



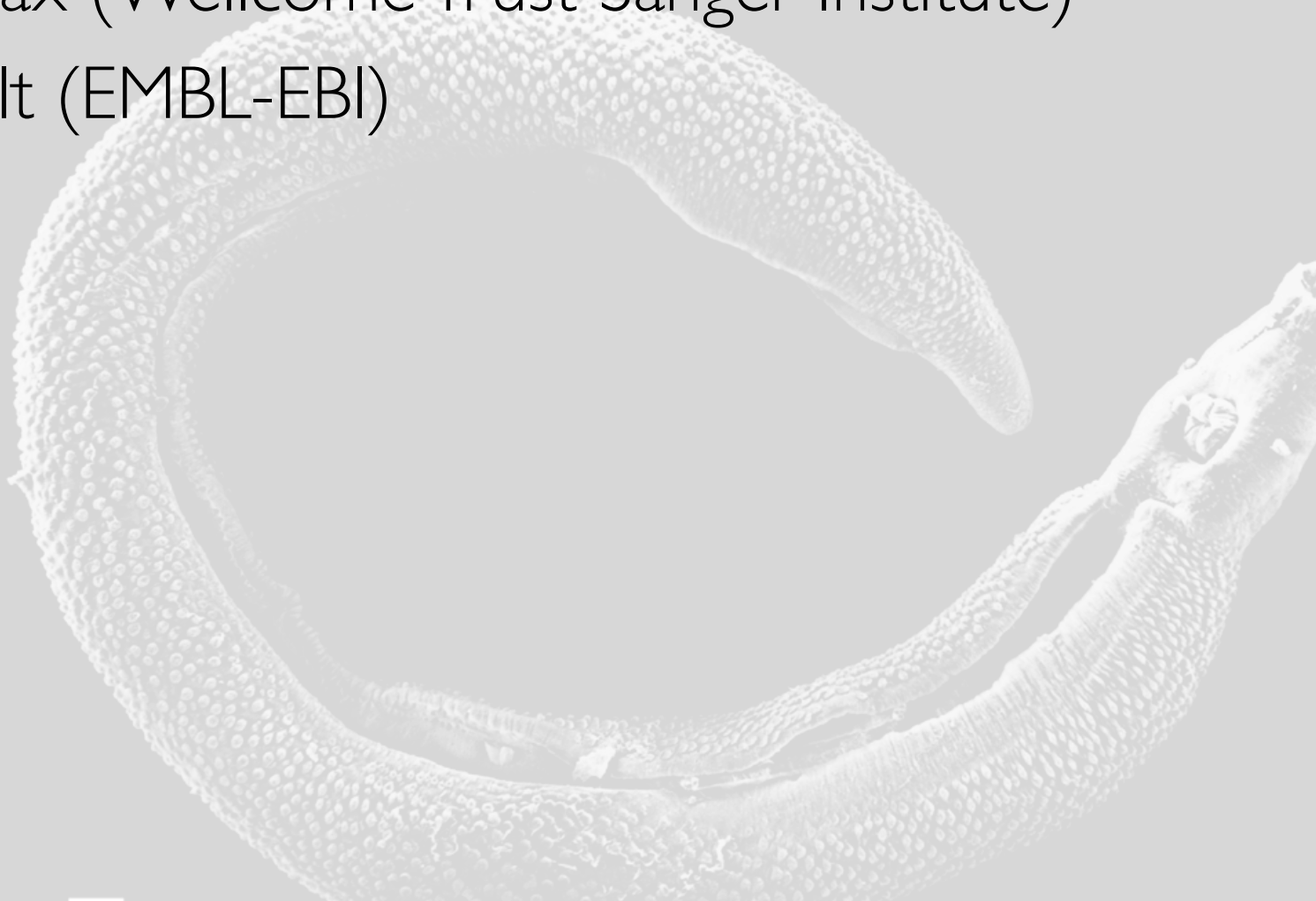
An Introduction to using WormBase ParaSite

Jane Lomax, Bruce Bolt
Wellcome Trust Sanger Institute and
EMBL-EBI

Course trainers

Jane Lomax (Wellcome Trust Sanger Institute)

Bruce Bolt (EMBL-EBI)



Course Outline

10:30 - 12:00 (Jane)

Using the website: Practical exercises

12:00 - 13:00

Lunch Break

13:00 - 13:45 (Bruce)

Sequence searching with BLAST: Practical exercises

13:45 - 14:30 (Bruce)

Data export with BioMart (Part 1): Practical exercises

14:30 - 14:50

Tea & Coffee Break

14:50 - 15:20 (Jane)

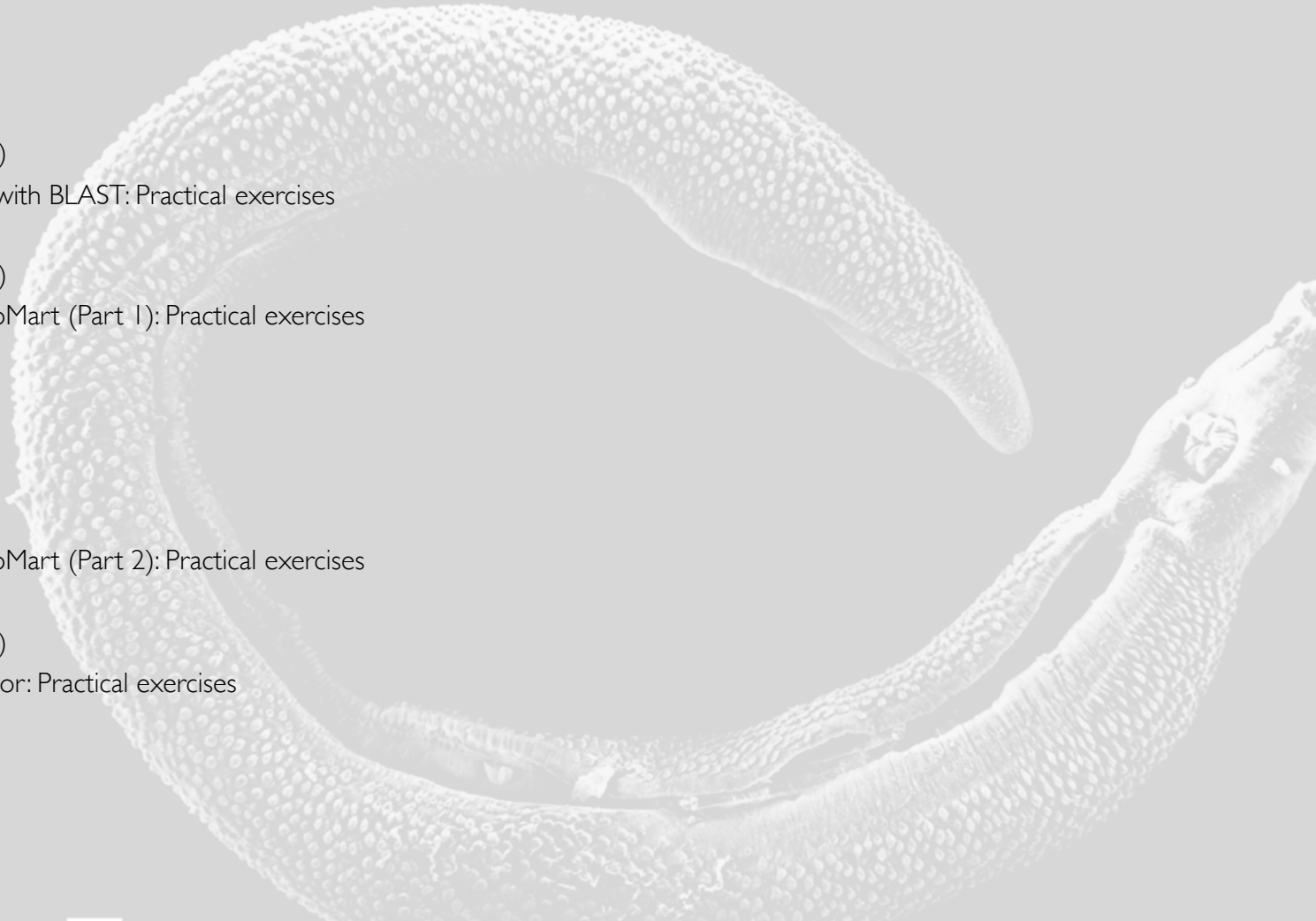
Data export with BioMart (Part 2): Practical exercises

15:20 - 16:00 (Bruce)

Variant Effect Predictor: Practical exercises

16:00 - 16:30

Q&A Session





Feedback forms

What is WormBase ParaSite?



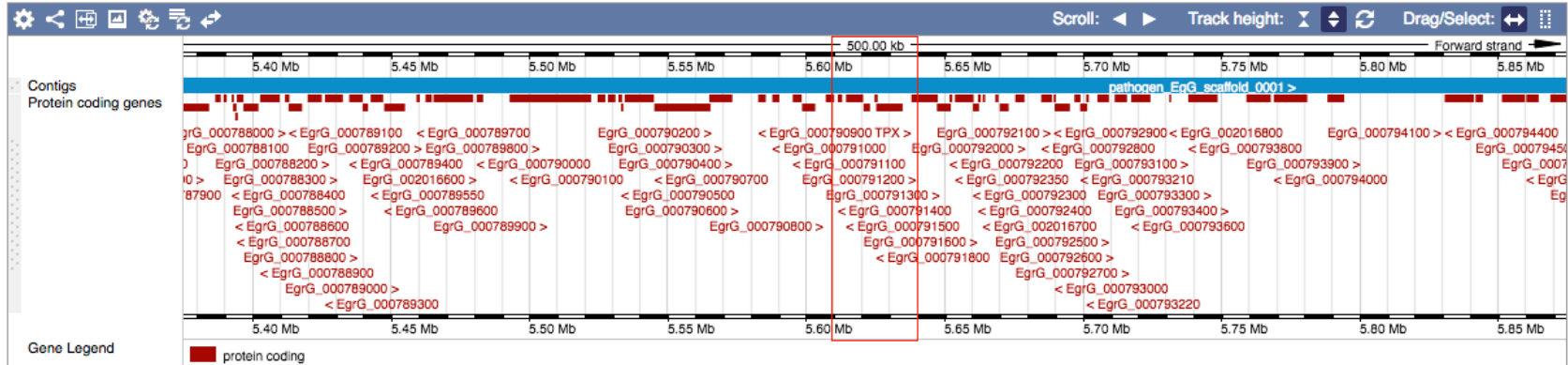


I. Genome browser for helminth species

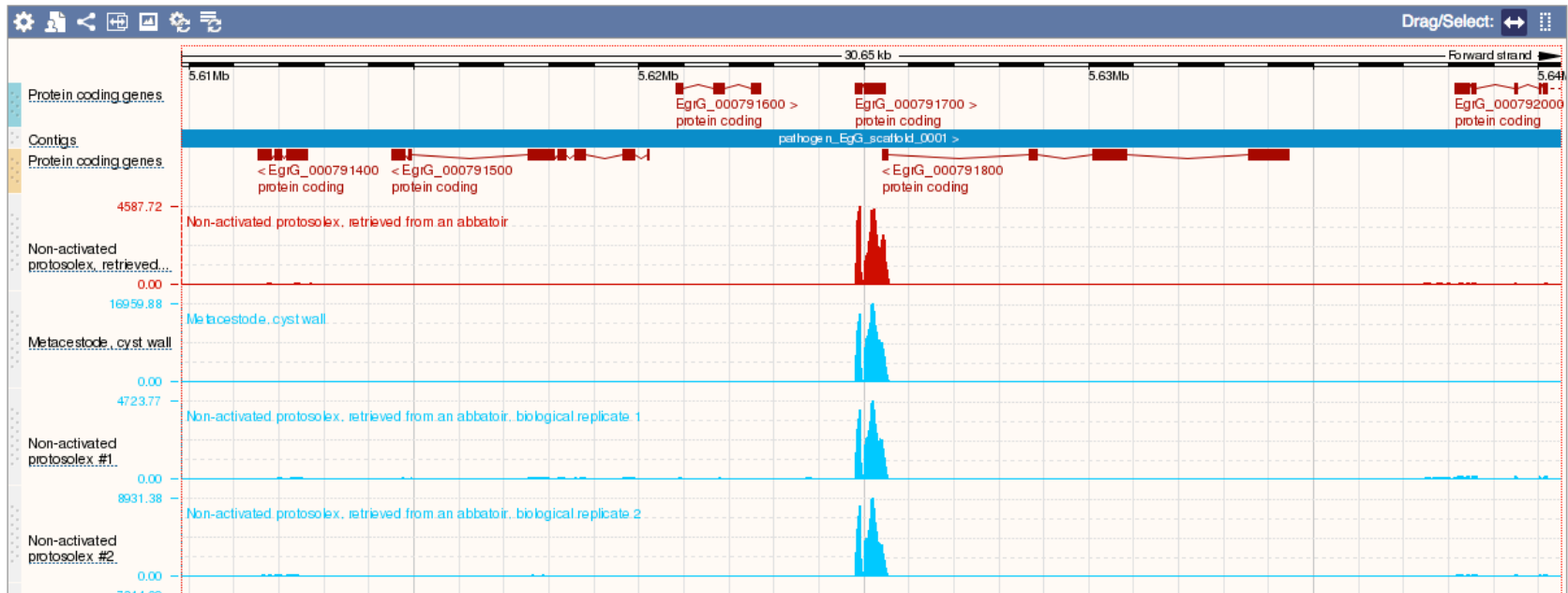
Scaffold pathogen_EgG_scaffold_0001: 5,609,817-5,640,467

Genome browser navigation bar with search field containing "scaffold pathogen_EgG..." and a red selection box.

Region in detail



Location: pathogen_EgG_scaffold_0001:5609817-5640467 Go Gene: Go



2. Set of tools for interacting with helminth genomes



3. Portal for downloading helminth genomic data



Where does the data come from?







What data does WormBase ParaSite contain?

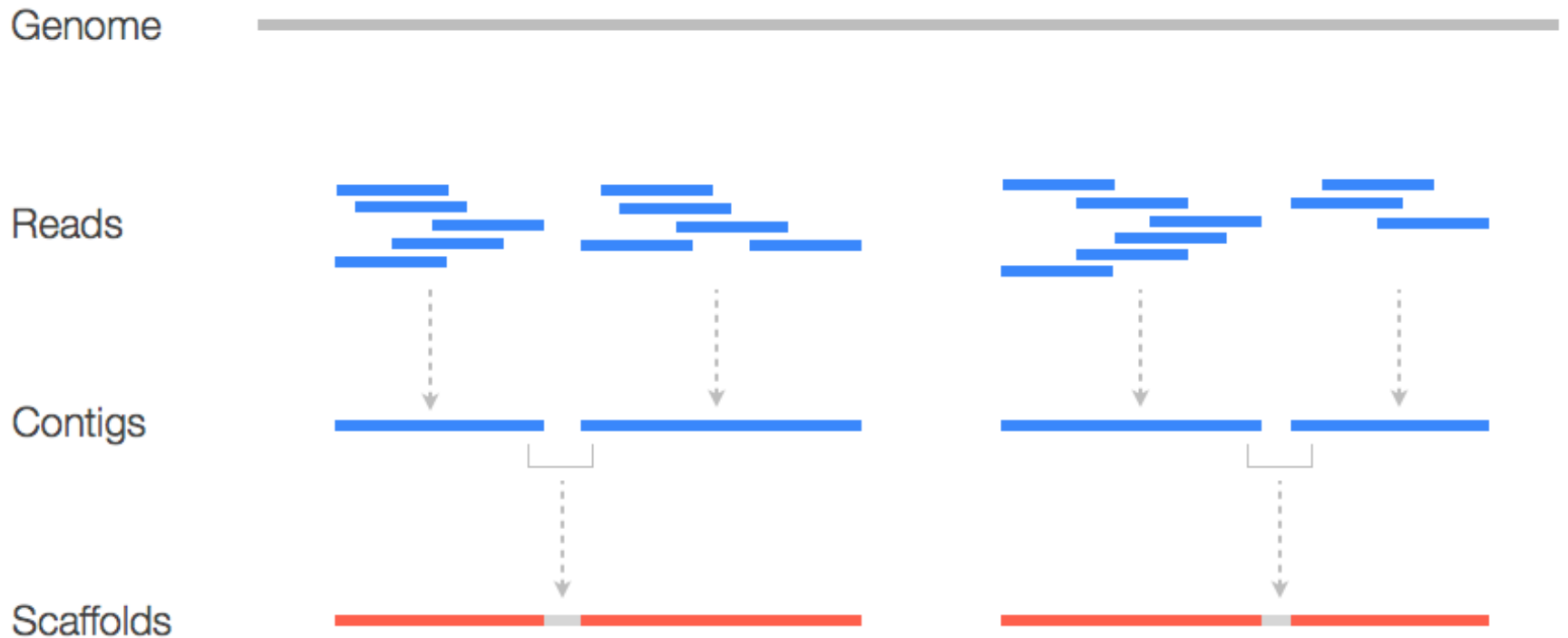
- Genomic:
 - protein-coding genes
 - transcripts
 - proteins
- Transcriptomic
- ncRNAs
- Variation (coming soon)





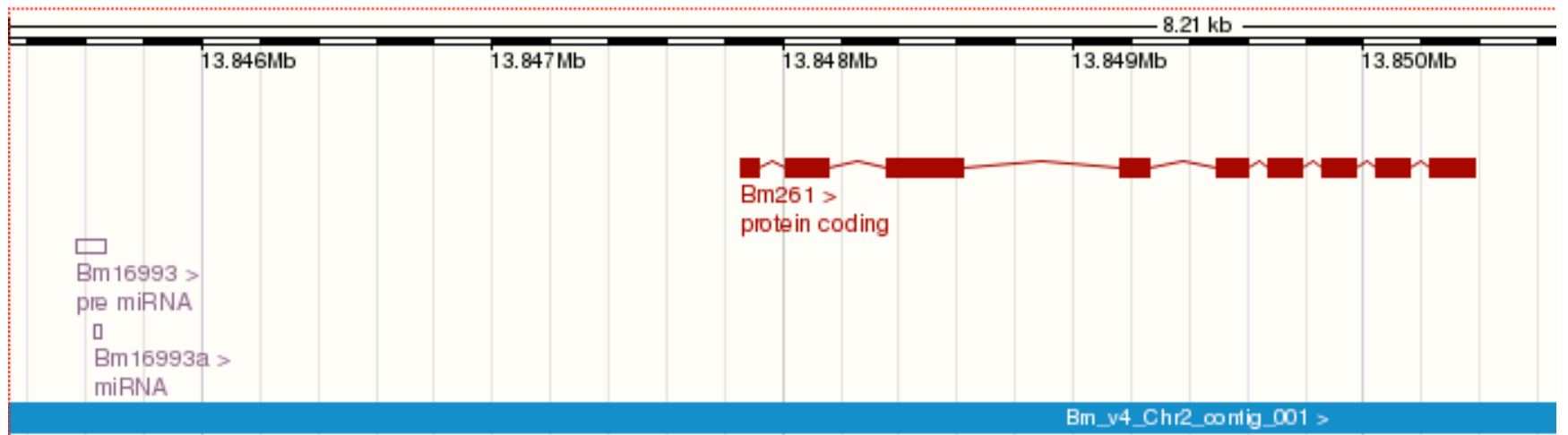
What is a genome assembly?

Genome assembly





Genome annotation





How can the data be accessed?

There are various ways for interacting with data In ParaSite:

- genome browser
- BLAST
- BioMart (data export)
- VEP
- REST API





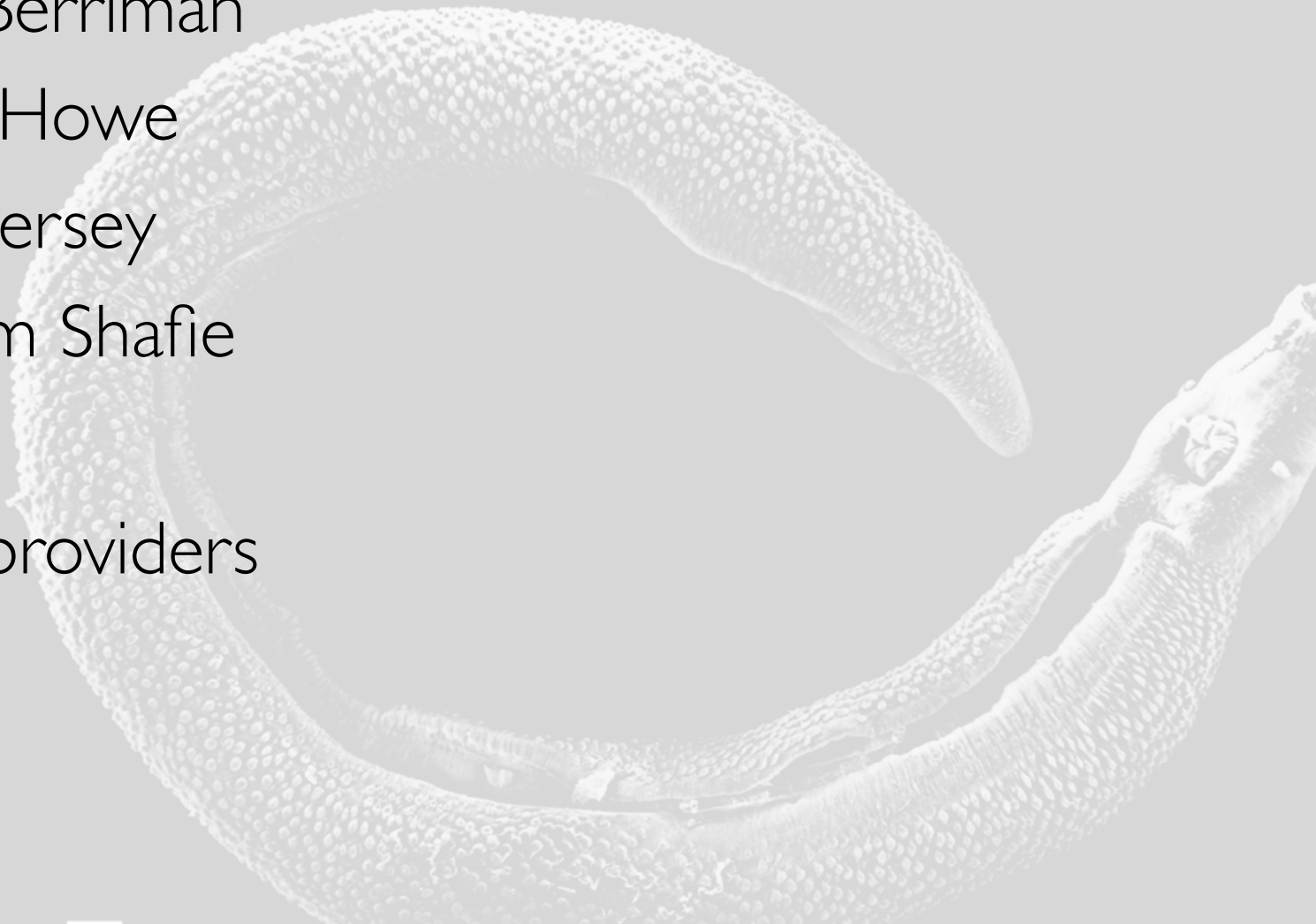
Where is WormBase ParaSite
developed?

- Joint project between Wellcome Trust Sanger Institute and WormBase team at EMBL-EBI
- BBSRC-funded
- Based on ENSEMBL technology



Acknowledgements


- Matt Berriman
- Kevin Howe
- Paul Kersey
- Myriam Shafie
- Data providers



Using the website



Summary

1. Searching
 2. Finding genomes
 3. Navigating genes, transcripts and scaffolds
 4. Comparative genomics
 5. RNASeq data tracks
 6. Adding your own data tracks
 7. User accounts
- 

I. Searching



Searching

Species



BLAST



BioMart



API



Downloads



WormBase



Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

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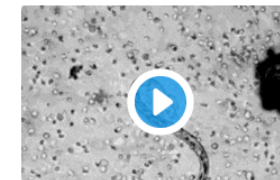
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Searching

SUGGESTED TERM
cystathionine
cystatin
cysteine
cysteines
cystinosin

Species

BLAST

BioMart

API

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WormBase

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Searching



New Search

Search WormBase ParaSite

- New Search
- Gene (485)
 - WormBase ParaSite (480)
 - WormBase (5)

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Search results for 'cystatin'

Showing 1-10 of 480 Genes found in WormBase ParaSite

Filter by species:

EEL_0000399501

Description *Cystatin* [Source:UniProtKB/TrEMBL;Acc:A0A0R3RQN0]
Gene ID [EEL_0000399501](#)
Species [Elaeophora elaphi \(PRJEB502\)](#)
Location [EEL_scaffold0000034:53318-53512](#)
Gene tree [View gene tree](#)

ALUE_0002323401

Description *Cystatin* [Source:UniProtKB/TrEMBL;Acc:A0A0M3IWW6]
Gene ID [ALUE_0002323401](#)
Species [Ascaris lumbricoides \(PRJEB4950\)](#)
Location [ALUE_scaffold0008948:353-2918](#)
Gene tree [View gene tree](#)

HPLM_0001052101

Description *Cystatin* [Source:UniProtKB/TrEMBL;Acc:A0A0N4WHX7]
Gene ID [HPLM_0001052101](#)
Species [Haemonchus placei \(PRJEB509\)](#)
Location [HPLM_scaffold0001226:46905-48974](#)
Gene tree [View gene tree](#)
***C. elegans* orthologues** [cpi-2](#), [cpi-1](#)

BPAG_0000497001

Description *Cystatin* [Source:UniProtKB/TrEMBL;Acc:A0A0N4T9T3]
Gene ID [BPAG_0000497001](#)
Species [Brugia pahangi \(PRJEB497\)](#)
Location [BPAG_contig0002942:40-2465](#)
Gene tree [View gene tree](#)

Searching

WormBase ParaSite

Species List BLAST BioMart REST API

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Search WormBase ParaSite

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 - WormBase ParaSite (480)
 - WormBase (5)

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Showing 1-10 of 480 results

Filter by species

EEL_000399	Description	nydaturiga taeniaiformis (PRJEB534)
	Gene ID	Hymenolepis diminuta (PRJEB507)
	Species	Hymenolepis microstoma (PRJEB124)
	Location	Hymenolepis nana (PRJEB508)
	Gene tree	Litomosoides sigmodontis (PRJEB3075)
		Loa loa (PRJNA246086)
		Loa loa (PRJNA60051)
		Meloidogyne floridensis (PRJEB6016)
		Meloidogyne hapla (PRJNA29083)
		Mesocostoides corti (PRJEB510)
		Necator americanus (PRJNA72135)
		Nippostrongylus brasiliensis (PRJEB511)
		Oesophagostomum dentatum (PRJNA72579)
		Onchocerca flexuosa (PRJEB512)
		Onchocerca ochengi (PRJEB1204)
		Onchocerca ochengi (PRJEB1809)
		Onchocerca volvulus (PRJEB513)
		Opisthorchis viverrini (PRJNA22628)
		Panagrellus redivivus (PRJNA186477)
		Parastrongyloides trichosuri (PRJEB515)
		Pristionchus exspectatus (PRJEB6009)
		Pristionchus pacificus (PRJNA12644)
		Protopolystoma xenopodis (PRJEB1201)
		Rhabditophanes sp. KR3021 (PRJEB1297)
		Romanomeris culicivora (PRJEB1358)
		Schistocephalus solidus (PRJEB527)
		Schistosoma haematobium (PRJNA78265)
		Schistosoma japonicum (PRJEA34885)
		Schistosoma mansoni (PRJEA36577)
		Schistosoma margrebowiei (PRJEB522)
		Schistosoma rodhaini (PRJEB526)
		Schmidtea mediterranea (PRJNA12585)
		Soboliphyme baturini (PRJEB516)
		Spirometra erinaceieuropaei (PRJEB1202)
		Steinernema carpocapsae (PRJNA202318)
		Steinernema feltiae (PRJNA204661)
		Steinernema glaseri (PRJNA204943)
		Steinernema monticolum (PRJNA205067)
		Steinernema scapteris (PRJNA204942)
		Strongyloides papillosus (PRJEB525)
		Strongyloides ratti (PRJEB125)
		Strongyloides stercoralis (PRJEB528)
		Strongyloides venezuelensis (PRJEB530)
		Strongylus vulgaris (PRJEB531)
		Syphacia muris (PRJEB524)
		Taenia asiatica (PRJEB532)
		Taenia solium (PRJNA170813)
		Teladorsagia circumcincta (PRJNA72569)
		Thelazia callipaeda (PRJEB1205)
		Toxocara canis (PRJEB533)
		Trichinella nativa (PRJNA179527)
		Trichinella spiralis (PRJNA12603)
		Trichuris muris (PRJEB126)
		Trichuris suis (PRJNA179528)
		Trichuris suis (PRJNA208415)
		Trichuris suis (PRJNA208416)
		Trichuris trichiura (PRJEB535)
		Wuchereria bancrofti (PRJEB536)

Search WormBase ParaSite...

e.g. *O. volvulus*, PRJNA60051, WBGene00282434, Bma-eat-4, eat-4 or metallopeptidase

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Searching



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Search WormBase ParaSite

- New Search
- Gene (485)
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 - WormBase (5)

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Search results for 'cystatin'

Showing 6 Genes found in WormBase ParaSite (filtered)

Filtered by species: **Strongyloides ratti (PRJEB125)** ✕

SRAE_2000370000 [WBGene00263925]

Description Proteinase inhibitor I25, *cystatin* domain-containing protein [Source:UniProtKB/TrEMBL;Acc:A0A090LLJ9]
Gene ID [WBGene00263925](#)
Species [Strongyloides ratti \(PRJEB125\)](#)
Location [SRAE_chr2:11581338-11581697](#)
[\[View region in WormBase JBrowse\]](#)
Gene tree [View gene tree](#)
C. elegans orthologues [cpi-2](#), [cpi-1](#)

SRAE_2000495700 [WBGene00265204]

Description Proteinase inhibitor I25, *cystatin* domain-containing protein [Source:UniProtKB/TrEMBL;Acc:A0A090LQ75]
Gene ID [WBGene00265204](#)
Species [Strongyloides ratti \(PRJEB125\)](#)
Location [SRAE_chr2:15634295-15634777](#)
[\[View region in WormBase JBrowse\]](#)
Gene tree [View gene tree](#)


SRAE_X000107250 [WBGene00266636]

Description Proteinase inhibitor I25, *cystatin* domain-containing protein [Source:UniProtKB/TrEMBL;Acc:A0A090KVQ2]
Gene ID [WBGene00266636](#)
Species [Strongyloides ratti \(PRJEB125\)](#)
Location [SRAE_chrX_scaffold2:377256-379294](#)
[\[View region in WormBase JBrowse\]](#)

SRAE_2000523500 [WBGene00265495]

Description Proteinase inhibitor I25, *cystatin* domain-containing protein [Source:UniProtKB/TrEMBL;Acc:A0A090LLL2]
Gene ID [WBGene00265495](#)
Species [Strongyloides ratti \(PRJEB125\)](#)
Location [SRAE_chr2:16571628-16571924](#)
[\[View region in WormBase JBrowse\]](#)

Searching

Advanced

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UniProtKB - G4VBC8 (G4VBC8_SCHMA)

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Display

- Entry
- Feature viewer
- Feature table

None

- Function
- Names & Taxonomy
- Subcellular location
- Pathology & Biotech
- PTM / Processing
- Expression
- Interaction
- Structure
- Family & Domains
- Sequence
- Cross-references
- Publications
- Entry information
- Miscellaneous
- Similar proteins

[Top](#)

Protein Submitted name: **Putative cystatin**

Gene **Smp_034420.1**

Organism *Schistosoma mansoni* (Blood fluke)

Status Unreviewed - Annotation score: ○○○○ - Protein predictedⁱ

Functionⁱ

GO - Molecular functionⁱ

- cysteine-type endopeptidase inhibitor activity [Source: InterPro](#)

[Complete GO annotation...](#)

Searching

G4VBC8



e.g. *O. volvulus*, PR:INA0051, WBGen00282434, Bma-ant-4, eat-4 or metalloproteinase

Species

BLAST

BioMart

API

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WormBase

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Searching

New Search

Search WormBase ParaSite

- New Search
- Gene (1)
 - WormBase ParaSite (1)
 - WormBase (0)

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Search results for 'G4VBC8'

Showing 1 Gene found in WormBase ParaSite
Smp_034420

Description	DIF_6; Putative cystatin [Source:UniProtKB/TrEMBL;Acc:B8Y6H4]
Gene ID	Smp_034420
Species	Schistosoma mansoni (PRJEA36577)
Location	Smp.Chr. 2:7321609-7322171
Gene tree	View gene tree

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2. Finding genomes



Finding a genome

Species 	BLAST 	BioMart 
API 	Downloads 	WormBase 

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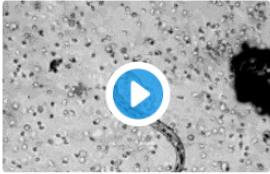
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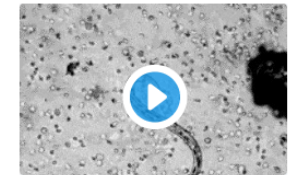
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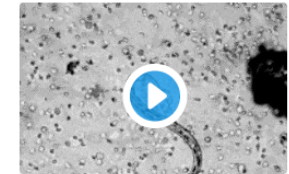
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pic.twitter.com/zqAIUZMYDx



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Release 6 - April 2016



WormBase ParaSite is funded by the [UK Biotechnology and Biological Sciences Research Council](#) under grant numbers BB/K020080/1 and BB/K020048/1.

Finding a genome


WormBase ParaSite

Version: WBPS6 (WS252)


Search WormBase ParaSite...
e.g. *O. volvulus*, PFLJNA60051, WBGene00262434, Bma-eat-4, eat-4 or metalloproteinase

Species List BLAST BioMart REST API VEP Downloads WormBase Login Register Help and Documentation


Species




BLAST




BioMart




API



Downloads



WormBase



Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

Statistics

- Version: WBPS6 (April 2016)
- WormBase Version: WS252
- 109 genomes, representing 100 species
- 2,189,841 genes

Announcements

Announcing WormBase ParaSite release 6

posted 2 months ago

We are pleased to announce the sixth release of WormBase ParaSite.

Blog

Featured Paper: Glucose and Glycogen Metabolism in *B. malayi* Is Associated with Wolbachia Symbiont Fitness

posted 1 month ago

We would like to draw your attention to a paper published by Denis Voronin, et. al on the influence of host metabolism on symbiont fitness: Denis Voronin, Saheed Bachu, Michael Shlossman, Thomas R. Unnasch, Elodie Ghedin, Sara Lustigman "Glucose and Glycogen Metabolism in *Brugia malayi* Is Associated with Wolbachia Symbiont Fitness", PLoS One. 2016 Apr [...]

Brugia malayi assembly update

posted 2 months ago

The new release of WormBase (WS252) is the first one to feature the new and updated version 4 of the *Brugia malayi* assembly. Due to additional optical mapping, as well as new long-range PacBio sequencing and additional reassembly work conducted to integrate all available data, it was possible to scaffold the 88.2Mbp assembly into 5 chromosomes [...]

Register for a WormBase ParaSite workshop

posted 2 months ago

To help our users make the most of this valuable resource, we are visiting universities and institutes to provide hands-on training sessions.

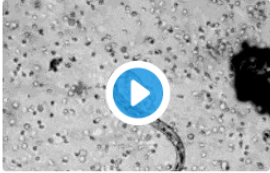
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WormBase ParaSite is funded by the UK Biotechnology and Biological Sciences Research Council under grant numbers BB/K020080/1 and BB/K020048/1.

Genomes list



Species List

Contents

[Nematoda \(80\)](#)
[Platyhelminthes \(29\)](#)

Nematoda

Species Name	Provider	Assembly	BioProject ID	Taxonomy ID
Acanthocheilonema viteae	University of Edinburgh	nAv.1.0	PRJEB4306	6277
Ancylostoma caninum	Genome Institute at Washington University	A_caninum_9.3.2.ec.cg.pg	PRJNA72585	29170
Ancylostoma ceylanicum	Cornell University	Acey_2013.11.30.genDNA	PRJNA231479	53326
Ancylostoma ceylanicum	Genome Institute at Washington University	A_ceylanicum1.3.ec.cg.pg	PRJNA72583	53326
Ancylostoma duodenale	Genome Institute at Washington University	A_duodenale_2.2.ec.cg.pg	PRJNA72581	51022
Angiostrongylus cantonensis	Wellcome Trust Sanger Institute	A_cantonensis_Taipei_v1_5_4	PRJEB493	6313
Angiostrongylus costaricensis	Wellcome Trust Sanger Institute	A_costaricensis_Costa_Rica_v1_5_4	PRJEB494	334426
Anisakis simplex	Wellcome Trust Sanger Institute	A_simplex_v1_5_4	PRJEB496	6269
Ascaris lumbricoides	Wellcome Trust Sanger Institute	A_lumbricoides_Ecuador_v1_5_4	PRJEB4950	6252
Ascaris suum	University of Colorado School of Medicine	ASU_2.0	PRJNA62057	6253
Ascaris suum	University of Melbourne	AscSuum_1.0_submitted	PRJNA80881	6253
Brugia malayi	WormBase	Bmal-4.0	PRJNA10729	6279
Brugia pahangi	Wellcome Trust Sanger Institute	B_pahangi_Glasgow_v1_5_4	PRJEB497	6280
Brugia timori	Wellcome Trust Sanger Institute	B_timori_Indonesia_v1_0_4	PRJEB4663	42155
Bursaphelenchus xylophilus	Wellcome Trust Sanger Institute	ASM23113v1_submitted	PRJEA64437	6326
Caenorhabditis angaria	WormBase	13mar2012	PRJNA51225	860376
Caenorhabditis brenneri	WormBase	C_brenneri-6.0.1b	PRJNA20035	135651
Caenorhabditis briggsae	WormBase	CB4	PRJNA10731	6238
Caenorhabditis elegans	WormBase	WBcel235	PRJNA13758	6239
Caenorhabditis japonica	WormBase	C_japonica-7.0.1	PRJNA12591	281687

Genome pages

Schistosoma mansoni (PRJEA36577) ▾

Schistosoma mansoni

BioProject [PRJEA36577](#) | Data Source [Wellcome Trust Sanger Institute](#) | Taxonomy ID [6183](#)

Search Schistosoma mansoni (PRJEA36577)...

About Schistosoma mansoni

The trematode *Schistosoma mansoni* is one of the three major infectious agents responsible for the chronic debilitating disease schistosomiasis found throughout Africa and South America. The intermediate host for the parasite is a freshwater snail from the genus Biomphalaria, and the definitive host is a human. Schistosomiasis is widely considered to be second only to malaria as a global health problem and an incalculable drain on the economic development of endemic countries.

Genome assembly: [ASM23792v2](#)

The *S. mansoni* reference genome was sequenced by a consortium led by the Wellcome Trust Sanger Institute, as described by [Berriman et al. \(2009\)](#). The assembly version represented here is the v5.0 freeze from [GeneDB](#) (December 2013), published in [Protasio et al 2012](#) and which corresponds with INSDC assembly [ASM23792v2](#).



Example region

Gene annotation

The gene predictions were initially made by a consortium led by the Wellcome Trust Sanger Institute, as described by [Berriman et al. \(2009\)](#). The gene models have since been iteratively improved, and the version represented here is the v5.0 freeze from [GeneDB](#) (December 2013) and described in [Protasio et al 2012](#).



Example gene

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

Comparative genomics

What can I find? Orthologues, paralogues, and gene trees across multiple species.

More information and statistics



Example gene tree

Key Publications

Berriman M, Haas BJ, LoVerde PT, Wilson RA, Dillon GP, Cerqueira GC, Mashiyama ST, Al-Lazikani B, Andrade LF, Ashton PD, Aslett MA, Bartholomew DC, Blandin G, Caffrey CR, Coghlan A, Coulson R, Day TA, Delcher A, DeMarco R, Djikeng A, Eyre T, Gamble JA, Ghedin E, Gu Y, Hertz-Fowler C, Hirai H, Hirai Y, Houston R, Ivans A, Johnston DA, Lacerda D, Macedo CD, McVeigh P, Ning Z, Oliveira G, Overington JP, Parkhill J, Pertea M, Pierce RJ, Protasio AV, Quail MA, Rajandream MA, Rogers J, Sajid M, Salzberg SL, Stanke M, Tivey AR, White O, Williams DL, Wortman J, Wu W, Zamanian M, Zerlotini A, Fraser-Liggett CM, Barrell BG, El-Sayed NM. [The genome of the blood fluke Schistosoma mansoni](#). *Nature*, 2009;460(7253):352-358

Protasio AV, Tsai IJ, Babbage A, Nichol S, Hunt M, Aslett MA, De Silva N, Velarde GS, Anderson TJ, Clark RC, Davidson C, Dillon GP, Holroyd NE, LoVerde PT, Lloyd C, McQuillan J, Oliveira G, Otto TD, Parker-Manuel SJ, Quail MA, Wilson RA, Zerlotini A, Dunne DW, Berriman M. [A systematically improved high quality genome and transcriptome of the human blood fluke Schistosoma mansoni](#). *PLoS Negl Trop Dis*, 2012;6(1):e1455

Statistics

Summary

Assembly:	ASM23792v2, GCA_000237925.2
Database version:	84.1
Base Pairs:	362,511,929
Genome Size:	364,538,298
Data source:	Wellcome Trust Sanger Institute
Genebuild version:	2014-05-WormBase

Gene counts

Coding genes:	10,831
Gene transcripts:	11,828

Downloads

- [Genomic Sequence \(FASTA\)](#)
- [Hard-masked Genomic Sequence \(FASTA\)](#)
- [Soft-masked Genomic Sequence \(FASTA\)](#)
- [Annotations \(GFF3\)](#)
- [Proteins \(FASTA\)](#)
- [Full-length transcripts \(FASTA\)](#)
- [CDS transcripts \(FASTA\)](#)

Tools

- [Search for sequences in the genome and proteome using BLAST](#)
- [Work with lists of data using the WormBase ParaSite BioMart data-mining tool](#)
- [Programmatically access WormBase ParaSite data using the REST API](#)
- [Predict the effects of variants using the Variant Effect Predictor](#)

3. Navigating genes, transcripts and scaffolds



Gene pages

Schistosoma mansoni (PRJEA36577) Location: Smp.Chr._4:31,987,438-31,988,870 Gene: SAT1 Transcript: Smp_090120.1

- Gene-based displays
 - Summary
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 - Sequence
 - External references
 - Ontology
 - GO: biological process
 - GO: molecular function
 - GO: cellular component
 - Comparative Genomics
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 - Paralogues
- Configure this page
- Add your data
- Export data
- Share this page
- Bookmark this page

Gene: SAT1 Smp_090120

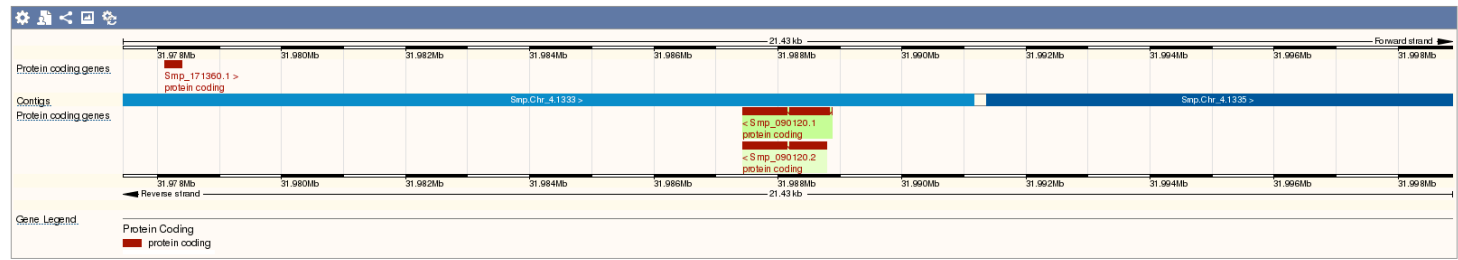
Description Putative alpha tubulin (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VHT1]
Location Scaffold Smp.Chr_4:31,987,438-31,988,870 reverse strand.
About this gene This gene has 2 transcripts ([splice variants](#)), [358 orthologues](#) and [4 paralogues](#).
Gene type Protein coding
Annotation Method Gene models from Wellcome Trust Sanger Institute [Reference Helminth Genomes project](#)
Transcripts [Hide transcript table](#)

Show/hide columns (1 hidden)

Name	Transcript ID	bp	Protein	Translation ID	Biotype	UniProt
Novel	Smp_090120.1	1356	451aa	Smp_090120.1	Protein coding	G4VHT1 Q26595
Novel	Smp_090120.2	1311	436aa	Smp_090120.2	Protein coding	G4VHT1

Summary

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



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

Viewing sequence

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e.g. *O. volvulus*, PRJNA60051, WBGene00262434, Ema-eat-4, eat-4 or metallopeptidase
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Schistosoma mansoni (PRJEA36577) Location: Smp.Chr_4:31,987,438-31,988,870 Gene: SAT1

Gene-based displays

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- Sequence**
- External references
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 - GO: Cellular component
 - GO: Biological process
- Comparative Genomics
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 - Paralogues

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Gene: SAT1 Smp_090120

Description Putative alpha tubulin (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VHT1]

Location Scaffold Smp.Chr_4: 31,987,438-31,988,870 reverse strand.

About this gene This gene has 2 transcripts ([splice variants](#)), [340 orthologues](#) and [4 paralogues](#).

Gene type Protein coding

Annotation Method Gene models from Wellcome Trust Sanger Institute [Reference Helminth Genomes project](#)

Transcripts [Show transcript table](#)

Marked-up sequence

[Download sequence](#) [BLAST this sequence](#)


Exons SAT1 exons All exons in this region

```
>scaffold:ASM23792v2:Smp.Chr_4:31986838:31989470:-1
GAGACTGCATCTCCTCAGCATGATCCACTGCCTTATAGATCAGATCTTTGAGTCAAAGGC
TCCAGGTGTGGCCTCCTAAAAAACTATCTGCTTCAGTTTGGTCACTGGTCAGTATCAC
ATCCCTCACACAAATCAAATGAGATTTGTGTGGCGCATATGTATCTGATGCTTCTTTGTA
CCAAATTTTATATGTTTAAATAAATAAATAAATTTCAATTATTGCTTCATCAGGTCAAT
CATGAGAATATTATCTTTGGGCTCTTCATGAAATTCAGATATGAAGTCAAATACAGGC
TGAATAAGGCGGTTTGGTTCCTTTTTTTTTTCCACCATCCATTCAAATGGCAACATAAA
TTTTCCAAATATATTCACCTCCAGTTTGAAGTAAGAACAATAGAATTCCTAGAAATGAA
GACATAACATTAATTAACCAATCAACGCAAGTAATGGTAATGAATTAACCAATAGAAT
TTAAATAATAGATGTTCAATAACATATAATAACATGAGGCGGCCATATTTGTTAGATTC
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ATGTTAAGCAATGAATAACATTTAATTTATATTTACACCGTGAATGATCAGTGTAC
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ATGGTATCAACCTGATGGACAGATGCCAAGTGATAAACTATTGGAGGTGGTATGACT
CGTTCAATACATCTTCAGTGAGACAGGAGCTGGAAAACATGTGCCACGAGCTTTTTCC
```

Viewing sequence

Gene-based displays

- Summary
- Splice variants
- Sequence**
- External references
- Ontologies
 - GO: Molecular function
 - GO: Cellular component
 - GO: Biological process
- Comparative Genomics
 - Gene tree
 - Orthologues
 - Paralogues



Marked-up sequence

[Download sequence](#) [BLAST this sequence](#)

Exons SAT1 exons All exons in this region

```
>scaffold:ASM23792v2:Smp.Chr_4:31986838:31989470:-1
GAGACTGCATCTCCTCACGATGATCCACTGCCTTAGATCAGATCTTTGAGTCAAAGGC
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ATCCCTCACACAAATCAAATGAGATTTGTGGGCGCATATGTATCTGATGCTCTTTGTA
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ATGTTGGTCAAGCTGGTGTACAATGGGAAATGCTTGTGGGAGTGTATGTTTGAAC
ATGGTATTCACCTGATGGACAGATGCCAAGTGTAAACTATTGGAGGTGGTGTGACT
CGTCAAEACATTTCTCAGTGAGACAGGAGCTGGAAACATGTCCACGAGCTGTTTTCG
TAGATTTAGAACCAACTGTAGTAGAAGTGCAGCTGGAACCTTATCGTCACTTTTTCC
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CCATTTATGATATTTGTCGTAAGTTGCTGTTTCAGTGAATTAACAATGTTTTTAGAC
GGAATCTAGATATAGAGCGTCCAACCTACACAAATTAATCGTCAATTTGGTCAGATAG
TGAGTTCATTAAGTGCATCACTGCGCTTCGATGGTGGCCTAAATGGGATTTGACGGAAT
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TAAAACTAAACGTACTATCCAGTTTGGGATTTGGTCCAAACAGGTTCAAGGTAGGTA
TAAACTACCAACCACCAACAGTTGCTTGGCGGTTGTTGGCAAAAGTTCAACGTGCTG
TCTGTATGTTGAGTAATACAACCGCAATAGCCGAGCTGGGCGGCTCAGATATAAAT
TTGATTTGATGTACGCAAAACGTCGCTTTGTACACTGGTATGTTGGTGAAGGTATGGAAG
AGGGTGAATTCCTGAGGCTCGTGAAGATCTGGCCGCACTTGAGAAAGATTACGAGGAGG
TCGGTGTGACAGCGTTGATGGCGAGGCGCAAGGGGAAGGTGAAGATATTAGTTTCAT
TTCTTTTGGTGTATGTTTTCTGGTTGTACTGCTTCCATAATACTTATCTATAACTA
CTTGTGGTTTTTCCGTGTGCCATTTGTGCAATGCTGTGGAGTTTTCCCTGTGTAGCGTCT
TAACTGTTGATAAGACTAGCATCTAATATAGGCTTTTTGATTAAGGTAAGTTGCTTAAAA
CATTCCACTGGTGCCAACGCACTACTAAACGAGTACTAGATGCTCTTGGAAATGAATTA
```

GO terms

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Schistosoma mansoni (PRJEA36577) Location: Smp.Chr_4:31,987,438-31,988,870 Gene: SAT1

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Annotation Method Gene models from Wellcome Trust Sanger Institute [Reference Helminth Genomes project](#)

Transcripts [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Biotype	UniProt
Novel	Smp_090120.1	1356	451aa	Protein coding	G4VHT1 Q26595
Novel	Smp_090120.2	1311	436aa	Protein coding	G4VHT1

GO: Molecular function

Accession	Term	Evidence	Annotation Source	Transcript IDs
GO:0000166	nucleotide binding	IEA	UniProtKB/TrEMBL:Q26595_SCHMA	Smp_090120.1 Smp_090120.2 • Search Biomart
GO:0003924	GTPase activity	IEA	UniProtKB/TrEMBL:Q26595_SCHMA	Smp_090120.1 Smp_090120.2 • Search Biomart
GO:0005200	structural constituent of cytoskeleton	IEA	UniProtKB/TrEMBL:Q26595_SCHMA	Smp_090120.1 Smp_090120.2 • Search Biomart
GO:0005525	GTP binding	IEA	UniProtKB/TrEMBL:Q26595_SCHMA	Smp_090120.1 Smp_090120.2 • Search Biomart

Transcripts



Brugia malayi (PRJNA10729) Location: Bmal_v3_scaffold83:109,351-111,179 Gene: Bm97 **Transcript: Bm97.2** [\[View at WormBase central\]](#)

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 - Domains & features
- External data

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Transcript: Bm97.2

Description Larval allergen [Source:UniProtKB/TrEMBL;Acc:Q8IS06]

Location [SuperContig Bmal_v3_scaffold83:109,351-111,177](#) reverse strand.

About this transcript This transcript has [5 exons](#) and is annotated with [7 domains and features](#).

Gene This transcript is a product of gene [WBGene00220358](#) [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Translation ID	Biotype	UniProt
Bm97.2	Bm97.2	975	247aa	Bm97.2	Protein coding	Q8IS06
Bm97.1	Bm97.1	965	247aa	Bm97.1	Protein coding	Q8IS06

Summary

Statistics Exons: 5 Coding exons: 4 Transcript length: 975 bps Translation length: 247 residues

Prediction Method Protein-coding model imported from [WormBase](#)

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Transcripts

Brugia malayi (PRJNA10729) Location: Bmal_v3_scaffold83:109,351-111,179 Gene: Bm97 Transcript: **Bm97.2** [\[View at WormBase central\]](#)

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Transcript: Bm97.2

Description Larval allergen [Source:UniProtKB/TrEMBL;Acc:Q8I506]

Location [SuperContig Bmal_v3_scaffold83:109,351-111,177](#) reverse strand.

About this transcript This transcript has [5 exons](#) and is annotated with [7 domains and features](#).

Gene This transcript is a product of gene [WBGene00220358](#) [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Translation ID	Biotype	UniProt
Bm97.2	Bm97.2	975	247aa	Bm97.2	Protein coding	Q8I506
Bm97.1	Bm97.1	965	247aa	Bm97.1	Protein coding	Q8I506

Summary

Statistics Exons: 5 Coding exons: 4 Transcript length: 975 bps Translation length: 247 residues

Prediction Method Protein-coding model imported from [WormBase](#)

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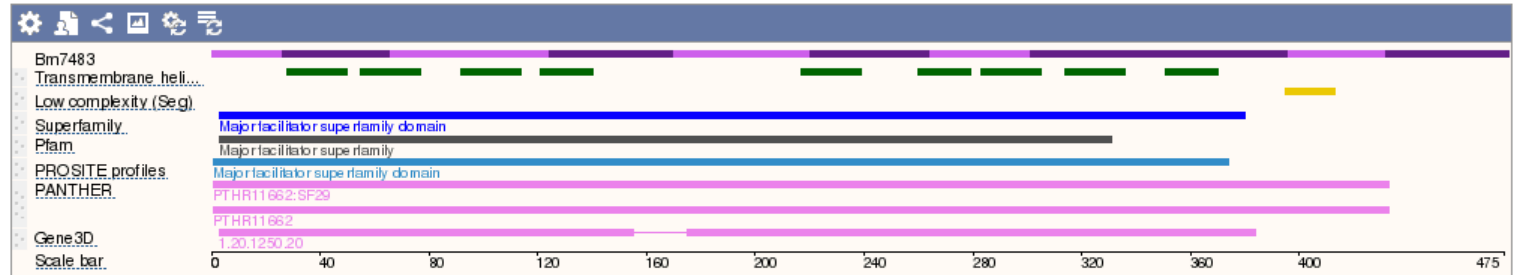
protein domains

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Protein summary

Protein domains for Bm7483.1



Statistics

Ave. residue weight: 109.833 g/mol
Charge: 4.5
Isoelectric point: 7.7239
Molecular weight: 52,170.59 g/mol
Number of residues: 475 aa

Location

WormBase ParaSite Search WormBase ParaSite...
e.g. *O. volvulus*, PRJNA60051, WBGene00262434, Bma-eat-4, eat-4 or metalloproteinase

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Brugia malayi (PRJNA10729) Location: Bmal_v3_scaffold83:109,351-111,179 Gene: Bm97 Transcript: Bm97.2

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- External data

Transcript: Bm97.2

Location [SuperContig Bmal_v3_scaffold83:109,351-111,177 reverse strand.](#)

About this transcript This transcript has [5 exons](#) and is annotated with [7 domains and features](#).

Gene This transcript is a product of gene [WBGene00220358](#) [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Biotype	UniProt
Bm97.2	Bm97.2	975	247aa	Protein coding	A0A0J9XM47 Q8IS06
Bm97.1	Bm97.1	965	247aa	Protein coding	A0A0J9XM47 Q8IS06

Summary

Statistics Exons: 5 Coding exons: 4 Transcript length: 975 bps Translation length: 247 residues

Prediction Method Protein-coding model imported from [WormBase](#)

Information

- [Help and Documentation](#)
- [Citing WormBase ParaSite](#)
- [About WormBase ParaSite](#)
- [Data Usage](#)
- [Contact Us](#)
- [Disclaimer](#)

Release 5 - January 2016

EMBL-EBI

WormBase ParaSite is funded by the [UK Biotechnology and Biological Sciences Research Council](#) under grant numbers BB/K020080/1 and BB/K020048/1.

Location view: zooming

Location: Bmal_v3_scaffold83:108,886-111,920 Gene: Bm97 [\[View region in WormBase JBrowse\]](#)

SuperContig Bmal_v3_scaffold83: 74,678-76,964

S'ctg Bmal_v3_scaffold83

Region in detail

Contigs
Protein coding genes

Gene Legend
protein coding

Location: Bmal_v3_scaffold83:108886-111920 Go Gene: Go

Contigs
Protein coding genes

%GC

Gene Legend
Protein Coding
protein coding

There are currently 15 tracks turned off.
WormBase ParaSite: Brugia malayi (PRJNA10729) version 251 (B_malayi-3.1). Supercontig Bmal_v3_scaffold83:108.886-111.920

Information
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[Citing WormBase ParaSite](#)
[About WormBase ParaSite](#)

Viewing gene/transcript info in browser

The screenshot displays the WormBase ParaSite web interface. At the top, the site logo and navigation menu are visible. The search bar contains the text "Search WormBase ParaSite...". The main navigation bar includes links for "Species List", "BLAST", "BioMart", "REST API", "Downloads", and "WormBase". The current page is for *Brugia malayi* (PRJNA10729), with the location set to "Bmal_v3_scaffold83:51,712-147,279" and the gene identified as "Bm97".

On the left side, there is a "Location-based displays" menu with options: "Whole genome", "Region in detail", "Configure this page", "Add your data", "Export data", "Share this page", and "Bookmark this page". A red arrow points to the "Region in detail" option.

The main content area is titled "SuperContig Bmal_v3_scaffold83: 109,351-111,179". Below this, there is a "Region in detail" section. The top part of this section shows a genomic map with contigs and protein coding genes. The contigs are labeled as CAPY01001590.2, CAPY01001591.2, CAPY01001592.2, and CAPY01001594.2. The protein coding genes are represented by red bars with labels such as Bm14102, Bm14104, Bm13347, Bm14103, Bm8196, Bm13965, Bm8197, Bm16940, Bma-polg-1, Bm8198, Bm8199, Bm13348, Bm13349, Bm1109, Bm97, and Bma-mps-22, Bm2317. A red arrow points to the Bm97 gene.

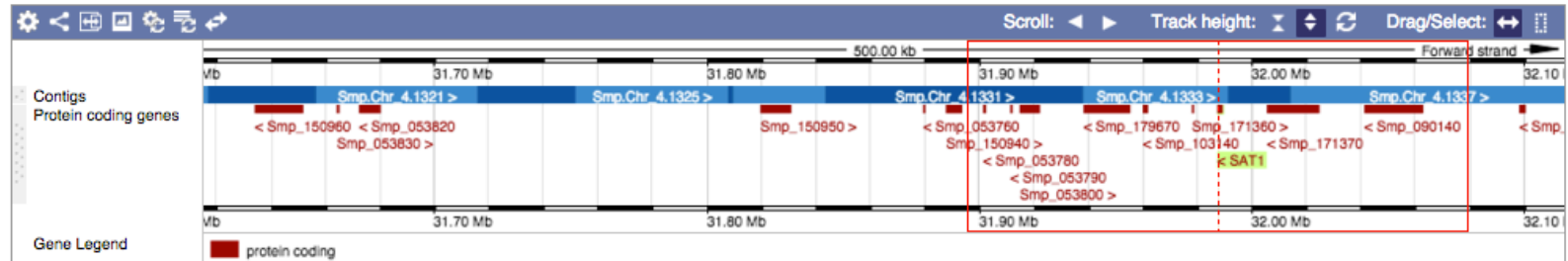
Below the genomic map, there is a "Gene Legend" section with a red square indicating "protein coding".

The bottom part of the "Region in detail" section shows a zoomed-in view of the region. The top part shows "Protein coding genes" with labels for Bm8197, Bm8199d, Bm8199b, Bm8199c, Bm13348, Bm1109, Bm2317a, Bm2317b, and Bm2317c. The middle part shows "Contigs" with labels for CAPY01001591.2, CAPY01001592.2, CAPY01001593.2, and CAPY01001594.2. The bottom part shows "%GC" content and a "Gene Legend" with a red square indicating "Protein Coding".

At the bottom of the page, there is a footer with the text: "There are currently 15 tracks turned off. WormBase ParaSite: *Brugia malayi* (PRJNA10729) version 251 (B_mabyi3.1). Supercontig Bmal_v3_scaffold83:51,712-147,279".

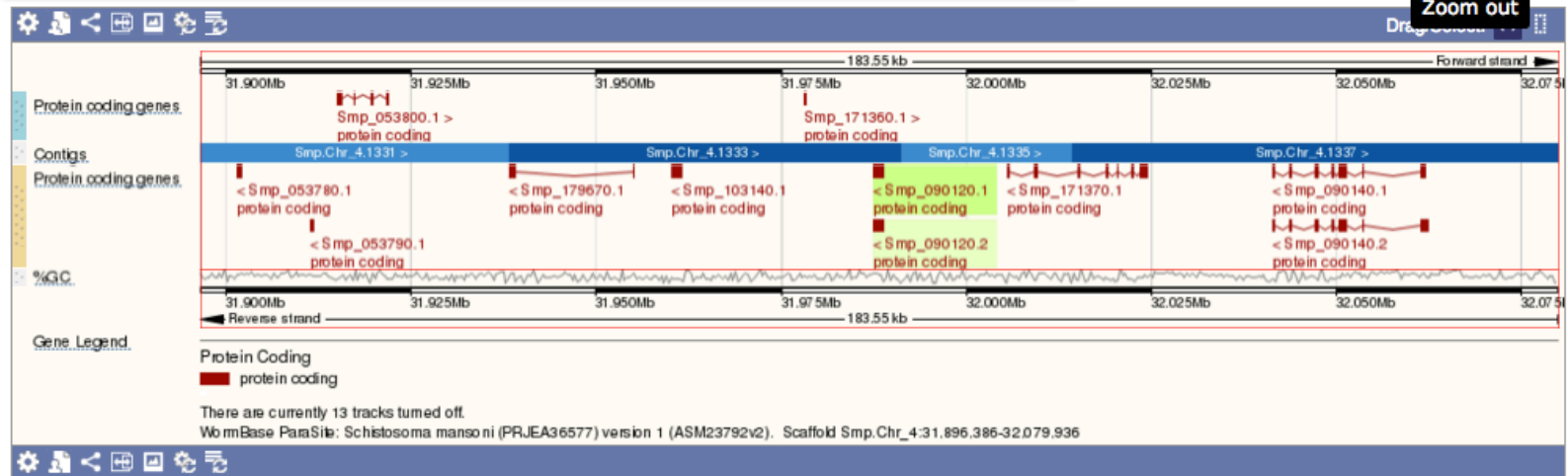
Jump to a chromosome location

Region in detail



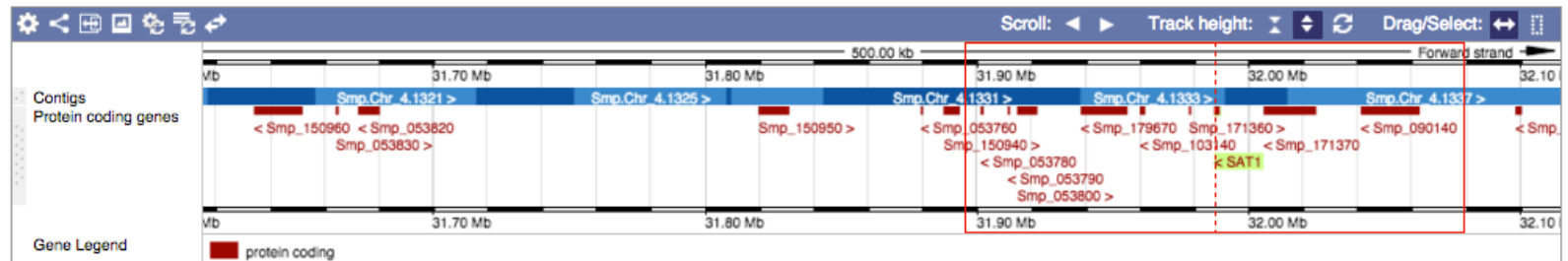
Location: Go Gene: Go

Navigation controls: Home, Previous, Next, End, Refresh, Drag/Select, Zoom in, Zoom out.

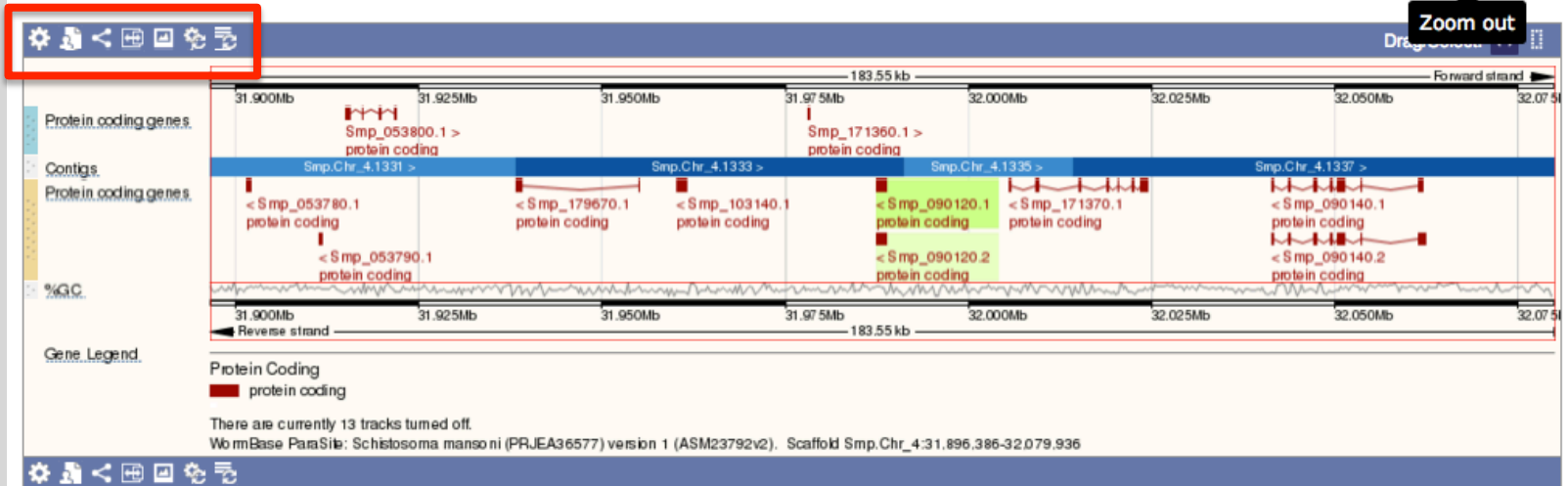


Sharing, options for browser

Region in detail



Location: Go Gene: Go



Export data



WormBase ParaSite Search WormBase ParaSite...

Species List BLAST BioMart REST API Downloads WormBase e.g. *O. volvulus*, PRJNA60051, WBGene00282434, Bma-eat-4, eat-4 or metalloproteinase

Location: Bmal_v3_scaffold83:124,072-163,019 Gene: Bm97 Login Register Help and Documentation

Location-based displays
Whole genome
Region in detail

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

SuperContig Bmal_v3_scaffold83: -352,720-147,279

Stctg Bmal_v3_scaffold83

Region in detail

Contigs
Protein coding genes

Gene Legend
protein coding

Location: Bmal_v3_scaffold83:124072-163019 Go Gene: Go

Protein coding genes

Contigs
Protein coding genes

%GC

Gene Legend
Protein Coding
protein coding

There are currently 8 tracks turned off.
WormBase ParaSite: Brugia malayi (PRJNA10729) version 251 (B_malayi3.1). Supercontig Bmal_v3_scaffold83:124.072-147.279

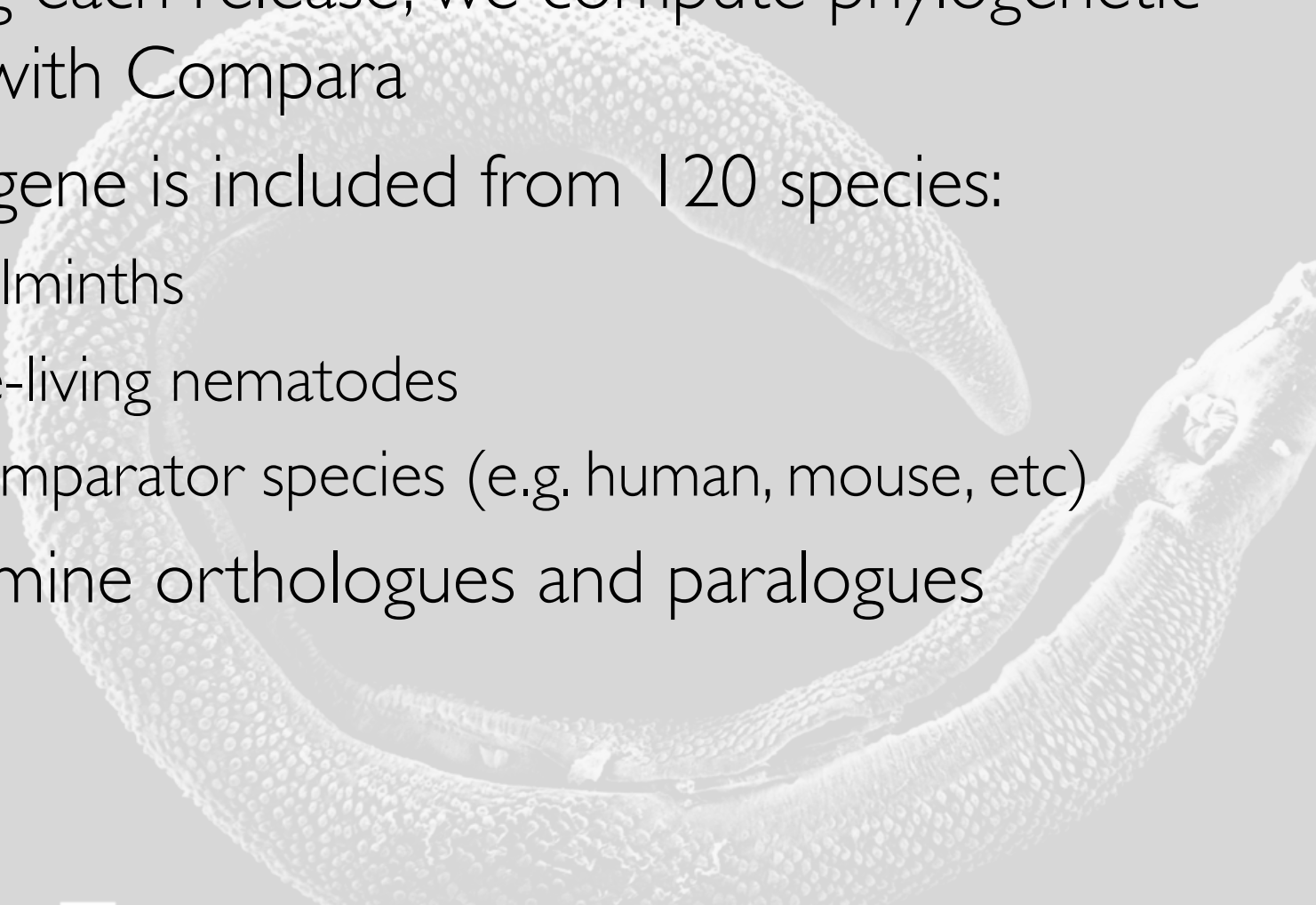
Information
Help and Documentation

4. Comparative Genomics



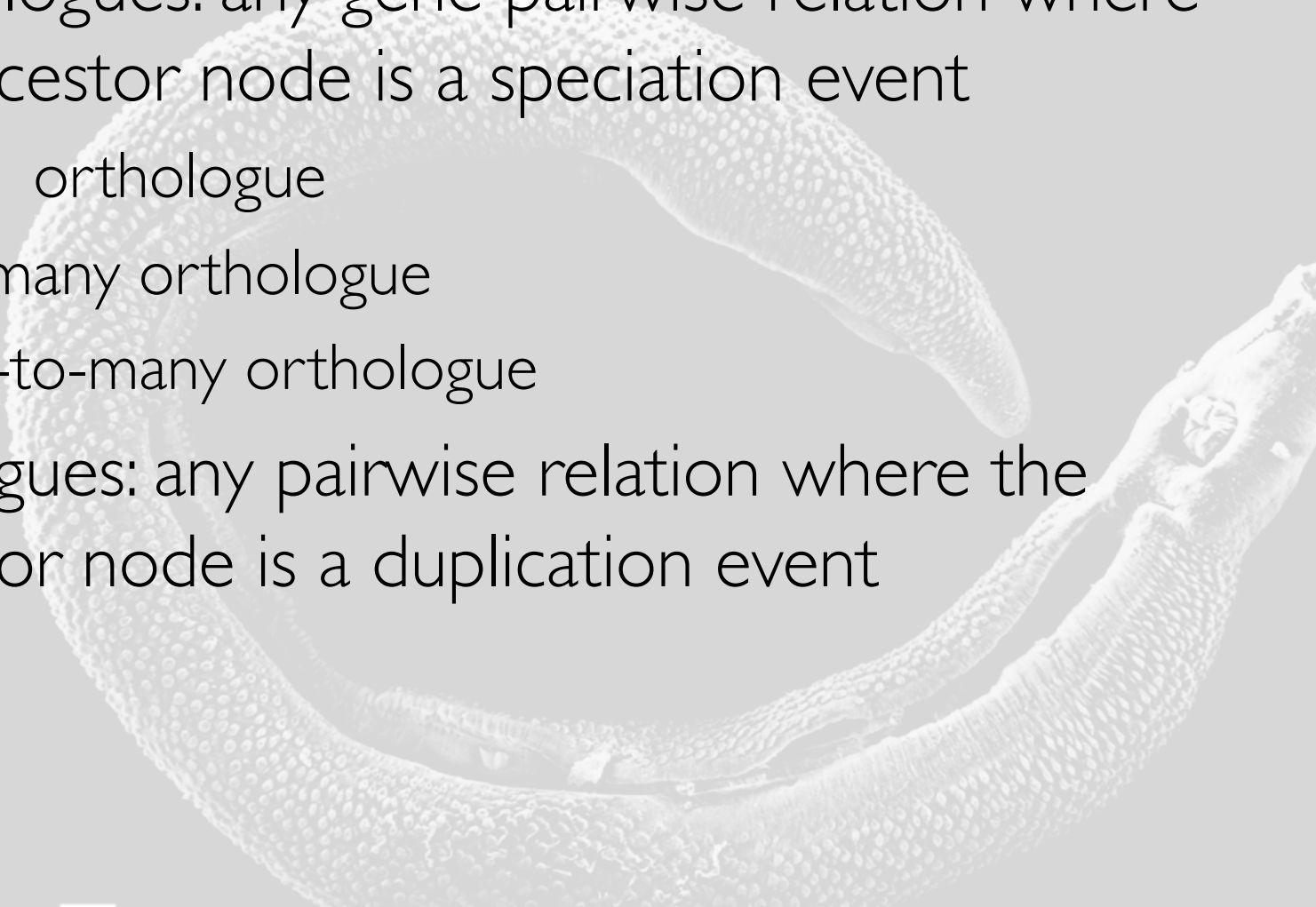
Introduction

- During each release, we compute phylogenetic trees with Compara
- Every gene is included from 120 species:
 - 99 helminths
 - 9 free-living nematodes
 - 12 comparator species (e.g. human, mouse, etc)
- Determine orthologues and paralogues

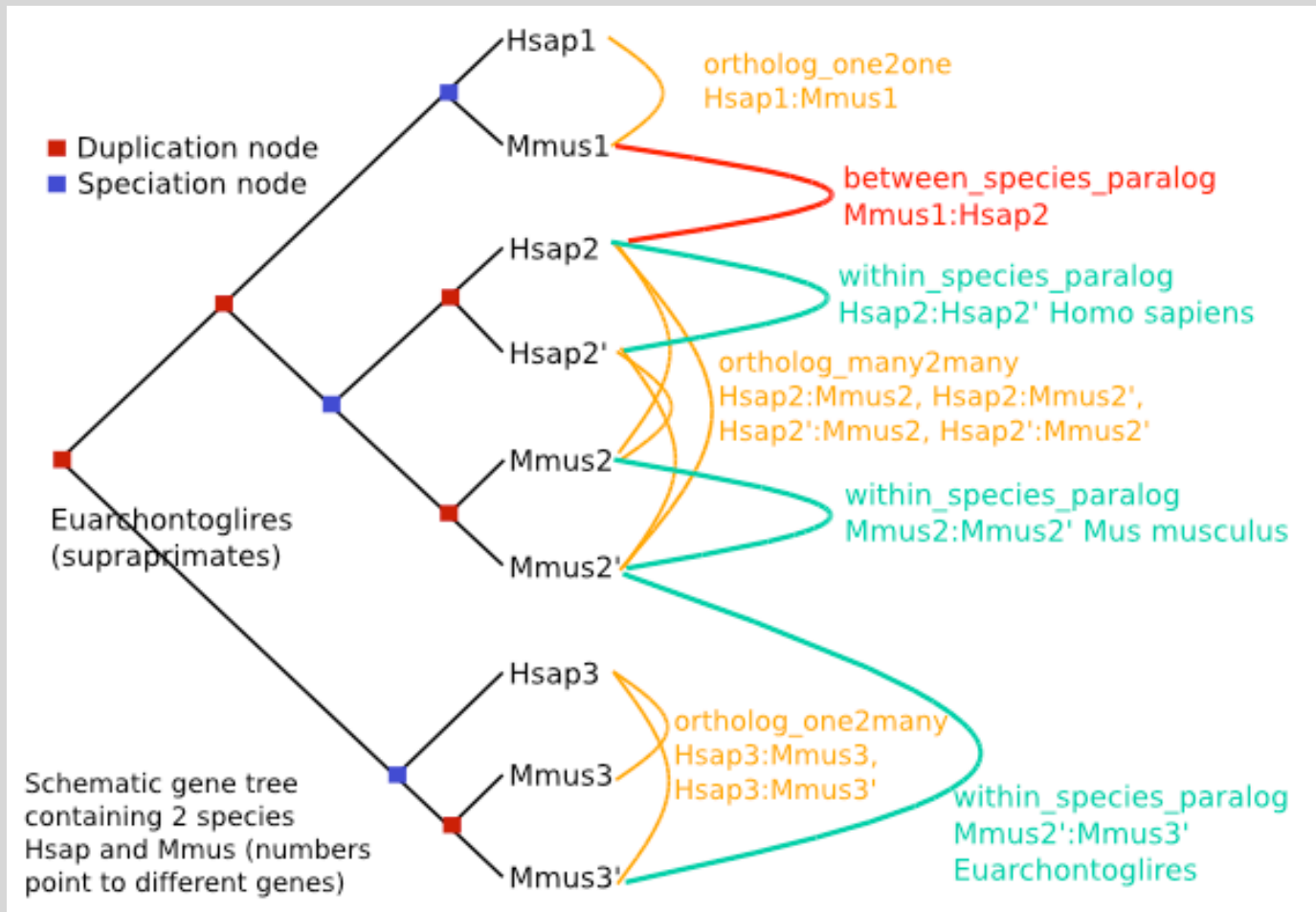


Homology types

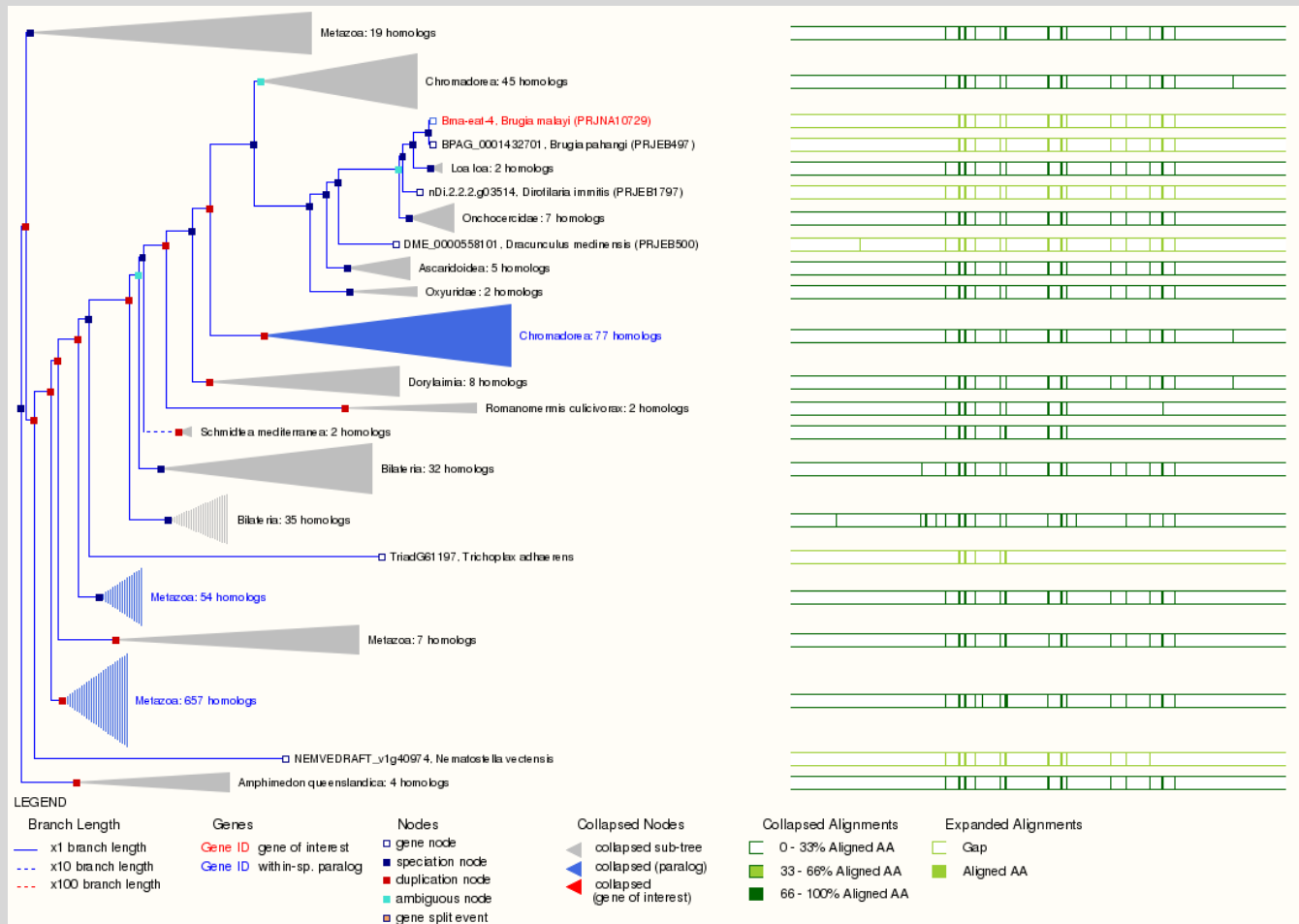
- Orthologues: any gene pairwise relation where the ancestor node is a speciation event
 - 1-to-1 orthologue
 - 1-to-many orthologue
 - Many-to-many orthologue
- Paralogues: any pairwise relation where the ancestor node is a duplication event



Understanding the gene tree



Visual access to the trees



Tabular access to tree data

Selected orthologues

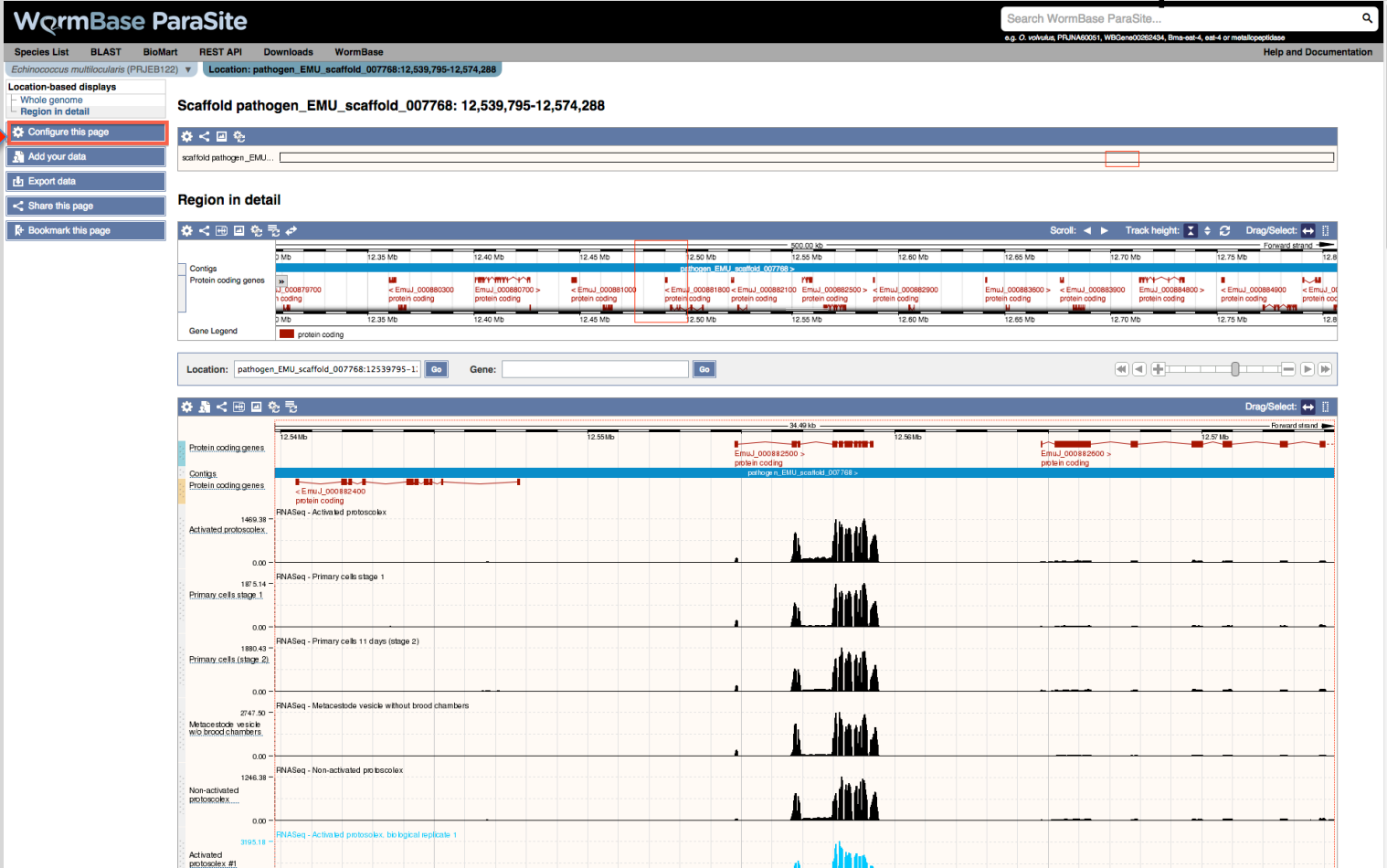
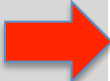
[View protein alignments of all orthologues](#)

Show <input type="button" value="All"/> entries		Show/hide columns		Filter <input type="text"/>			
Species	Type	dN/dS	Stable ID & gene name	Compare	Location	Target %id	Query %id
Acanthocheilonema viteae (PRJEB4306)	1-to-1	n/a	nAv.1.0.1.g03135 <small>Probable vesicular glutamate transporter eat-4 (inferred by orthology to a C. elegans protein) [Source: UniProtKB; acc: P34644]</small>	<ul style="list-style-type: none"> Alignment (protein) Alignment (cDNA) Gene Tree (image) 	nAv.1.0.scaf00057:63087-67685:1	73	76
Amphimedon queenslandica	Many-to-many	n/a	Aqu1.218710 <small>No description</small>	<ul style="list-style-type: none"> Alignment (protein) Alignment (cDNA) Gene Tree (image) 	Contig13347:93913-96460:1	27	28
Amphimedon queenslandica	Many-to-many	n/a	Aqu1.218711 <small>No description</small>	<ul style="list-style-type: none"> Alignment (protein) Alignment (cDNA) Gene Tree (image) 	Contig13347:96728-99289:-1	26	29
Amphimedon queenslandica	Many-to-many	n/a	Aqu1.219143 <small>No description</small>	<ul style="list-style-type: none"> Alignment (protein) Alignment (cDNA) Gene Tree (image) 	Contig13358:105162-108191:1	28	23
Amphimedon queenslandica	Many-to-many	n/a	Aqu1.219145 <small>No description</small>	<ul style="list-style-type: none"> Alignment (protein) Alignment (cDNA) Gene Tree (image) 	Contig13358:109023-112077:1	28	30
Ancylostoma caninum (PRJNA72585)	1-to-1	n/a	ANCCAN_09055 <small>Probable vesicular glutamate transporter eat-4 (inferred by orthology to a C. elegans protein) [Source: UniProtKB; acc: P34644]</small>	<ul style="list-style-type: none"> Alignment (protein) Alignment (cDNA) Gene Tree (image) 	ANCCANDFT_Contig116:390303-392960:1	68	60
Ancylostoma ceylanicum (PRJNA231479)	1-to-1	n/a	Acey_s0107.g3812 <small>Probable vesicular glutamate transporter eat-4 (projected from Caenorhabditis elegans ortholog eat-4)[Source: UniProtKB/Swiss-Prot; acc: P34644]</small>	<ul style="list-style-type: none"> Alignment (protein) Alignment (cDNA) Gene Tree (image) 	Acey_s0107_scaf:399963-412768:-1	56	67

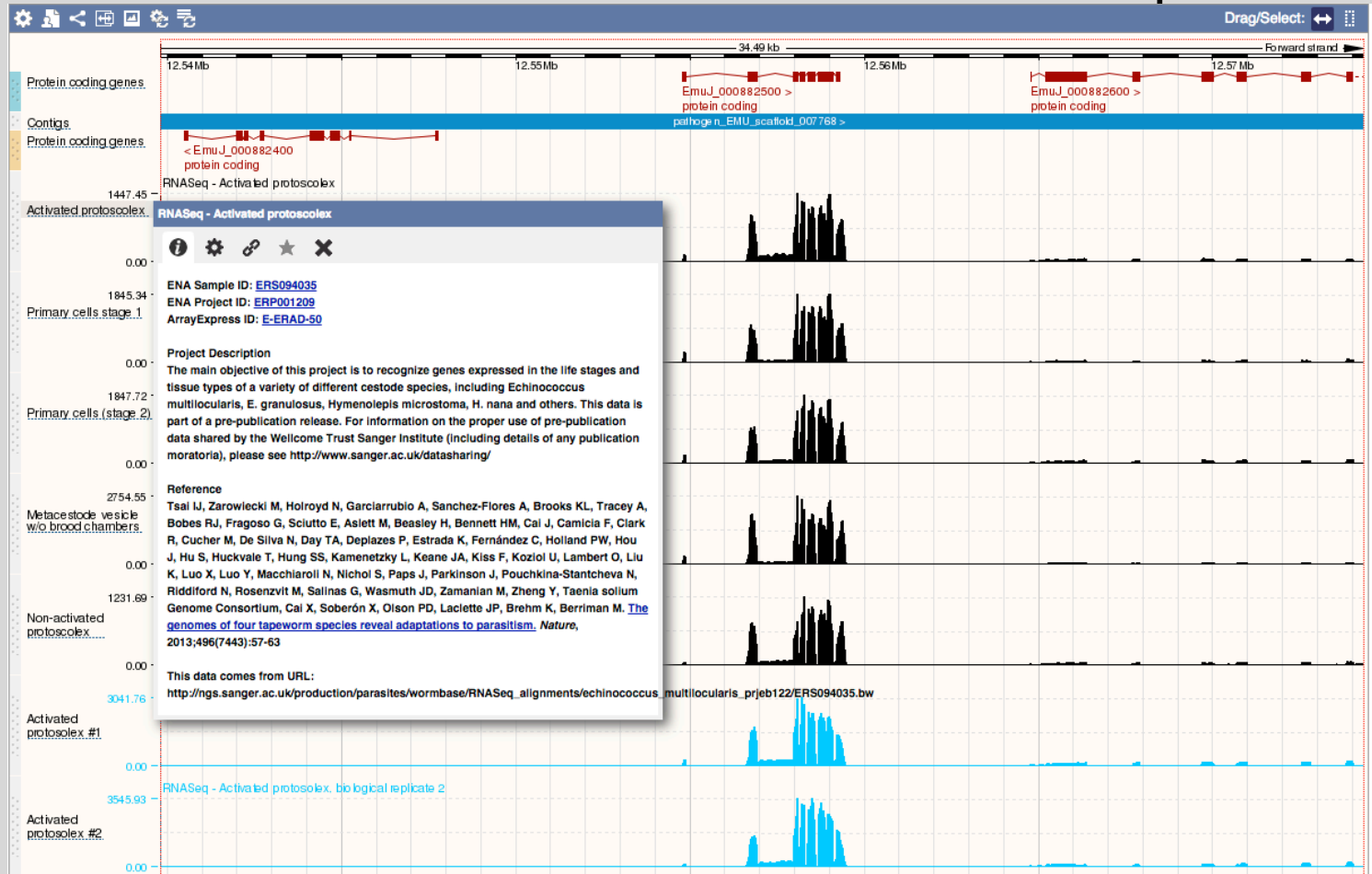
5. RNASeq tracks



Data tracks - RNASeq



Data tracks - RNASeq



6. Adding your own data



Adding your own data



WormBase ParaSite Search WormBase ParaSite...
e.g. C. volutus, PRJNA60051, WBGene00282434, Bin-eat-4, eat-4 or metalloproteinase

Species List BLAST BioMart REST API Downloads WormBase Help and Documentation

Brugia timori (PRJEB4683) Location: BTMF_scaffold0000001:2,457-34,400

Location-based displays
Whole genome
Region in detail

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

Scaffold BTMF_scaffold0000001: 2,457-34,400

scaffold BTMF_scaffold...

Region in detail

Contigs
Protein coding genes
Gene Legend

Location: BTMF_scaffold0000001:2457-34400 Gene: Go

Protein coding genes
Contigs
Protein coding genes
%GC
Gene Legend

There are currently 6 tracks turned off.
WormBase ParaSite: Brugia timori version 80.1 (B_timori_Indonesia_v1_0_4) Scaffold BTMF_scaffold0000001: 2,457 - 34,400

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Release 4 - November 2015
EMBL-EBI Sanger EMBL-EBI BBSRC
WormBase ParaSite is funded by the UK Biotechnology and Biological Sciences Research Council under grant numbers BB/K020080/1 and BB/K020048/1.

Adding your own data

Account Settings

- Edit Details
- View a group
- Edit a group
- Create new group
- Join existing group
- Invite new members
- Edit bookmark
- Create new bookmark
- Share bookmark

Custom Data

- Add your data**
- Manage Data
- Features on Karyotype

Manage Configurations

- Configurations for this page
- All configurations
- Configuration sets

Logout

Add a custom track

Name for this data (optional):

Species:

Assembly: TMUE2.2

Data:

Or upload file (max 20MB) No file chosen

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

Adding your own data

The screenshot shows the 'Add a custom track' page in the WormBase web interface. The page is divided into a left-hand navigation menu and a main content area. The navigation menu includes sections for 'Account Settings', 'Custom Data', 'Manage Configurations', and 'Logout'. The 'Custom Data' section is expanded, showing 'Add your data' as the active option. The main content area contains the following fields and options:

- Add a custom track**: The main heading for the form.
- Name for this data (optional):**: An empty text input field.
- Species:**: A dropdown menu currently set to 'Trichuris muris (PRJEB126)'.
- Assembly:**: A dropdown menu currently set to 'TMUE2.2'.
- Data:**: A text area containing the URL 'http://ngs.sanger.ac.uk/production/parasites/wormbase/RNASeq_alignments/trichuris_muris_prjeb126/ERS092077.bw'.
- Or upload file (max 20MB)**: A section with a 'Choose File' button and the text 'No file chosen'.
- Data format:**: A dropdown menu currently set to 'BigWig'.
- Help on supported formats, display types, etc**: A blue hyperlink.
- Add data**: A blue button at the bottom of the form.

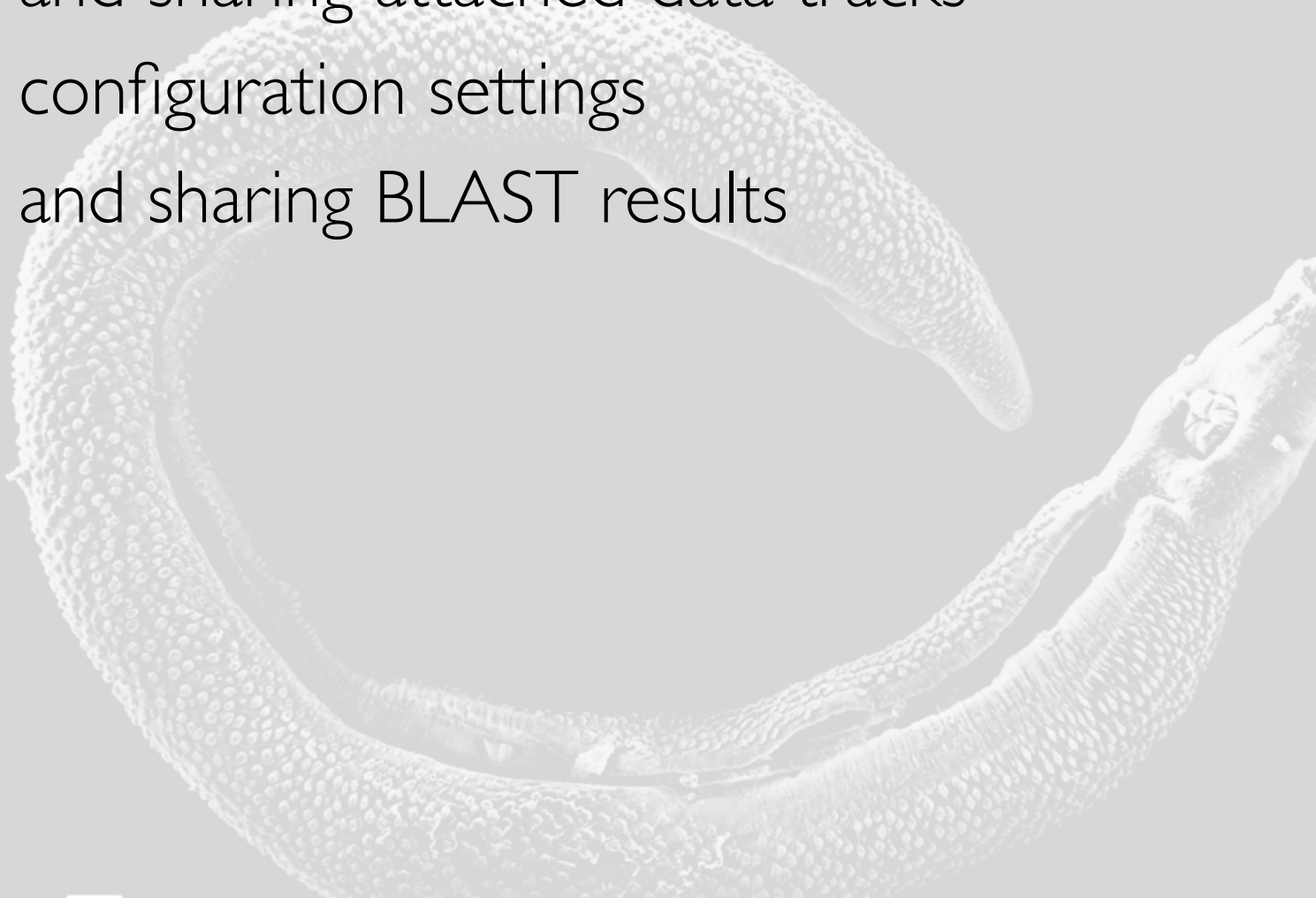
The interface also features a top navigation bar with links for 'BLAST', 'BioMart', 'REST API', 'Downloads', 'WormBase', 'My Account', and 'Logout'. A bottom track visualization is partially visible, showing genomic coordinates and data tracks.

7. User Accounts



User accounts

- Saving and sharing attached data tracks
- Saving configuration settings
- Saving and sharing BLAST results



User accounts

Species



BLAST



BioMart



API



Downloads



WormBase



Find a genome

[-] Nematoda (Roundworms)

[-] Clade I

Romanomermis culicivorax
PRJEB1358

Soboliphyme baturini
PRJEB516

Trichinella nativa
PRJNA179527

Trichinella spiralis
PRJNA179527

Announcements

[Announcing WormBase ParaSite release 5](#)

posted 1 month ago

We are pleased to announce the fifth release of WormBase ParaSite.

Blog

[British Society for Parasitology Spring Meeting 2016](#)

posted 6 days ago

Registration is now open for the 2016 Spring Meeting of the British Society for Parasitology (BSP), which will be held from 11th April to 13th April at Imperial College London. A WormBase ParaSite workshop will feature as part of the schedule.

[Published Strongyloides genomes in WormBase ParaSite](#)

posted 17 days ago

Complete genomic and transcriptomic data from the new Nature Genetics paper "The Genomic Basis of Parasitism in the Strongyloides Clade of Nematodes" Hunt et al. (2016) is available in WormBase ParaSite.

[Announcing the WormBase ParaSite Roadshow](#)

posted 1 month ago

Want to learn more about WormBase ParaSite? Sign-up or host one of our hands-on workshops at your university or institution.

[Brugia malayi papers of interest](#)

posted 1 month ago

A number of newly published *Brugia malayi* papers are featured in the new WormBase release, WS251.

[\[Older \]](#)

Twitter

Tweets

[Follow](#)

WormBase ParaSite @WBParasite 15h
Sign up for Wormbase ParaSite Workshop at the BSP Spring Meeting in April - bsp.uk.net/news-and-event... @parasitegenomes @BSPparasitology
Expand

BUG Consortium @BUGConsortium 17 Feb
Looking forward to hosting the @WBParasite Roadshow in Glasgow - a week today! See wp.me/p6yN4l-2y for more info #helminth #genomics
Retweeted by WormBase ParaSite
Show Summary

WormBase ParaSite @WBParasite 16 Feb
Whole genome resequencing of the human parasite #Schistosoma mansoni...population history...effects of selection nature.com/articles/srep2...
Show Summary

Tweet to @WBParasite

User accounts: registering

WormBase ParaSite Search WormBase ParaSite...
e.g. *O. volvulus*, PRJNA60051, WBGene00262434, Bma-est-4, est-4 or metallopeptidase

Species List BLAST BioMart REST API Downloads WormBase Login Register Help and Documentation

Strongyloide **Register**

Location-based
Whole genome
Region in

Configure
Add your data
Manage Data
Features on Karyotype

Manage

Export data

Share this

Bookmarks

Register
Login
Lost Password

Custom Data
Add your data
Manage Data
Features on Karyotype

Manage Configurations
Configurations for this page
All configurations
Configuration sets

Name:

Email Address:

You'll use this to log in to WormBase ParaSite.

Organisation:

Country:

Register

Fields marked * are required

%GC

< 5 YK_2014000.1 protein coding
< 5 YK_1227500.1 protein coding

User accounts

WormBase ParaSite Search WormBase ParaSite...
e.g. *O. volvulus*, PRJNA60051, WBGene00262434, Bma-est-4, est-4 or metalloproteinase

Species List BLAST BioMart REST API Downloads WormBase My Account - wormbase.test@gmail.com Logout Help and Documentation

Strongyloide **My Account - wormbase.test@gmail.com**

Location-based
Whole genome
Region in

Account Settings
Edit Details
View a group
Edit a group
Create new group
Join existing group
Invite new members
Edit bookmark
Create new bookmark
Share bookmark

Custom Data
Add your data
Manage Data
Features on Karyotype

Manage Configurations
Configurations for this page
All configurations
Configuration sets

Logout

User Details ✎

Name	Test
Email	wormbase.test@gmail.com
Organisation	
Country	
Login via	WormBase ParaSite: wormbase.test@gmail.com Change password

Groups 🗑️ 📄

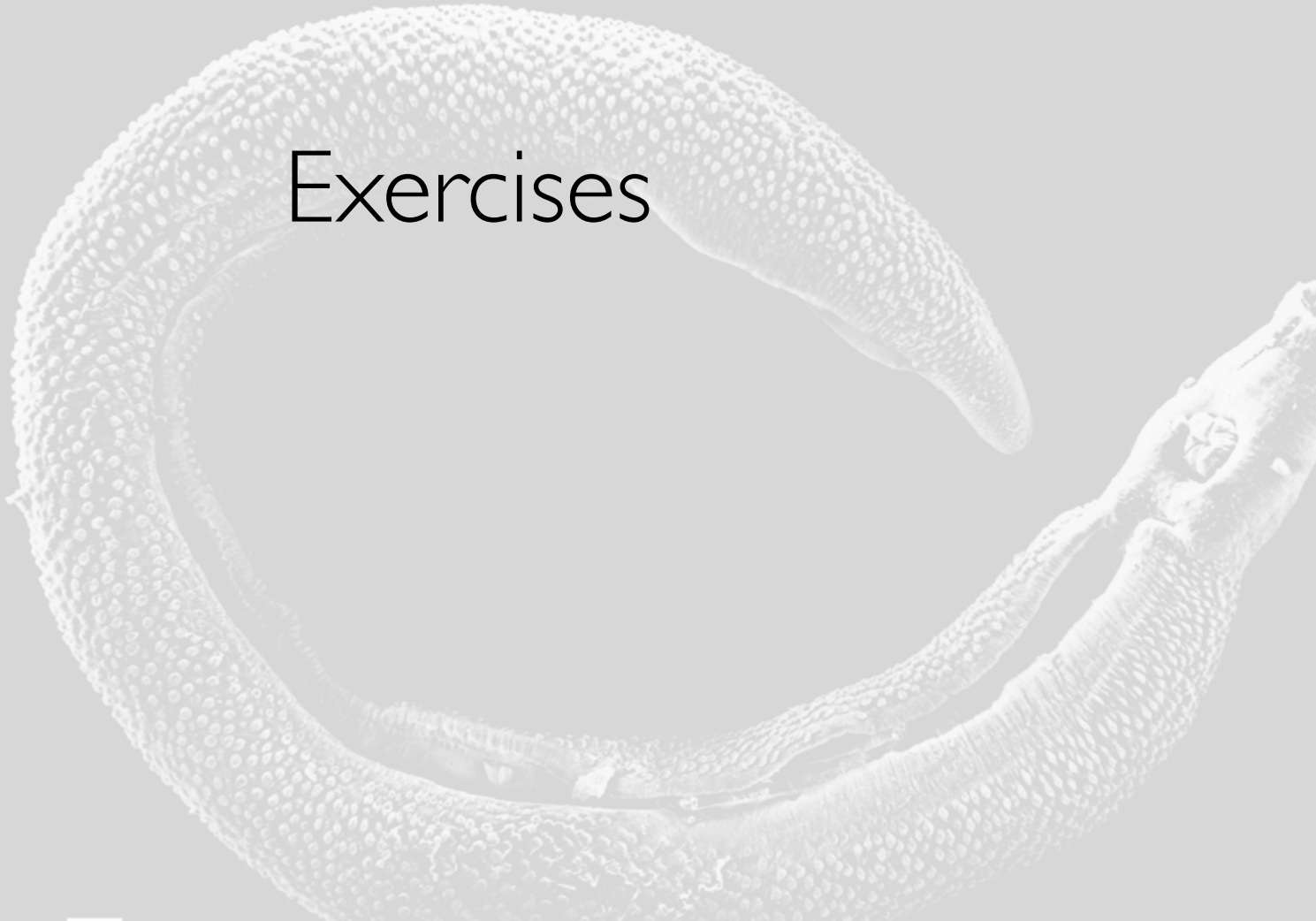
You are not a member of any group.

My bookmarks 📌

You have not saved any bookmarks to your account.

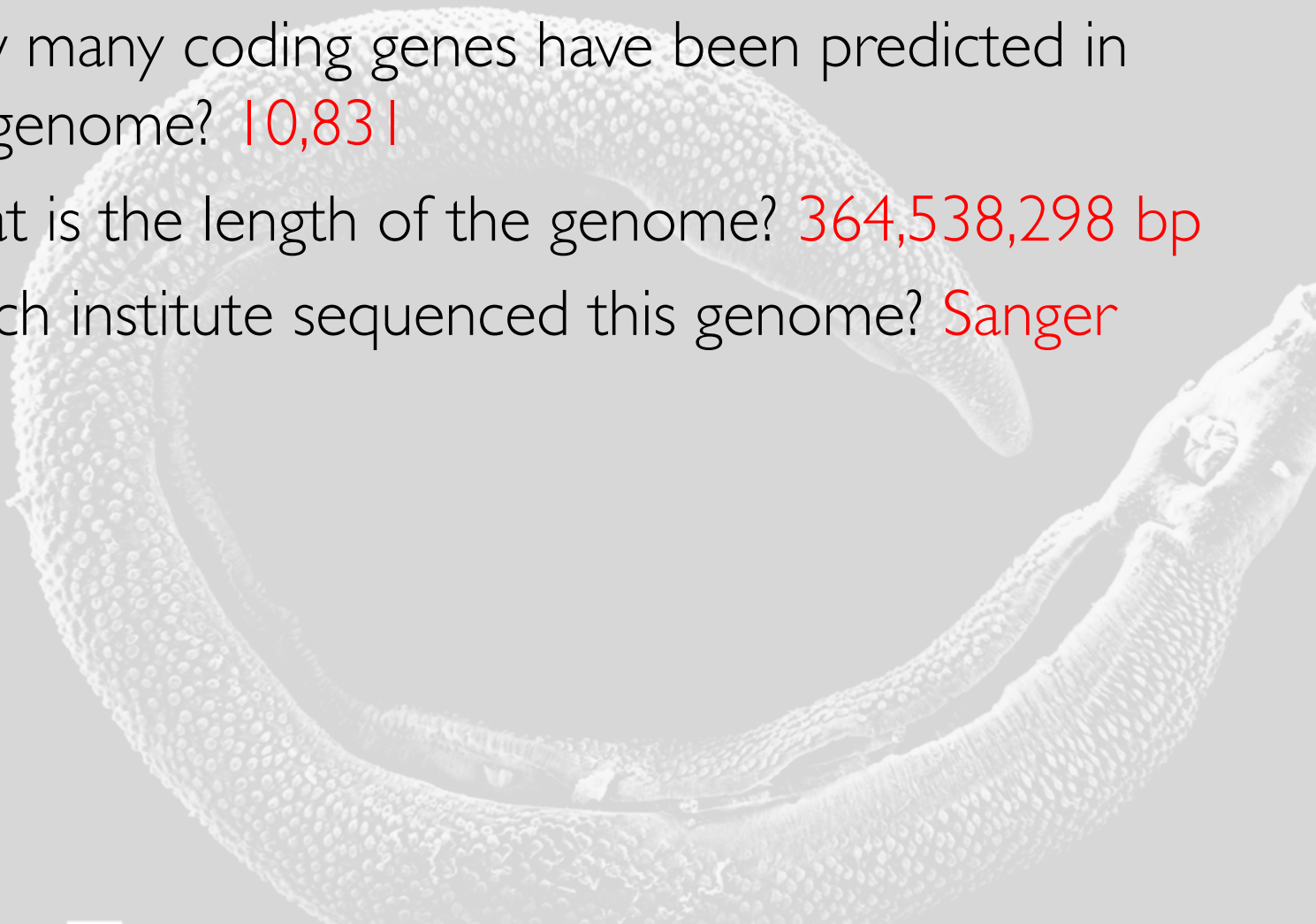
Genomic track showing protein coding regions: <3 VE_2014000.1 protein coding, <3 VE_1227500.1 protein coding

Exercises



Answers to exercises

- I. Navigate to the page for *Schistosoma mansoni*
 - How many coding genes have been predicted in this genome? 10,831
 - What is the length of the genome? 364,538,298 bp
 - Which institute sequenced this genome? Sanger





Species 	BLAST 	BioMart
API 	Downloads 	WormBase

Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

Statistics

- Version: WBPS6 (April 2016)
- WormBase Version: WS252
- 109 genomes, representing 100 species
- 2,189,841 genes

Announcements

[Announcing WormBase ParaSite release 6](#)
posted 2 months ago

We are pleased to announce the sixth release of WormBase ParaSite.

Blog

[Featured Paper: Glucose and Glycogen Metabolism in *B. malayi* Is Associated with Wolbachia Symbiont Fitness](#)
posted 2 months ago

We would like to draw your attention to a paper published by Denis Voronin, et. al on the influence of host metabolism on symbiont fitness: Denis Voronin, Saheed Bachu, Michael Shlossman, Thomas R. Unnasch, Elodie Ghedin, Sara Lustigman "Glucose and Glycogen Metabolism in *Brugia malayi* Is Associated with Wolbachia Symbiont Fitness", PLoS One. 2016 Apr [...]

[Brugia malayi assembly update](#)
posted 2 months ago

The new release of WormBase (WS252) is the first one to feature the new and updated version 4 of the *Brugia malayi* assembly. Due to additional optical mapping, as well as new long-range PacBio sequencing and additional reassembly work conducted to integrate all available data, it was possible to scaffold the 88.2Mbp assembly into 5 chromosomes [...]

[Register for a WormBase ParaSite workshop](#)
posted 2 months ago

To help our users make the most of this valuable resource, we are visiting universities and institutes to provide hands-on training sessions.

[\[Older\]](#)

Twitter

Tweets by @WBParasite

WormBase ParaSite Retweeted

British Parasitology @BSPparasitology

Job opportunity: Filarial Diseases Research Scientist, Northwick Park Institute for Medical Research (NPIMR). bsp.uk.net/jobs/

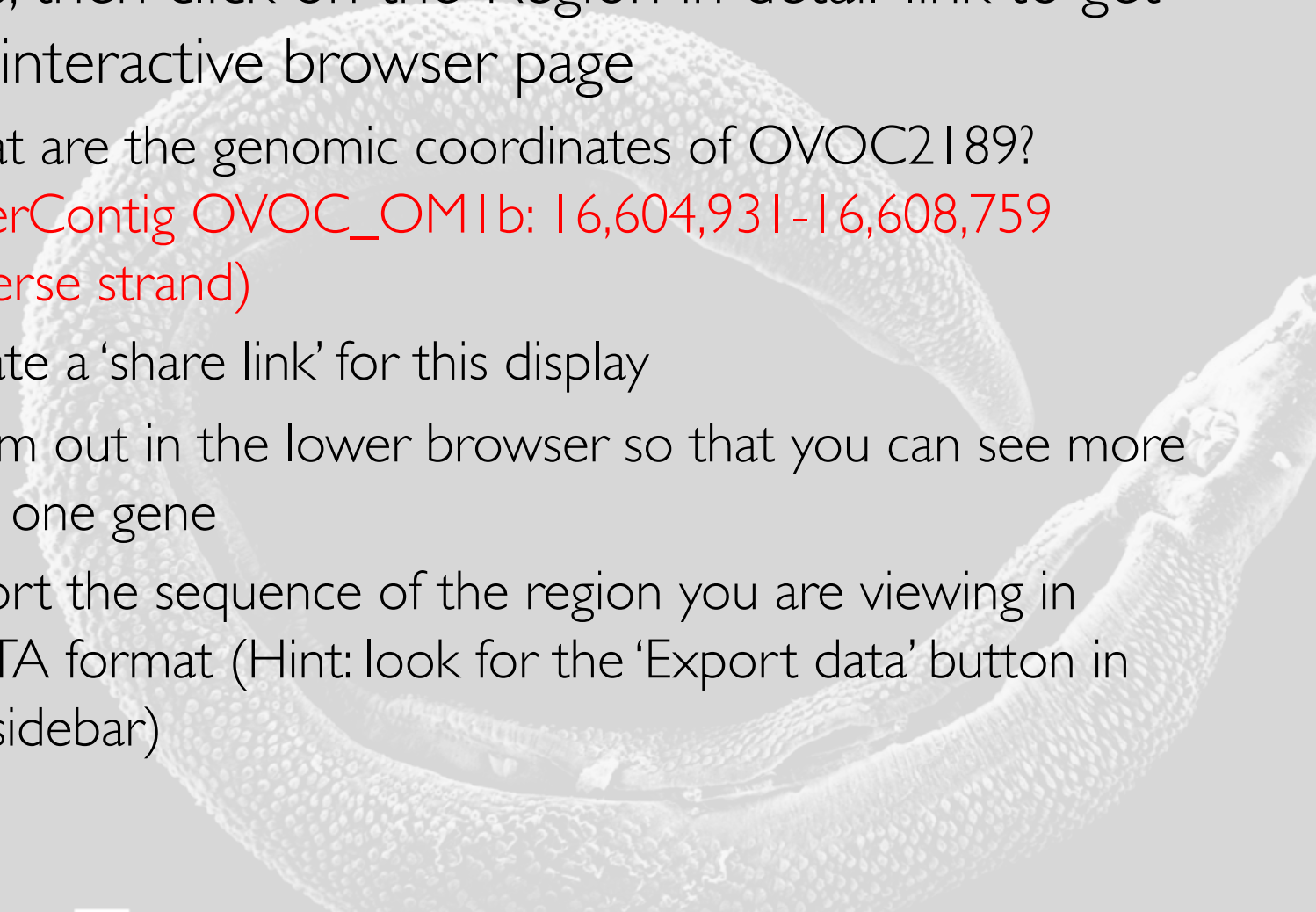
WormBase ParaSite Retweeted

Science @scienmag

White blood cells attacking a parasite. pic.twitter.com/zqAIUZMYDx

[Embed](#) [View on Twitter](#)

Answers to exercises

2. Navigate to gene OVOC2189 from *Onchocerca volvulus*, then click on the 'Region in detail' link to get to the interactive browser page
 - What are the genomic coordinates of OVOC2189?
SuperContig OVOC_OM1b: 16,604,931-16,608,759
(reverse strand)
 - Create a 'share link' for this display
 - Zoom out in the lower browser so that you can see more than one gene
 - Export the sequence of the region you are viewing in FASTA format (Hint: look for the 'Export data' button in the sidebar)
- 

Species 	BLAST 	BioMart
API 	Downloads 	WormBase

Find a genome

Statistics

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- WormBase Version: WS252
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We would like to draw your attention to a paper published by Denis Voronin, et. al on the influence of host metabolism on symbiont fitness: Denis Voronin, Saheed Bachu, Michael Shlossman, Thomas R. Unnasch, Elodie Ghedin, Sara Lustigman "Glucose and Glycogen Metabolism in *Brugia malayi* Is Associated with Wolbachia Symbiont Fitness", *PLoS One*. 2016 Apr [Link]

***Brugia malayi* assembly update**
posted 2 months ago

The new release of WormBase (WS252) is the first one to feature the new and updated version 4 of the *Brugia malayi* assembly. Due to additional optical mapping, as well as new long-range PacBio sequencing and additional reassembly work conducted to integrate all available data, it was possible to scaffold the 88.2Mbp assembly into 5 chromosomes [Link]

Register for a WormBase ParaSite workshop
posted 2 months ago

To help our users make the most of this valuable resource, we are visiting universities and institutes to provide hands-on training sessions.

[Order]

Twitter

Tweets by @WBParasite

WormBase ParaSite Retweeted

British Parasitology @BSPparasitology
 Job opportunity: Filarial Diseases Research Scientist, Northwick Park Institute for Medical Research (NPIMR). bsp.uk.net/jobs/

WormBase ParaSite Retweeted

Science @sciencemag
 White blood cells attacking a parasite. pic.twitter.com/zqAIUZMYDx

Embed View on Twitter

Release 6 - April 2016

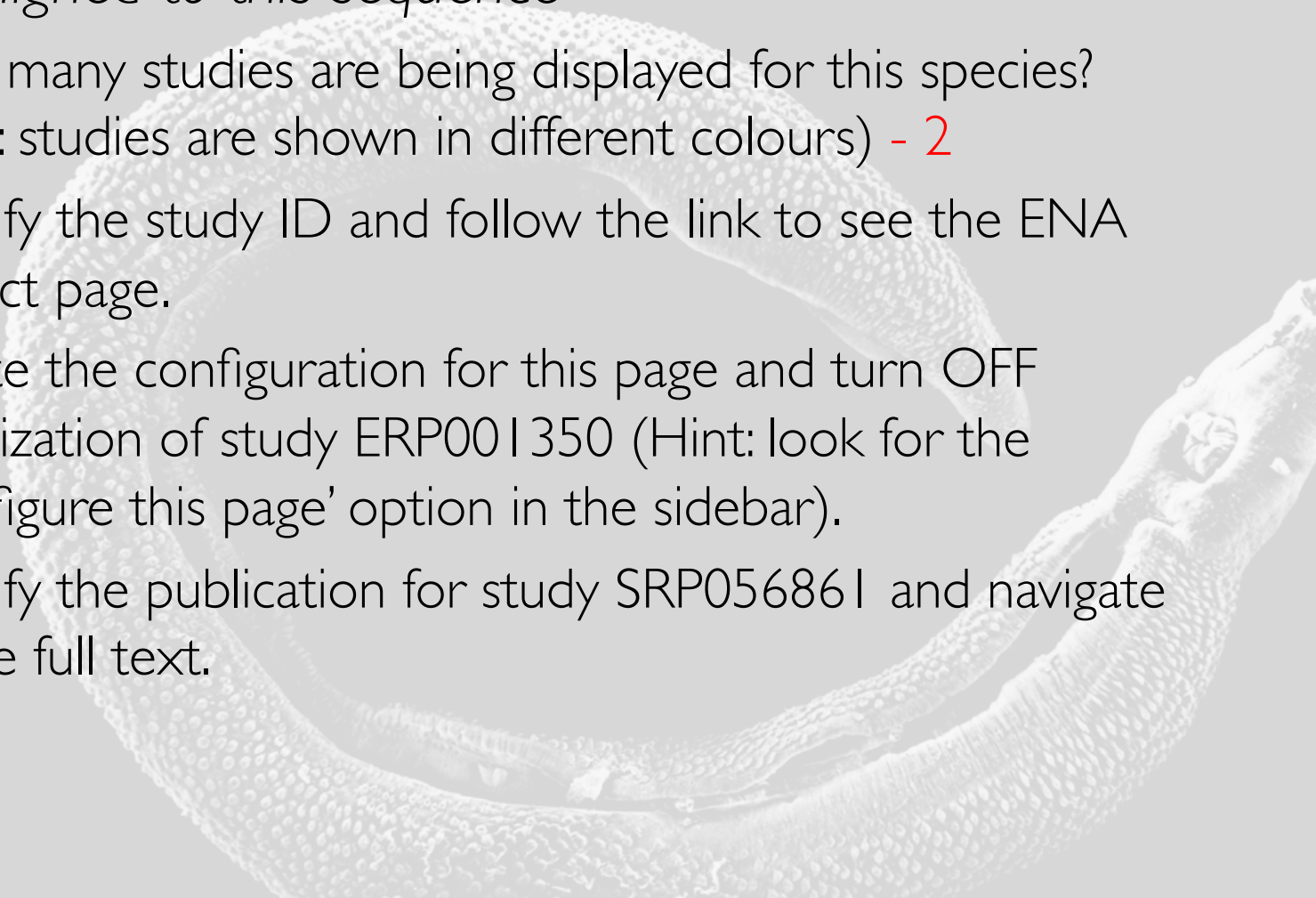


WormBase ParaSite is funded by the UK Biotechnology and Biological Sciences Research Council under grant numbers BB/K020080/1 and BB/K020048/1.

Information

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- Citing WormBase ParaSite
- About WormBase ParaSite
- Data Usage
- Contact Us
- Disclaimer

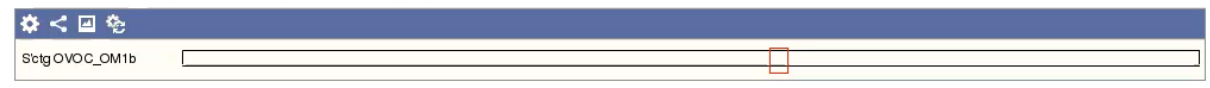
Answers to exercises

3. *Scroll down the page you are on to see the RNASeq tracks aligned to this sequence*
- How many studies are being displayed for this species? (Hint: studies are shown in different colours) - 2
 - Identify the study ID and follow the link to see the ENA project page.
 - Locate the configuration for this page and turn OFF visualization of study ERP001350 (Hint: look for the 'Configure this page' option in the sidebar).
 - Identify the publication for study SRP056861 and navigate to the full text.
- 

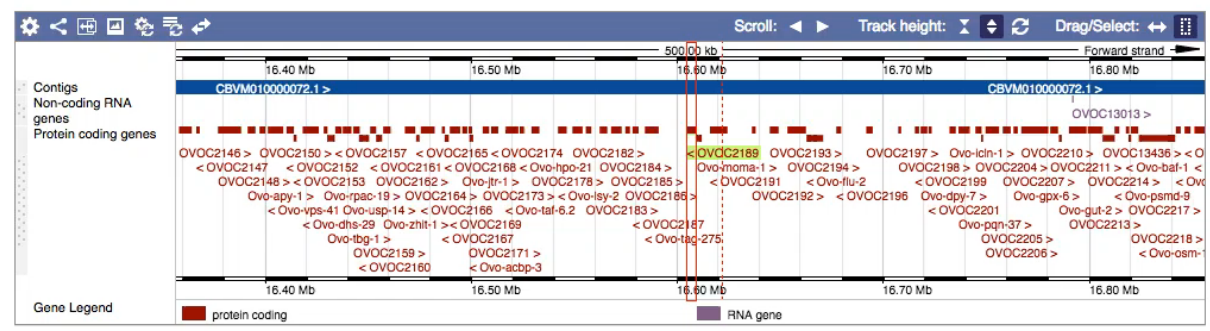
Onchocerca volvulus (PRJEB513) Location: OVOC_OM1b:16,604,931-16,608,759 Gene: OVOC2189 Transcript: OVOC2189

- Location-based displays
 - Whole genome
 - Region in detail
- Configure this page
- Add your data
- Export data
- Share this page
- Bookmark this page

SuperContig OVOC_OM1b: 16,604,931-16,608,759



Region in detail



Location: OVOC_OM1b:16604931-16608759 Go
Gene: Go

Answers to exercises

4. Navigate to the *Trichuris muris* genome page, and click on the 'Example region' link in the Genome assembly information box:
- Open up the 'Add your Data' window by clicking the link in the sidebar
 - Attach one of the BigWig files located at:
<http://www.ebi.ac.uk/~jane/testdata/>
by pasting the URL in to the Data box (Hint: to copy the URL, right-click file name and 'Copy link address')
 - Navigate to gene TMUE_s0016004100 and have a look at the RNASeq track. How would you judge the existing gene model? (Hint: go to the 'Region in Detail' view to see the tracks and zoom in) (no evidence for first two exons, no evidence for intron 4)

Species 

BLAST 

BioMart 

API 

Downloads 

WormBase 

Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

Statistics

- Version: WBPS6 (April 2016)
- WormBase Version: WS252
- 109 genomes, representing 100 species

Announcements

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posted 2 months ago

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17 Jun

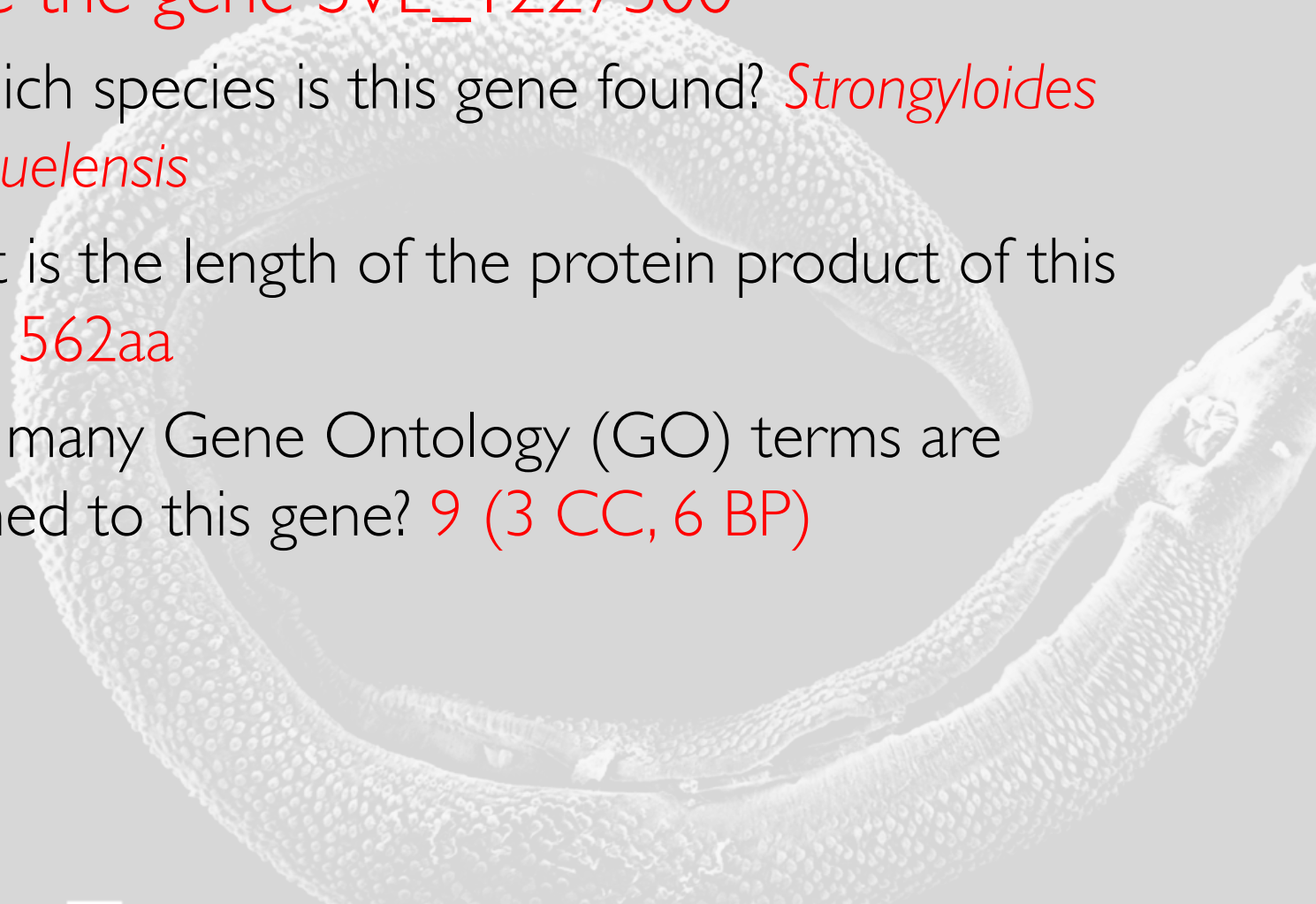
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Answers to exercises

5. Locate the gene SVE_I227300

- In which species is this gene found? *Strongyloides venezuelensis*
- What is the length of the protein product of this gene? 562aa
- How many Gene Ontology (GO) terms are assigned to this gene? 9 (3 CC, 6 BP)



Species 	BLAST 	BioMart
API 	Downloads 	WormBase

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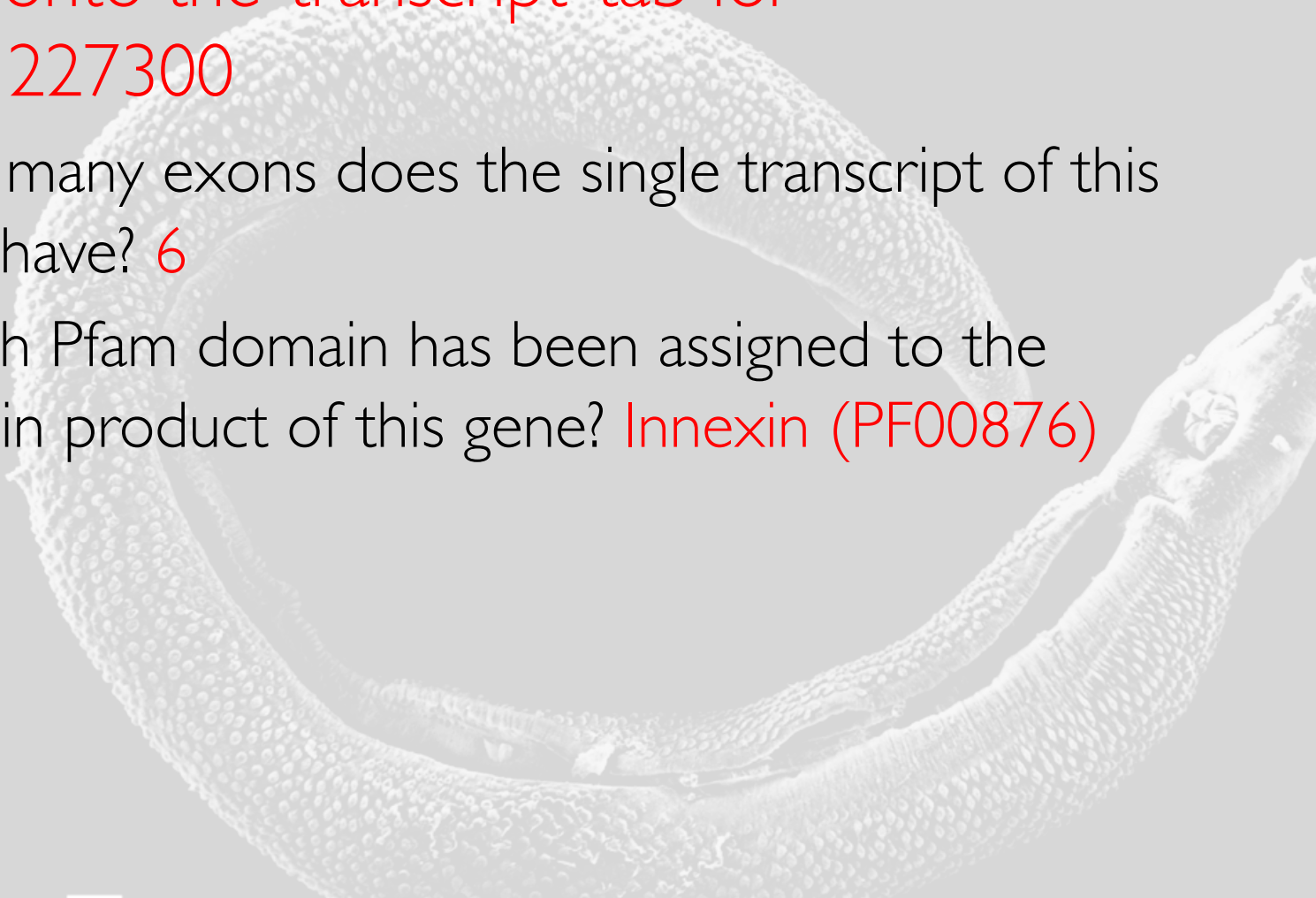
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Answers to exercises

6. Move onto the 'transcript' tab for [SVE_I227300](#)

- How many exons does the single transcript of this gene have? **6**
- Which Pfam domain has been assigned to the protein product of this gene? **Innexin (PF00876)**



- Gene-based displays**
- Summary
 - Splice variants
 - Sequence
 - External references
 - Ontologies
 - GO: Molecular function
 - GO: Cellular component
 - GO: Biological process
 - Literature
 - Comparative Genomics
 - Gene tree
 - Orthologues
 - Paralogues

- Configure this page
- Manage your data
- Export data
- Share this page
- Bookmark this page

Gene: SVE_1227300

Description Innexin unc-7 (projected from Caenorhabditis elegans ortholog unc-7) [Source:UniProtKB/Swiss-Prot;Acc:Q03412]

Location Scaffold SVE_contig0000018: 37,733-39,694 forward strand.

About this gene This gene has 1 transcript (splice variant), 89 orthologues and 16 paralogues.

Gene type Protein coding

Annotation Method Gene models from the Strongyloidea Nematode Genomes Project (unpublished) from the Parasite Genomics Group at the Wellcome Trust Sanger Institute

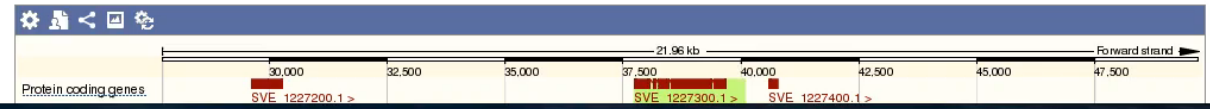
Transcripts [Hide transcript table](#)

Show/hide columns (2 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype
Novel	SVE_1227300.1	1689	562aa	Protein coding

Summary

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



7. Navigate to the gene page for the *Necator americanus* gene NECAME_00080


- How many orthologues have been predicted in flatworm genomes? 13
- Which species has an orthologue with the highest percentage identity? *Brugia timori* (PRJEB4663)
- View the alignment between this gene's protein product and the protein of the *Ancylostoma duodenale* orthologue.


QuickTime Player File Edit View Window Help


WormBase ParaSite Version: WBPS6 (WS252)


Search WormBase ParaSite...
e.g. *O. volvulus*, PFJNA60051, WBGene00262434, Bms-eat-4, eat-4 or metallopeptidase


Species List BLAST BioMart REST API VEP Downloads WormBase Login Register Help and Documentation


Species 

BLAST 

BioMart 

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WormBase 

Find a genome

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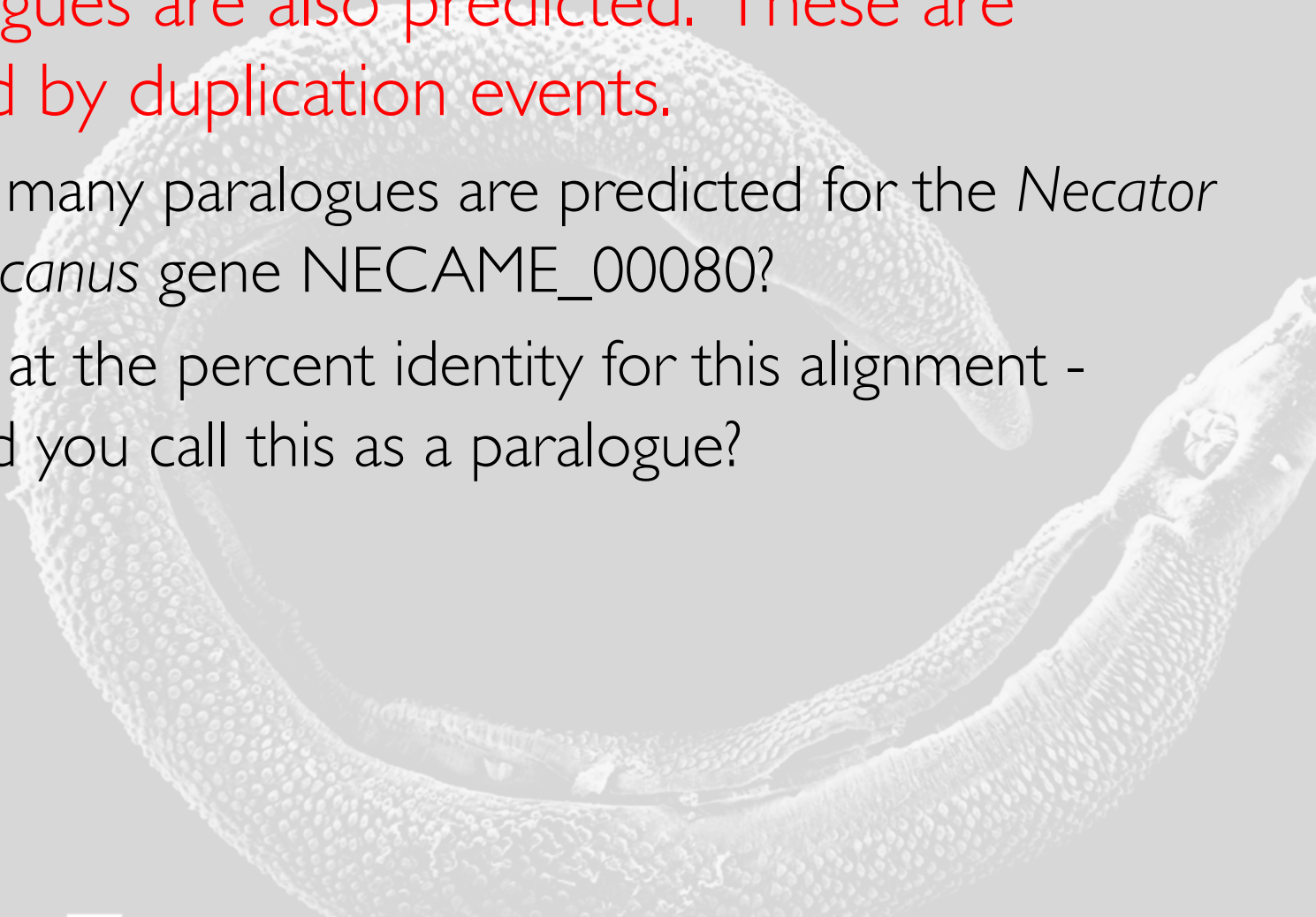
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Windows taskbar: Firefox, Chrome, Safari, Edge, Word, Excel, PowerPoint, Outlook, OneDrive, Teams, Zoom, Slack, Jira, Confluence, etc.

8. Paralogues are also predicted. These are caused by duplication events.

- How many paralogues are predicted for the *Necator americanus* gene NECAME_00080?
- Look at the percent identity for this alignment - would you call this as a paralogue?



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 - Sequence
 - External references
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 - GO: Molecular function
 - GO: Cellular component
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 - Gene tree
 - Orthologues**
 - Paralogues

Gene: NECAME_00080

Description HMG box [Source:UniProtKB/TrEMBL;Acc:W2U1H1]

Location Scaffold KI657455: 914,690-916,914 reverse strand.

About this gene This gene has 1 transcript (splice variant), 85 orthologues and 1 paralogue.

Gene type Protein coding

Annotation Method Get models produced by the Mitreva laboratory at the Genome Institute of Washington University, as described in Tang et al (2014)

Transcripts [Hide transcript table](#)

- Configure this page
- Manage your data
- Export data
- Share this page
- Bookmark this page

Show/hide columns (2 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	UniProt
Novel	NECAME_00080	498	166aa	Protein coding	W2U1H1

Orthologues

[Download orthologues](#)

Summary of orthologues of this gene

Click on 'Show' to display the orthologues for one or more groups, or click on 'Configure this page' to choose a custom list of species

Species set	Show details	1-to-1	1-to-many	many-to-many
Human	<input type="checkbox"/>	0	1	0
<i>C. elegans</i>	<input type="checkbox"/>	1	0	0

9. Locate the *Fasciola hepatica* (PRJNA179522) orthologue of the human gene BRCA2. Using the gene trees:

- How close in evolutionary history is this gene located to its orthologue?
- Are there any duplication events in the evolution of this gene and its homologues? **Yes, 2**

Species 	BLAST 	BioMart
API 	Downloads 	WormBase

Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

Statistics

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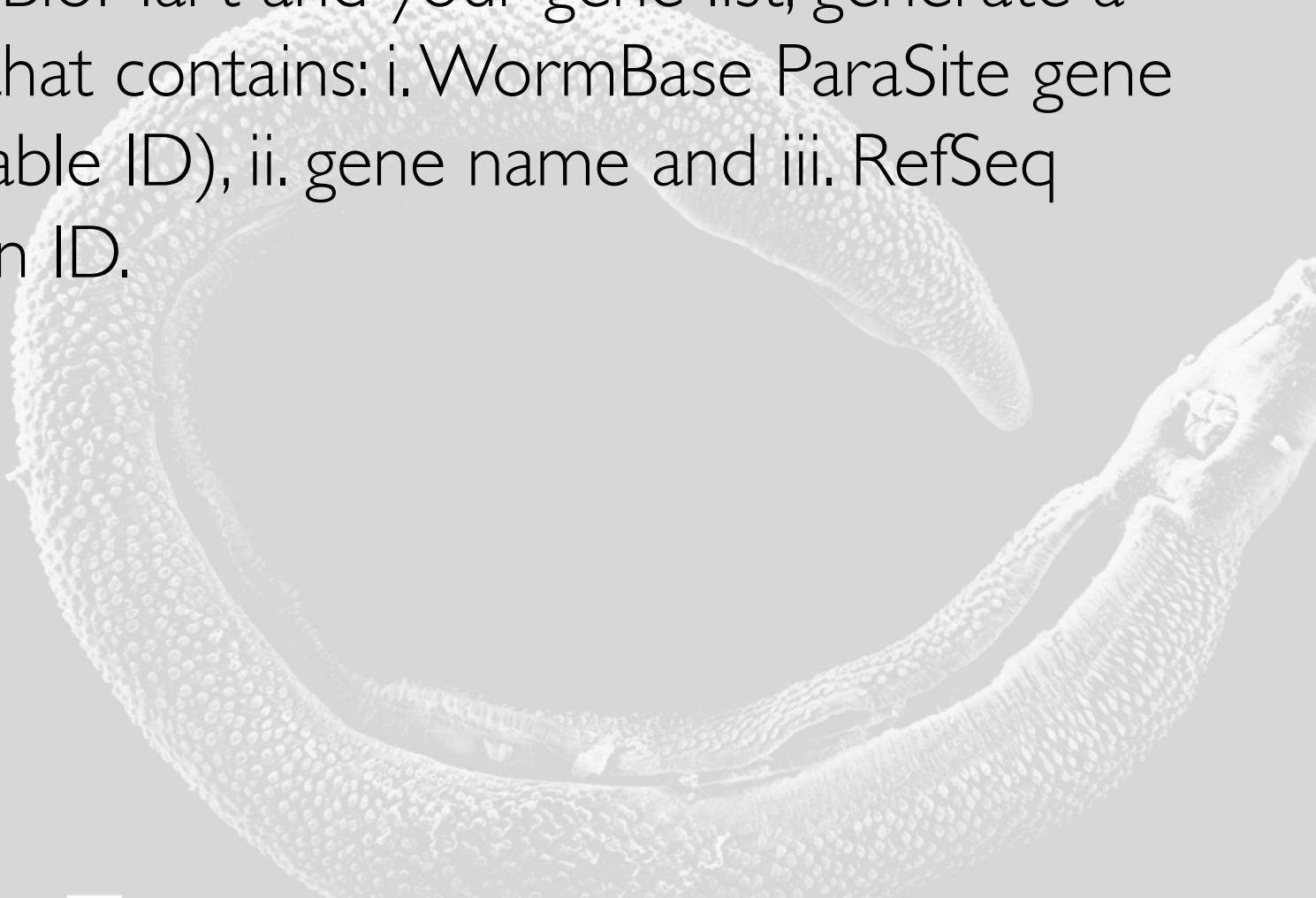
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10. Click on the 'Register' link in the horizontal toolbar under the search box

- Enter your details and create an account (if you don't want to create an account, skip to c. and use the test account:
email: wormbase.test@gmail.com
password: W0rmbase)
- Verify your account via your email address
- Log in to your account via the 'Login' link
- Go to 'Manage your data' and save the data track you added to your account (Hint: use the floppy disk icon under 'Actions')
- Try logging out and logging back in again. Does your data track persist?

BioMart part II answers

- I. Using BioMart and your gene list, generate a table that contains: i. WormBase ParaSite gene ID (stable ID), ii. gene name and iii. RefSeq Protein ID.





Species 	BLAST 	BioMart
API 	Downloads 	WormBase

Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

Statistics

- Version: WBPS6 (April 2016)
- WormBase Version: WS252
- 109 genomes, representing 100 species
- 2,189,841 genes

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- [Help and Documentation](#)
- [Citing WormBase ParaSite](#)
- [About WormBase ParaSite](#)

BioMart part II answers

2. Using BioMart, generate a table showing i. the WormBase ParaSite gene ID (stable ID), ii. *O. volvulus* gene name, iii. *C. elegans* orthologue gene stable ID and iv. human orthologue gene stable ID.
 - How many of these genes have an orthologue defined in both *C. elegans* and human? 4

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

1. Query Filters
 Gene stable ID(s): [ID-list specified]
2. Output Attributes

- Genome project
- Gene stable ID
- Gene name
- RefSeq protein ID

Export all results to Unique results only

Email notification to

View rows as Unique results only

Genome project	Gene stable ID	Gene name	RefSeq protein ID
onchocerca_volvulus_prieb513	WBGene00249437	OVOC12628	NP_008370
onchocerca_volvulus_prieb513	WBGene00249438	OVOC12629	NP_008371
onchocerca_volvulus_prieb513	WBGene00249440	OVOC12631	NP_008374
onchocerca_volvulus_prieb513	WBGene00249441	OVOC12632	NP_008375
onchocerca_volvulus_prieb513	WBGene00249442	OVOC12633	NP_008377
onchocerca_volvulus_prieb513	WBGene00249445	OVOC12636	NP_008368
onchocerca_volvulus_prieb513	WBGene00249446	OVOC12637	NP_008369
onchocerca_volvulus_prieb513	WBGene00249820	OVOC12995	NP_008373
onchocerca_volvulus_prieb513	WBGene00249821	OVOC12996	NP_008376



BioMart part II answers

3. Using BioMart, get the sequence for the region 500bp upstream of each gene in your list. Export this as a FASTA file.



WormBase ParaSite

Search WormBase ParaSite...

WormBase Home | ParaSite Home

BLAST | BioMart | Downloads

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3. Hit the 'Results' button at the top of this page

1. Query Filters

[None selected]

2. Output Attributes

Genome project
Gene stable ID

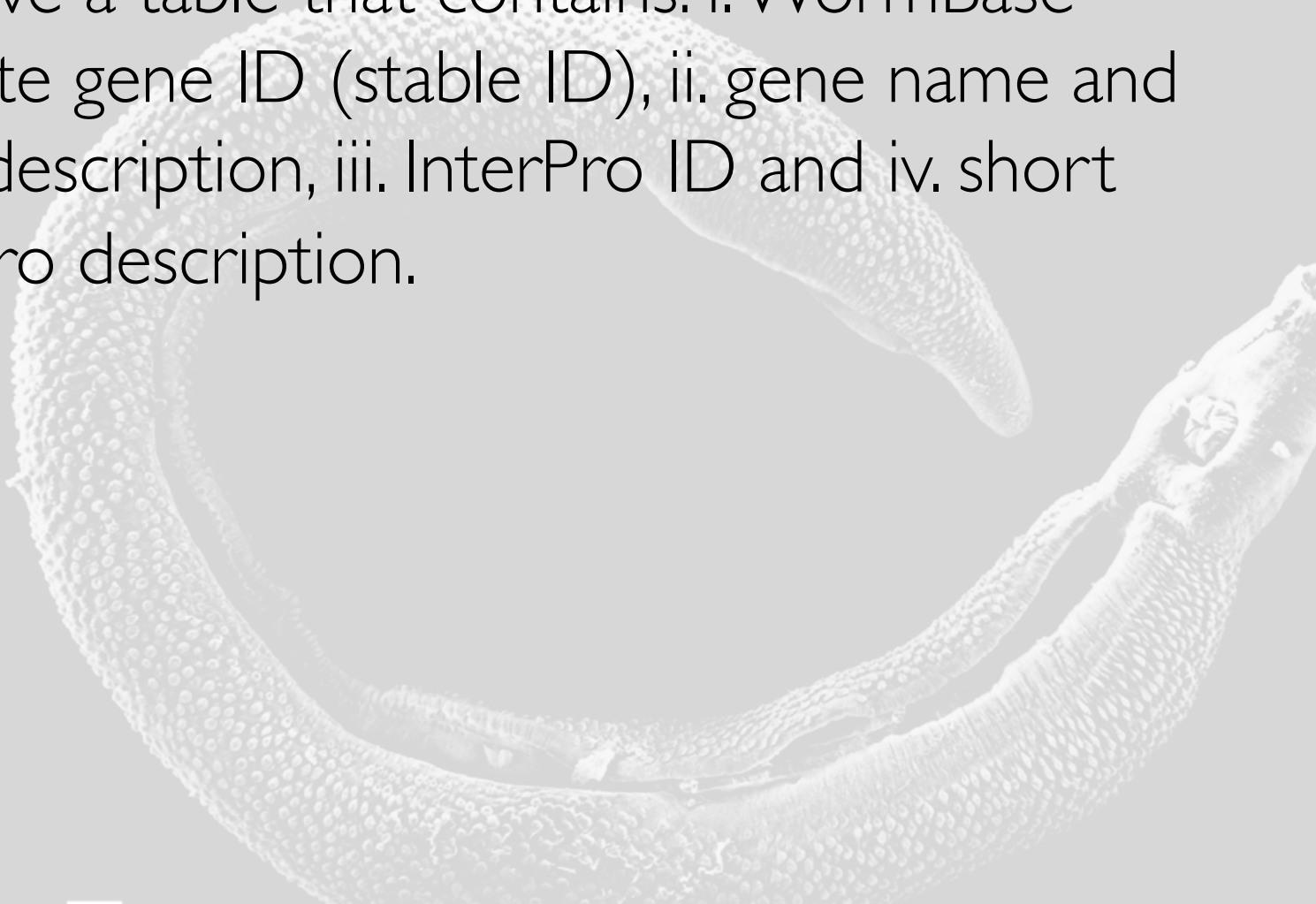
Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)
For guidance, see the [relevant pages](#) of our documentation.

- SPECIES
- REGION (use only when selecting one species)
- GENE
- GENE ONTOLOGY (GO)
- HOMOLOGY (ORTHOLOGUES AND PARALOGUES)
- PROTEIN DOMAINS



BioMart part II answers

4. Retrieve a table that contains: i. WormBase ParaSite gene ID (stable ID), ii. gene name and gene description, iii. InterPro ID and iv. short InterPro description.



WormBase ParaSite

Search WormBase ParaSite...

WormBase Home | ParaSite Home

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URL XML Perl Help

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[None selected]

2. Output Attributes

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Gene stable ID

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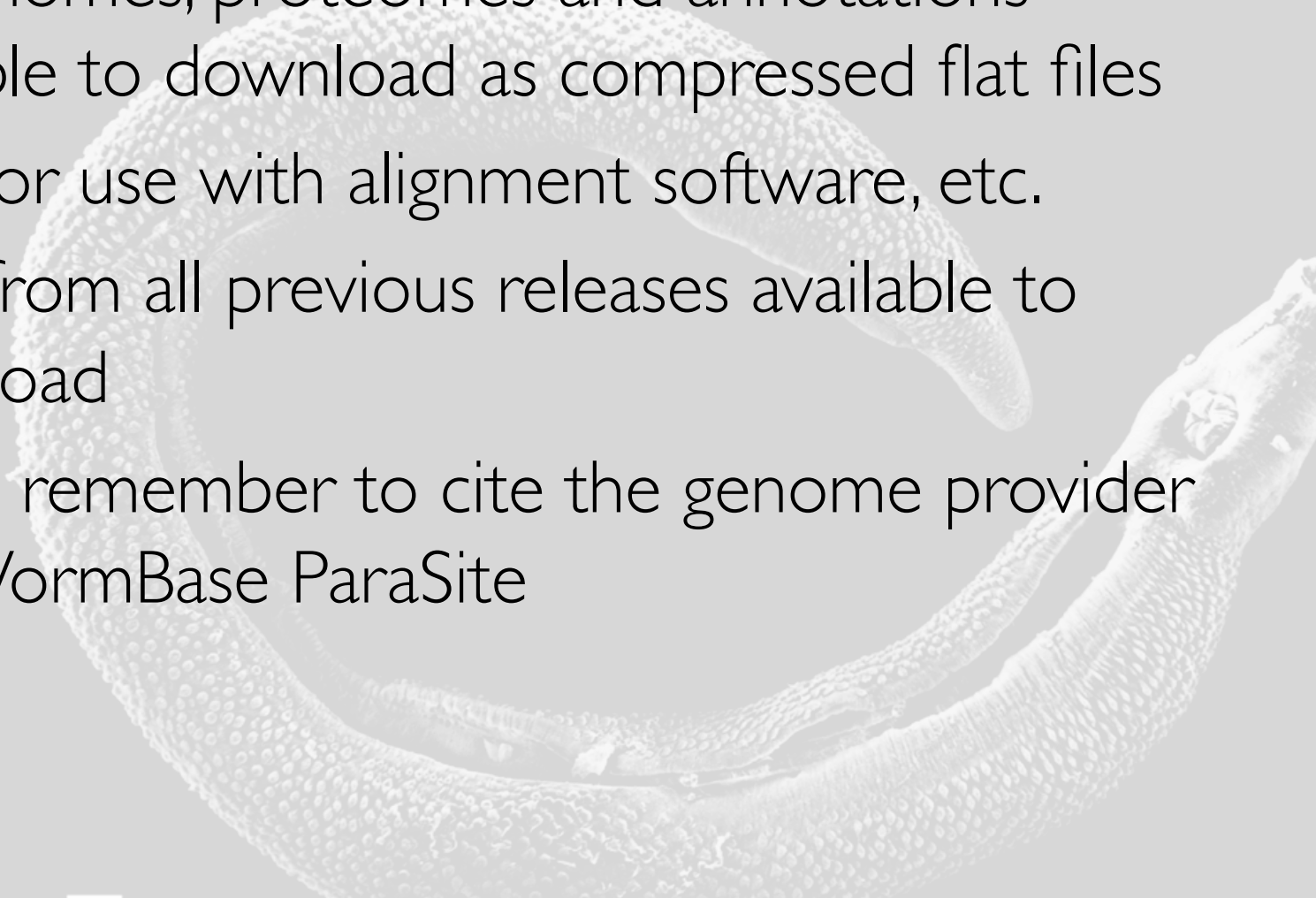




Bulk downloads and programmatic access

Downloads

- All genomes, proteomes and annotations available to download as compressed flat files
- Ideal for use with alignment software, etc.
- Data from all previous releases available to download
- Please remember to cite the genome provider and WormBase ParaSite



Downloads – File Formats

Genomic	Raw FASTA genome file
Masked Genomic	Genome FASTA with repeat regions hard-masked
Soft-masked Genomic	Genome FASTA with repeat regions soft-masked
Annotations	GFF3 file containing all annotations
Proteins	FASTA protein file
mRNA Transcripts	FASTA of the spliced full-length transcripts
CDS Transcripts	FASTA of the spliced CDS-portion of the protein coding transcripts

Access using R

- Access our database directly from R, via the biomaRt package
- Syntax identical to Ensembl
- Very quick access to large amounts of data
- Please don't use excessively (i.e. download the results once then store them locally for processing)

WormBase ParaSite in R

- Install the biomaRt package:

```
source("http://bioconductor.org/biocLite.R")  
biocLite("biomaRt")
```

- Install the biomaRt package:

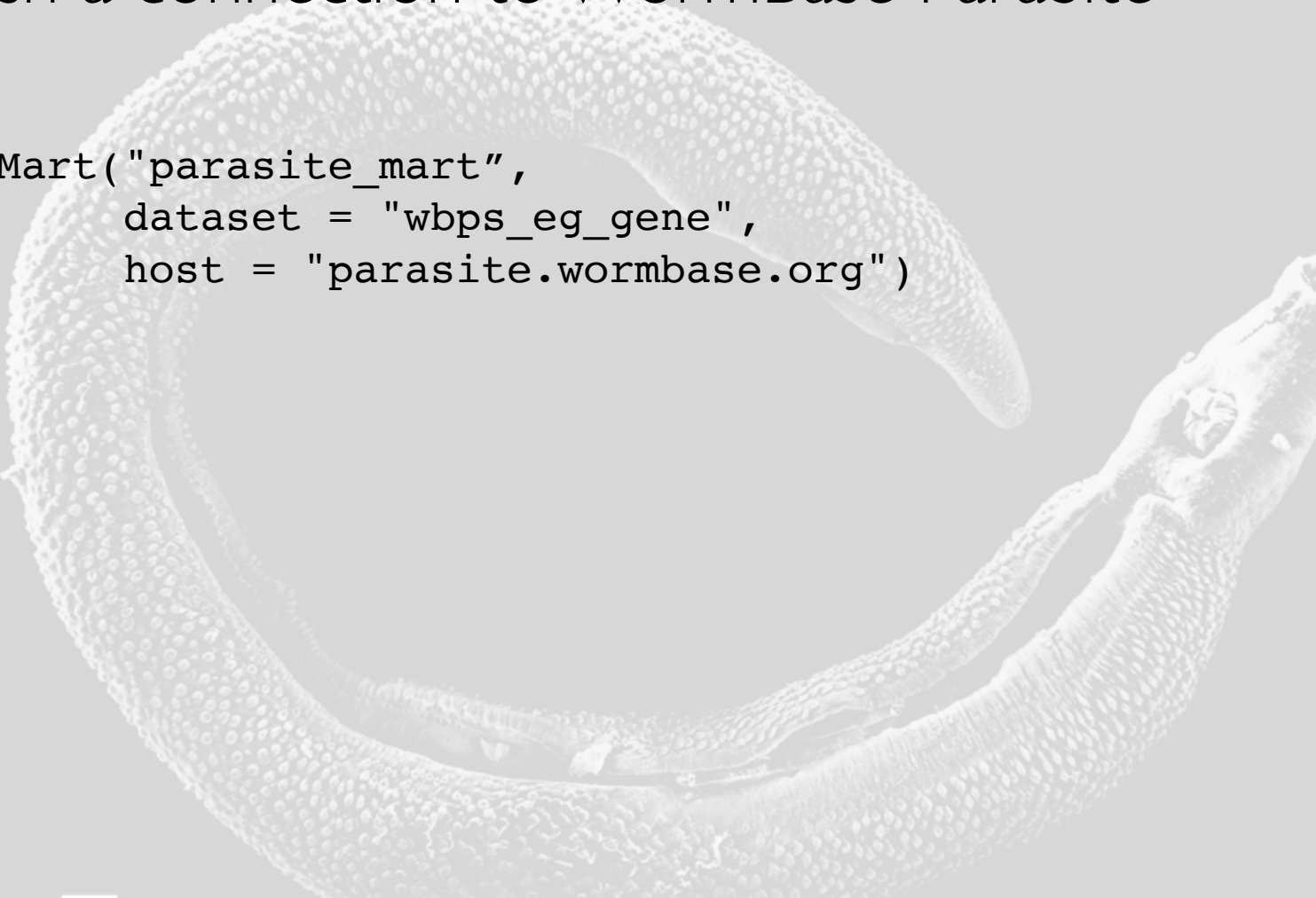
```
library(biomaRt)
```



WormBase ParaSite in R

- Establish a connection to WormBase ParaSite

```
mart <- useMart("parasite_mart",  
               dataset = "wbps_eg_gene",  
               host = "parasite.wormbase.org")
```



WormBase ParaSite in R

- Example: get all the *Schistosoma mansoni* genes with a *C. elegans* orthologue:

```
genes <- getBM(mart = mart,  
               filters = c("species_id_1010",  
                           "with_celegans_eg_homologue"),  
               value = list("prjea36577", TRUE),  
               attributes = c("ensembl_gene_id",  
                              "celegans_eg_gene"))
```

```
head(genes)
```

	ensembl_gene_id	celegans_eg_gene
1	Smp_078570	WBGene00009448
2	Smp_063300	WBGene00004450
3	Smp_210640	WBGene00009305
4	Smp_049930	WBGene00010465
5	Smp_132740	WBGene00001395
6	Smp_132740	WBGene00001396

Language neutral queries

- REST API allows access using any programming language
- For processing large amounts of data: consider whether making one query to BioMart may be more suitable
- Examples provided in Perl, Python, Ruby, Java, Curl and Wget

Endpoint Catalogue

Comparative Genomics

Resource	Description
GET /rest/genetree/id/:id	Retrieves a gene tree dump for a gene tree stable identifier
GET /rest/genetree/member/id/:id	Retrieves a gene tree that contains the stable identifier
GET /rest/genetree/member/symbol/:species/:symbol	Retrieves a gene tree containing the gene identified by a symbol
GET /rest/homology/id/:id	Retrieves homology information (orthologues) by gene id
GET /rest/homology/symbol/:species/:symbol	Retrieves homology information (orthologues) by symbol

Endpoint Specifics

GET `genetree/member/id/:id`

Retrieves a gene tree that contains the stable identifier

Parameters

Required

Name	Type	Description	Default	Example Values
id	String	A stable ID	-	WBGene00225050

Endpoint Examples

Example Requests

[/rest/genetree/member/symbol/brugia_malayi_prjna10729](#)

[/Bma-unc-1?content-type=text/x-phyloxml%2Bxml](#)

Example output

[Perl](#)

[Python2](#)

[Python3](#)

[Ruby](#)

[Java](#)

[Curl](#)

[Wget](#)

```
<?xml version="1.0" encoding="UTF-8"?>
<phyloxml xsi:schemaLocation="http://www.phyloxml.org http://www.phyloxml.org/1.10/phyloxml.xsd"
xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.phyloxml.org">
  <phylogeny rooted="true" type="gene tree">
    <clade branch_length="0">
      <confidence type="duplication_confidence_score">0.7311</confidence>
      <taxonomy>
        <id>33208</id>
        <scientific_name>Metazoa</scientific_name>
      </taxonomy>
      <events>
        <type>speciation_or_duplication</type>
        < duplications>1</ duplications>
      </events>
    <clade branch_length="0.003861">
      <confidence type="duplication_confidence_score">0.1584</confidence>
      <taxonomy>
```

Code Examples

Example Requests

[/rest/genetree/member/symbol/brugia_malayi_prjna10729](#)

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Perl

Python2

Python3

Ruby

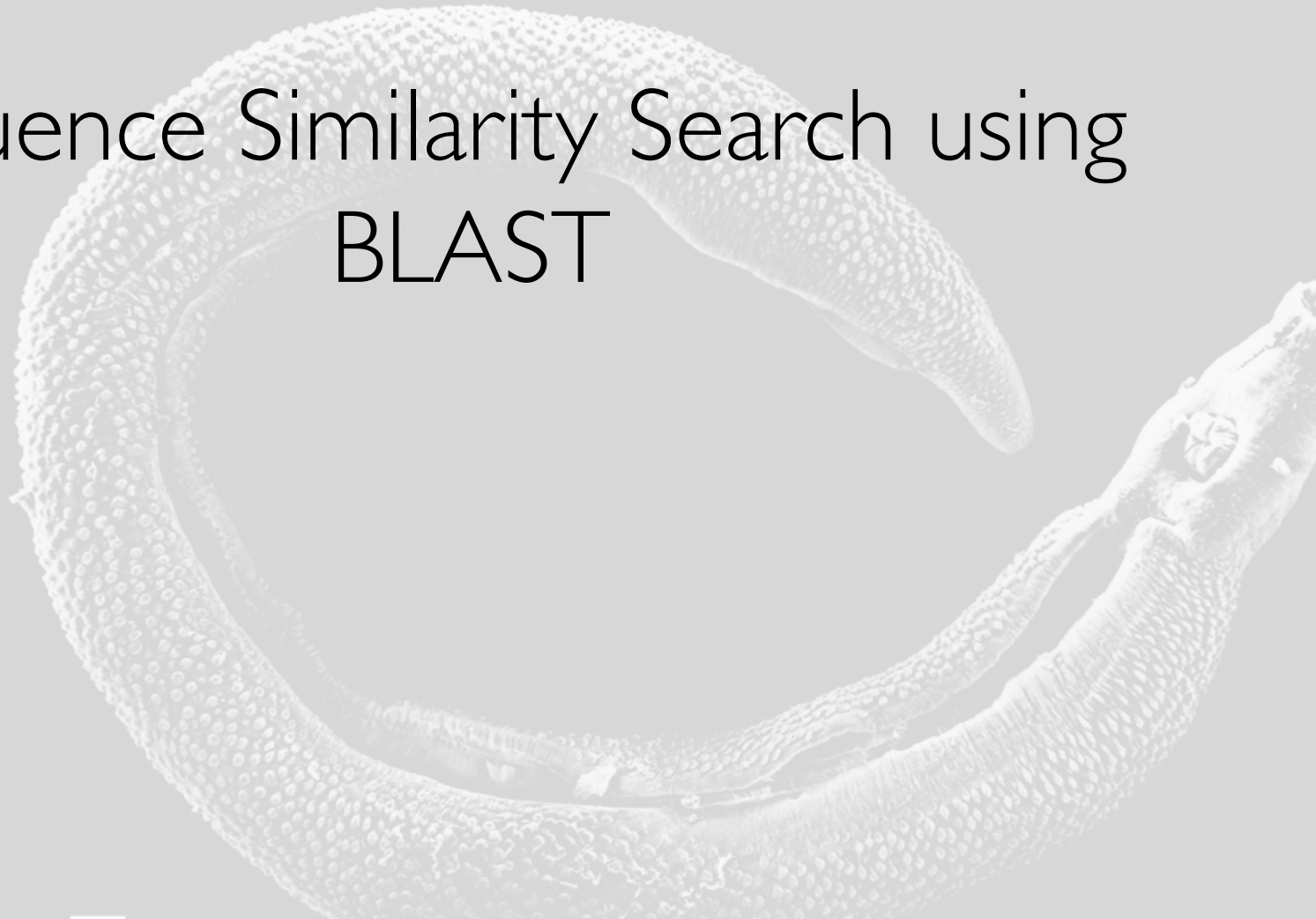
Java

Curl

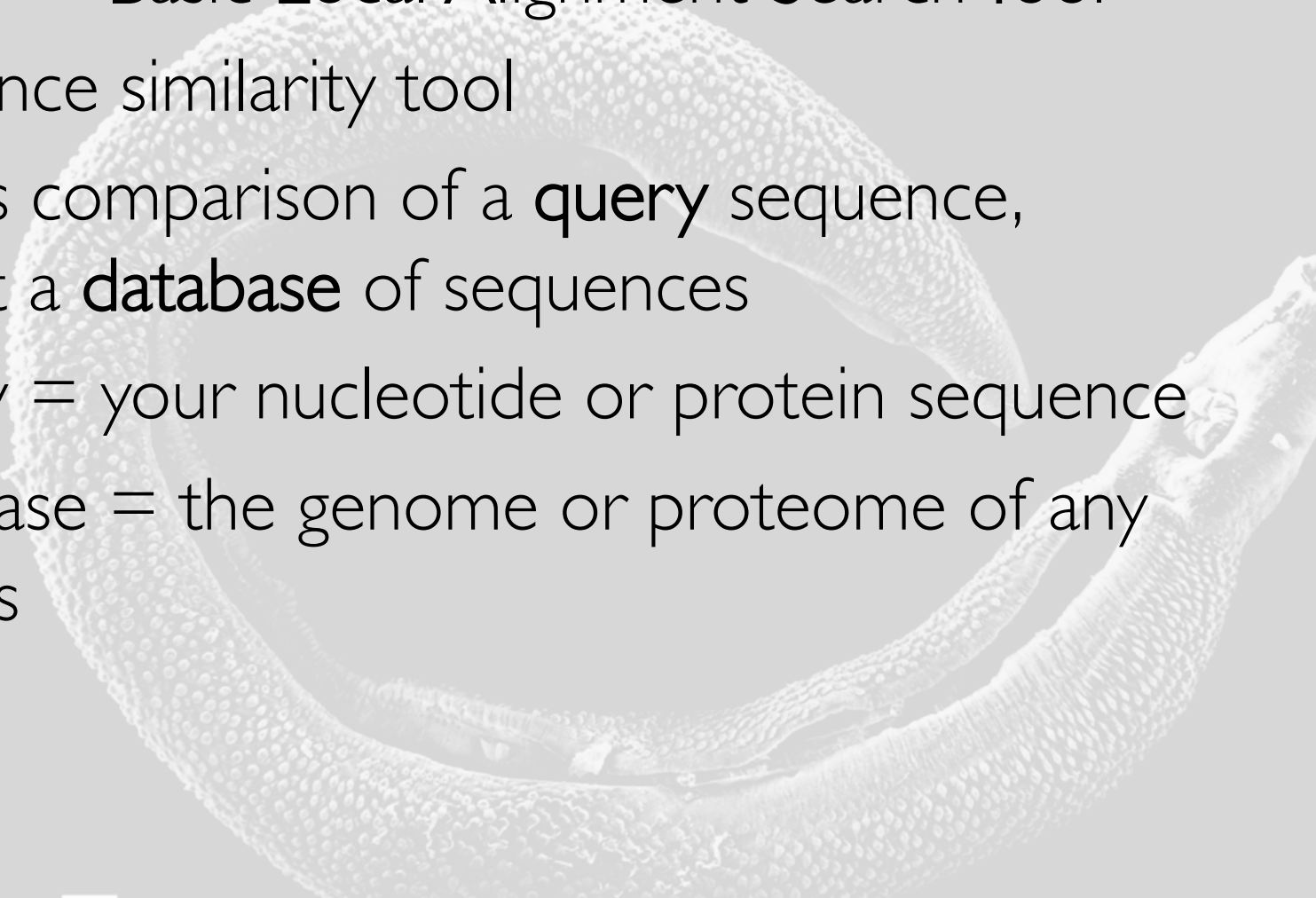
Wget

```
1. use strict;
2. use warnings;
3.
4. use HTTP::Tiny;
5.
6. my $http = HTTP::Tiny->new();
7.
8. my $server = 'http://parasite.wormbase.org';
9. my $ext = '/genetree/member/symbol/brugia_malayi_prjna10729/Bma-unc-1?';
10. my $response = $http->get($server.$ext, {
11.     headers => { 'Content-type' => 'text/x-phyloxml+xml' }
12. });
13.
14. die "Failed!\n" unless $response->{success};
15.
16.
17. print "$response->{status} $response->{reason}\n";
18.
```


Sequence Similarity Search using BLAST

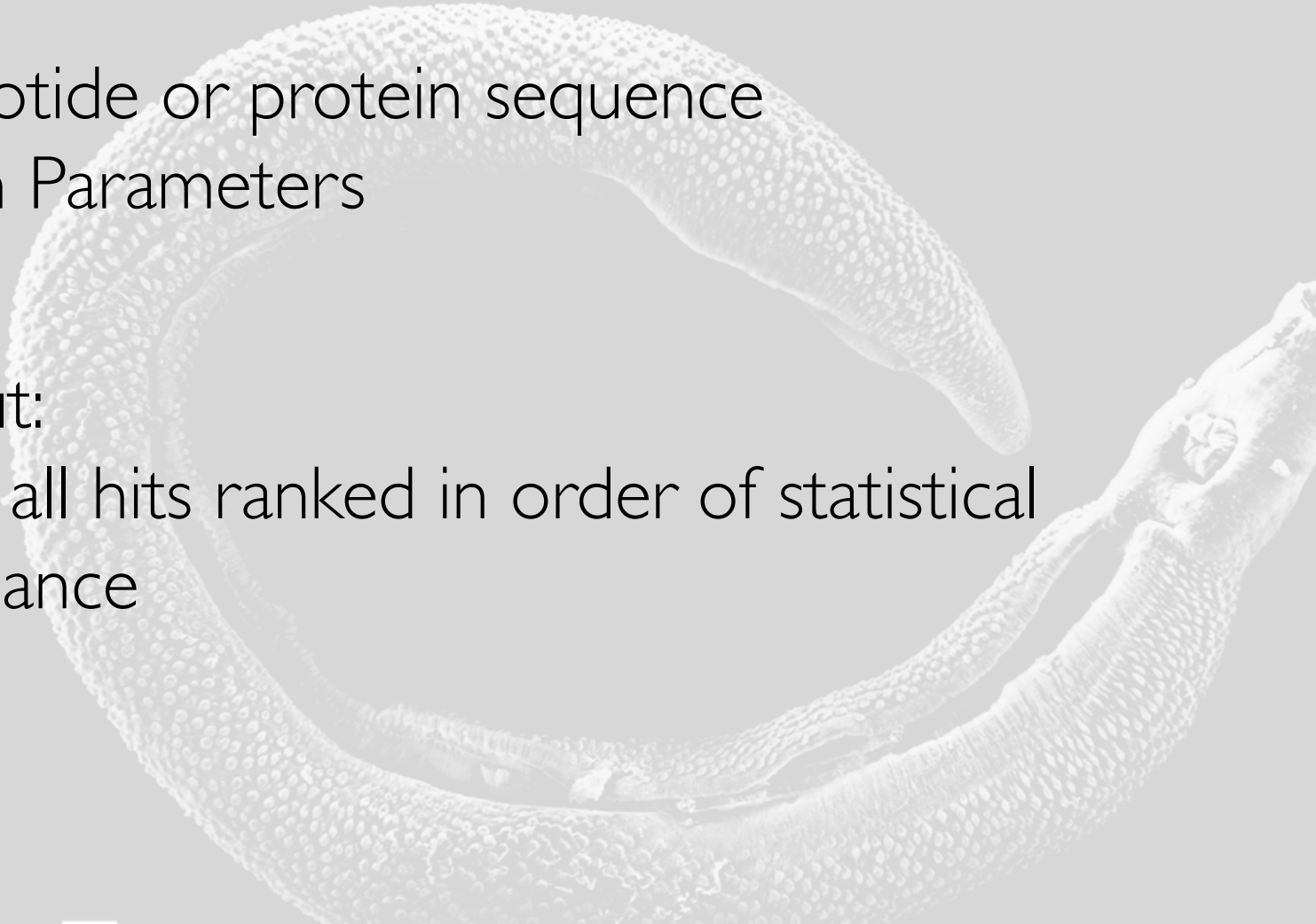


What is BLAST?

- BLAST = **B**asic **L**ocal **A**lignment **S**earch **T**ool
 - Sequence similarity tool
 - Allows comparison of a **query** sequence, against a **database** of sequences
 - Query = your nucleotide or protein sequence
 - Database = the genome or proteome of any species
- 

What is BLAST?

- Input:
Nucleotide or protein sequence
Search Parameters
- Output:
List of all hits ranked in order of statistical significance



Types of BLAST

BLAST Type	Query Sequence	Target Database
BLASTN	Nucleotide	Genome (nucleotide)
BLASTP	Peptide	Proteome (peptide)
BLASTX	Six frame translation of a nucleotide sequence	Proteome (peptide)
TBLASTX (slowest)	Six frame translation of a nucleotide sequence	Six frame translation of genome
TBLASTN	Peptide	Six frame translation of genome

Using the ParaSite BLAST

WormBase ParaSite

Species List **BLAST** BioMart REST API Downloads WormBase

Brugia malayi (PR:INA10729) Location: Bmal_v3_scaffold1:3,207,430-3,210,542 Gene: Bm2147

Gene-based displays

- Summary
- Splice variants
- Sequence**
- External references
- Ontologies
 - GO: Molecular function
 - GO: Cellular component

Gene: Bm2147 WBGene00222408

Location [SuperContig Bmal_v3_scaffold1:3,207,430-3,210,542 forward](#)

About this gene This gene has 2 transcripts ([splice variants](#)) and [112 orthologues](#)

Gene type Protein coding

Defaults to the species you are currently browsing

Using the ParaSite BLAST

The screenshot displays the ParaSite BLAST interface. On the left, there is a sidebar with navigation options: 'References', 'Molecular function', 'Molecular component', 'Biological process', 'Genomics', 'Genes', 'Download this page', 'Data', 'Data', 'This page', and 'Link this page'. The main content area is divided into several sections:

- Location:** SuperContig Bmal_v3 scaffold1: 3,207,430-3,210,542 forward strand.
- About this gene:** This gene has 2 transcripts ([splice variants](#)) and [112 orthologues](#).
- Gene type:** Protein coding
- Annotation Method:** Protein-coding model imported from [WormBase](#)
- Transcripts:** A button labeled 'Show transcript table'.
- Marked-up sequence:** A section containing two buttons: 'Download sequence' and 'BLAST this sequence'. The 'BLAST this sequence' button is highlighted with a red rectangle.
- Exons:** A section with three tabs: 'Exons', 'Bm2147 exons', and 'All exons in this region'. The 'All exons in this region' tab is selected.
- Sequence:** A block of DNA sequence text starting with '>supercontig:B_malayi-3.1:Bmal_v3_scaffold1:3206830:3211142:1'. The sequence is mostly in black, but a specific segment is highlighted in red: **ATGGACGCTGGCAGTTAGTTGCTGGGTACATTACTTAG**.

Using the ParaSite BLAST

ecular function
lular component
ological process
ve Genomics
ee
gues
ues

Gene type: Protein coding
Annotation Method: Protein-coding model imported from [WormBase](#)
Transcripts: [Show transcript table](#)

Marked-up sequence

[Download sequence](#) [BLAST this sequence](#)

Exons Bm2147 exons **All exons in this region**

```
>supercontig:B_malayi-3.1:Bmal_v3_scaffold1:3206830:3211142:1  
ATTACTTCTGTATTTTTTCATGATCTTATCCAAACCATTATTTTTGAACTTCTTTTGT  
CTACTCTAAGTCTACTCTACAGAGATCAGCCCTTTTGTATTTAGAAACACCAAGCTAAAC  
TCGAGAGTTACTGTATTGTTTTGACATTGTGTCGTTGATGCTTCTACCATGTCACTGAT  
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  
TTAAATAATTTCAAGTGATTTAGACATTAATATCAGGCAATATCTGTAAGAACATAAGTCA  
TTACAACATTTGCTGTTCCACGGTAAACTGTCATTTTTTTTCATCTCGTTGCATTATATTG  
CAATTTCTATCATATTCGCAAGTTAATAAATATTGATGTTGCTTCATTT  
CAGTTTTAGTACGAAGTTCAGTATTTCTTGAAAGCTTTGGTTTCATTA  
TGGTTTGTTTCAGTTGCGCAAATTTTGAAGTACAATTTTCGATCAGCTATTTTTAAAAA  
TATGTTTATTAAGCAAAATATACGACAAAAGAAGTATTTGATATAATTCGTTTGGAT  
ATGGACGCTGGCAGTTTAGTTGCTGGGTCACATTACTTAGGTAATGTTCTGTGTTTGAT  
TAAATGAGTTGACTTCTATTTTTTCGATCCCTTTTCTGTTTATAAAGGATAGTAATCCAA  
ATGAATGATTCAACAATTTATTGTTAATTCCTTTAATAACTTACGTAGTGTGTAATA
```

[BLAST selected sequence](#)

Using the ParaSite BLAST

WormBase ParaSite Search WormBase ParaSite...
e.g. *O. volvulus*, PRJNA60051, WBGene00262434, Bma-eat-4, eat-4 or metallopeptidase

Species List BLAST BioMart REST API Downloads WormBase My Account - bbolt@ebi.ac.uk Logout Help and Documentation

Brugia malayi (PRJNA10729) Location: Bmal_v3_scaffold525:2,308-5,498 Gene: Bma-eat-4 Transcript: Bm7483

Gene-based displays

- Summary
- Splice variants
- Sequence**
- External references
- Ontologies
 - GO: Molecular function
 - GO: Cellular component
 - GO: Biological process
- Comparative Genomics
 - Gene tree
 - Orthologues
 - Paralogues

Gene: Bma-eat-4 WBGene00227744

Location [SuperContig Bmal_v3_scaffold525:2,308-5,498](#) forward strand.

About this gene This gene has 1 transcript ([splice variant](#)), [126 orthologues](#) and [7 paralogues](#).

Gene type Protein coding

Annotation Method Protein-coding model imported from [WormBase](#)

Transcripts [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Biotype	UniProt
Bm7483	Bm7483	1459	475aa	Protein coding	A0A0H5SF60

Marked-up sequence

[Download sequence](#) [BLAST this sequence](#)

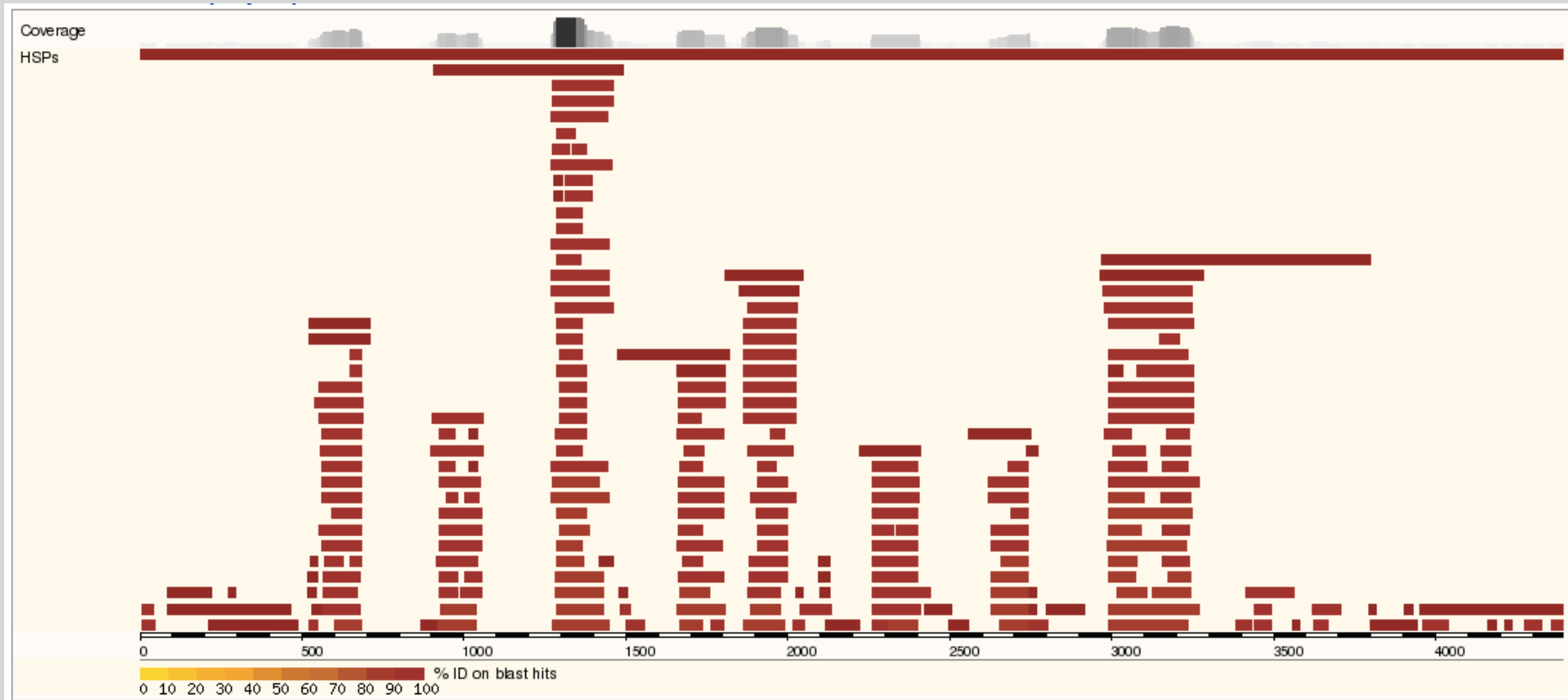
Exons [Bma-eat-4 exons](#) [All exons in this region](#)

```
>supercontig:B_malayi-3.1:Bmal_v3_scaffold525:1708:6098:1
ATTTCAACTTCAAAAATAACTATATCATAATTTTGTGTTGCTAAAAATATAAAAAAGTGA
AATAATGAAAAACATTAAAAAATAAAAAAATAAAAAAATGAACAAAATAAAATAAAAATATAA
TTCCAGATTAAAGCAGAAAGCAATGCAACAAATTAATATCATAAAAAGTTGATTTATGT
GAATTTAATTTATACTTTAGCTATTAGAGTTAAAAAAGAAAGAGAGAAAATCATTAA
TAAAAATATTGCTCAATAATCTTTTATATTTAAAAATATATTTTGAATGAATCATAA
AAATTAGAATTTGATTACAATTAACAATTAATATATTTAATCATAATGATAAGAATAAAA
TATTTATATGGAATAATCCGGAAAAGTTAATAAATCTCCGGAATAATTACGCTAGAAA
CAGAAACAAATTCACCTGTTTTCTTTCTTTTTTTTTTTGTTTTATTTTTCTGTTTT
GATTTTATTTTATTTCAATTCAAAATATGAGAAAAAATAATTTTTTTTTTTTTTAAATATA
```


Making sense of the results

- Score
Used to assess the biological relevance by describing the alignment quality
Higher score = higher similarity
- *E*-value
Similar to (but not the same as) a *p*-value that has been corrected for multiple testing - decreases exponentially as the score increases
Lower *E*-value = more significant result
- %ID
Percentage of your query sequence that matches the genome/proteome database

Making sense of the results



Practical Exercises

1. Locate the peptide sequence for the *Brugia malayi* gene Bma-eat-4. Using BLAST, find which other nematode(s) this peptide sequence occurs in at 100% similarity?
2. Locate the cDNA sequence for the *Clonorchis sinensis* gene csin111107. Using BLAST, find which other genomes the six-frame translation of this sequence occurs in with a %ID of more than 90%. Which BLAST tool is most appropriate here?
3. Use the 'Edit' button to populate the input form with the sequence from (2). There are many advanced options that can be set. In most cases, these can be left at the default values. Decrease the maximum number of alignments displayed to 5 and run the query. Why are there more than five results in the table?
4. Find a gene of choice from your favourite species. BLAST the sequence of the first exon against the database of all helminth transcriptomes.

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WormBase ParaSite Version: WBPS6 (WS252)

Search WormBase ParaSite...
e.g. *O. volvulus*, PFJNA80051, WBGene00262434, Bma-eat-4, eat-4 or metalloproteinase

Species List BLAST BioMart REST API VEP Downloads WormBase My Account - bbolt@ebi.ac.uk Logout Help and Documentation

Species **BLAST** **BioMart**

API **Downloads** **WormBase**

Find a genome

- [+] Nematoda (Roundworms)
- [+] Platyhelminthes (Flatworms)

Statistics

- Version: WBPS6 (April 2016)
- WormBase Version: WS252
- 109 genomes, representing 100 species
- 2,189,841 genes

Announcements

[Announcing WormBase ParaSite release 6](#)
posted 2 months ago

We are pleased to announce the sixth release of WormBase ParaSite.

Blog

[Featured Paper: Glucose and Glycogen Metabolism in *B. malayi* Is Associated with Wolbachia Symbiont Fitness](#)
posted 1 month ago

We would like to draw your attention to a paper published by Denis Voronin, et. al on the influence of host metabolism on symbiont fitness: Denis Voronin, Saheed Bachu, Michael Shlossman, Thomas R. Unnasch, Elodie Ghedin, Sara Lustigman "Glucose and Glycogen Metabolism in *Brugia malayi* Is Associated with Wolbachia Symbiont Fitness", PLoS One. 2016 Apr [...]

[Brugia malayi assembly update](#)
posted 2 months ago

The new release of WormBase (WS252) is the first one to feature the new and updated version 4 of the *Brugia malayi* assembly. Due to additional optical mapping, as well as new long-range PacBio sequencing and additional reassembly work conducted to integrate all available data, it was possible to scaffold the 88.2Mbp assembly into 5 chromosomes [...]

[Register for a WormBase ParaSite workshop](#)
posted 2 months ago

To help our users make the most of this valuable resource, we are visiting universities and institutes to provide hands-on training sessions.

[\[Older\]](#)

Twitter

Tweets by @WBParasite

WormBase ParaSite @WBParasite
This maintenance is now complete. Thank you for your patience. [twitter.com/WBParasite/sta...](https://twitter.com/WBParasite/status/711111111) 3h

WormBase ParaSite @WBParasite
Important notice: due to essential server maintenance, WormBase ParaSite will be unavailable tomorrow (7th June) between 10:00-11:30 (BST). 23h

WormBase ParaSite Retweeted
Havlev Bennett

[Embed](#) [View on Twitter](#)

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BLASTX or TBLASTX

WormBase ParaSite Version: WBPS6 (WS252)

Search WormBase ParaSite...

e.g. *O. volvulus*, PFJNA80051, WBGene00262434, Bma-eat-4, eat-4 or metallopeptidase

Species List BLAST BioMart REST API VEP Downloads WormBase Login Register Help and Documentation

Species **BLAST** **BioMart**

API **Downloads** **WormBase**

Find a genome

[+] Nematoda (Roundworms)

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posted 2 months ago

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[Older]

Twitter

Tweets by @WBParasite

WormBase ParaSite @WBParasite
This maintenance is now complete. Thank you for your patience. [twitter.com/WBParasite/sta...](https://twitter.com/WBParasite/status/711111111)

WormBase ParaSite @WBParasite
Important notice: due to essential server maintenance, WormBase ParaSite will be unavailable tomorrow (7th June) between 10:00-11:30 (BST).

WormBase ParaSite Retweeted
Havley Bennett

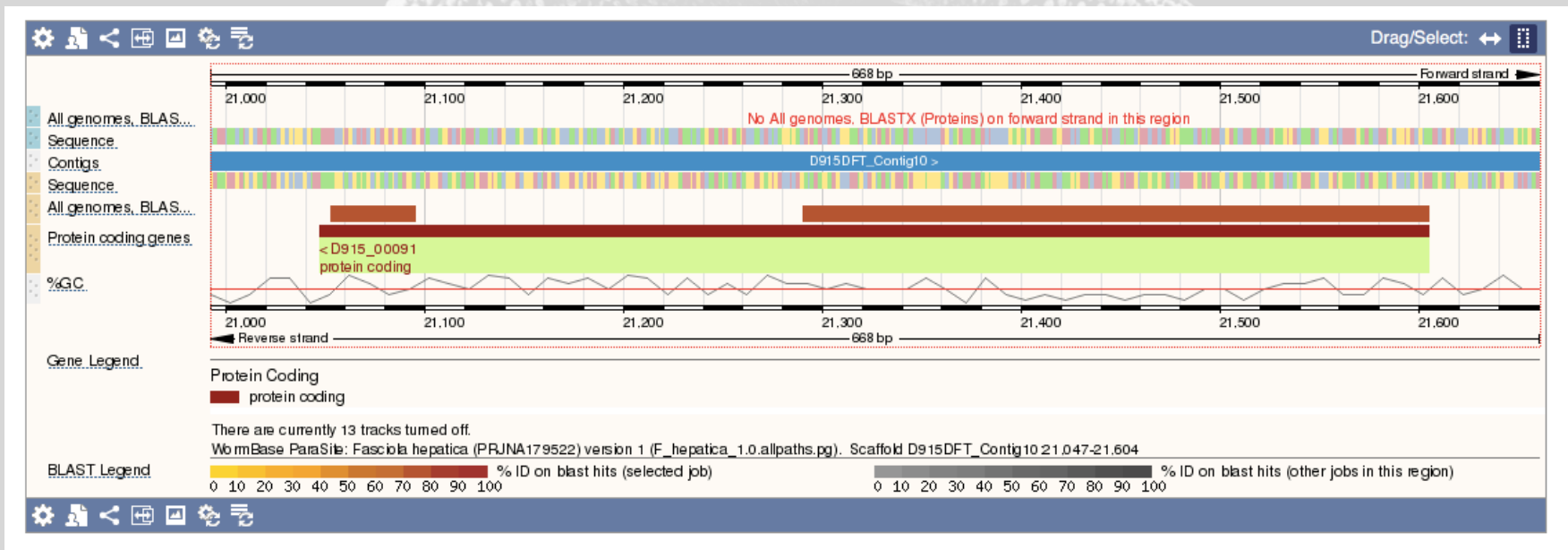
Embed View on Twitter

- Use the 'Edit' button to populate the input form with the sequence from (2). There are many advanced options that can be set. In most cases, these can be left at the default values. Decrease the maximum number of alignments displayed to 5. Why are there more than five results in the table?

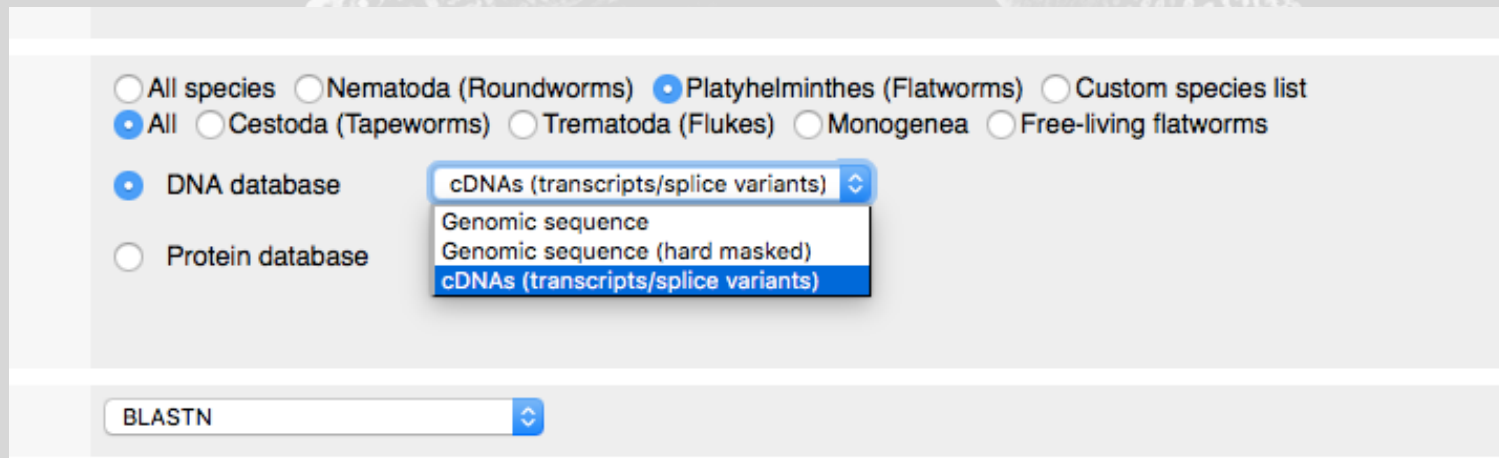
Show/hide columns (8 hidden)		Filter							
Genome	Subject name	Subject description	Gene hit	Query start	Length	Score	E-val	%ID	
Clonorchis sinensis (PRJDA72781)	csin111107	DNA-binding protein A	csin111107	427	128 [Sequence]	677	7.1E-144	100.0	[Alignment]
Clonorchis sinensis (PRJDA72781)	csin111107	DNA-binding protein A	csin111107	1	108 [Sequence]	478	7.1E-144	100.0	[Alignment]
Opisthorchis viverrini (PRJNA222628)	T265_14198		T265_14198	427	17 [Sequence]	95	2.4E-57	100.0	[Alignment]
Opisthorchis viverrini (PRJNA222628)	T265_14198		T265_14198	1	105 [Sequence]	434	2.4E-57	96.2	[Alignment]
Fasciola hepatica (PRJNA179522)	D915_00091		D915_00091	1	105 [Sequence]	334	9.8E-38	72.4	[Alignment]
Fasciola hepatica (PRJEB6687)	BN1106_s1641B000184.mRNA-1		BN1106_s1641B000184	1	105 [Sequence]	330	3.6E-37	72.4	[Alignment]
Echinostoma caproni (PRJEB1207)	ECPE_0000786301-mRNA-1		ECPE_0000786301	1	105 [Sequence]	314	7.9E-35	72.4	[Alignment]
Fasciola hepatica (PRJEB6687)	BN1106_s1641B000184.mRNA-1		BN1106_s1641B000184	433	14 [Sequence]	51	3.6E-37	71.4	[Alignment]
Fasciola hepatica (PRJNA179522)	D915_00091		D915_00091	433	14 [Sequence]	51	9.8E-38	71.4	[Alignment]
Echinostoma caproni (PRJEB1207)	ECPE_0000786301-mRNA-1		ECPE_0000786301	427	16 [Sequence]	50	7.9E-35	56.3	[Alignment]

This parameter specifies the maximum number of objects in the subject database (i.e. genome or proteome). In this case, the query sequence has matched twice to each gene. This suggests there may be two conserved sequences within the query.

3. Use the 'Edit' button to populate the input form with the sequence from (2). There are many advanced options that can be set. In most cases, these can be left at the default values. Decrease the maximum number of alignments displayed to 5. Why are there more than five results in the table?



4. Find a gene of choice from your favourite flatworm species. BLAST the sequence of the first exon against the database of all flatworm transcriptomes.



The image shows a screenshot of a BLAST search interface. The background is a grayscale image of a flatworm, possibly a planarian, showing its characteristic segmented body and head region. The interface is a white rectangular box with a light gray border. It contains several radio buttons and a dropdown menu. The 'DNA database' section is selected, and the 'cDNAs (transcripts/splice variants)' option is highlighted in the dropdown menu. The 'BLASTN' search type is also visible in a dropdown menu at the bottom left.

All species Nematoda (Roundworms) Platyhelminthes (Flatworms) Custom species list
 All Cestoda (Tapeworms) Trematoda (Flukes) Monogenea Free-living flatworms

DNA database Protein database

cDNAs (transcripts/splice variants)
Genomic sequence
Genomic sequence (hard masked)
cDNAs (transcripts/splice variants)

BLASTN

Data Discovery & Export with BioMart

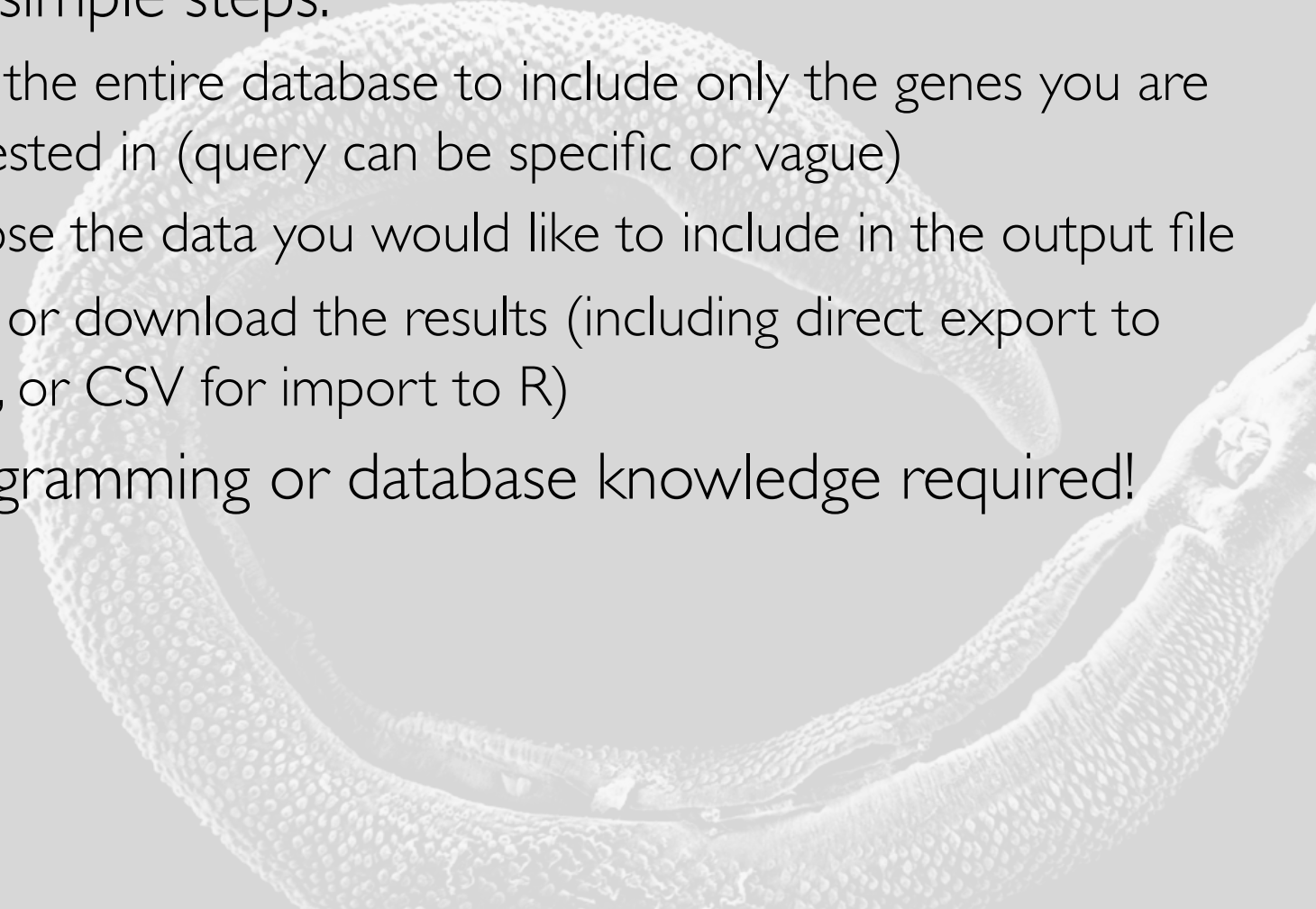


Basics of BioMart

- Advanced search and data export tool
- Produces tables of data or files containing sequence
- Table contents are entirely customisable
- Ideal for working with, or generating, lists of data

Gene stable ID	Chromosome/scaffold name	Gene start (bp)	Gene end (bp)	Exon ID	Exon region start (bp)	Exon region end (bp)	cDNA coding start	cDNA coding end
A01321	Scaffold1052	8861	10795	A01321.e1	8861	9057	1	197
A01321	Scaffold1052	8861	10795	A01321.e2	9212	9353	198	339
A01321	Scaffold1052	8861	10795	A01321.e3	10646	10795	340	489
A01322	Scaffold1052	19019	19861	A01322.e1	19019	19266	1	248
A01322	Scaffold1052	19019	19861	A01322.e2	19663	19861	249	447
A02773	Scaffold1159	9064	10222	A02773.e1	10184	10222	1	39
A02773	Scaffold1159	9064	10222	A02773.e2	9064	9354	40	330
A03307	Scaffold118	185300	190808	A03307.e1	190768	190808	1	41
A03307	Scaffold118	185300	190808	A03307.e2	190413	190656	42	285
A03307	Scaffold118	185300	190808	A03307.e3	188719	188878	286	445
A03307	Scaffold118	185300	190808	A03307.e4	188038	188180	446	588
A03307	Scaffold118	185300	190808	A03307.e5	187378	187413	589	624
A03307	Scaffold118	185300	190808	A03307.e6	185300	185401	625	726
A03308	Scaffold118	191713	191954	A03308.e1	191817	191954	1	138
A03308	Scaffold118	191713	191954	A03308.e2	191713	191775	139	201
A04991	Scaffold127	310799	318815	A04991.e1	318652	318815	1	164
A04991	Scaffold127	310799	318815	A04991.e2	315979	316050	165	236
A04991	Scaffold127	310799	318815	A04991.e3	314309	314432	237	360
A04991	Scaffold127	310799	318815	A04991.e4	313695	313832	361	498
A04991	Scaffold127	310799	318815	A04991.e5	310799	311017	499	717

Three simple steps...

- Three simple steps:
 1. Filter the entire database to include only the genes you are interested in (query can be specific or vague)
 2. Choose the data you would like to include in the output file
 3. View or download the results (including direct export to Excel, or CSV for import to R)
 - No programming or database knowledge required!
- 

Data available for export

- Sequences (genomic, cDNA, UTR, flanking, cDNA, peptide)
- Gene IDs, names and descriptions
- Identifiers for data from external databases (e.g. UniProt)
- Gene structure (e.g. exons)
- Protein domains and function (e.g. InterPro, Gene3D, PANTHER etc.)
- Gene ontology terms
- Orthologues and paralogues (in all nematodes, flatworms and a number of non-worm comparators, e.g. human, mouse and rat)

BioMart Interface

WormBase ParaSite
WormBase Home | ParaSite Home

New Count Results

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

Please restrict your query using criteria (If filter values are truncated in any lists, hover over the list for more information. For guidance, see the [relevant pages](#) of our documentation.)

- SPECIES
- REGION (use only when selecting one species)
- GENE
- GENE ONTOLOGY (GO)
- HOMOLOGY (ORTHOLOGUES AND PARALOGUES)
- PROTEIN DOMAINS

1. Query Filters
[None selected]

2. Output Attributes
Genome project
Gene stable ID

Filters and attributes appear here

Control buttons:
New = reset form
Count = count results
Results = preview results

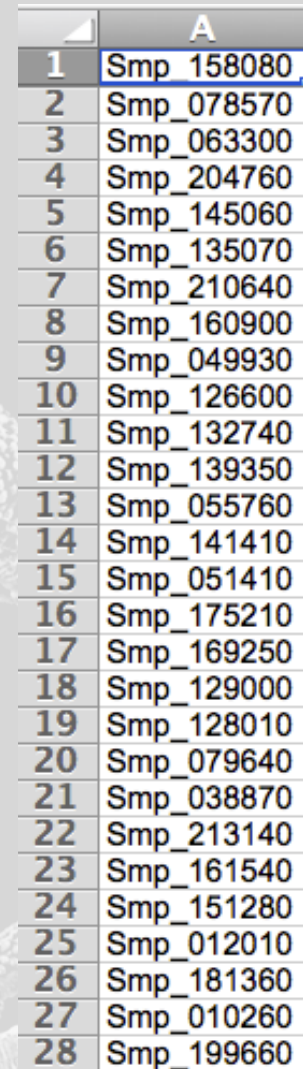
Query filters = search terms to restrict the query

Output attributes = select data to add into results (i.e. which columns would you like to appear in your table)

BioMart Example 1 – Working with a list

I have a list of *Schistosoma mansoni* genes and would like to find:

1. The gene name and gene description
2. How many of these genes have a human orthologue?
3. The functional annotation of the genes with a human orthologue?



	A
1	Smp_158080
2	Smp_078570
3	Smp_063300
4	Smp_204760
5	Smp_145060
6	Smp_135070
7	Smp_210640
8	Smp_160900
9	Smp_049930
10	Smp_126600
11	Smp_132740
12	Smp_139350
13	Smp_055760
14	Smp_141410
15	Smp_051410
16	Smp_175210
17	Smp_169250
18	Smp_129000
19	Smp_128010
20	Smp_079640
21	Smp_038870
22	Smp_213140
23	Smp_161540
24	Smp_151280
25	Smp_012010
26	Smp_181360
27	Smp_010260
28	Smp_199660

BioMart Example 1 – Working with a list

Save time by using BioMart!

The image shows three overlapping screenshots of the WormBase ParaSite website, illustrating the process of working with a list of genes. A large red 'no' symbol is overlaid on the screenshots, indicating that the traditional way of viewing individual gene pages is inefficient. The screenshots show the following information:

- Gene: GLUCL** (Transcript: Smp_104890.1)
- Description:** Putative cys-loop ligand gated ion channel subunit (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V7T2]
- Location:** Scaffold Smp_Chr_1:42,206,486-42,214,230 reverse strand.
- About this gene:** This gene has 1 transcript (splice variant), 375 orthologues and 3 paralogues.
- Gene-based displays:** Summary, Splice variants, Sequence, External references, Ontologies (GO: Molecular function, GO: Cellular component, GO: Biological process), Comparative Genomics (Gene tree, Orthologues, Paralogues).
- Table:** A table with columns for Transcript ID, bp, Protein, Biotype, and UniProt. The row for Smp_104890.1 shows 1515 bp, protein 504aa, and UniProt accession G4V7T2. T2CSW6.
- GO: Molecular function:** A table with columns for Accession, Term, Evidence, Annotation Source, and Transcript IDs. The row for GO:0005230 shows the term 'extracellular ligand-gated ion channel activity' with evidence from IEA and UniProtKB/TrEMBL/T2CSW6.

I have a list of *Schistosoma mansoni* genes and would like to find:
 2. How many of these genes have a human orthologue?

100 / 2550346 Genes

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

1. Query Filters

Gene stable ID(s): [ID-list specified]

2. Output Attributes

- Genome project
- Gene stable ID
- Gene name
- Gene description

Export all results to Unique results only

Email notification to

View rows as Unique results only

Genome project	Gene stable ID	Gene name	Gene description
schistosoma_mansoni_prjea36577	Smp_002160		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4VLL1]
schistosoma_mansoni_prjea36577	Smp_007180		Sr-related ctd associated factor (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VB15]
schistosoma_mansoni_prjea36577	Smp_010260		
schistosoma_mansoni_prjea36577	Smp_012010	FOXO	Forkhead transcription factor (inferred by orthology to a protein) [Source:UniProtKB;Acc:A6XDL3]
schistosoma_mansoni_prjea36577	Smp_013610		
schistosoma_mansoni_prjea36577	Smp_018150		Putative mannosyl-oligosaccharide alpha-1,2-mannosidase (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VP10]
schistosoma_mansoni_prjea36577	Smp_029520		Villin, putative (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4LW89]
schistosoma_mansoni_prjea36577	Smp_036550		
schistosoma_mansoni_prjea36577	Smp_038870		NADH-ubiquinone oxidoreductase, putative (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4LUK7]
schistosoma_mansoni_prjea36577	Smp_044010		Tropomyosin-1 [Source:UniProtKB/Swiss-Prot;Acc:P42637]
schistosoma_mansoni_prjea36577	Smp_045420		Adiponectin receptor, putative (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4LXQ3]
schistosoma_mansoni_prjea36577	Smp_046890		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4VCLB]
schistosoma_mansoni_prjea36577	Smp_048430	TGR	Thioredoxin glutathione reductase (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V8J4]
schistosoma_mansoni_prjea36577	Smp_049930		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4LWN1]
schistosoma_mansoni_prjea36577	Smp_051410		Septate junction protein (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4LY05]
schistosoma_mansoni_prjea36577	Smp_055760		ATP-dependent zinc metalloprotease YME1 homolog [Source:UniProtKB/Swiss-Prot;Acc:P54813] (projected from Caenorhabditis elegans ortholog ymel-1)
schistosoma_mansoni_prjea36577	Smp_058780		
schistosoma_mansoni_prjea36577	Smp_060480		Putative copine (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V6J0]
schistosoma_mansoni_prjea36577	Smp_063300		60S ribosomal protein L36-like protein; Putative 60s ribosomal protein L36e [Source:UniProtKB/TrEMBL;Acc:Q15ET2]
schistosoma_mansoni_prjea36577	Smp_069170		Putative cation efflux protein/ zinc transporter (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VIP1]
schistosoma_mansoni_prjea36577	Smp_074990		Regulator of chromosome condensation-related (inferred by orthology to a protein) [Source:UniProtKB;Acc:C4QHH6]
schistosoma_mansoni_prjea36577	Smp_075110		Putative rad1 DNA damage checkpoint protein (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VH02]
schistosoma_mansoni_prjea36577	Smp_077790		Putative histone H2B (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VL73]
schistosoma_mansoni_prjea36577	Smp_078570		Putative zinc finger protein (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VM27]
schistosoma_mansoni_prjea36577	Smp_079640		Putative monocarboxylate transporter (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V7W3]
schistosoma_mansoni_prjea36577	Smp_085080		
schistosoma_mansoni_prjea36577	Smp_093760		Strain Puerto Rico chromosome W, complete genome [Source:UniProtKB/TrEMBL;Acc:G4VTD3]
schistosoma_mansoni_prjea36577	Smp_120620		Amine GPCR, putative (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4LW20]

I have a list of *Schistosoma mansoni* genes and would like to find:
 3. The functional annotation of the genes with a human orthologue?

47 / 2550346 Genes

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

1. Query Filters

Gene stable ID(s): [ID-list specified]

Orthologue(s) in Human: With

2. Output Attributes

- Genome project
- Gene stable ID
- Gene name
- Gene description
- Human gene stable ID

Export all results to XLS Unique results only Go

Email notification to

View rows as Unique results only

Genome project	Gene stable ID	Gene name	Gene description	Human gene stable ID
schistosoma_mansoni_prj36577	Smp_002160		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4VLL1]	ENSG00000178028
schistosoma_mansoni_prj36577	Smp_007180		Sr-related ctd associated factor (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VB15]	ENSG00000085872
schistosoma_mansoni_prj36577	Smp_010260			ENSG00000136936
schistosoma_mansoni_prj36577	Smp_013610			ENSG00000170264
schistosoma_mansoni_prj36577	Smp_013610			ENSG00000156050
schistosoma_mansoni_prj36577	Smp_018150		Putative mannosyl-oligosaccharide alpha-1,2-mannosidase (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VP10]	ENSG00000111885
schistosoma_mansoni_prj36577	Smp_018150		Putative mannosyl-oligosaccharide alpha-1,2-mannosidase (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VP10]	ENSG00000198162
schistosoma_mansoni_prj36577	Smp_018150		Putative mannosyl-oligosaccharide alpha-1,2-mannosidase (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4VP10]	ENSG00000117643
schistosoma_mansoni_prj36577	Smp_038870		NADH-ubiquinone oxidoreductase, putative (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4LUK7]	ENSG00000023228
schistosoma_mansoni_prj36577	Smp_044010		Tropomyosin-1 [Source:UniProtKB/Swiss-Prot;Acc:P42637]	ENSG00000167460
schistosoma_mansoni_prj36577	Smp_044010		Tropomyosin-1 [Source:UniProtKB/Swiss-Prot;Acc:P42637]	ENSG00000140416
schistosoma_mansoni_prj36577	Smp_044010		Tropomyosin-1 [Source:UniProtKB/Swiss-Prot;Acc:P42637]	ENSG00000198467
schistosoma_mansoni_prj36577	Smp_044010		Tropomyosin-1 [Source:UniProtKB/Swiss-Prot;Acc:P42637]	ENSG00000143549
schistosoma_mansoni_prj36577	Smp_045420		Adiponectin receptor, putative (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4LXQ3]	ENSG00000006831
schistosoma_mansoni_prj36577	Smp_045420		Adiponectin receptor, putative (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4LXQ3]	ENSG00000159346
schistosoma_mansoni_prj36577	Smp_046890		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4VCL8]	ENSG00000196850
schistosoma_mansoni_prj36577	Smp_048430	TGR	Thioredoxin glutathione reductase (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V8J4]	ENSG00000197763
schistosoma_mansoni_prj36577	Smp_048430	TGR	Thioredoxin glutathione reductase (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V8J4]	ENSG00000198431
schistosoma_mansoni_prj36577	Smp_049930		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4LWN1]	ENSG00000148343
schistosoma_mansoni_prj36577	Smp_049930		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4LWN1]	ENSG00000180488
schistosoma_mansoni_prj36577	Smp_058780			ENSG00000105617
schistosoma_mansoni_prj36577	Smp_060480		Putative copine (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V6J0]	ENSG00000139117
schistosoma_mansoni_prj36577	Smp_060480		Putative copine (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V6J0]	ENSG00000144550
schistosoma_mansoni_prj36577	Smp_060480		Putative copine (inferred by orthology to a protein) [Source:UniProtKB;Acc:G4V6J0]	ENSG00000124772
schistosoma_mansoni_prj36577	Smp_063300		60S ribosomal protein L36-like protein; Putative 60s ribosomal protein L36e [Source:UniProtKB/TrEMBL;Acc:G415E2]	ENSG00000130255

BioMart Example 2 – Generating a list

I think a novel drug targets transmembrane signalling receptor activity in *Brugia* species. I would like to model this in *C. elegans*, so would like a list of orthologues.

Therefore I want to generate a list of *Brugia* genes, which:

- Do not have an orthologue in humans
- Are associated with transmembrane signalling receptor activity
- Annotated with the *C. elegans* orthologue, if available

I want to generate a list of *Brugia* genes, which do not have an orthologue in humans, are associated with transmembrane signalling receptor activity and annotated with the *C. elegans* orthologue, if available

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

[1. Query Filters](#)

[None selected]

[2. Output Attributes](#)

Genome project
Gene stable ID

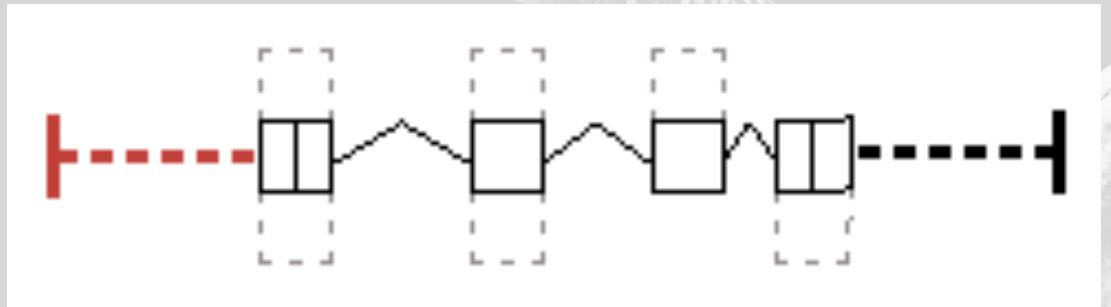
Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)
For guidance, see the [relevant pages](#) of our documentation.

- SPECIES
- REGION (use only when selecting one species)
- GENE
- GENE ONTOLOGY (GO)
- HOMOLOGY (ORTHOLOGUES AND PARALOGUES)
- PROTEIN DOMAINS



BioMart Example 3 – Retrieving sequences

I would like to retrieve the sequence located 500bp upstream of each *Brugia malayi* gene



I would like to retrieve the sequence located 500bp upstream of each *Brugia malayi* gene

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

[1. Query Filters](#)

[None selected]

[2. Output Attributes](#)

Genome project
Gene stable ID

Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)
For guidance, see the [relevant pages](#) of our documentation.

- SPECIES
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- HOMOLOGY (ORTHOLOGUES AND PARALOGUES)
- PROTEIN DOMAINS



BioMart Summary

- Use when working with lists of data, for generating lists of genes and for retrieving sequence
- All data from the website is available
- No programming knowledge required
- Export directly to Excel or CSV for import to R
- Contact us if you are unsure how to construct a query (contact link at bottom of website)

Coming soon... (release 7 in August)

HOMOLOGY (ORTHOLOGUES AND PARALOGUES)

Restrict results to genes with orthologues in...

Caenorhabditis elegans [WS252]
Drosophila melanogaster
Human
Mouse
Saccharomyces cerevisiae
Zebrafish
Acanthocheilonema viteae (PRJEB4306)
Amphimedon queenslandica
Ancylostoma caninum (PRJNA72585)
Ancylostoma ceylanicum (PRJNA231479)
Ancylostoma ceylanicum (PRJNA72583)
Ancylostoma duodenale (PRJNA72581)
Angiostrongylus cantonensis (PRJEB493)
Angiostrongylus costaricensis (PRJEB494)
Anisakis simplex (PRJEB496)
Ascaris lumbricoides (PRJEB4950)
Ascaris suum (PRJNA62057)
Ascaris suum (PRJNA80881)
Brugia malayi (PRJNA10729) [WS252]
Brugia pahangi (PRJEB497)

Restrict results to genes without orthologues in...

Caenorhabditis elegans [WS252]
Drosophila melanogaster
Human
Mouse
Saccharomyces cerevisiae
Zebrafish
Acanthocheilonema viteae (PRJEB4306)
Amphimedon queenslandica
Ancylostoma caninum (PRJNA72585)
Ancylostoma ceylanicum (PRJNA231479)
Ancylostoma ceylanicum (PRJNA72583)
Ancylostoma duodenale (PRJNA72581)
Angiostrongylus cantonensis (PRJEB493)
Angiostrongylus costaricensis (PRJEB494)
Anisakis simplex (PRJEB496)
Ascaris lumbricoides (PRJEB4950)
Ascaris suum (PRJNA62057)
Ascaris suum (PRJNA80881)
Brugia malayi (PRJNA10729) [WS252]
Brugia pahangi (PRJEB497)

Restrict results to genes with/without...

paralogues With Without

PROTEIN DOMAINS

Exercises – Part I

- <http://parasite.wormbase.org/workshop>



Exercise 1

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
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Please restrict your query using criteria below
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- SPECIES
- REGION (use only when selecting one species)
- GENE
- GENE ONTOLOGY (GO)
- HOMOLOGY (ORTHOLOGUES AND PARALOGUES)
- PROTEIN DOMAINS

[1. Query Filters](#)

[None selected]

[2. Output Attributes](#)

Genome project
Gene stable ID

Exercise 2

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

1. Query Filters

[None selected]

2. Output Attributes

Genome project
Gene stable ID

Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)
For guidance, see the [relevant pages](#) of our documentation.

- SPECIES
- REGION (use only when selecting one species)
- GENE
- GENE ONTOLOGY (GO)
- HOMOLOGY (ORTHOLOGUES AND PARALOGUES)
- PROTEIN DOMAINS

Exercise 3

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

1. Query Filters

[None selected]

2. Output Attributes

Genome project
Gene stable ID

Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)
For guidance, see the [relevant pages](#) of our documentation.

- SPECIES
- REGION (use only when selecting one species)
- GENE
- GENE ONTOLOGY (GO)
- HOMOLOGY (ORTHOLOGUES AND PARALOGUES)
- PROTEIN DOMAINS

Exercise 4

WormBase ParaSite Search WormBase ParaSite...

WormBase Home | ParaSite Home BLAST | BioMart | Downloads

[New](#) [Count](#) [Results](#) [★ URL](#) [XML](#) [Perl](#) [Help](#)

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

[1. Query Filters](#)
[None selected]

[2. Output Attributes](#)
Genome project
Gene stable ID

Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)
For guidance, see the [relevant pages](#) of our documentation.

<input type="checkbox"/> SPECIES
<input type="checkbox"/> REGION (use only when selecting one species)
<input type="checkbox"/> GENE
<input type="checkbox"/> GENE ONTOLOGY (GO)
<input type="checkbox"/> HOMOMOLOGY (ORTHOLOGUES AND PARALOGUES)
<input type="checkbox"/> PROTEIN DOMAINS

WormBase ParaSite © EBI & WTSI



Exercise 5

BioMart allows the fast export of data tables and sequence in just a few steps:

1. Select your 'Query Filters' (these are search parameters that define your results)
2. Choose your 'Output Attributes' (what you would like to include in your results table or file)
3. Hit the 'Results' button at the top of this page

[1. Query Filters](#)

[None selected]

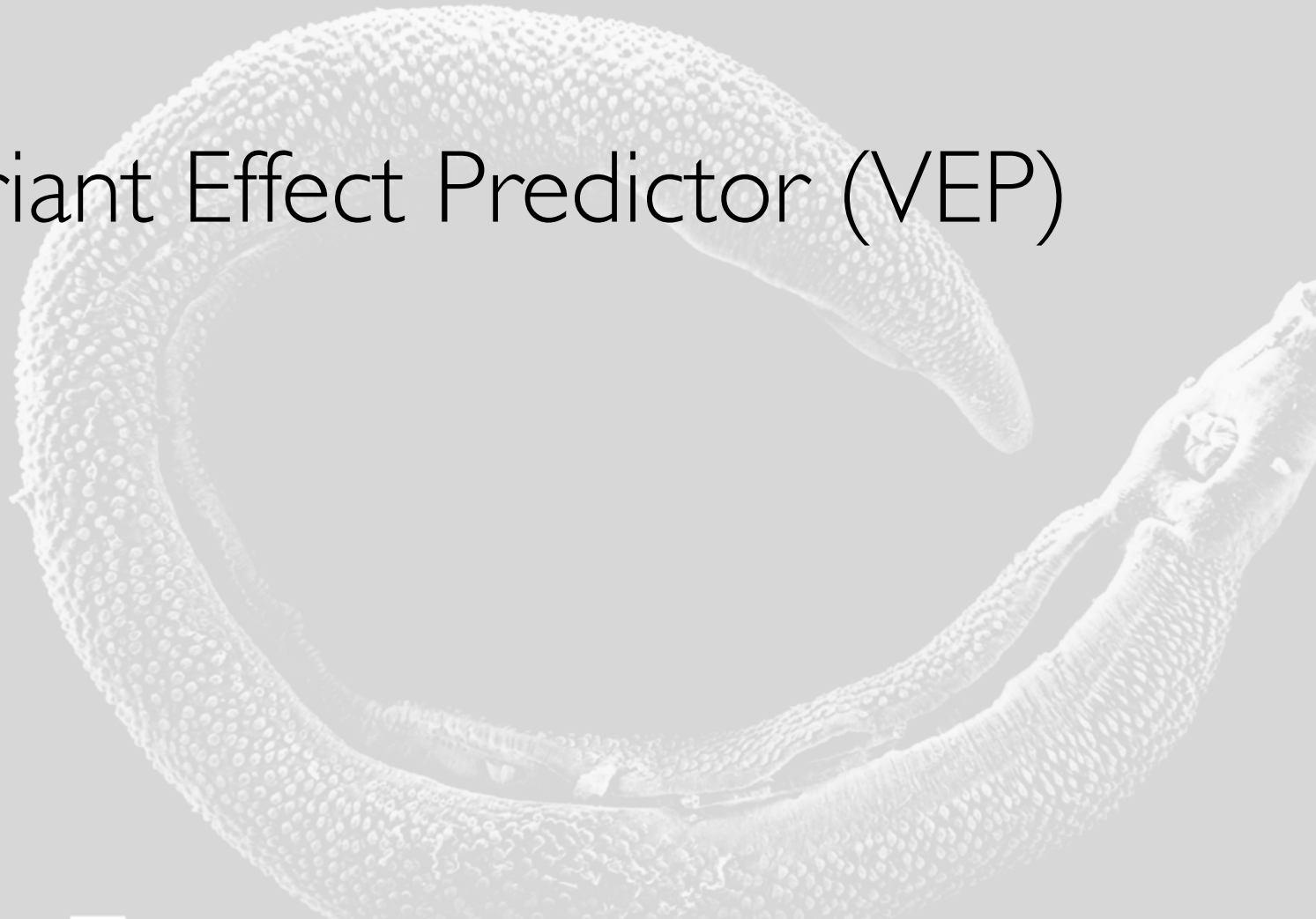
[2. Output Attributes](#)

Genome project
Gene stable ID

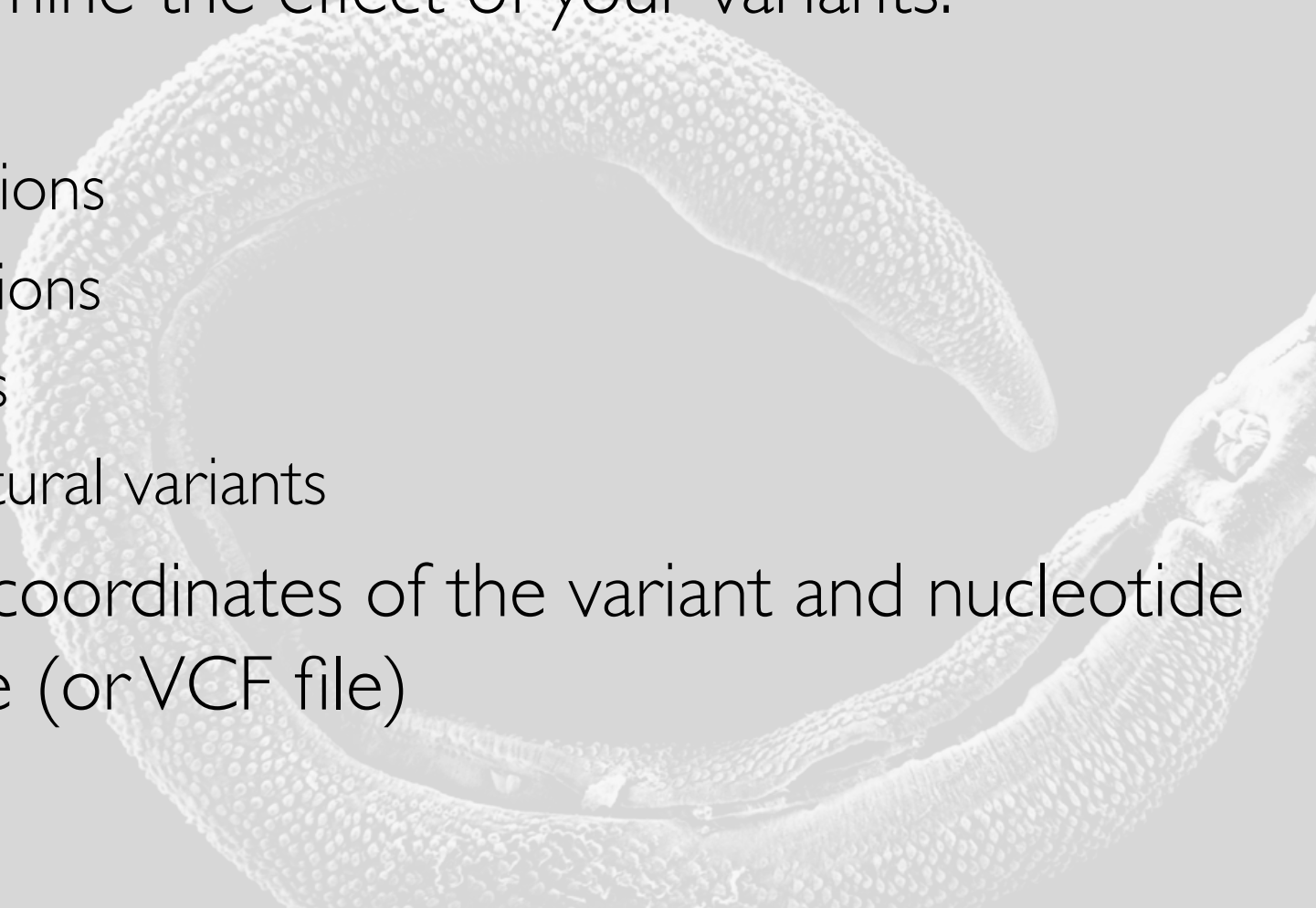
Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)
For guidance, see the [relevant pages](#) of our documentation.

- SPECIES
- REGION (use only when selecting one species)
- GENE
- GENE ONTOLOGY (GO)
- HOMOLOGY (ORTHOLOGUES AND PARALOGUES)
- PROTEIN DOMAINS

Variant Effect Predictor (VEP)



Introduction to the VEP

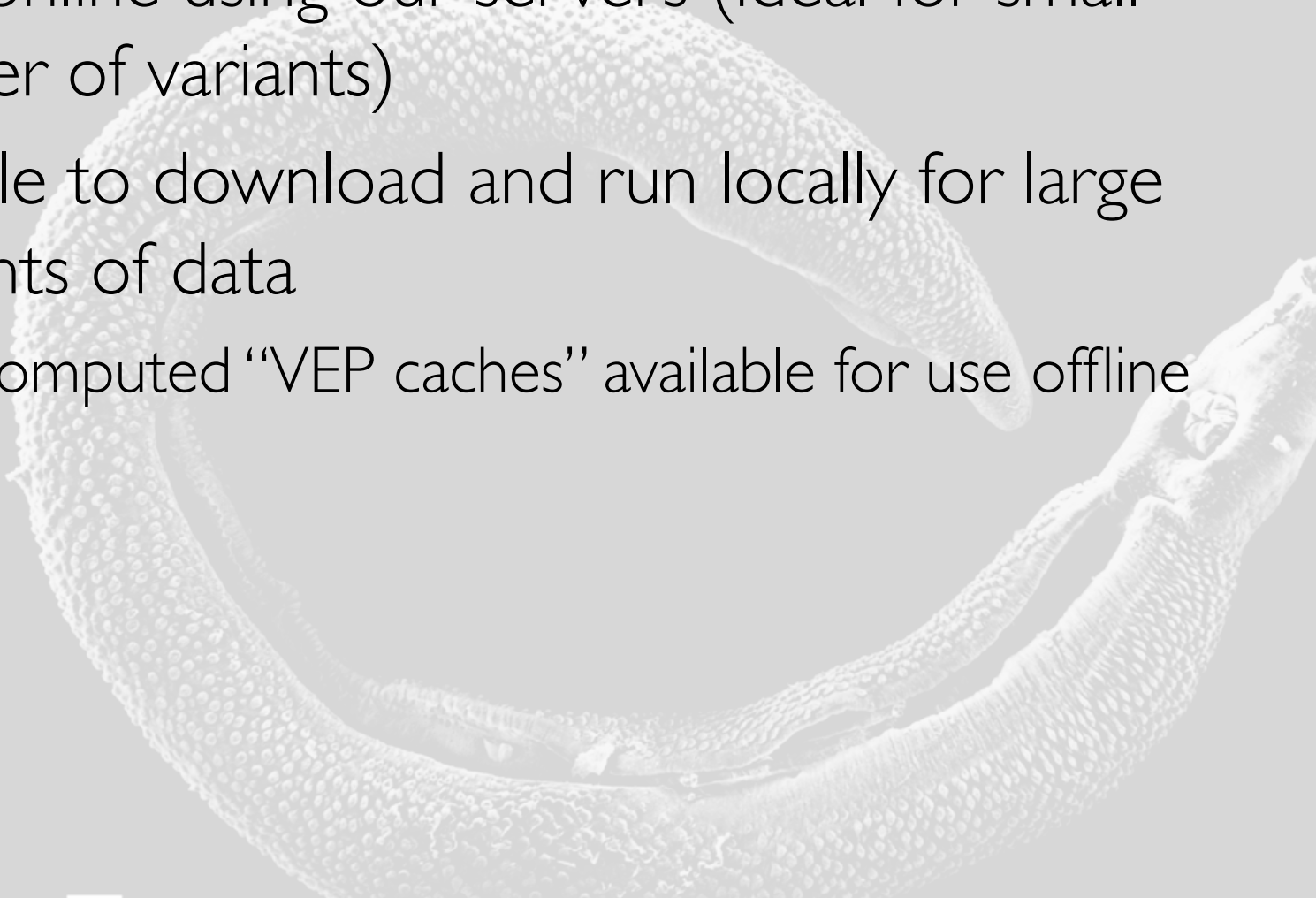
- Determine the effect of your variants:
 - SNPs
 - Insertions
 - Deletions
 - CNVs
 - Structural variants
 - Input: coordinates of the variant and nucleotide change (or VCF file)
- 

Introduction to the VEP

- Output:
 - Genes and transcripts affected by the variants
 - Location of the variants (e.g. upstream of a transcript, in coding sequence, in ncRNA, etc)
 - Consequence of the variant on protein sequence (e.g. stop gained/lost, missense, frameshift, synonymous, non-synonymous, etc)
- View results in table and on genome browser

Introduction to VEP

- Runs online using our servers (ideal for small number of variants)
- Possible to download and run locally for large amounts of data
 - Pre-computed “VEP caches” available for use offline



Using the VEP

WormBase ParaSite

 Version: WBPS6 (WS252)

Search WormBase ParaSite...
e.g. *O. volvulus*, PRJNA60051, WBGene00262434, Bma-eat-4, eat-4 or metalloproteinase

Species List BLAST BioMart REST API VEP Downloads WormBase Login Register Help and Documentation

Species

BLAST

BioMart

API

Downloads

WormBase

Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

Statistics

- Version: WBPS6 (April 2016)
- WormBase Version: WS252
- 109 genomes, representing 100 species
- 2,189,841 genes

Announcements

[Announcing WormBase ParaSite release 6](#)

posted 1 month ago

We are pleased to announce the sixth release of WormBase ParaSite.

Blog

[Featured Paper: Glucose and Glycogen Metabolism in *B. malayi* Is Associated with Wolbachia Symbiont Fitness](#)

posted 1 month ago

We would like to draw your attention to a paper published by Denis Voronin, et. al on the influence of host metabolism on symbiont fitness: Denis Voronin, Saheed Bachu, Michael Shlossman, Thomas R. Unnasch, Elodie Ghedin, Sara Lustigman "Glucose and Glycogen Metabolism in *Brugia malayi* Is Associated with Wolbachia Symbiont Fitness", PLoS One. 2016 Apr [...]

[Brugia malayi assembly update](#)

posted 2 months ago

The new release of WormBase (WS252) is the first one to feature the new and updated version 4 of the *Brugia malayi* assembly. Due to additional optical mapping, as well as new long-range PacBio sequencing and additional reassembly work conducted to integrate all available data, it was possible to scaffold the 88.2Mbp assembly into 5 chromosomes [...]

[Register for a WormBase ParaSite workshop](#)

posted 2 months ago

To help our users make the most of this valuable resource, we are visiting universities and institutes to provide hands-on training sessions.

[Featured Paper: Allergy the Price of Immunity](#)

posted 3 months ago

We would like to draw your attention to a paper recently published in PLOS Computational Biology: Comparisons of Allergenic and Metazoan Parasite Proteins: Allergy the Price of Immunity by Nidhi Tyagi It is thought that part of our immune system has evolved to combat and provide immunity against infection by parasitic worms. However, in the absence [...]

Twitter

Tweets by @WBParasite

WormBase ParaSite Retweeted

Hayley Bennett @HayleyMBennett
Wow @ProtocolsIO publishing neat&reproducible research methods! Great parasitology example-how to culture tapeworms. [twitter.com/GigaScience/st...](https://twitter.com/GigaScience/status/711111111111111111)

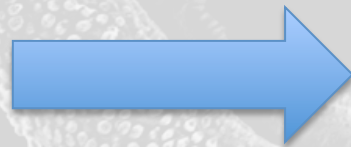
WormBase ParaSite Retweeted

NaturalHistoryMuseum @NHM_London
You can learn more about Schistosomes and their fellow parasites at #ParasitesDay, Fri 1 Jun nhm.ac.uk/visit/exhibiti...

Embed View on Twitter

Other variation data

- Starting in WBPS7 (due August 2016), we will display data from the European Variation Archive (EVA)
- Simply deposit your own variation data in EVA and it will display automatically in the next release of WormBase ParaSite



WormBase ParaSite

Gene Variation Table

WormBase ParaSite Version: WBPS31 (WS254)

e.g. *O. volvulus*, PRJNA60051, WBGene00282434, Bma-eat-4, eat-4 or metalloproteinase

HMMER Species List BLAST BioMart REST API VEP Downloads WormBase

[Login](#) [Register](#) [Help and Documentation](#)

Sorghum bicolor Location: 1:257,765-268,116 Gene: Sb01g000355

Gene-based displays

- Summary
- Splice variants
- Sequence
- External references
- Ontologies
 - GO: Molecular function
 - GO: Cellular component
 - GO: Biological process
- Literature
- Comparative Genomics
 - Gene tree
 - Orthologues
 - Paralogues
- Variation
 - Variation Table
 - Variation Image

[Export data](#)

[Share this page](#)

[Ensembl Plants is produced in collaboration with Gramene](#)

Gene: Sb01g000355

Description RNA-binding ASCH domain protein [Source:Projected from Arabidopsis thaliana (AT2G20410) TAIR;Acc:AT2G20410]

Location [Chromosome 1: 251,508-255,065](#) reverse strand.

About this gene This gene has 2 transcripts ([splice variants](#)).

Gene type Protein coding

Annotation Method Gene annotation by [JGI](#) through a process of automatic and manual curation

Transcripts [Hide transcript table](#)

Show/hide columns (2 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype
Novel	Sb01g000355.1	1457	342aa	Protein coding
Novel	Sb01g000355.2	1447	318aa	Protein coding

Variation Table

Show All entries Show/hide columns Filter

Variant ID	Study	Genomic Position	Type	Alleles	Most Severe Consequence	Transcript
vc22KJ20E	PRJEB9507	247192	SNV	T/A	downstream_gene_variant	Sb01g000355.2
vc22KJ20E	PRJEB9507	247192	SNV	T/A	downstream_gene_variant	Sb01g000355.1
vc22KJ20F	PRJEB9507	247220	SNV	T/A	downstream_gene_variant	Sb01g000355.2
vc22KJ20F	PRJEB9507	247220	SNV	T/A	downstream_gene_variant	Sb01g000355.1
vc22KJ20G	PRJEB9507	247508	SNV	C/T	downstream_gene_variant	Sb01g000355.2
vc22KJ20G	PRJEB9507	247508	SNV	C/T	downstream_gene_variant	Sb01g000355.1
vc22KJ20H	PRJEB9507	247542	SNV	C/A	downstream_gene_variant	Sb01g000355.2
vc22KJ20H	PRJEB9507	247542	SNV	C/A	downstream_gene_variant	Sb01g000355.1

Variant Information Page

WormBase ParaSite Version: WBPS31 (WS254)

HMMER Species List BLAST BioMart REST API VEP Downloads WormBase

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Sorghum bicolor Location: 1:257,765-268,116

Location-based displays

- Whole genome
- Region in detail
- Other genome browsers
- Phytozome [↗](#)

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Variant Information

Variant ID	Scaffold/Chromosome	Start	End	Reference Allele	Alternative Allele
vcZ2KJ26I	1	260344	-	T	C

Consequences

This variant affects 3 transcripts

Show/hide columns Filter <input style="width: 50px;" type="text"/>									
Gene ID	Transcript ID	Strand	Biotype	cDNA Position	CDS Position	AA Position	AA Change	Codon Change	SO Term(s)
Sb01g000365	Sb01g000365.1	-	protein_coding	-	-	-	-	-	downstream_gene_variant
Sb01g000360	Sb01g000360.1	+	protein_coding	142	142	48	S/P	Tct/Cct	missense_variant
Sb01g000357	Sb01g000357.1	+	protein_coding	-	-	-	-	-	downstream_gene_variant

Study PRJEB9507_ERZ115806

Quality Overview

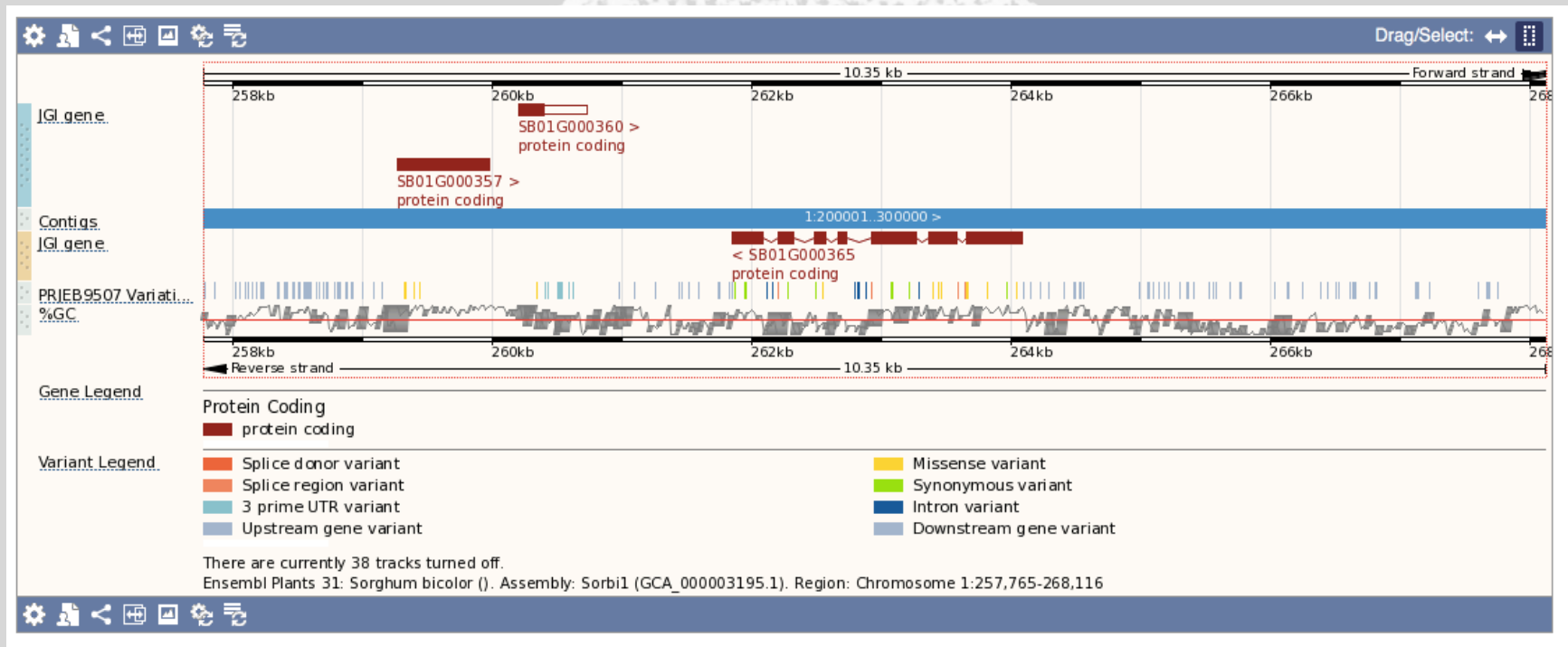
QUAL	DP	FILTER	AF	NS
33.0	278	PASS	0.0645	47

Genotypes

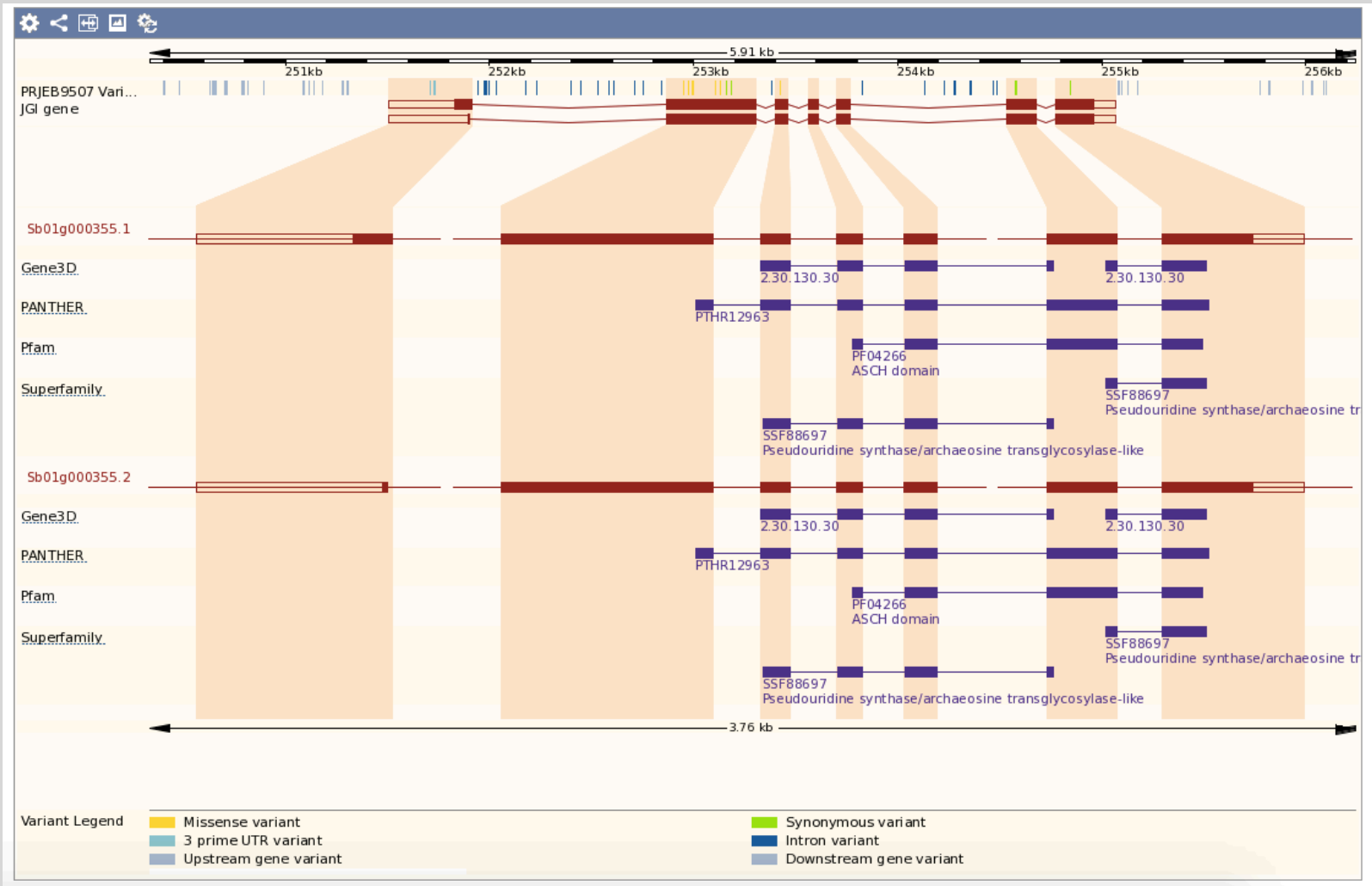
This study included 47 individuals. The genotype for each is shown in the table below.

Show All entries Filter <input style="width: 50px;" type="text"/>	
Sample Name	Genotype
B35	CIC
SC23	CIC
SC326-6	TIT
IS8525	TIT
B923296	TIT
Greenleaf	TIT
PI586430	TIT
Kilo	TIT
SC56-14E	TIT
Malisor84-7	TIT
SC62C	TIT
Rio	TIT
M35-1	TIT
S. bicolor subsp. Verticilliflorum(PI300119)	TIT

Genome Browser Tracks

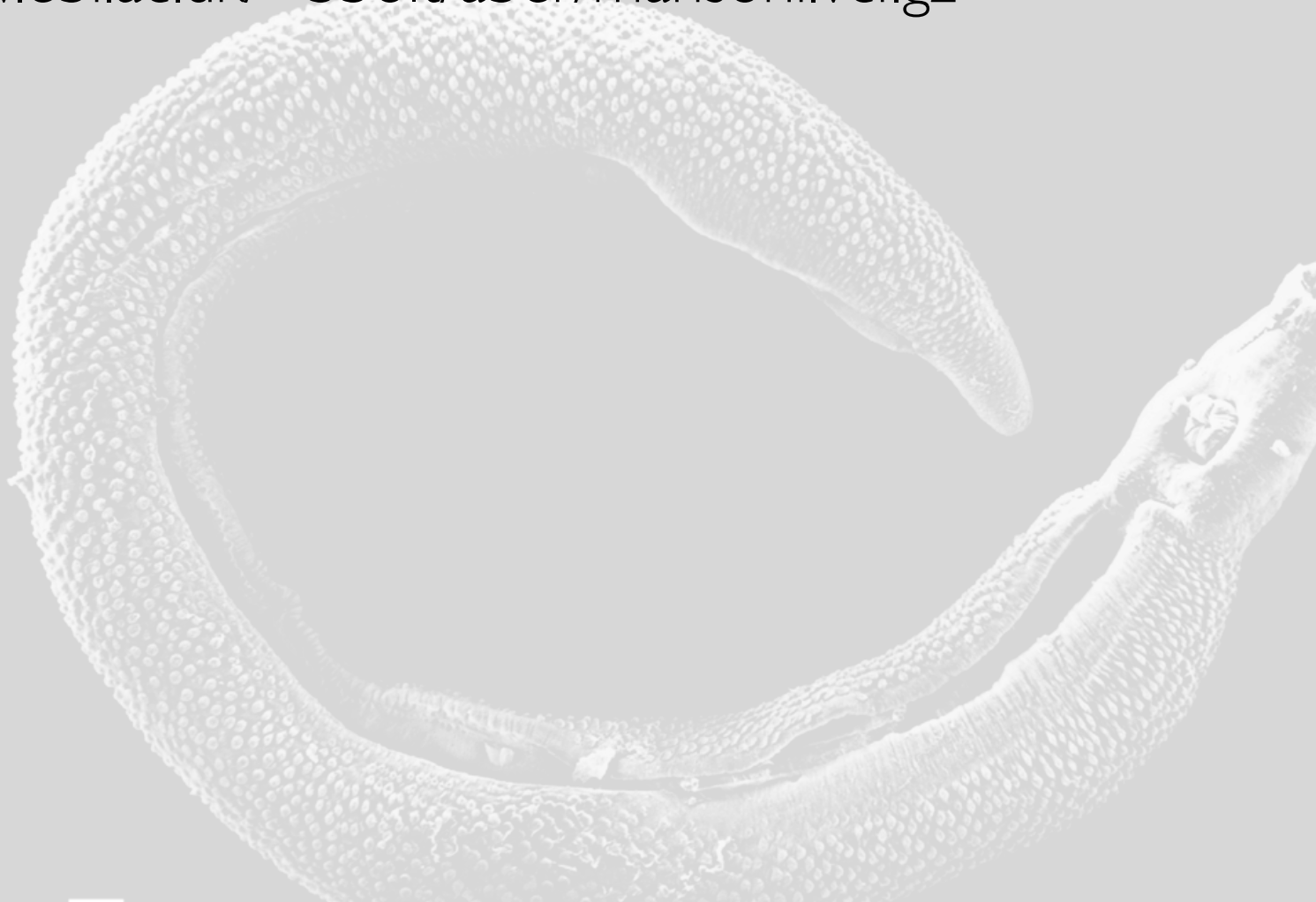


Variant/Transcript Image



Exercises

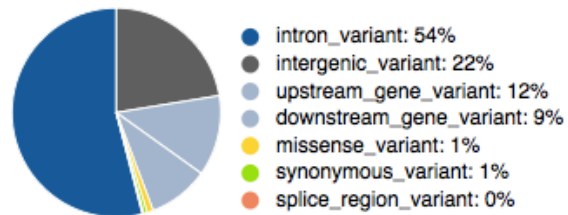
<http://www.ebi.ac.uk/~bbolt/aber/mansoni.vcf.gz>



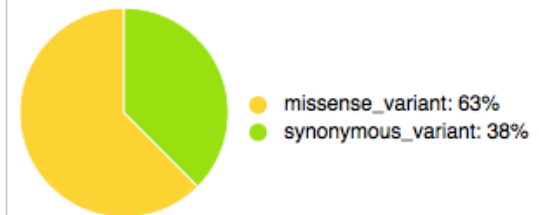
Exercise Solutions

Category	Count
Variants processed	499
Variants remaining after filtering	499
Novel / existing variants	-
Overlapped genes	5
Overlapped transcripts	5
Overlapped regulatory features	-

Consequences (all)



Coding consequences



Exercise Solutions

Navigation: Show: 1 5 10 50 All variants

Filters: Gene is Smp_160490

Download: All: VCF VEP TXT Filtered: VCF VEP TXT

Uploaded variant is defined Add

Show/hide columns

Uploaded variant	Location	Allele	Consequence	Impact	Symbol	Gene	Feature type	Feature	Biotype	HG
.	Smp.Chr 1:118335-118335	G	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:118771-118771	G	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:118772-118772	T	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:118973-118973	C	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119104-119104	T	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119118-119118	G	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119483-119483	T	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119484-119484	G	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119485-119485	G	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119573-119573	C	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119738-119738	T	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119775-119775	C	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:119946-119946	A	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:120098-120098	A	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-
.	Smp.Chr 1:120380-120380	T	downstream_gene_variant	MODIFIER	-	Smp_160490	Transcript	Smp_160490.1	protein_coding	-

Scroll to see more columns »