Sequence Viewer and Genome Workbench – Sequence Display and Analysis Tools

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Computer Demo 1

PAG XXIII January 10-14, 2015

NCBI Sequence Display Tools

Sequence Viewer

- Online
- Display NCBI
- Import your data
- Customize the display
- Search, pan, zoom
- Display a single accession
- BLAST analysis
- Export high quality PDF
- API to embed tool in any website

Genome Workbench

- Downloadable application
- Display NCBI data
- Import your data
- Customize the display
- Search, pan, zoom
- Load a whole genome
- BLAST analysis
- More analysis and display options than Sequence Viewer

Sequence Viewer (sviewer)

A general purpose tool for online viewing of sequence, annotation, alignments, graphs.

- Used to display:
  - Genome annotation
  - Alignments
  - Histograms
  - BED, WIG, GFF
- Features:
  - Search, Zoom, Pan, Add tracks
  - Click/drag to move tracks
  - Compare objects (discover differences)
  - Generate, or Import, BLAST results
  - Import local data
  - Download sequence
  - Download high resolution PDF

Gene

Chromosome context

Genome annotation

Intermediate updates

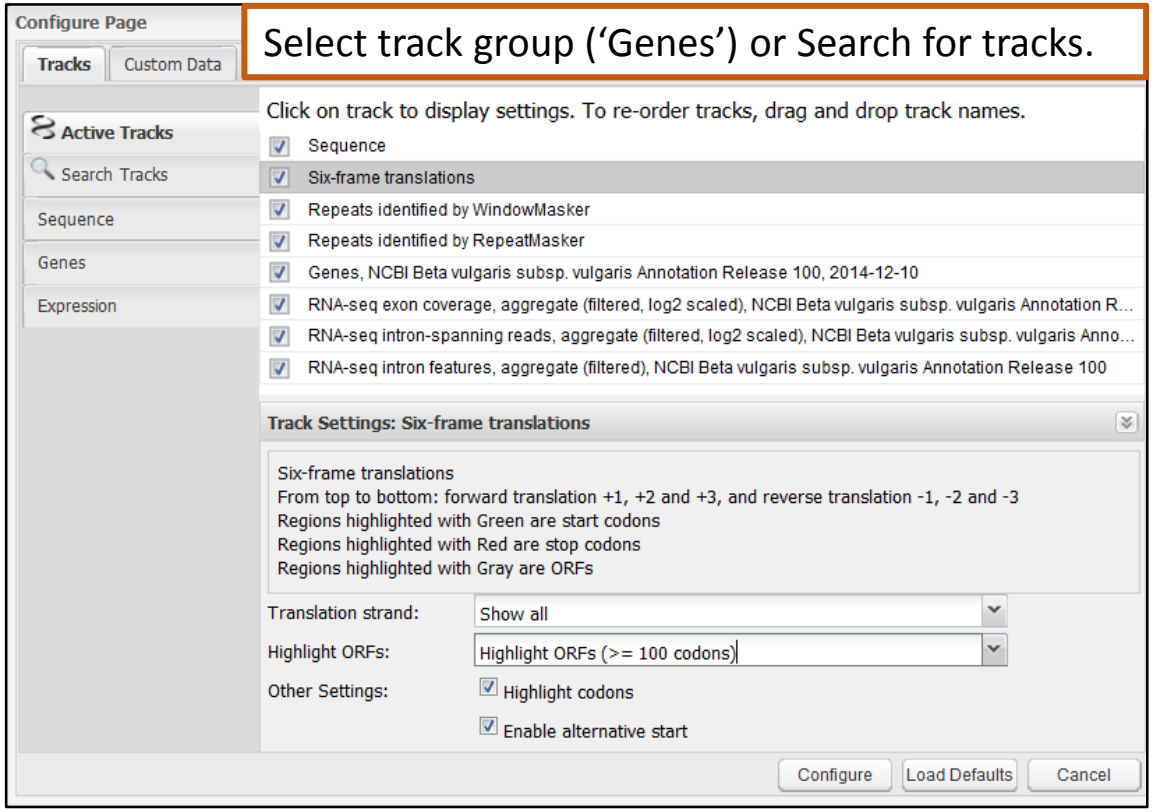
Consensus CDS

Ensembl annotation

Variation tracks

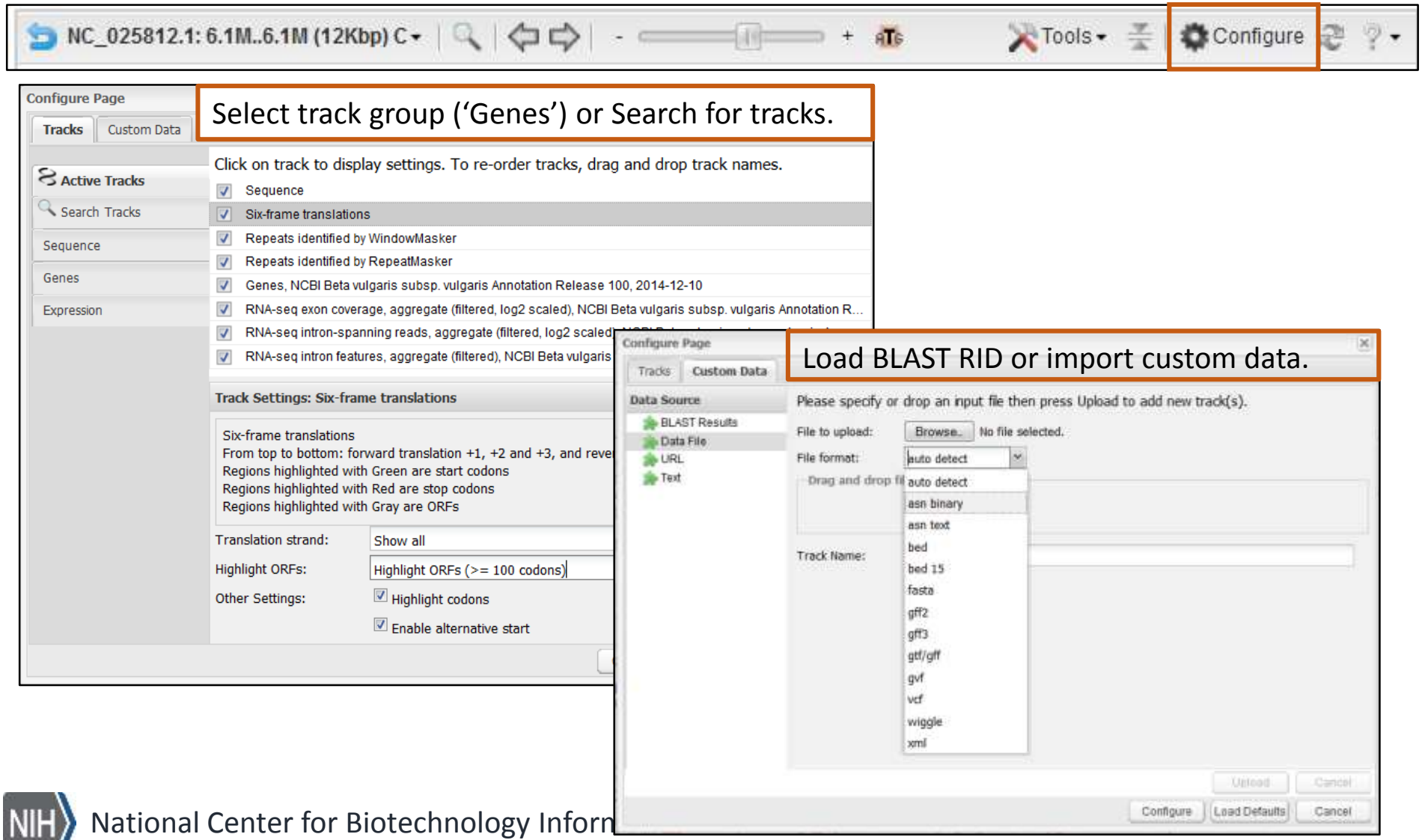
RNA-Seq tracks

Configuring the display

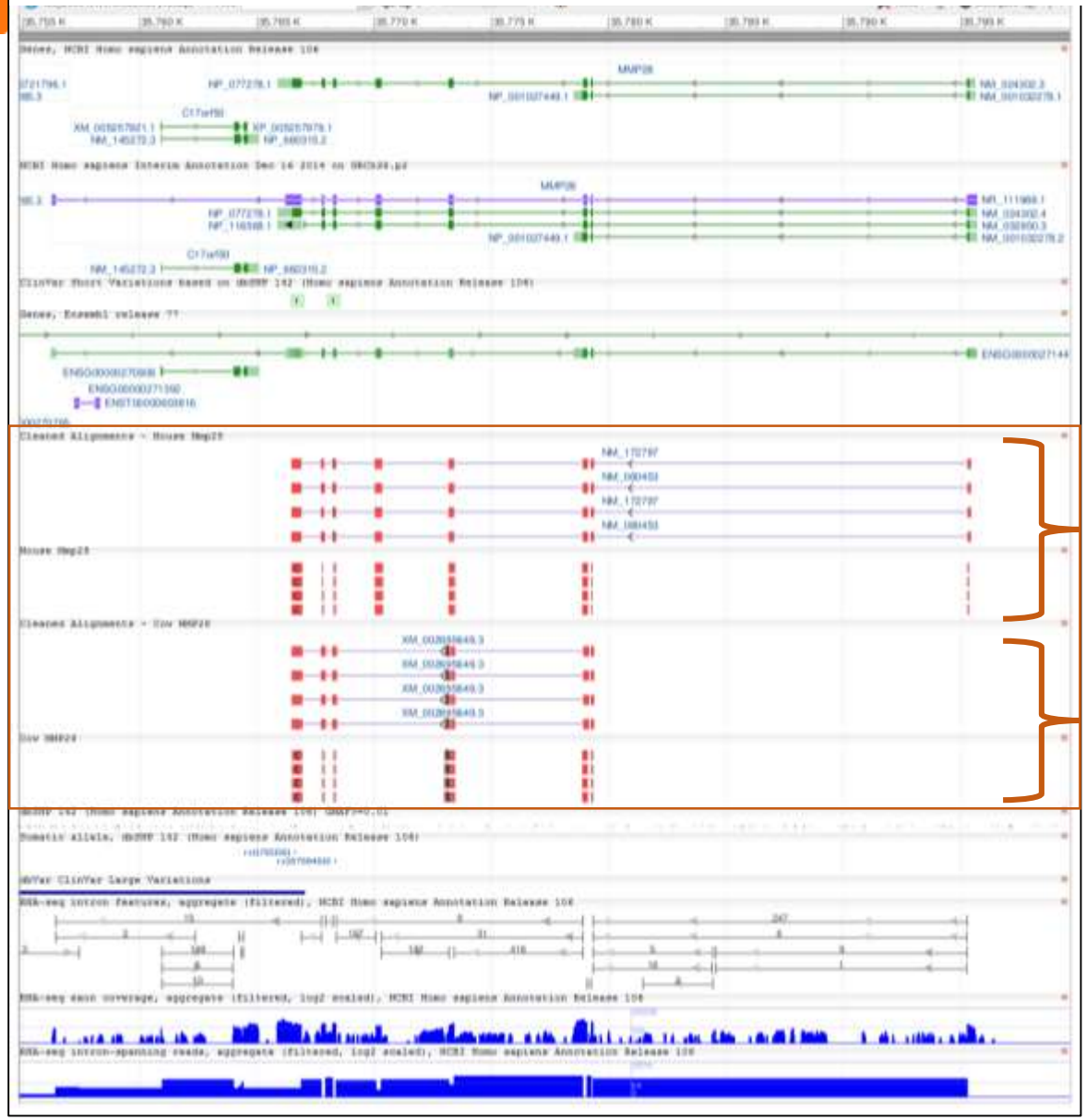


Select track group ('Genes') or Search for tracks.

Configuring the display



Human MMP28 gene (GeneID:79148), chromosome 17, GRCh38 primary assembly

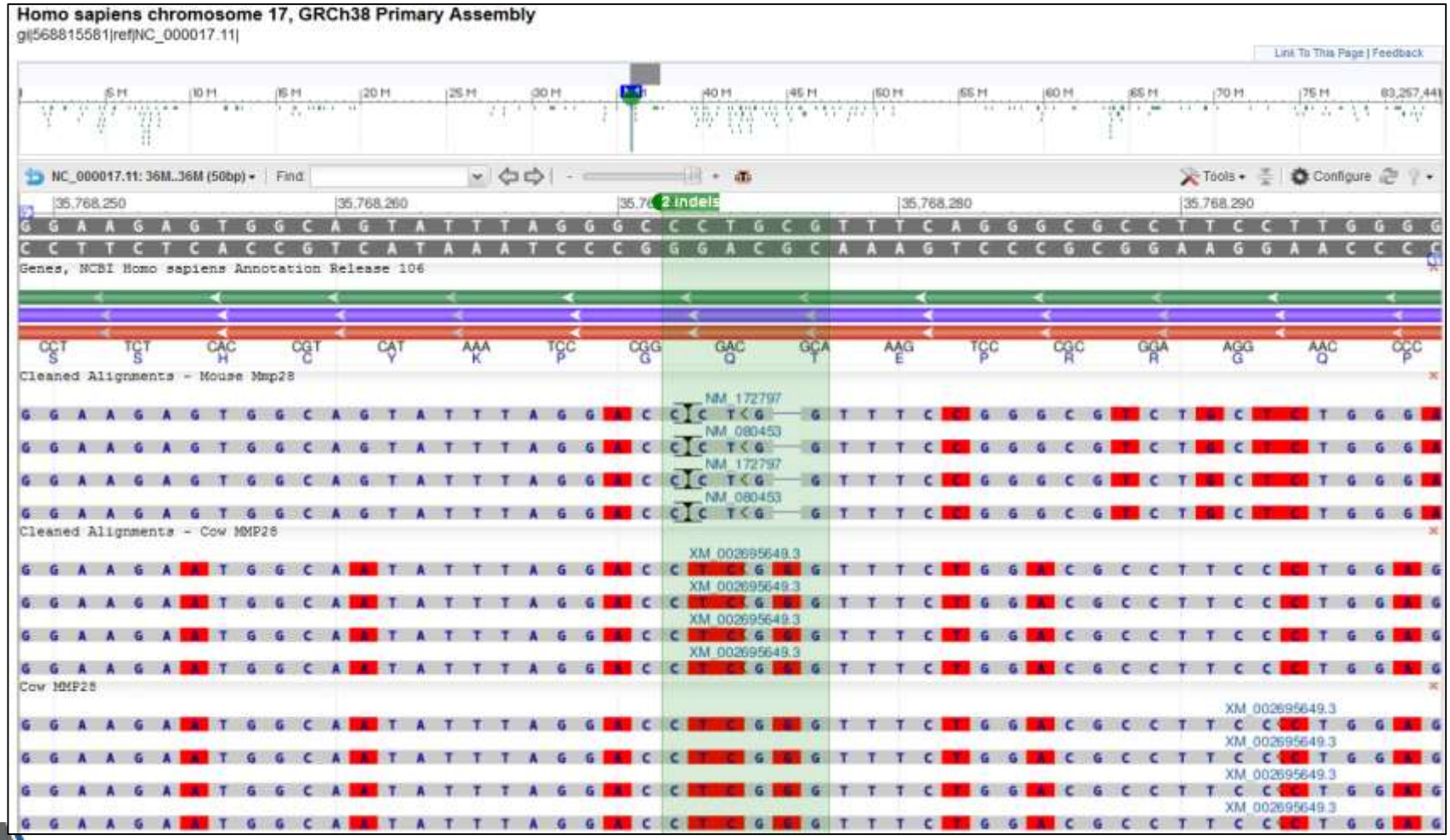


Loaded BLAST RIDs

mouse Mmp28
NM_172797.2
NM_080453.2

cow MMP28
XM_002695649.3

Zoom to sequence, add markers



Displaying submitted Map Data

Nucleotide | Nucleotide | Search
Advanced | Help

Display Settings: GenBank | Send to: | Change region shown

Staphylococcus epidermidis NIH04008, AflII whole genome map

GenBank: MAP_000012.1

FASTA | Graphics

Go to:

Analyze this sequence

```
LOCUS       MAP_000012            292919 bp    DNA     linear   BCT 23-OCT-2013
DEFINITION  Staphylococcus epidermidis NIH04008 chromosome, AflII whole genome
            map.
ACCESSION   MAP_000012 REGION: 1..292919
VERSION     MAP_000012.1  GI:551059683
DBLINK      BioProject: PRJNA62395
            BioSample: SAMN00993294
KEYWORDS    Whole_Genome_Map.
SOURCE      Staphylococcus epidermidis NIH04008
  ORGANISM  Staphylococcus epidermidis NIH04008
            Bacteria; Firmicutes; Bacilli; Bacillales; Staph
REFERENCE   1  (bases 1 to 292919)
  AUTHORS   Conlan,S., Mijares,L.A., Becker,J., Blakesley,R.
            Brooks,S., Gupta,J., Gurson,N., Park,M., Schmidt
            Young,A., Otto,M., Kong,H.H., Murray,P.R. and Se
  TITLE     Genome-wide recombination drives diversification
            strains of Acinetobacter baumannii
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 292919)
  AUTHORS   Segre,J. and Mullican,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-SEP-2013) NIH Intramural Sequencin
            Fishers Lane, Rockville, MD 20852, USA
COMMENT     This map has 332 pieces:
            *     3681    5403: fragment of 1723 bp in lengt
            *     5404   16274: fragment of 10871 bp in length
            *    16275   21013: fragment of 4739 bp in length
```

Follow the 'Graphics' link in Nucleotide & Protein

Nucleotide | Nucleotide
Advanced

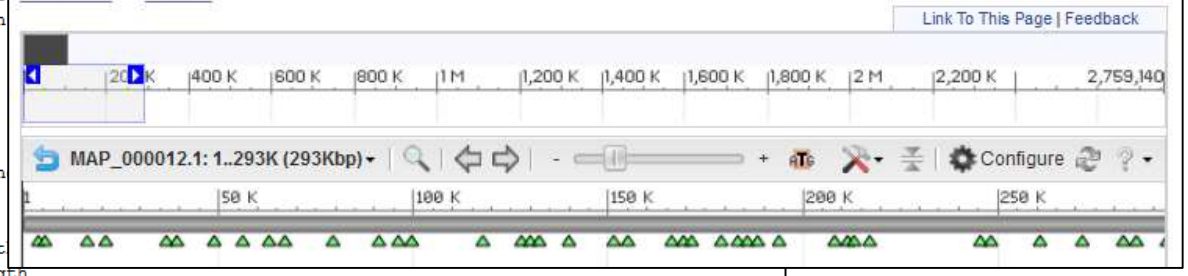
Display Settings: Graphics | Send to:

Staphylococcus epidermidis NIH04008, AflII whole genome map

GenBank: MAP_000012.1

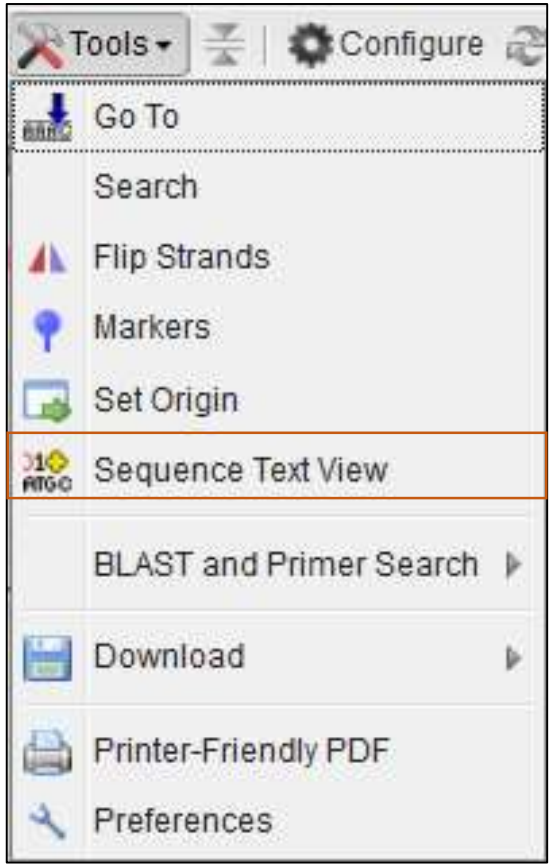
GenBank | FASTA

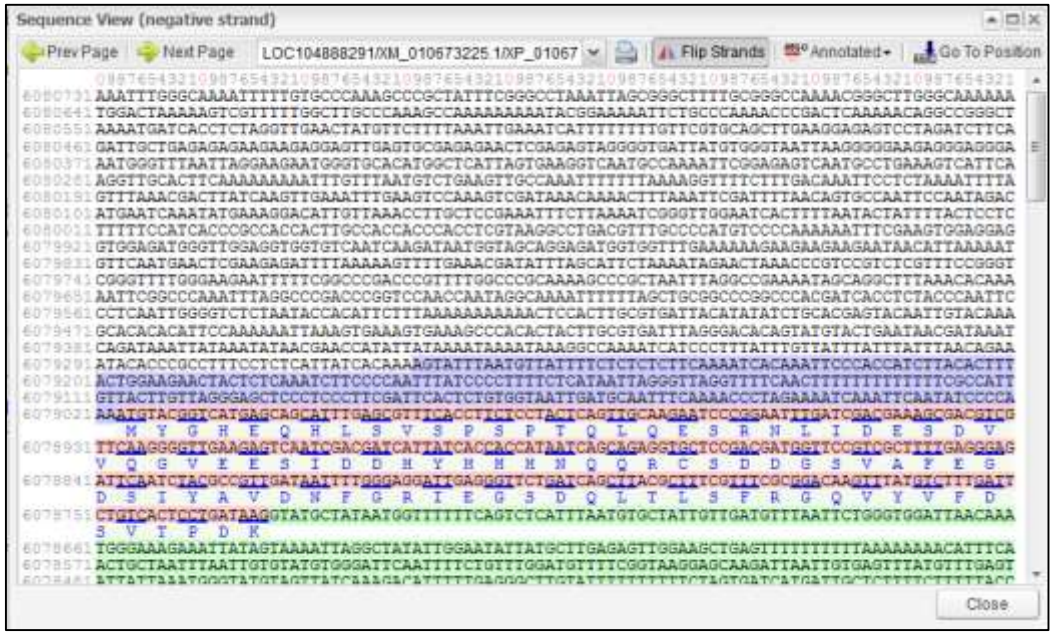
Link To This Page | Feedback



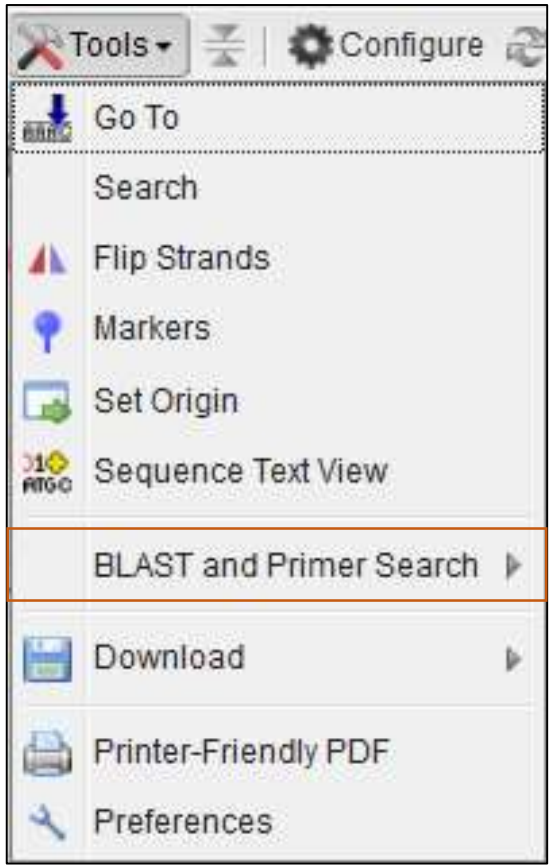
www.ncbi.nlm.nih.gov/nuccore/MAP_000012

NC_025812.1: 6.1M..6.1M (12Kbp) C
Tools
Configure


Tools
Configure
Go To
Search
Flip Strands
Markers
Set Origin
Sequence Text View
BLAST and Primer Search
Download
Printer-Friendly PDF
Preferences


Sequence View (negative strand)
Prev Page
Next Page
Flip Strands
Annotated
Go To Position
Close

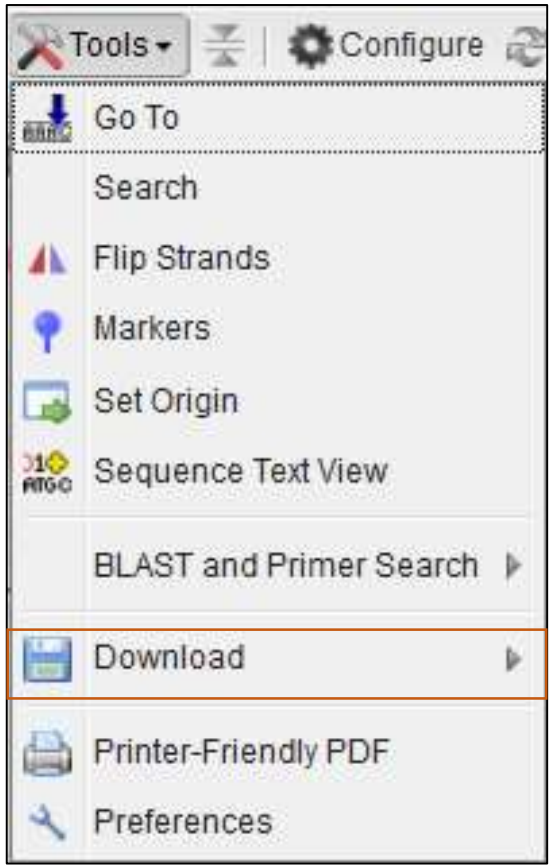
NC_025812.1: 6.1M..6.1M (12Kbp) C
Tools
Configure


Tools
Configure
Go To
Search
Flip Strands
Markers
Set Origin
Sequence Text View
BLAST and Primer Search
Download
Printer-Friendly PDF
Preferences

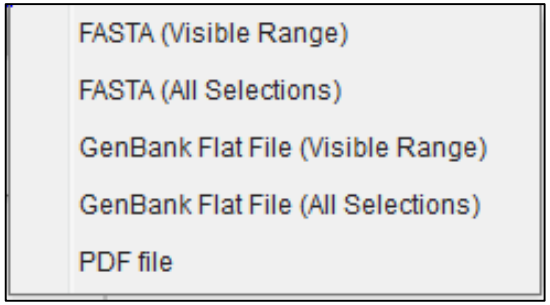
Analyze

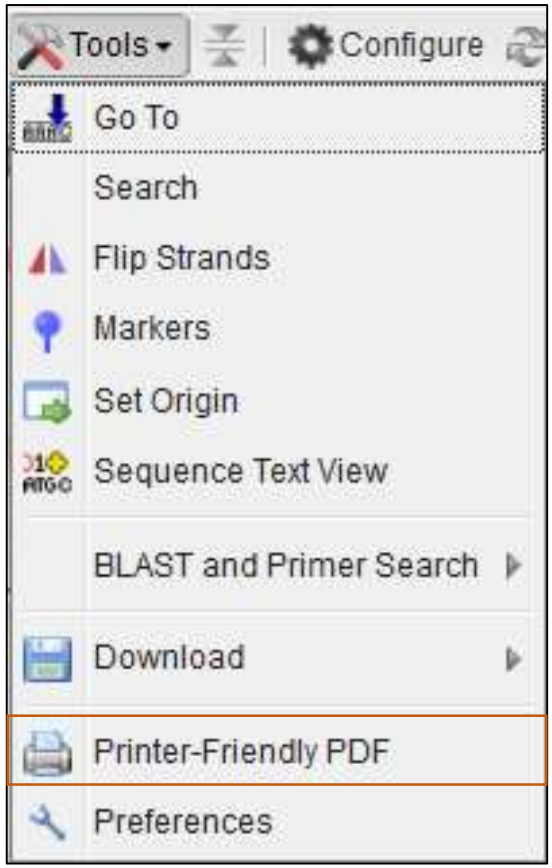
BLAST Search (Visible Range)
Primer BLAST (Visible Range)
BLAST Search (Selection)
Primer BLAST (Selection)

NC_025812.1: 6.1M..6.1M (12Kbp) C
Tools
Configure

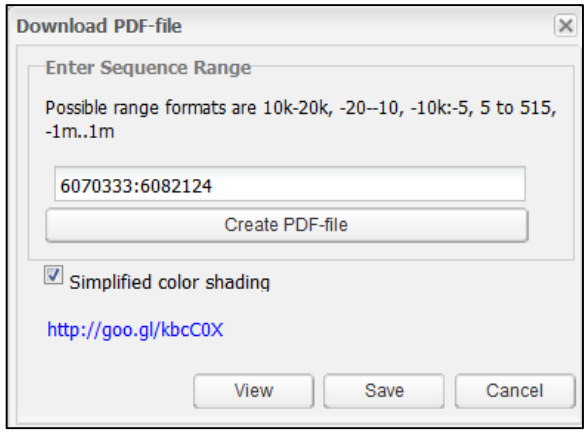

Tools
Configure
Go To
Search
Flip Strands
Markers
Set Origin
Sequence Text View
BLAST and Primer Search
Download
Printer-Friendly PDF
Preferences

Download

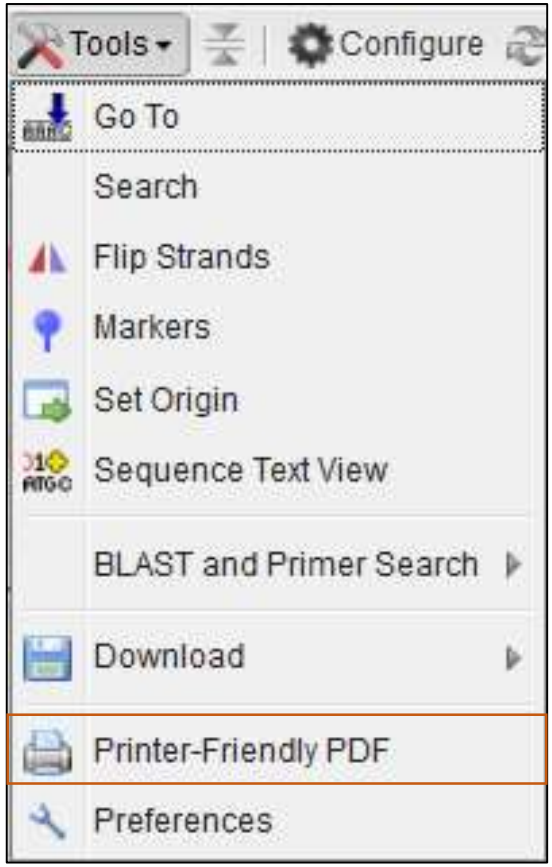

FASTA (Visible Range)
FASTA (All Selections)
GenBank Flat File (Visible Range)
GenBank Flat File (All Selections)
PDF file

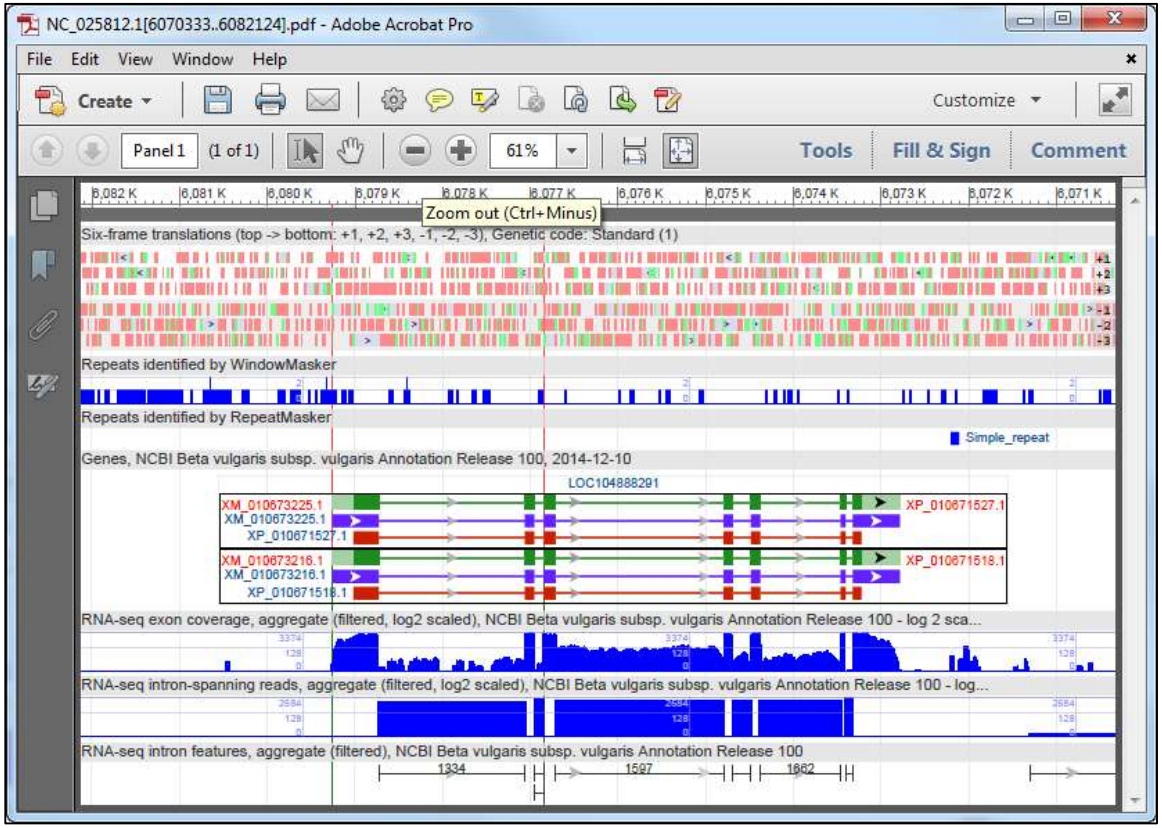


Make a figure



NC_025812.1: 6.1M..6.1M (12Kbp) C
Tools
Configure

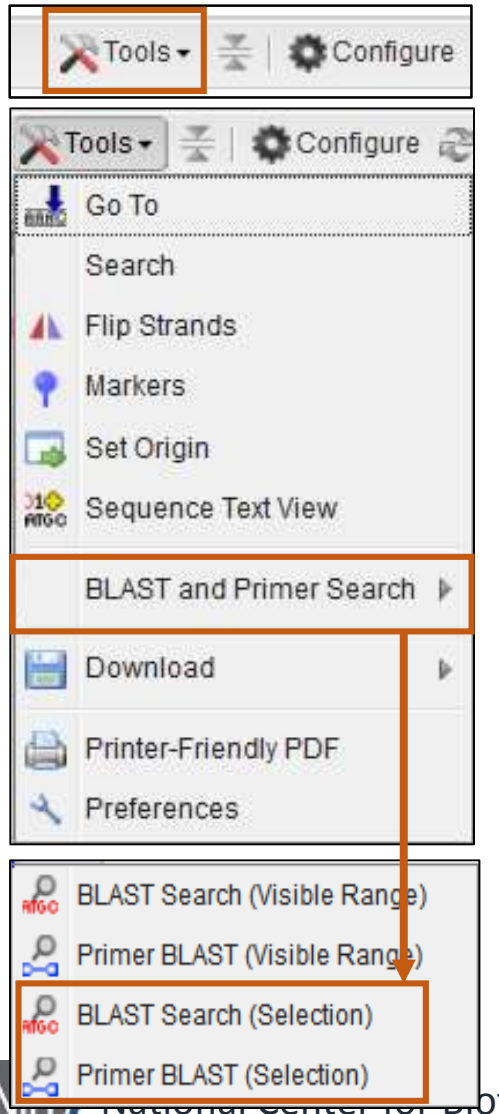

Tools
Configure
Go To
Search
Flip Strands
Markers
Set Origin
Sequence Text View
BLAST and Primer Search
Download
Printer-Friendly PDF
Preferences

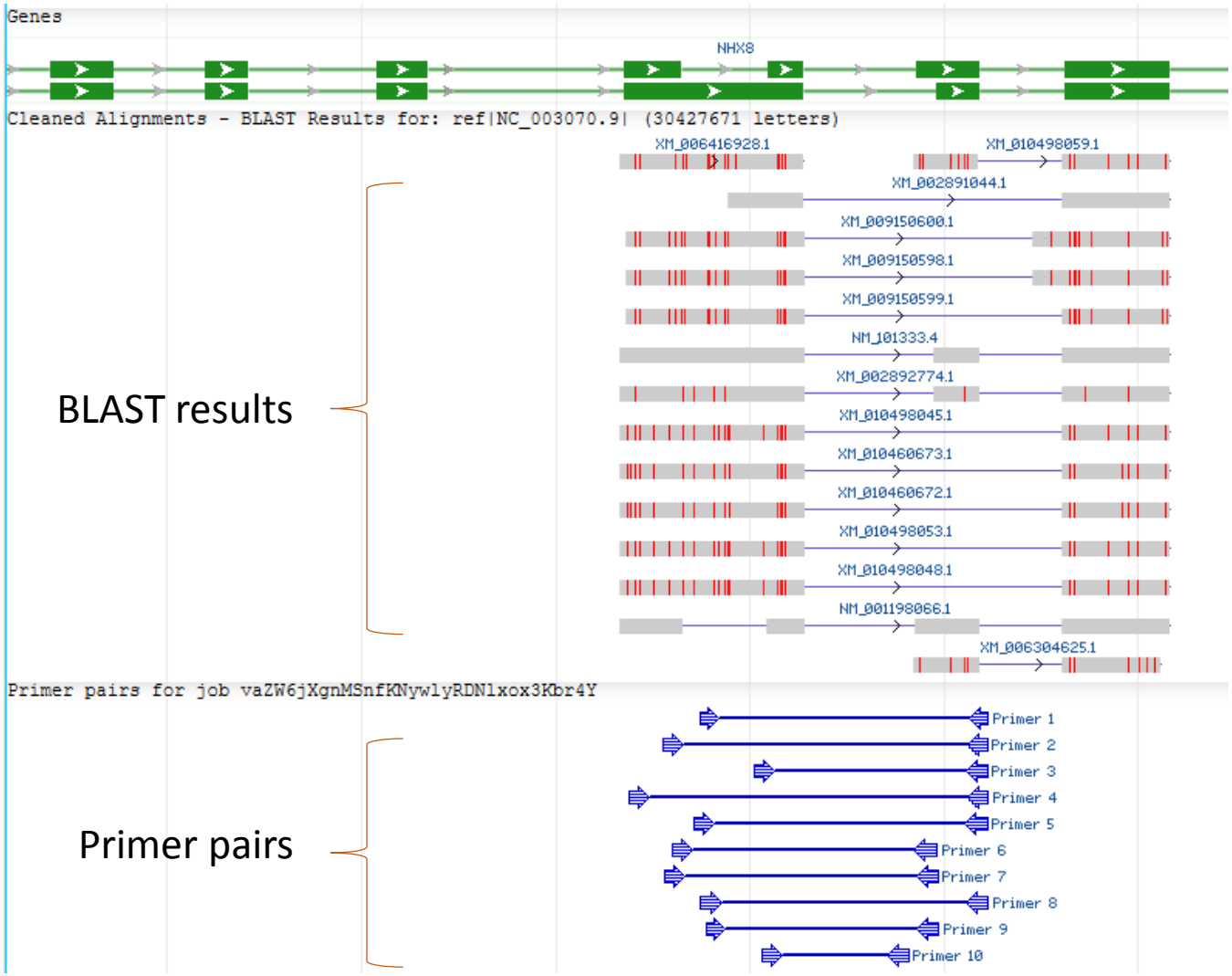

NC_025812.1[6070333..6082124].pdf - Adobe Acrobat Pro
File Edit View Window Help
Create
Customize
Panel 1
(1 of 1)
61%
Tools
Fill & Sign
Comment
Zoom out (Ctrl+Minus)
Six-frame translations (top -> bottom: +1, +2, +3, -1, -2, -3), Genetic code: Standard (1)
Repeats identified by WindowMasker
Repeats identified by RepeatMasker
Simple_repeat
Genes, NCBI Beta vulgaris subsp. vulgaris Annotation Release 100, 2014-12-10
LOC104888291
RNA-seq exon coverage, aggregate (filtered, log2 scaled), NCBI Beta vulgaris subsp. vulgaris Annotation Release 100 - log 2 sca...
RNA-seq intron-spanning reads, aggregate (filtered, log2 scaled), NCBI Beta vulgaris subsp. vulgaris Annotation Release 100 - log...
RNA-seq intron features, aggregate (filtered), NCBI Beta vulgaris subsp. vulgaris Annotation Release 100

BLAST

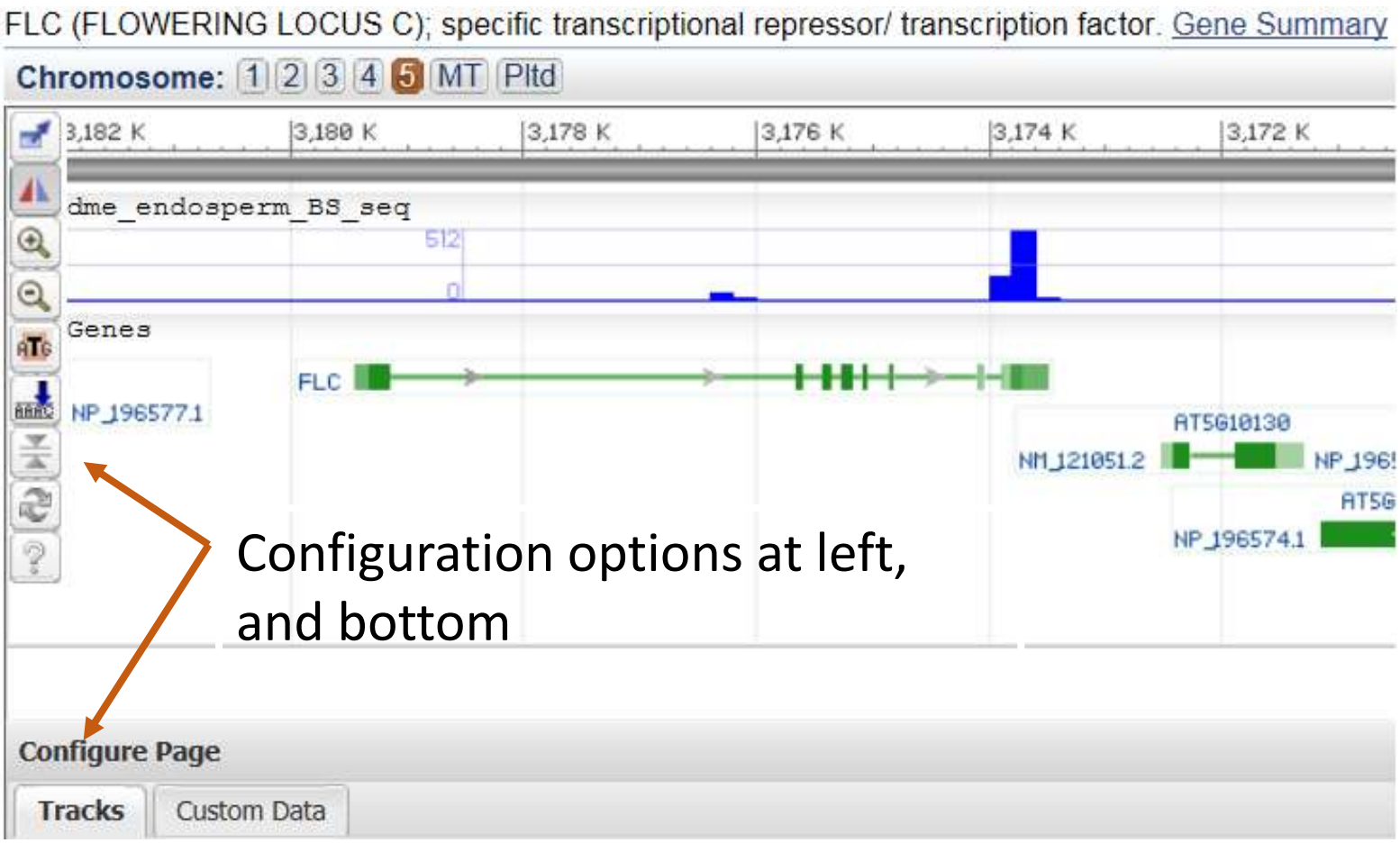
Arabidopsis thaliana NHX8 gene

- Click-drag on sequence coordinate line to select range
- Tools Menu -> BLAST Search (Selection)
- Tools Menu -> Primer BLAST (Selection)





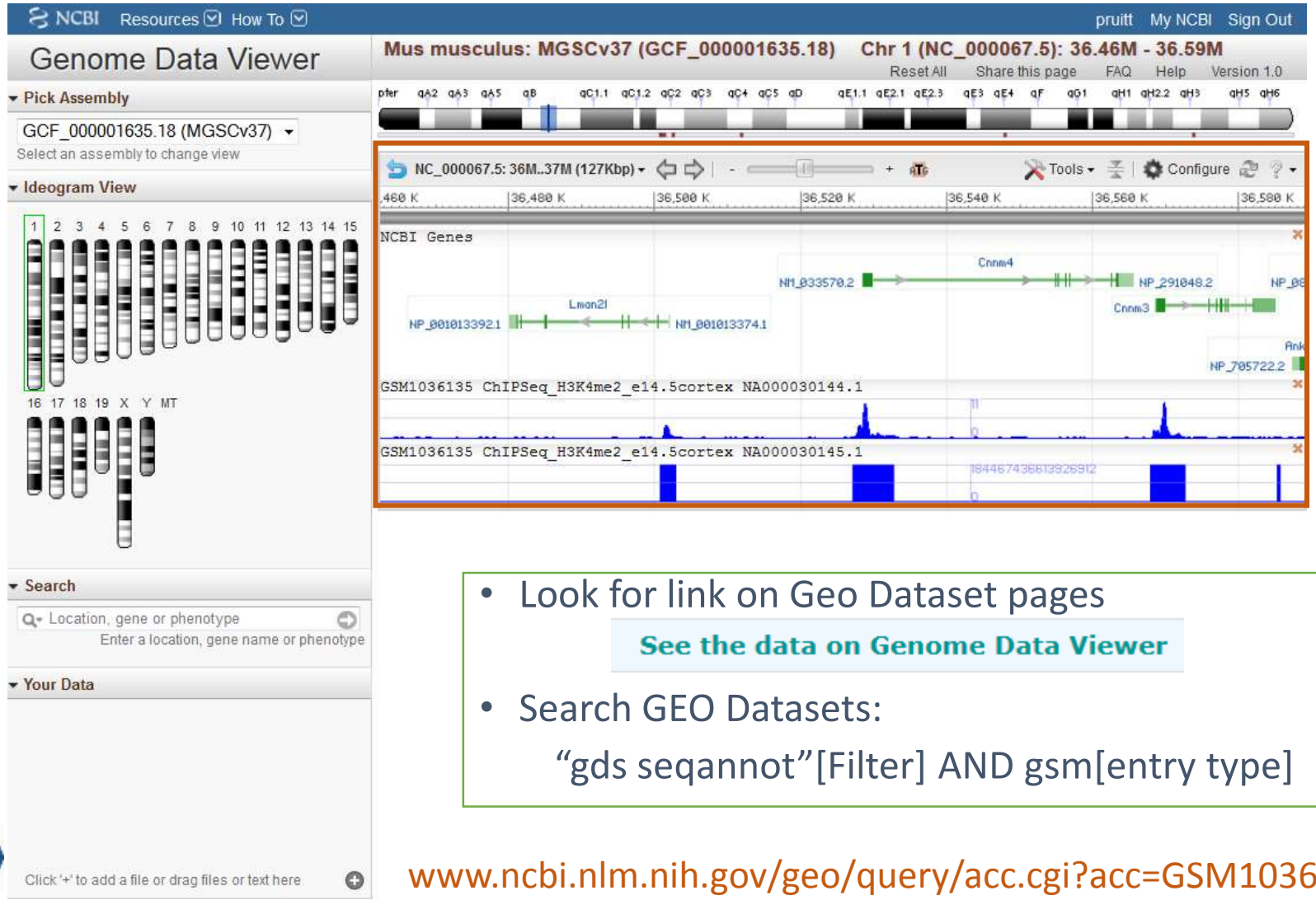
Epigenomics



Configuration options at left, and bottom

GEO Genome Data Viewer (GDV)

GSM1036135 (mouse ChIP-seq H3K4me2, embryonic cortex)



- Look for link on Geo Dataset pages

  See the data on Genome Data Viewer

- Search GEO Datasets:

  "gds seqannot"[Filter] AND gsm[entry type]

www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM1036135

Genome Workbench (gbench)

www.ncbi.nlm.nih.gov/tools/gbench/

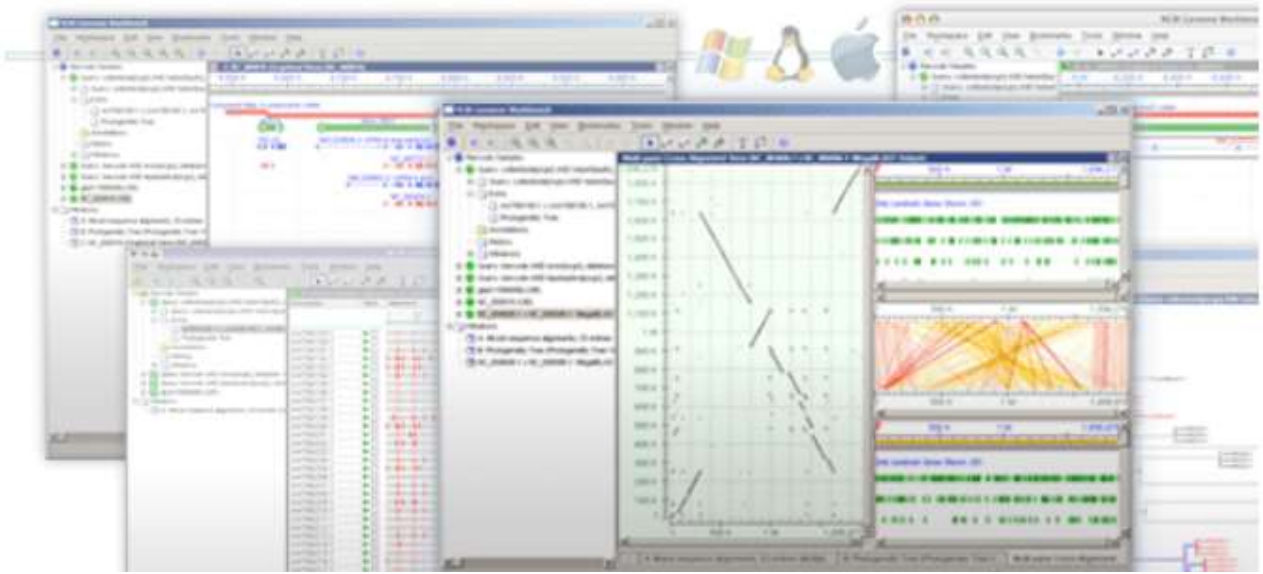
NCBI Genome Workbench

Search NCBI | Search

Home | Tutorials | Help | Videos | Manuals

Welcome to NCBI Genome Workbench!

NCBI Genome Workbench is an integrated application for viewing and analyzing sequence data. With Genome Workbench, you can view data in publically available sequence databases at NCBI, and mix this data with your own private data.



Download

Current Version is 2.8.0 (released August 18, 2014)

- Release Notes
- FTP site for all downloads
- Windows
  - Windows 7 (64-bit)
  - Windows 7 (32-bit)
- Mac OS X
  - Mac OS X 10.6+ 64-Bit (Snow Leopard, Lion, Mountain Lion)
- Linux (Ubuntu 12.04 (Precise Pangolin))
  - 64-bit DEB
  - 32-bit DEB
- Linux (Fedora 20)
  - 64-bit RPM

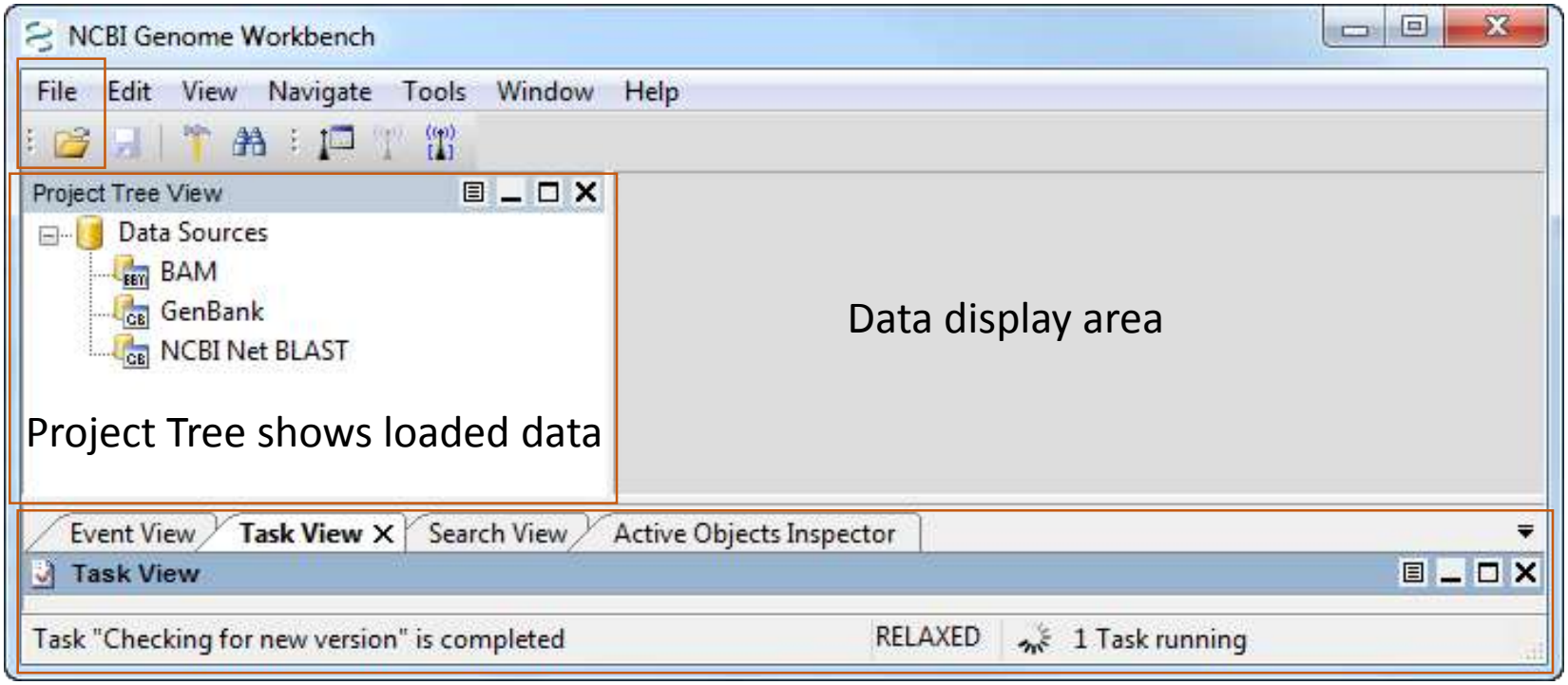
Genome Workbench

- Compiled for several operating systems
- Used to display:
    - Genome annotation
    - Alignments
    - Histograms
    - BED, WIG, GFF
- Features:
    - Search, Pan, Zoom
    - Configure the display
    - Run BLAST
    - View annotation tracks, multiple alignments
    - Generate and display phylogenetic trees
    - Import local data in a variety of formats
    - Merge NCBI data with uploaded private data to view both together

An application for viewing and analyzing sequence data from NCBI databases, or upload your data for analysis

NIH www.ncbi.nlm.nih.gov/tools/gbench/

General layout



Search for features, search the sequence, search for open reading frames
Monitor the progress of analysis tasks

General layout

NCBI Genome Workbench

File Edit View Navigate Tools Window Help

Project Tree View

Data Sources

BAM

GenBank

Open - Genome

Projects or Workspace
File Import
Genome
BAM/CSRA files
Data from GenBank
RIDs from NCBI Net BLAST

Enter a search term , then select genome(s) from the list.

Search term: Turkey

Find Genomes

Found Genomes

Name	Accession	Organism	Description	Class
Turkey_5.0	GCF_000146605.2	Meleagris ...		haploid
Turkey_5.0	GCA_000146605.3	Meleagris ...		haploid
Turkey_2.01 (melGal1)	GCF_000146605.1	Meleagris ...		haploid
Turkey_2.01 (melGal1)	GCA_000146605.2	Meleagris ...		haploid
Turkey_2.01	GCA_000146605.1	Meleagris ...		haploid

Release type

All RefSeq GenBank

Help Next > Cancel

Open - File Import

Projects or Workspace
File Import
Genome
BAM/CSRA files
Data from GenBank
RIDs from NCBI Net BLAST

File Format: Autodetect format

Filenames:

Autodetect format
AGP assembly files
NCBI ASN1 files
BED files (*.bed)
FASTA files
GFF/GVF files
Newick/Nexus Tree files
RepeatMasker files
Table files
Text Alignment files
VCF (Variant Call Format) files
WIG files (*.wig)
5 Column Feature files

Add files

Recently used Files:

Xenia_primaryTrs.gff3 last used Jan 02, 03:52 pm

HBA1 541307 1244967.asn last used Aug 07, 05:38 pm

Help Next > Cancel

Open - Data from GenBank

Projects or Workspace
File Import
Genome
BAM/CSRA files
Data from GenBank
RIDs from NCBI Net BLAST

Accessions to load:

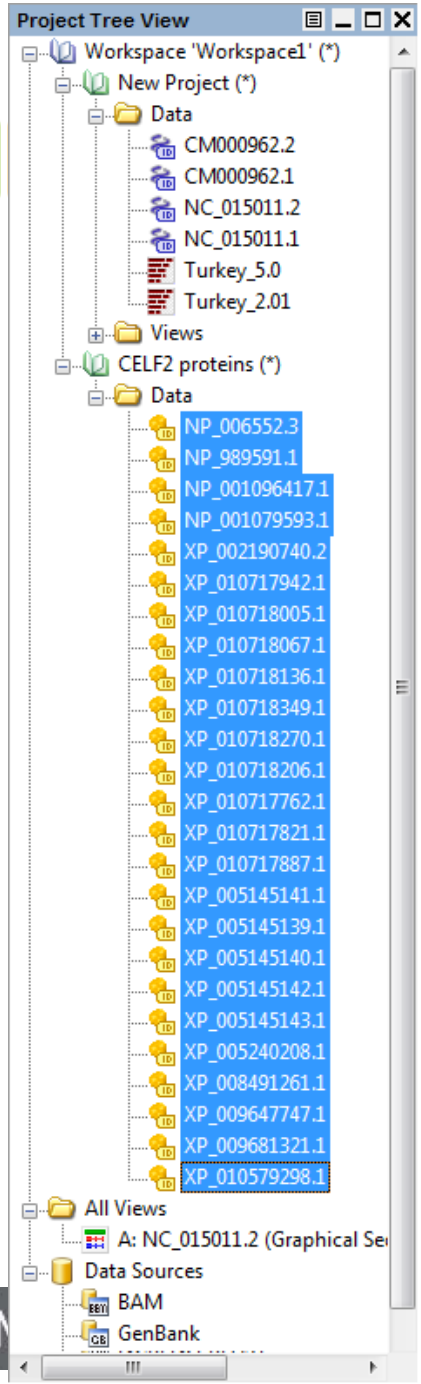
Separate accessions with spaces, tabs, commas or semicolons.
Add a range to accession after colon (NT_029999:5k-10k).

NP_006552.3
NP_989591.1
NP_001096417.1
NP_001079503.1
XP_002190740.2
XP_010717942.1
XP_010718005.1
XP_010718067.1
XP_010718136.1
XP_010718349.1
XP_010718270.1
XP_010718206.1

Recently loaded accessions:

XP_010579298.1 last loaded Jan 05, 03:01 pm
XP_009681371.1 last loaded Jan 05, 03:01 pm
XP_009647747.1 last loaded Jan 05, 03:01 pm
XP_008491261.1 last loaded Jan 05, 03:01 pm
XP_005240208.1 last loaded Jan 05, 03:01 pm
XP_005145143.1 last loaded Jan 05, 03:01 pm
XP_005145142.1 last loaded Jan 05, 03:01 pm

Help Next > Cancel



Load a set of protein accession.version numbers
Select accessions to include in your analysis
Select the analysis option from the Tool menu

r Biotechnology Information

Project Tree View

- Workspace 'Workspace1' (*)
  - New Project (*)
    - Data
      - CM000962.2
      - CM000962.1
      - NC_015011.2
      - NC_015011.1
      - Turkey_5.0
      - Turkey_2.01
    - Views
  - CELF2 proteins (*)
    - Data
      - NP_006552.3
      - NP_989591.1
      - NP_001096417.1
      - NP_001079593.1
      - XP_002190740.2
      - XP_010717942.1
      - XP_010718005.1
      - XP_010718067.1
      - XP_010718136.1
      - XP_010718349.1
      - XP_010718270.1
      - XP_010718206.1
      - XP_010717762.1
      - XP_010717821.1
      - XP_010717887.1
      - XP_005145141.1
      - XP_005145139.1
      - XP_005145140.1
      - XP_005145142.1
      - XP_005145143.1
      - XP_005240208.1
      - XP_008491261.1
      - XP_009647747.1
      - XP_009681321.1
      - XP_010579298.1
- All Views
  - A: NC_015011.2 (Graphical Se
- Data Sources
  - BAM
  - GenBank

NCBI Genome Workbench

File Edit View Navigate Tools Window

Run Tool

Filter: Reset Filter

Recent Tools (3 tools)

- BLAST Search
- Clean Up Alignments
- ClustalW (Multiple Sequence Alignment)

Alignment Creation (14 tools)

- BLAST Search
- BLAST Sequences
- Clean Up Alignments
- ClustalW (Multiple Sequence Alignment)
- Common taxonomic tree for sequences
- Create Gene Model
- Needleman-Wunsch Alignment
- Find Overlap between DNA Sequences
- Group Alignments
- Merge Alignments
- MUSCLE
- Genomic Aligner (NG Aligner)
- SPLIGN (SPliced aLIGNment)

Tree Building (1 tool)

- Phylogenetic Tree Builder Tool

Help

Project Tree View

- Data
  - CM000962.2
  - CM000962.1
  - NC_015011.2
  - NC_015011.1
  - Turkey_5.0
  - Turkey_2.01
- Views
- CELF2 proteins (*)
  - Data
    - NP_006552.3
    - NP_989591.1
    - NP_001096417.1
    - NP_001079593.1
    - XP_002190740.2
    - XP_010717942.1
    - XP_010718005.1
    - XP_010718067.1
    - XP_010718136.1
    - XP_010718349.1
    - XP_010718270.1
    - XP_010718206.1
    - XP_010717762.1
    - XP_010717821.1
    - XP_010717887.1
    - XP_005145141.1
    - XP_005145139.1
    - XP_005145140.1
    - XP_005145142.1
    - XP_005145143.1
    - XP_005240208.1
    - XP_008491261.1
    - XP_009647747.1
    - XP_009681321.1
    - XP_010579298.1
    - MUSCLE alignment: 25 sequences.
    - Phylogenetic tree: MUSCLE alignment: 25 sequences.
- All Views
  - A: NC_015011.2 (Graphical Sequence View) [New Project]
- Data Sources
  - BAM
  - GenBank
  - NCBI Net BLAST

r Biotechnology Information

NCBI Genome Workbench

File Edit View Navigate Tools Window Help

Display the phylogenetic tree calculated from selected CELF proteins.

MUSCLE alignment: 25 sequences.

Phylogenetic tree: MUSCLE alignment: 25 sequences.

CELF proteins

Search Tool: Feature Search

Search Context: Project Tree View

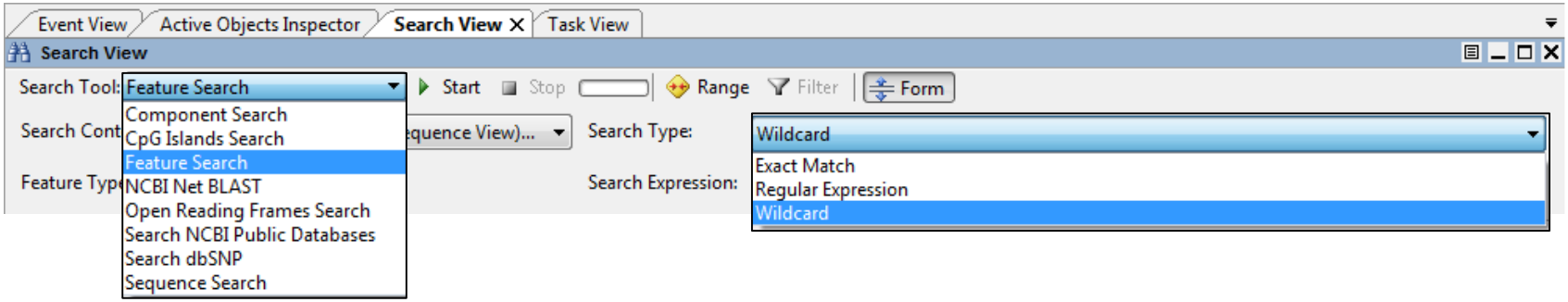
Search Type: Wildcard

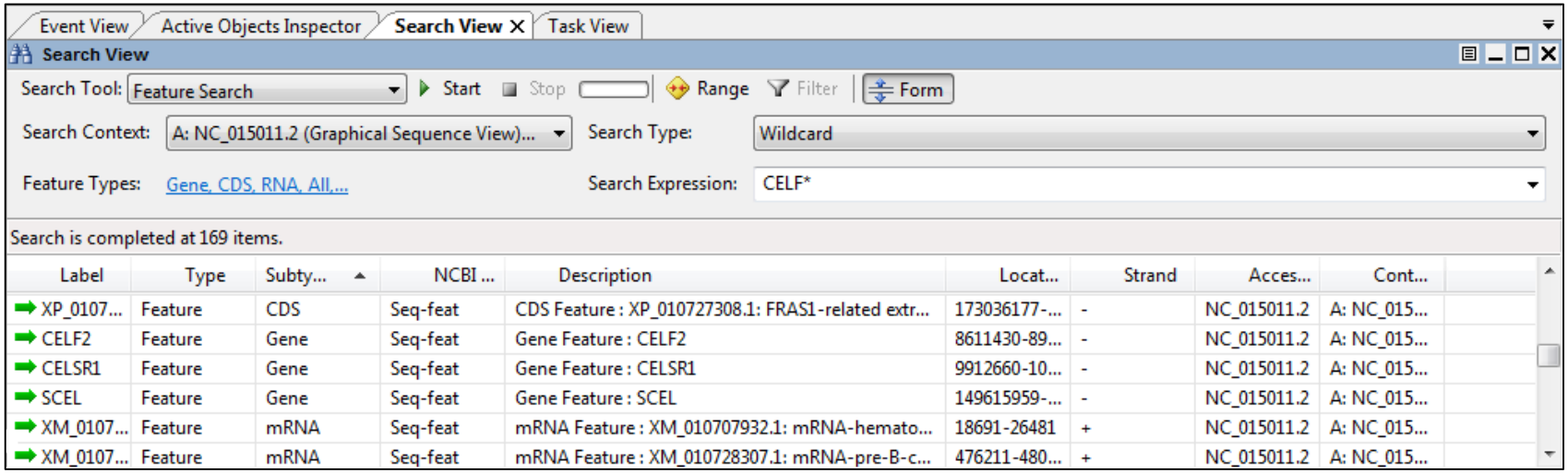
Feature Types: Gene, CDS, RNA, All...

Search Expression: CELF*

Task "Retrieving sequence descriptions" is completed

Search


Event View
Active Objects Inspector
Search View
Task View
Search View
Search Tool: Feature Search
Start
Stop
Range
Filter
Form
Component Search
CpG Islands Search
Feature Search
NCBI Net BLAST
Open Reading Frames Search
Search NCBI Public Databases
Search dbSNP
Sequence Search
Search Type:
Wildcard
Exact Match
Regular Expression
Wildcard
Search Expression:


Event View
Active Objects Inspector
Search View
Task View
Search View
Search Tool: Feature Search
Start
Stop
Range
Filter
Form
Search Context: A: NC_015011.2 (Graphical Sequence View)...
Search Type: Wildcard
Feature Types: Gene, CDS, RNA, All,...
Search Expression: CELF*
Search is completed at 169 items.
Label | Type | Subty... | NCBI ... | Description | Locat... | Strand | Acces... | Cont...
XP_0107... | Feature | CDS | Seq-feat | CDS Feature : XP_010727308.1: FRAS1-related extr... | 173036177-... | - | NC_015011.2 | A: NC_015...
CELF2 | Feature | Gene | Seq-feat | Gene Feature : CELF2 | 8611430-89... | - | NC_015011.2 | A: NC_015...
CELSR1 | Feature | Gene | Seq-feat | Gene Feature : CELSR1 | 9912660-10... | - | NC_015011.2 | A: NC_015...
SCEL | Feature | Gene | Seq-feat | Gene Feature : SCEL | 149615959-... | - | NC_015011.2 | A: NC_015...
XM_0107... | Feature | mRNA | Seq-feat | mRNA Feature : XM_010707932.1: mRNA-hemato... | 18691-26481 | + | NC_015011.2 | A: NC_015...
XM_0107... | Feature | mRNA | Seq-feat | mRNA Feature : XM_010728307.1: mRNA-pre-B-c... | 476211-480... | + | NC_015011.2 | A: NC_015...

Multiple sequence alignment

A: NC_015011.2 | B: MUSCLE alignment: 25 sequences. | C: Phylogenetic tree: MUSCLE alignment: 25 sequences. (49 nodes, 25 leaves)

B: MUSCLE alignment: 25 sequences. (Multiple Alignment View) [CELF2 proteins]

Description	Marker	Seq. Sta	First	Alignment	Org. Name	Last	Seq. End	Seq. Le
XP_008491261.1		1	1		Calypte anna	532	532	532
XP_009647747.1		1	1		Egretta garzetta	532	532	532
XP_005240208.1		1	1		Falco peregrinus	530	530	530
NP_989591.1		1	1		Gallus gallus	488	488	488
XP_010579298.1		1	1		Haliaeetus leucocephalus	519	519	519
NP_006552.3		1	1		Homo sapiens	521	521	521
XP_010718136.1		1	1		Meleagris gallopavo	521	521	521
XP_010718349.1		1	1		Meleagris gallopavo	490	490	490
XP_010718270.1		1	1		Meleagris gallopavo	490	490	490
XP_010718206.1		1	1		Meleagris gallopavo	490	490	490
XP_010717762.1		1	1		Meleagris gallopavo	490	490	490
XP_010717887.1		1	1		Meleagris gallopavo	484	484	484
XP_010718005.1		1	1		Meleagris gallopavo	530	530	530
XP_010717942.1		1	1		Meleagris gallopavo	532	532	532
XP_010718067.1		1	1		Meleagris gallopavo	526	526	526
XP_010717821.1		1	1		Meleagris gallopavo	488	488	488
XP_005145142.1		1	1		Melopsittacus undulatus	521	521	521
XP_005145139.1		1	1		Melopsittacus undulatus	530	530	530
XP_005145141.1		1	1		Melopsittacus undulatus	532	532	532
XP_005145140.1		1	1		Melopsittacus undulatus	526	526	526
XP_005145143.1		1	1		Melopsittacus undulatus	488	488	488
XP_009681321.1		1	1		Struthio camelus australis	530	530	530
XP_002190740.2		1	1		Taeniopygia guttata	490	490	490
NP_001096417.1		1	1		Xenopus (Silurana) tropicali	513	513	513
NP_001079593.1		1	1		Xenopus laevis	536	536	536

Quick zoom: ‘Control-V’+ mouse

A: NC_015011.2 | B: MUSCLE alignment: 25 sequences. | C: Phylogenetic tree: MUSCLE alignment: 25 sequences. (49 nodes, 25 leaves)

B: MUSCLE alignment: 25 sequences. (Multiple Alignment View) [CELF2 proteins]

Description	Marker	Seq. Sta	First	Alignment	Org. Name	Last	Seq. End	Seq. Le
XP_010718005.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Meleagris gallopavo	43	530	530
XP_008491261.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Calypte anna	43	532	532
XP_009647747.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Egretta garzetta	43	532	532
XP_005240208.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Falco peregrinus	43	530	530
NP_989591.1		1	1		Gallus gallus	1	488	488
XP_010579298.1		1	1	MTSSFKLDFLPEMMVDGRLLVSDRINGTANK	Haliaeetus leucocephalus	32	519	519
NP_006552.3		1	1	MTSAFKLDFLPDMMVEGRLLVPDRINGTANK	Homo sapiens	32	521	521
XP_010718136.1		1	1	MTSSFKLDFLPEMMVDGRLLVSDRINGTANK	Meleagris gallopavo	32	521	521
XP_010718349.1		1	1		Meleagris gallopavo	1	490	490
XP_010718270.1		1	1		Meleagris gallopavo	1	490	490
XP_010718206.1		1	1		Meleagris gallopavo	1	490	490
XP_010717762.1		1	1		Meleagris gallopavo	1	490	490
XP_010717887.1		1	1		Meleagris gallopavo	1	484	484
XP_010717942.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Meleagris gallopavo	43	532	532
XP_010718067.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Meleagris gallopavo	43	526	526
XP_010717821.1		1	1		Meleagris gallopavo	1	488	488
XP_005145142.1		1	1	MTSSFKLDFLPEMMVDGRLLVSDRINGTANK	Melopsittacus undulatus	32	521	521
XP_005145139.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Melopsittacus undulatus	43	530	530
XP_005145141.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Melopsittacus undulatus	43	532	532
XP_005145140.1		1	1	MFERTSELAFVENIGAESMRCPKSAVTMRNEELLLSNGTANK	Melopsittacus undulatus	43	526	526
XP_005145143.1		1	1		Melopsittacus undulatus	1	488	488
XP_009681321.1		1	1	MFERTSEPAFVANIGAESMRCPKSAVTMRNEELLLSNGTANK	Struthio camelus australis	43	530	530
XP_002190740.2		1	1		Taeniopygia guttata	1	490	490
NP_001096417.1		1	1	MMVDSRLLVSDRINGTTNK	Xenopus (Silurana) tropicali	20	513	513
NP_001079593.1		1	1	MFERTSKPAFVENICVESMRCPKSAVTMRNEELLFSNGTTNK	Xenopus laevis	43	536	536

Multi-pane cross alignment view

Event View | Active Objects Inspector | Search View | Task View

Search View

Search Tool: Feature Search | Start | Stop | Range | Filter | Form

Search Context: A: NC_015011.2 (Graphical Sequence View)...

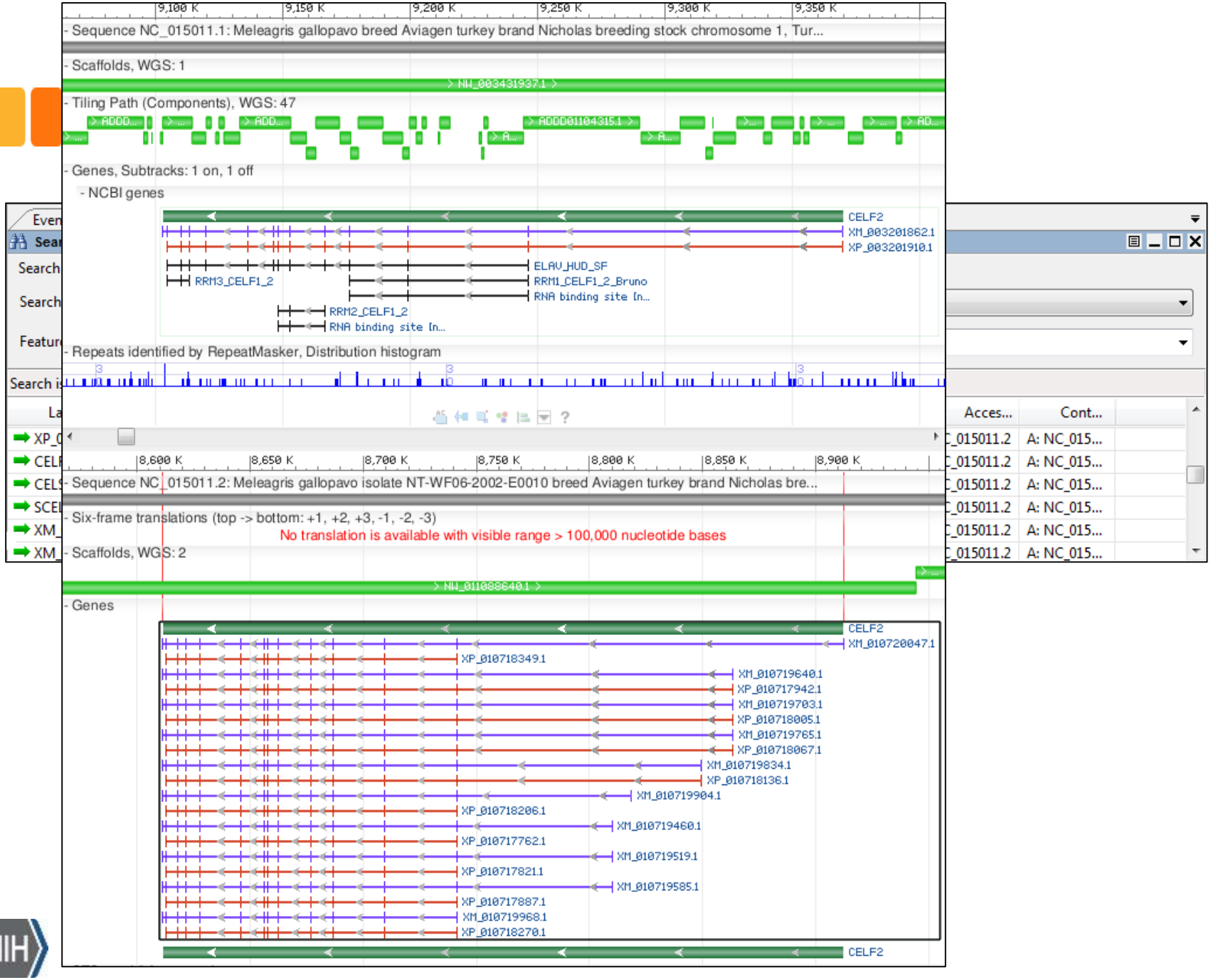
Search Type: Wildcard

Feature Types: Gene, CDS, RNA, All,...

Search Expression: CELF*

Search is completed at 169 items.

Label	Type	Subty...	NCBI ...	Description	Locat...	Strand	Acces...	Cont...
XP_0107...	Feature	CDS	Seq-feat	CDS Feature : XP_010727308.1: FRAS1-related extr...	173036177-...	-	NC_015011.2	A: NC_015...
CELF2	Feature	Gene	Seq-feat	Gene Feature : CELF2	8611430-89...	-	NC_015011.2	A: NC_015...
CELSR1	Feature	Gene	Seq-feat	Gene Feature : CELSR1	9912660-10...	-	NC_015011.2	A: NC_015...
SCEL	Feature	Gene	Seq-feat	Gene Feature : SCEL	149615959-...	-	NC_015011.2	A: NC_015...
XM_0107...	Feature	mRNA	Seq-feat	mRNA Feature : XM_010707932.1: mRNA-hemato...	18691-26481	+	NC_015011.2	A: NC_015...
XM_0107...	Feature	mRNA	Seq-feat	mRNA Feature : XM_010728307.1: mRNA-pre-B-c...	476211-480...	+	NC_015011.2	A: NC_015...


9,100 K
9,150 K
9,200 K
9,250 K
9,300 K
9,350 K
- Sequence NC_015011.1: Meleagris gallopavo breed Aviagen turkey brand Nicholas breeding stock chromosome 1, Tur...
- Scaffolds, WGS: 1
NW_003431937.1
- Tiling Path (Components), WGS: 47
- Genes, Subtracks: 1 on, 1 off
- NCBI genes
CELF2
XM_003201862.1
XP_003201910.1
ELAV_HUD_SF
RRM3_CELF1_2
RRM1_CELF1_2_Bruno
RNA binding site In...
RRM2_CELF1_2
RNA binding site In...
- Repeats identified by RepeatMasker, Distribution histogram
8,600 K
8,650 K
8,700 K
8,750 K
8,800 K
8,850 K
8,900 K
- Sequence NC_015011.2: Meleagris gallopavo isolate NT-WF06-2002-E0010 breed Aviagen turkey brand Nicholas bre...
- Six-frame translations (top -> bottom: +1, +2, +3, -1, -2, -3)
No translation is available with visible range > 100,000 nucleotide bases
- Scaffolds, WGS: 2
NW_011088640.1
- Genes
CELF2
XM_010720047.1
XP_010718349.1
XM_010719640.1
XP_010717942.1
XM_010719703.1
XP_010718005.1
XM_010719765.1
XP_010718067.1
XM_010719834.1
XP_010718136.1
XM_010719904.1
XP_010718206.1
XM_010719460.1
XP_010717762.1
XM_010719519.1
XP_010717821.1
XM_010719585.1
XP_010717887.1
XM_010719968.1
XP_010718270.1
CELF2
Acces...
Cont...
A: NC_015...

- Align NC_015011.1 x NC_015011.2
- Turkey_2.01 x Turkey_5.0
- Improved annotation of FGD6

NCBI Sequence Display Tools

Sequence Viewer

- Online
- Display NCBI
- Import your data
- Customize the display
- Search, pan, zoom
- Display a single accession
- Analysis tools
- Export high quality PDF
- API to embed tool in any website

Genome Workbench

- Downloadable application
- Display NCBI data
- Import your data
- Customize the display
- Search, pan, zoom
- Load a whole genome
- Analysis tools
- More analysis and display options than Sequence Viewer

Acknowledgements

- Sequence Viewer & Genome Workbench
  - David Falk
  - Mike DiCuccio
  - Anatoliy Kuznetsov

NCBI Posters (Titles paraphrased)

- P0051: Eukaryotic Genome Annotation Pipeline
- P0791: Genomic Resources for Arabidopsis Research
- P1105: From Genes to Genomes
- P1109: dbSNP and dbVAR
- P1112: Submissions to NCBI Sequence Repositories
- P1115: Annotation of Laurasitheria Genomes
- P1120: Resources for Plant Genomics
- P1142: Sequence Viewer and Genome Workbench

NCBI Genome Resources Workshop

- 12:50– 1:15 Improving the Flow of Data to National Center of Biotechnology Information Sequence Repositories, SRA and Genbank
  Ilene Mizrachi
- 1:15– 1:40 Variation at NCBI: Resources, Tools and Submissions
  Jennifer Lee
- 1:40– 2:05 Update on the Eukaryotic Genome Annotation Pipeline
  Francoise Thibaud-Nissen
- 2:05– 2:30 From Genes to Genomes – New Features and Data Access
  Kim D. Pruitt
- 2:30– 2:50 Annual Report
  Tatiana Tatusova
- 2:50-3:10 Questions & Discussion

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