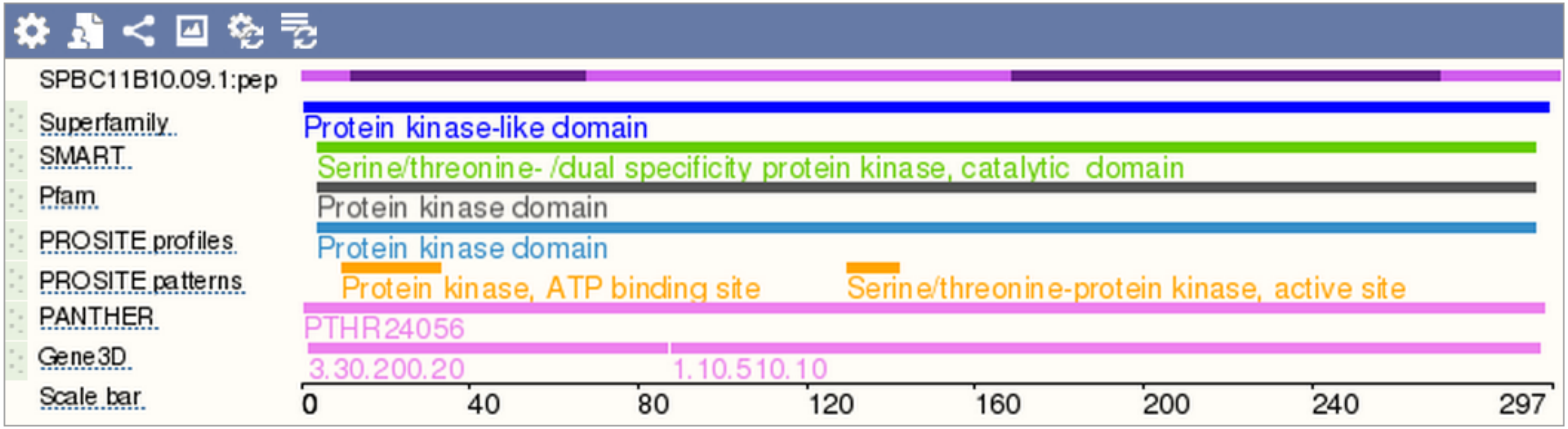
Translation

Protein summary

Protein domains for SPBC11B10.09.1:pep.1



Statistics

Ave. residue weight: 115.685 g/mol

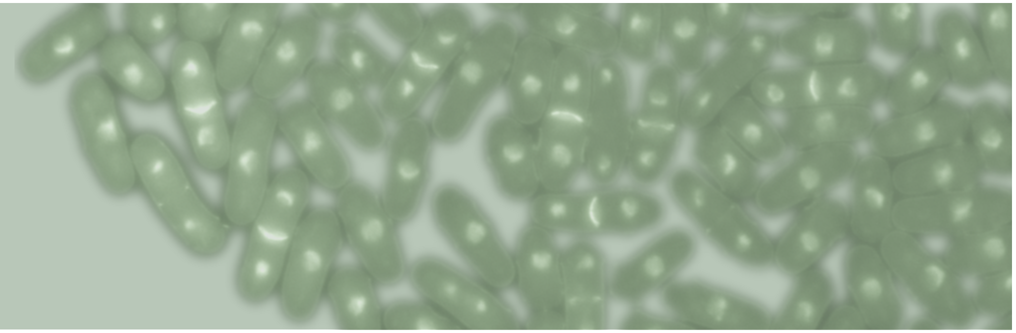
Charge: 4.5

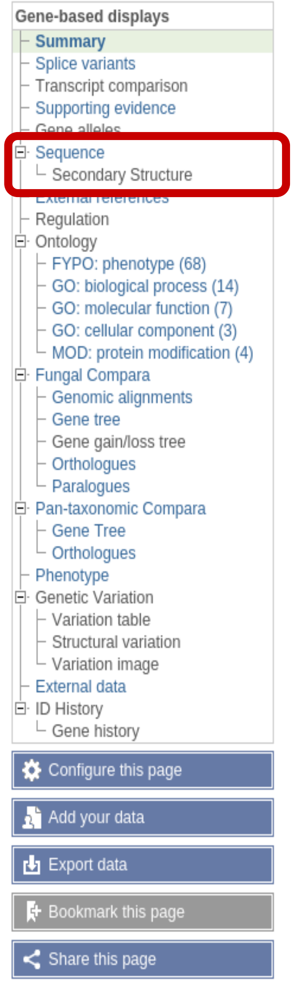
Isoelectric point: 7.6821

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)
GO: biological process (14)
GO: molecular function (7)
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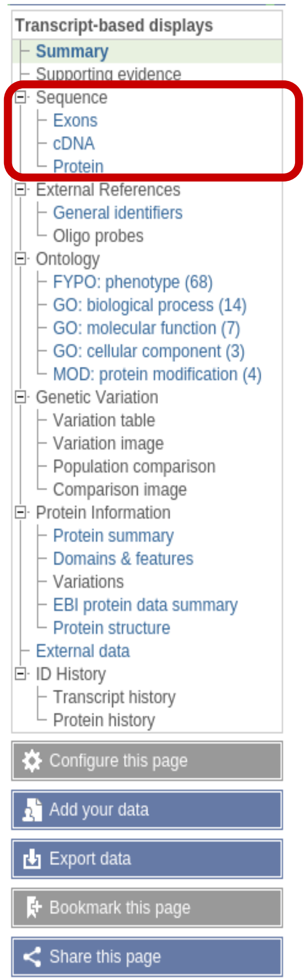
Fungal Compara
Genomic alignments
Gene tree
Gene gain/loss tree
Orthologues
Paralogues
Pan-taxonomic Compara
Gene Tree
Orthologues
Phenotype
Genetic Variation
Variation table
Structural variation
Variation image
External data
ID History
Gene history
Configure this page
Add your data
Export data
Bookmark this page
Share this page

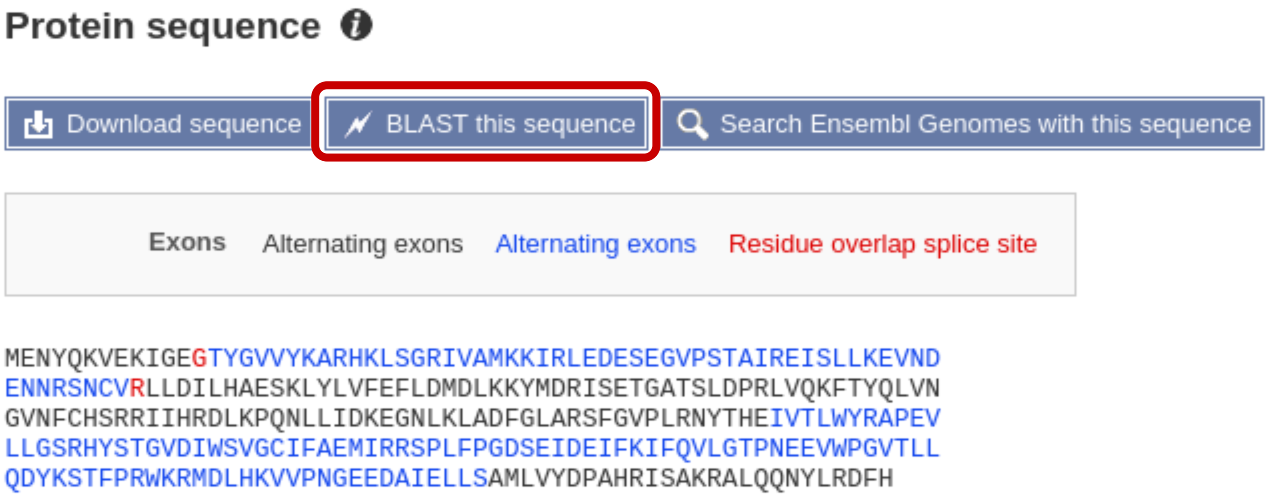

Transcript-based displays
Summary
Supporting evidence
Sequence
Exons
cDNA
Protein
External References
General identifiers
Oligo probes
Ontology
FYPO: phenotype (68)
GO: biological process (14)
GO: molecular function (7)
GO: cellular component (3)
MOD: protein modification (4)
Genetic Variation
Variation 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
Bookmark this page
Share this page

Sequences

Protein sequence

```
MENYQKVEKIGEGTYGVVYKARHKLSGRIVAMKKIRLEDESEGVPSTAIREISLLKEVND
ENNRSNCVRLLDILHAESKLYLVFEFLDMDLKKYMDRISETGATSLDPRLVQKFTYQLVN
GVNFCHSRRIIHRDLKPQNLLIDKEGNLKLADFGLARSFGVPLRNYTHEIVTLWYRAPEV
LLGSRHYSTGVDIWSVGCIFAEMIRRSPLFPGDSEIDEIFKIFQVLGTPNEEVWPGVTLL
QDYKSTFPRWKRMDLHKVVPNGEEDAIELLSAMLVYDPAHRISAKRALQQNYLRDFH
```

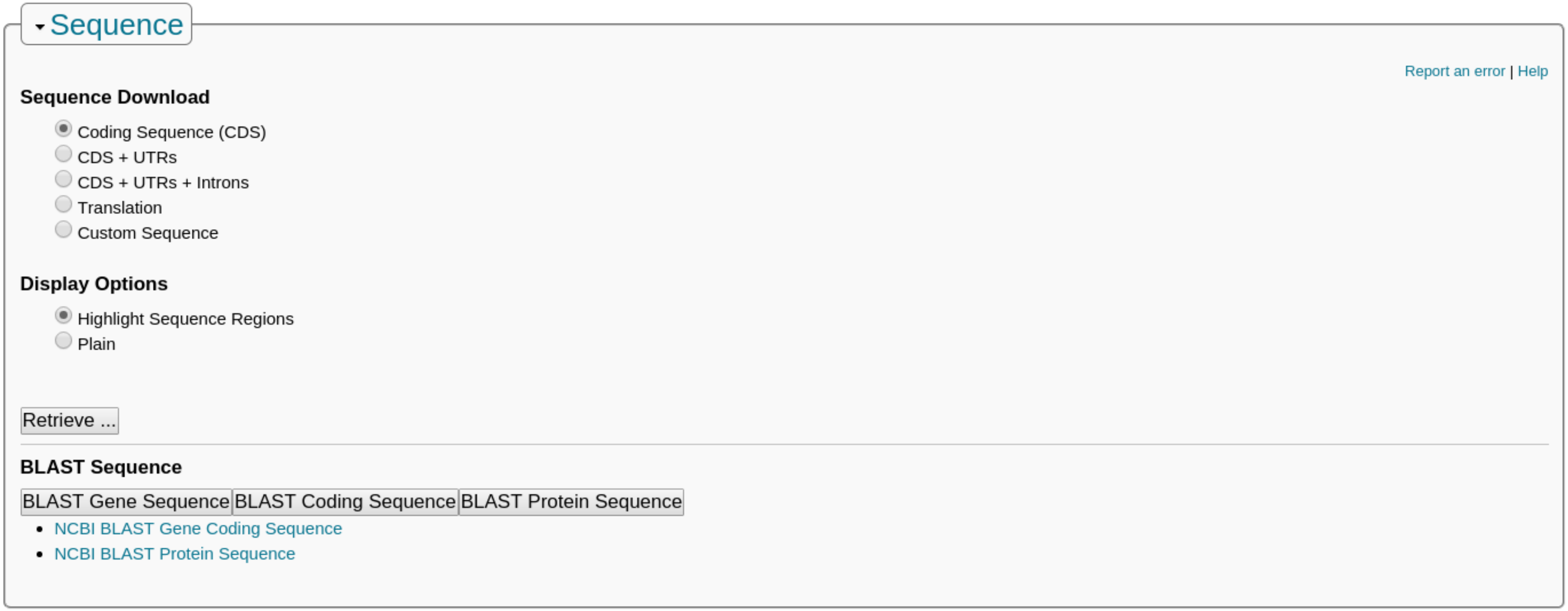
Sequence - BLAST



Protein sequence

```
MENYQKVEKIGEGTYGVVYKARHKLSGRIVAMKKIRLEDESEGVPSTAIREISLLKEVND
ENNRSNCVRLLDILHAESKLYLVFEFLDMDLKKYMDRISETGATSLDPRLVQKFTYQLVN
GVNFCHSRRIIHRDLKPQNLLIDKEGNLKLADFGLARSFGVPLRNYTHEIVTLWYRAPEV
LLGSRHYSTGVDIWSVGCIFAEMIRRSPLFPGDSEIDEIFKIFQVLGTPNEEVWPGVTLL
QDYKSTFPRWKRMDLHKVVPNGEEDAIELLSAMLVYDPAHRISAKRALQQNYLRDFH
```

From the gene page



Sequence Download

- ● Coding Sequence (CDS)
- ○ CDS + UTRs
- ○ CDS + UTRs + Introns
- ○ Translation
- ○ Custom Sequence

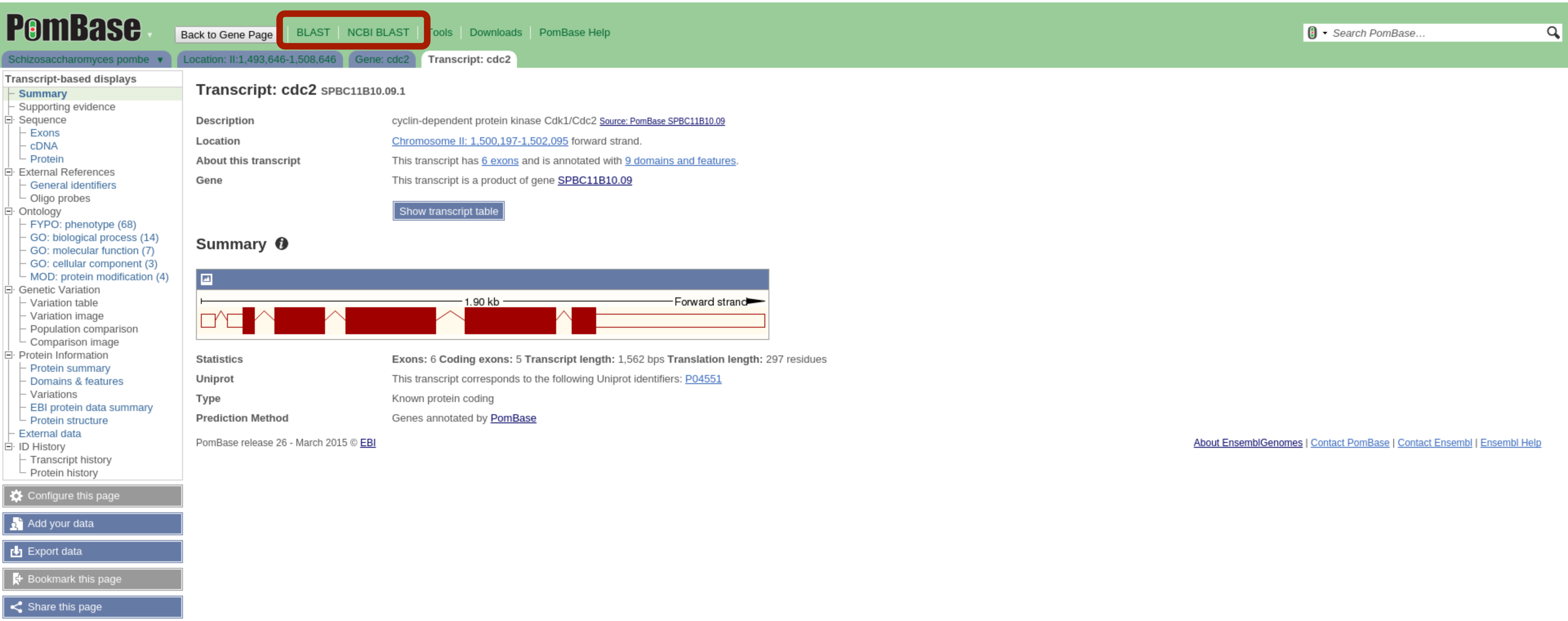
Display Options

- ● Highlight Sequence Regions
- ○ Plain

BLAST Sequence

- NCBI BLAST Gene Coding Sequence
- NCBI BLAST Protein Sequence

From the genome browser



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

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

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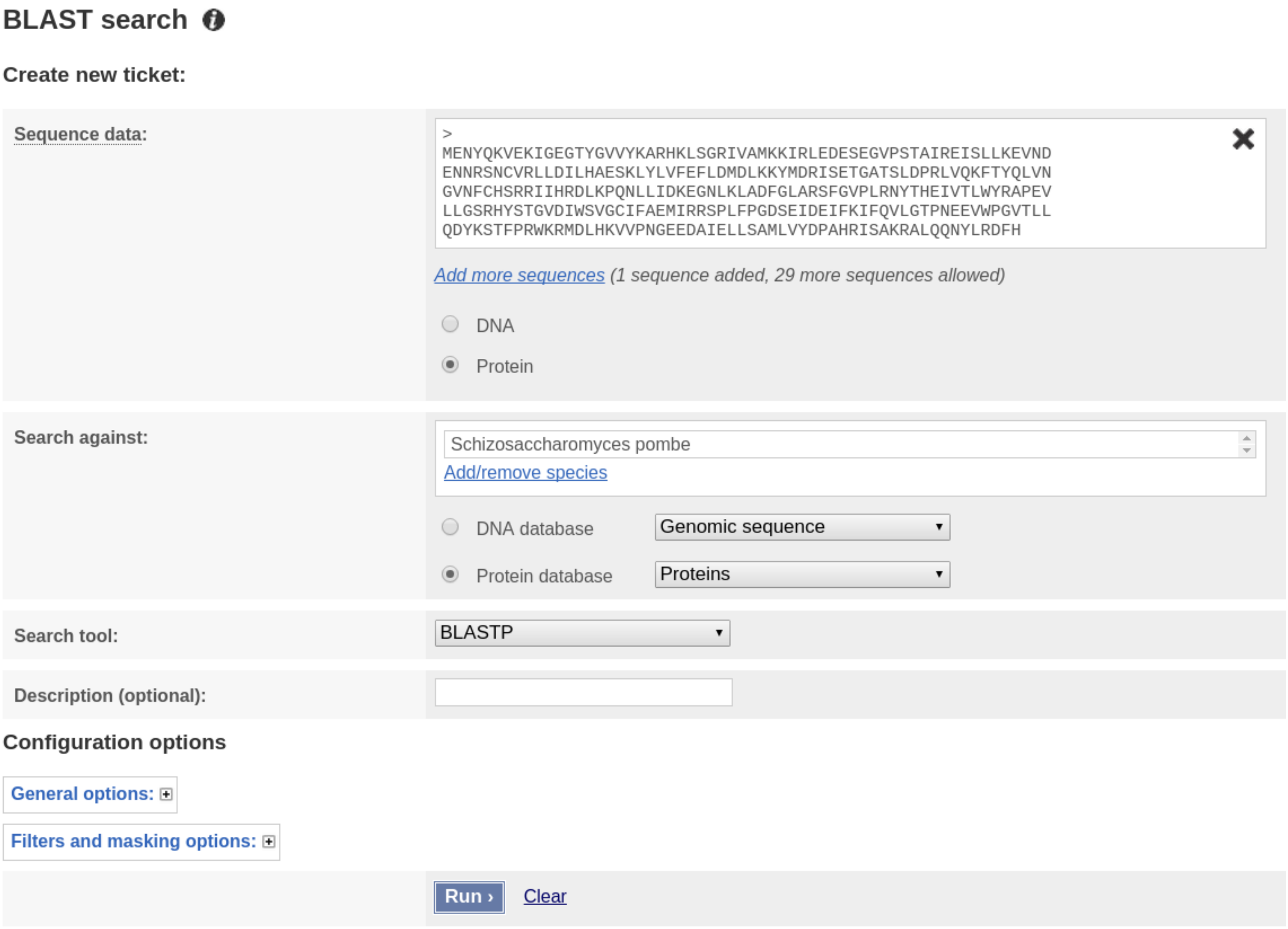
BLAST - Submitting a job



BLAST search

Create new ticket:

Sequence data:

```
>
MENYQKVEKIGEGTYGVVYKARHKLSGRIVAMKKIRLEDESEGVPSTAIREISLLKEVND
ENNRSNCVRLLDILHAESKLYLVFEFLDMDLKKYMDRISETGATSLDPRLVQKFTYQLVN
GVNFCHSRRIIHRDLKPQNLLIDKEGNLKLADFGLARSFGVPLRNYTHEIVTLWYRAPEV
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

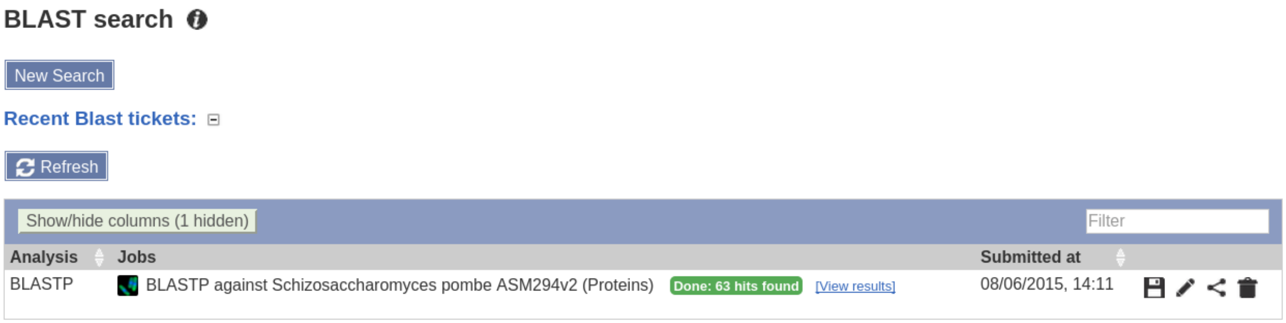
● Protein database: Proteins

Search tool: BLASTP

Description (optional):

Configuration options

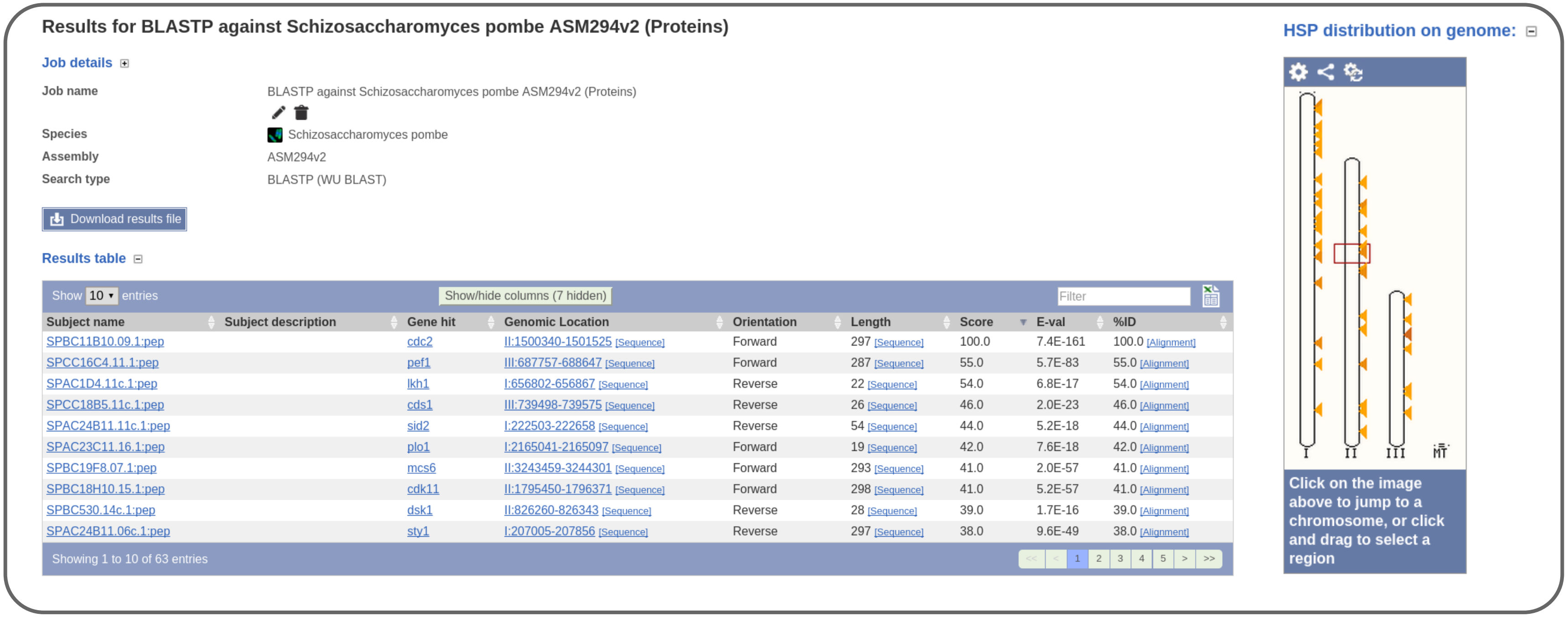
BLAST - Results



BLAST search

Recent Blast tickets:

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)

Results table

Subject name	Subject description	Gene hit	Genomic Location	Orientation	Length	Score	E-val	%ID
SPBC11B10.09.1:pep		cdc2	II:1500340-1501525 [Sequence]	Forward	297 [Sequence]	100.0	7.4E-161	100.0 [Alignment]
SPCC16C4.11.1:pep		pef1	III:687757-688647 [Sequence]	Forward	287 [Sequence]	55.0	5.7E-83	55.0 [Alignment]
SPAC1D4.11c.1:pep		lkh1	I:656802-656867 [Sequence]	Reverse	22 [Sequence]	54.0	6.8E-17	54.0 [Alignment]
SPCC18B5.11c.1:pep		cds1	III:739498-739575 [Sequence]	Reverse	26 [Sequence]	46.0	2.0E-23	46.0 [Alignment]
SPAC24B11.11c.1:pep		sid2	I:222503-222658 [Sequence]	Reverse	54 [Sequence]	44.0	5.2E-18	44.0 [Alignment]
SPAC23C11.16.1:pep		plo1	I:2165041-2165097 [Sequence]	Forward	19 [Sequence]	42.0	7.6E-18	42.0 [Alignment]
SPBC19F8.07.1:pep		mcs6	II:3243459-3244301 [Sequence]	Forward	293 [Sequence]	41.0	2.0E-57	41.0 [Alignment]
SPBC18H10.15.1:pep		cdk11	II:1795450-1796371 [Sequence]	Forward	298 [Sequence]	41.0	5.2E-57	41.0 [Alignment]
SPBC530.14c.1:pep		dsk1	II:826260-826343 [Sequence]	Reverse	28 [Sequence]	39.0	1.7E-16	39.0 [Alignment]
SPAC24B11.06c.1:pep		sty1	I:207005-207856 [Sequence]	Reverse	297 [Sequence]	38.0	9.6E-49	38.0 [Alignment]

Showing 1 to 10 of 63 entries

HSP distribution on genome:

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