Mini Courses NCBI Resources one course at a time

Map Viewer Quick Start
An NCBI Mini-Course

NCBI's Map Viewer can be used to visualize an organism's genome and annotation. The organisms represented in the Map Viewer include human, mouse, rat, zebrafish, mosquito, nematode, fruit fly, yeast, arabidopsis and others.

In this course, we will use the human genome Map Viewer to

- Locate a human gene
- Download the gene sequence along with its upstream sequence (to analyze promoter regions)
- Determine whether the sequence is in the draft or finished form
- Find a possible splice variant using Model Maker
- Identify whether variations in the gene are associated with a disease
- Obtain information about the mouse, rat and chimp homologs
- Obtain phenotype information

During the first hour, an overview will be given using one human gene, followed by an hour of hands-on session to practice using another human gene. The following handout contains the screenshots of the overview.

URL: http://www.ncbi.nlm.nih.gov/Class/minicourses/mapviewer.html

Instructor:
Dr. Wayne Matten, NCBI

Problem 1

We will use as an example the glial cell derived neurotrophic factor GDNF. GDNF may contribute to Hirschsprung disease when mutated. Search for "GDNF" in the Map Viewer. Access the Human Map Viewer page by clicking on Map Viewer and enter GDNF as a search term.

Name the chromosome on which this gene is located. Click on the Genes_seq map link of the map element GDNF in the reference assembly.
What is the map that is displayed? Turn on the ruler line for the map through the Maps & Options link. What are the nucleotide locations for the gene on the chromosome? What is the orientation of the gene on the chromosome? Download the gene sequence by using the "dl" link. (Change the strand, if necessary). In order to search for promoter elements, you may also download 5000 nucleotides of upstream sequence by adjusting the locations for the upstream 5000 nucleotides.

Add the Clone, Component and Contig maps for this region. Name the contig and GenBank accession numbers for the sequence covering this region. Are the sequences in the finished form? Is there a clone mapped to this region? If so, how can you order it?

Remove all the maps except Genes_seq and add the Ab initio (model) and Transcript (RNA) maps. Does the gene prediction match the current gene annotation? How many alternatively spliced transcripts have been annotated for the gene? Display the current data as "Data As Table View".

Using the Model Maker (mm), obtain a possible alternatively spliced product and its translated amino acid sequence. Search for similar proteins by using BLAST.

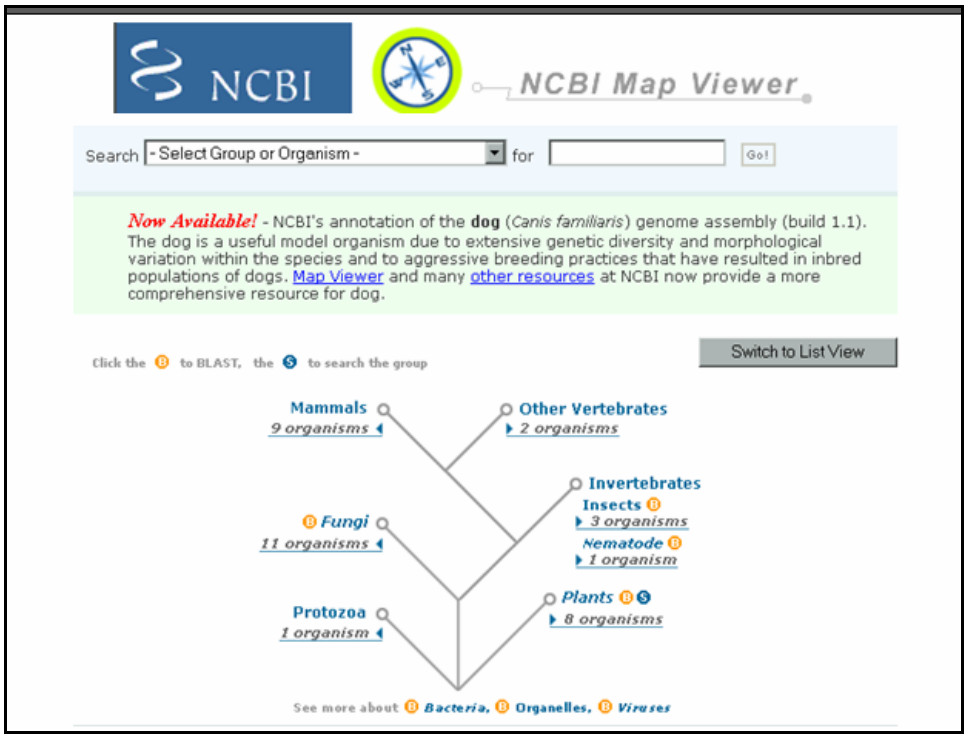
Remove all the maps except Genes_seq and add the Gene maps for mouse, chimp and rat. Are the gene structures in the three organisms similar?
Remove all the maps except the human Gene map, and add the phenotype map. Name the disease with which the GDNF gene is associated. Obtain more information about the disease by linking to the corresponding OMIM record.

NCBI Map Viewer

What is Map Viewer?

Map Viewer allows you to view and search an organism's complete genome, display chromosome maps, and zoom into progressively greater levels of detail, down to the sequence data for a region of interest.

It allows for the analysis of genes and genome annotation in graphical format.



NCBI

NCBI Map Viewer

- Locate a human gene
- Download the gene sequence along with its upstream region (for promoter analysis)
- Determine whether the sequence is in draft or finished form
- Find a possible splice variant via Model Maker
- Identify whether variations in the gene are associated with a disease
- Obtain information about mouse and rat homologues

Genome Assembly Accession Numbers

Intermediate Assemblies:

NT_ BAC (Bacterial Artificial Chromosome) sequence data
NW_ WGS (Whole Genome Shotgun) sequence data

Complete Chromosome/Contig Assembly:

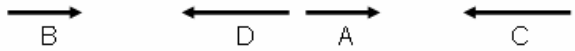
NC_

High Throughput Genomic Sequences

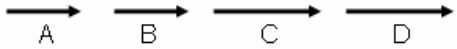
Sequencing of BACs:

Draft:

Phase 0 – single/few pass reads of a single clone
Phase 1 – unfinished, unordered BACs with gaps



Phase 2 – unfinished, ordered with gaps



Finished:

Phase 3 – high quality finished sequence with no gaps

Map Annotation

Type	Unit
Sequence	base pairs
Cytogenetic	p/q (short)/(long) arms
Genetic	centiMorgans (cM)
Radiation	centiRays (cR)

NCBI

NCBI Map Viewer

PubMed Nucleotide Protein Genome Gene Structure PopSet Taxonomy Help

Search for GDNF on chromosome(s) assembly All Find Advanced Search

Show related entries Help FTP Map Viewer home

Map Viewer
- Map Viewer Home
- Map Viewer Help
- Human Maps Help
- Release Notes

NCBI Resources
- Genome Project
- TaxPlot
- Consensus CoDing Sequence (CCDS)
- Human Genome Resources
- NCBI Handbook
- RefSeq
- Whole Genome Association (WGA)

BLAST search the human genome

Homo sapiens (human) genome view

Build 36.1 statistics Switch to previous build

1 2 3 4 5 6 7 8 9 10 11 12 13

14 15 16 17 18 19 20 21 22 X Y MT

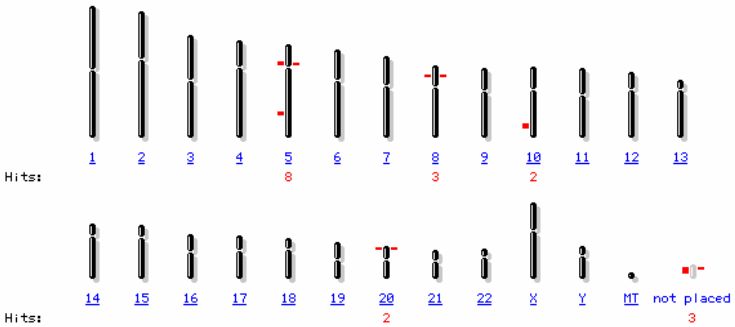
Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo; Homo sapiens

March 2006: NCBI released an update for the human genome (NCBI Build 36.1) that includes some changes to

Homo sapiens (human) genome view

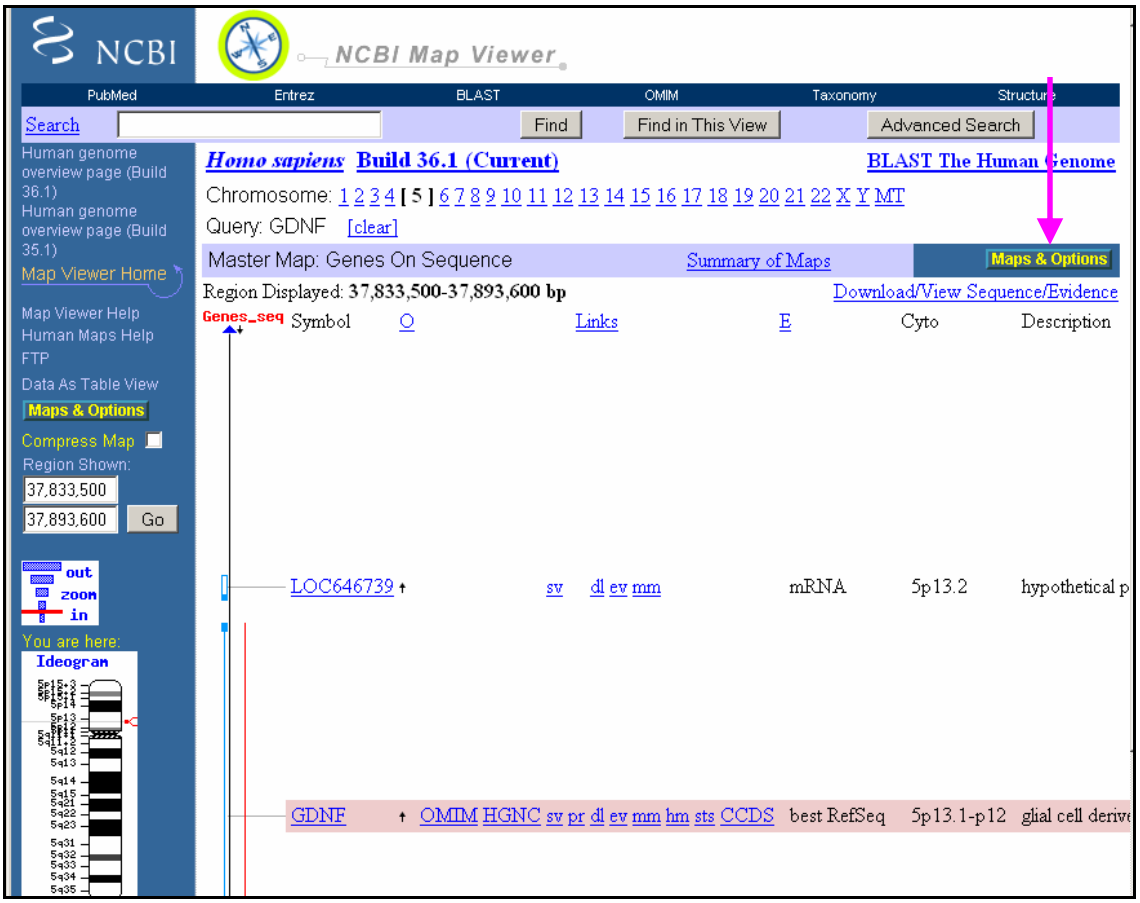
BLAST search the human genome

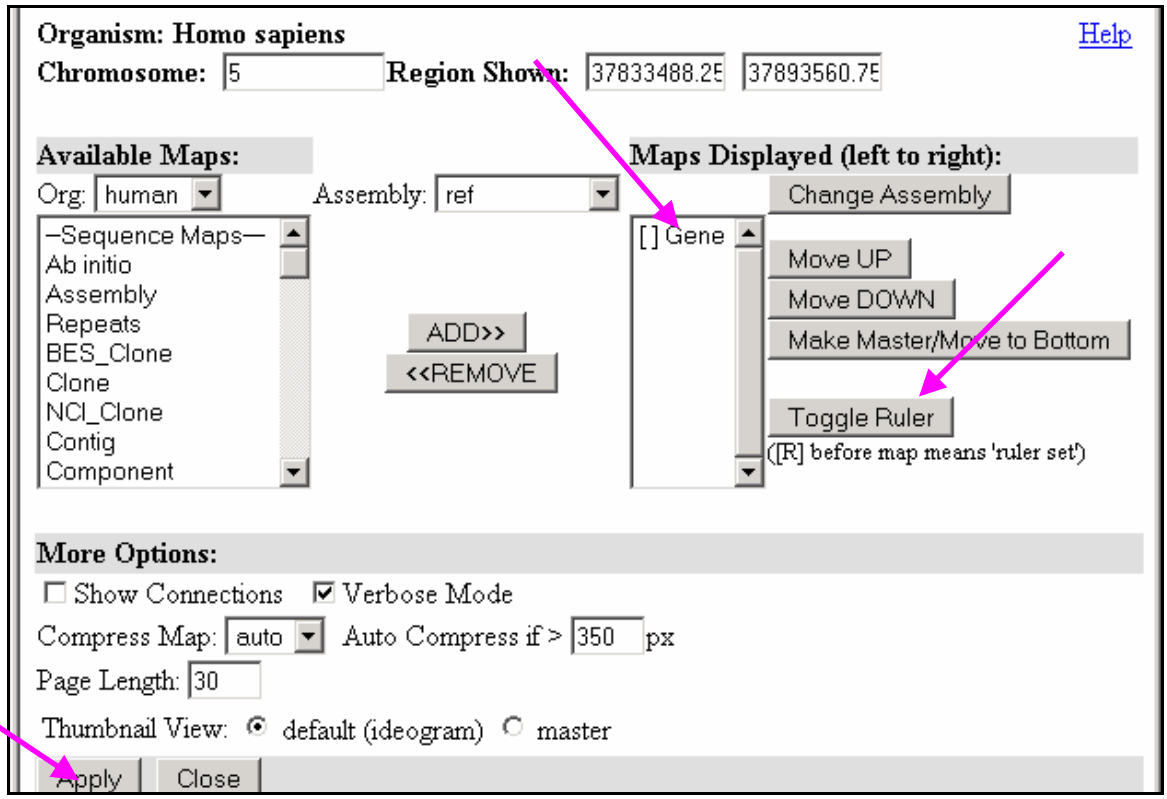
Build 36.1 statistics Switch to previous build



Search results for query "GDNF": 18 hits

Chr	Assembly	Match	Map element	Type	Maps
5	reference	all matches			
		GDNF	GDNF	PHENO	Pheno
		Gdnf	Gdnf	STS	STS
		GDNF family receptor alpha 3	GFRA3	GENE	Genes_cyto | Genes_seq
		GDNF : astrocyte-derived trophic factor	GDNF	GENE	Genes_cyto | Genes_seq
5	Celera	all matches			
		GDNF	GDNF	PHENO	Pheno
		Gdnf	Gdnf	STS	STS
		GDNF family receptor alpha 3	GFRA3	GENE	Genes_seq
		GDNF : astrocyte-derived trophic factor	GDNF	GENE	Genes_seq
8	reference	all matches			
		similar to GDNF family receptor alpha 2 precursor (GFR-alpha...	LOC653765	GENE	Genes_cyto | Genes_seq


NCBI
NCBI Map Viewer
PubMed
Entrez
BLAST
OMIM
Taxonomy
Structure
Search
Find
Find in This View
Advanced Search
Homo sapiens Build 36.1 (Current)
BLAST The Human Genome
Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT
Query: GDNF [clear]
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
Genes_seq
Symbol
O
Links
E
Cyto
Description
Human genome overview page (Build 36.1)
Human genome overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
LOC646739
sv
dl ev mm
mRNA
5p13.2
hypothetical p
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS
best RefSeq
5p13.1-p12
glial cell derive


Organism: Homo sapiens
Help
Chromosome: 5
Region Shown: 37833488.25
37893560.75
Available Maps:
Org: human
Assembly: ref
—Sequence Maps—
Ab initio
Assembly
Repeats
BES_Clone
Clone
NCI_Clone
Contig
Component
ADD>>
<<REMOVE
Maps Displayed (left to right):
[ ] Gene
Change Assembly
Move UP
Move DOWN
Make Master/Move to Bottom
Toggle Ruler
([R] before map means 'ruler set')
More Options:
Show Connections
Verbose Mode
Compress Map: auto
Auto Compress if > 350 px
Page Length: 30
Thumbnail View: default (ideogram) master
Apply
Close

NCBI NCBI Map Viewer

PubMed Entrez BLAST OMIM Taxonomy Structure

Search Find Find in This View Advanced Search

Human genome overview page (Build 36.1)
Human genome overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600 Go
out zoom in
You are here:
Ideogram
default

Homo sapiens Build 36.1 (Current) BLAST The Human Genome

Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

Query: GDNF [clear]

Master Map: Genes On Sequence Summary of Maps Maps & Options

Region Displayed: 37,833,500-37,893,600 bp Download/View Sequence/Evidence

Genes_seq	Symbol	O	Links	E	Cyto	Description
	LOC646739	+	sv dl ev mm	mRNA	5p13.2	hypothetical p
	GDNF	+	OMIM HGNC sv pr dl ev mm hm sts CCDS	best RefSeq	5p13.1-p12	glial cell deriv

Homo sapiens Genome (build 35.1)

Region to retrieve (in chromosome coordinates):

Chromosome: 5 Strand: plus

from: 37851510 adjust by: -0K

to: 37875539 adjust by: +0K Change Region/Strand

Sequence Format: FASTA

This chromosome region corresponds to the contig region(s):

Contig	start	stop	strand	
NT_006576.15	37788510	37812539	+	Display Save to Disk View Evidence ModelMaker

Homo sapiens Genome (build 35.1)

Region to retrieve (in chromosome coordinates):

Chromosome: 5 Strand: minus

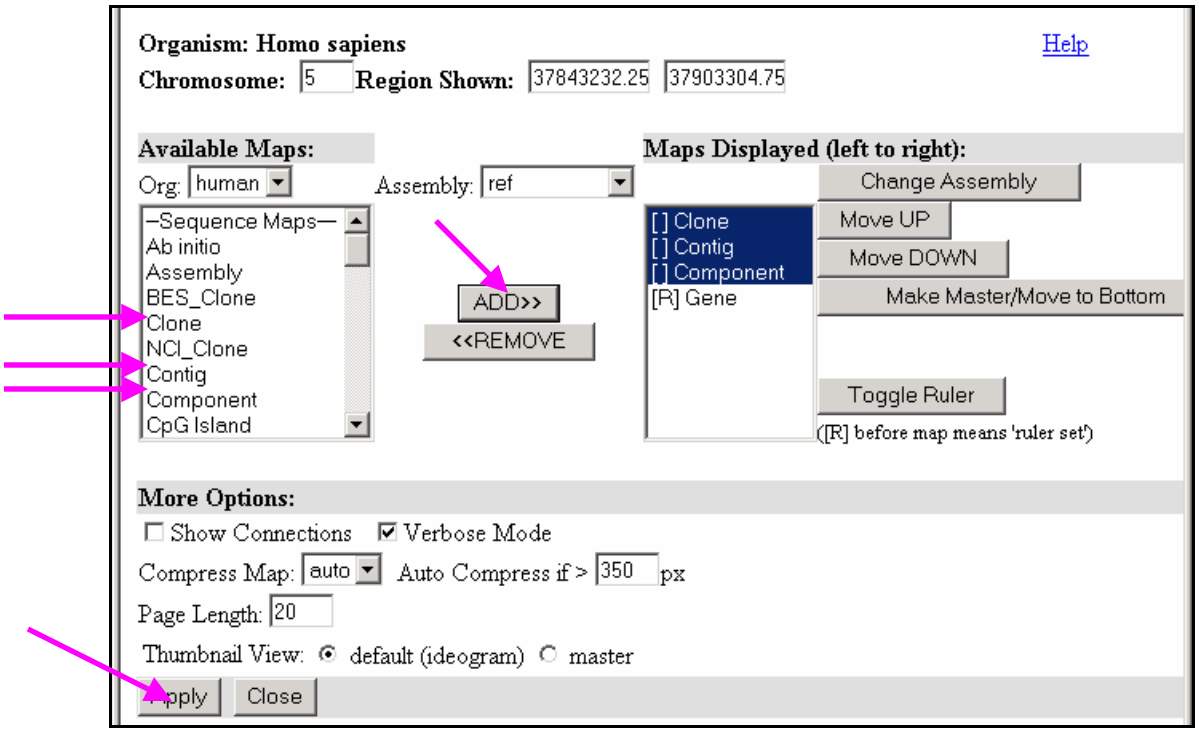
from: 37851510 adjust by: -0K

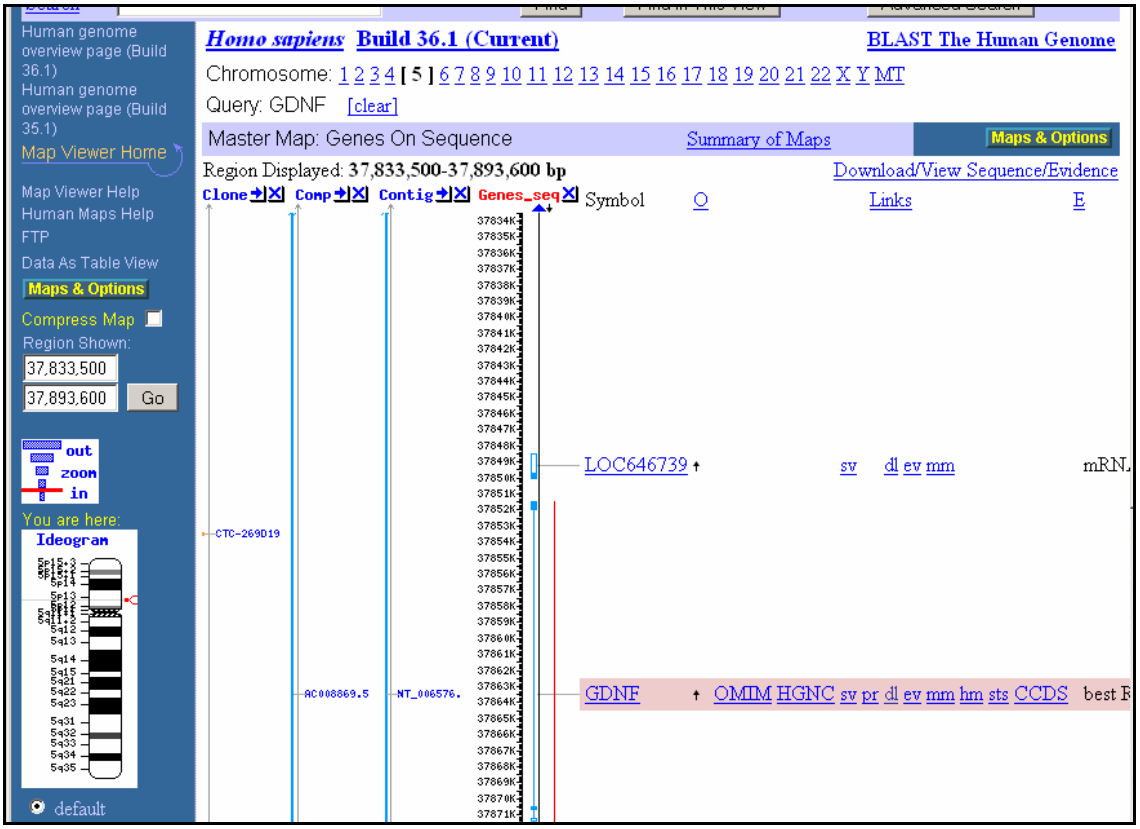
to: 37875539 adjust by: +0K Change Region/Strand

Sequence Format: FASTA

Reverse Complement of this chromosome region corresponds to the contig region(s):

Contig	start	stop	strand	
NT_006576.15	37788510	37812539	-	Display Save to Disk View Evidence ModelMaker


Organism: Homo sapiens
Help
Chromosome: 5 Region Shown: 37843232.25 37903304.75
Available Maps:
Org: human
Assembly: ref
–Sequence Maps–
Ab initio
Assembly
BES_Clone
Clone
NCI_Clone
Contig
Component
CpG Island
ADD>>
<<REMOVE
Maps Displayed (left to right):
[ ] Clone
[ ] Contig
[ ] Component
[R] Gene
Change Assembly
Move UP
Move DOWN
Make Master/Move to Bottom
Toggle Ruler
([R] before map means 'ruler set')
More Options:
Show Connections
Verbose Mode
Compress Map: auto
Auto Compress if > 350 px
Page Length: 20
Thumbnail View: default (ideogram) master
Apply
Close


Human genome overview page (Build 36.1)
Human genome overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
default
Homo sapiens Build 36.1 (Current)
BLAST The Human Genome
Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT
Query: GDNF [clear]
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
Clone
Comp
Contig
Genes_seq
Symbol
Links
LOC646739
sv
dl ev mm
mRNA
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS
best R

Human genome overview page (Build 36.1)
Human genome overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram

Homo sapiens **Build 36.1 (Current)** **BLAST The Human Genome**

Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

Query: GDNF [clear]

Master Map: Genes On Sequence Summary of Maps Maps & Options

Region Displayed: 37,833,500-37,893,600 bp Download/View Sequence/Evidence

Clone Comp Contig Genes_seq Symbol O Links E

LOC646739 sv dl ev mm mRN

CTC-269D19

Symbol: CTC-269D19
UniSTS: sts
Clone insert sequence: -
Clone end sequence: -
FISH: 5p13.2(UCSF)

AC008869.5 NT_006576.

GDNF OMIM HGNC sv pr dl ev mm hm sts CCDS best E

NCBI **Clone Registry**

PubMed Entrez BLAST OMIM Taxonomy Structure

Search CloneRegistry for Go

Clone Registry Home Page
Clone Nomenclature
BAC End Report
Distributor Information

Clone-ID: CTC-269D19 **CurrState:** Free
Comment: CloneMap processing

FingerPrint Information: No

Mapping Information

Chrom	Position	Map-Method	Center
5	5p13.2	FISH	UCSF
5	37.9 Mb	ePCR/BLAST	NCBI

STS Information

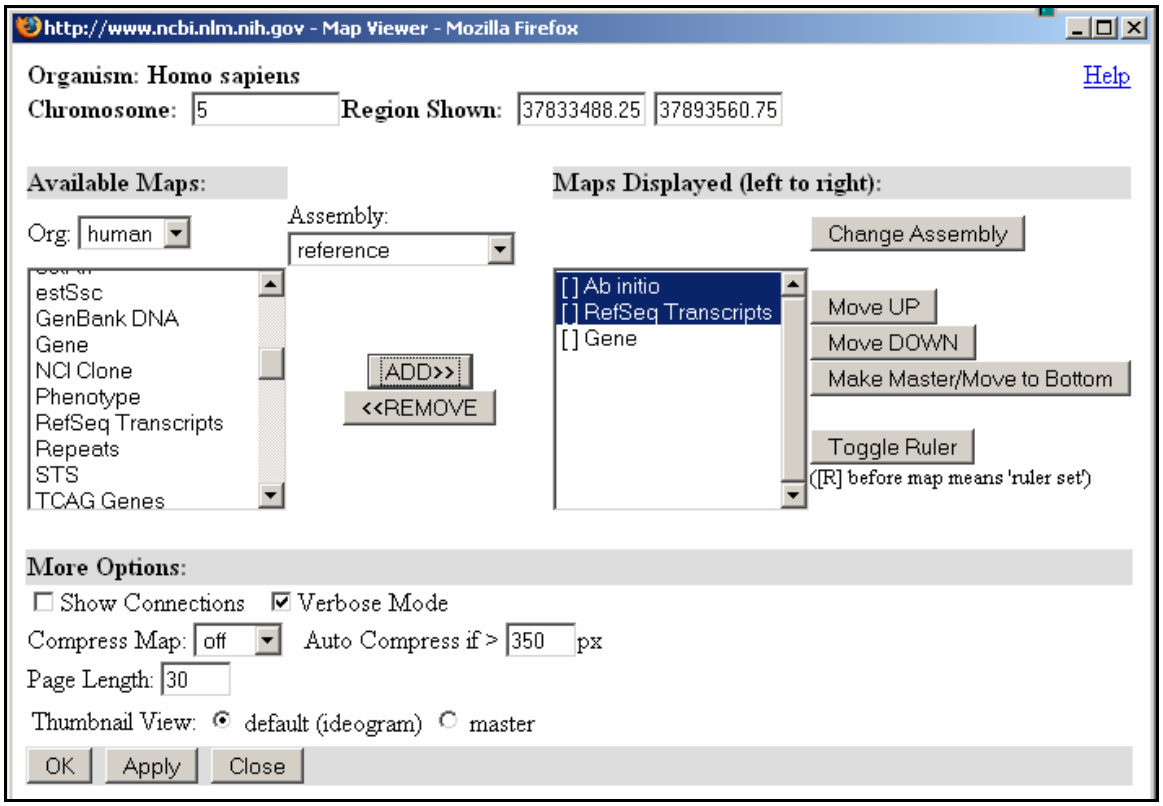
Chrom	STS-Name	Accession	Map-Method	Center
5	D5S2021		PCR/Hyb	UCSF

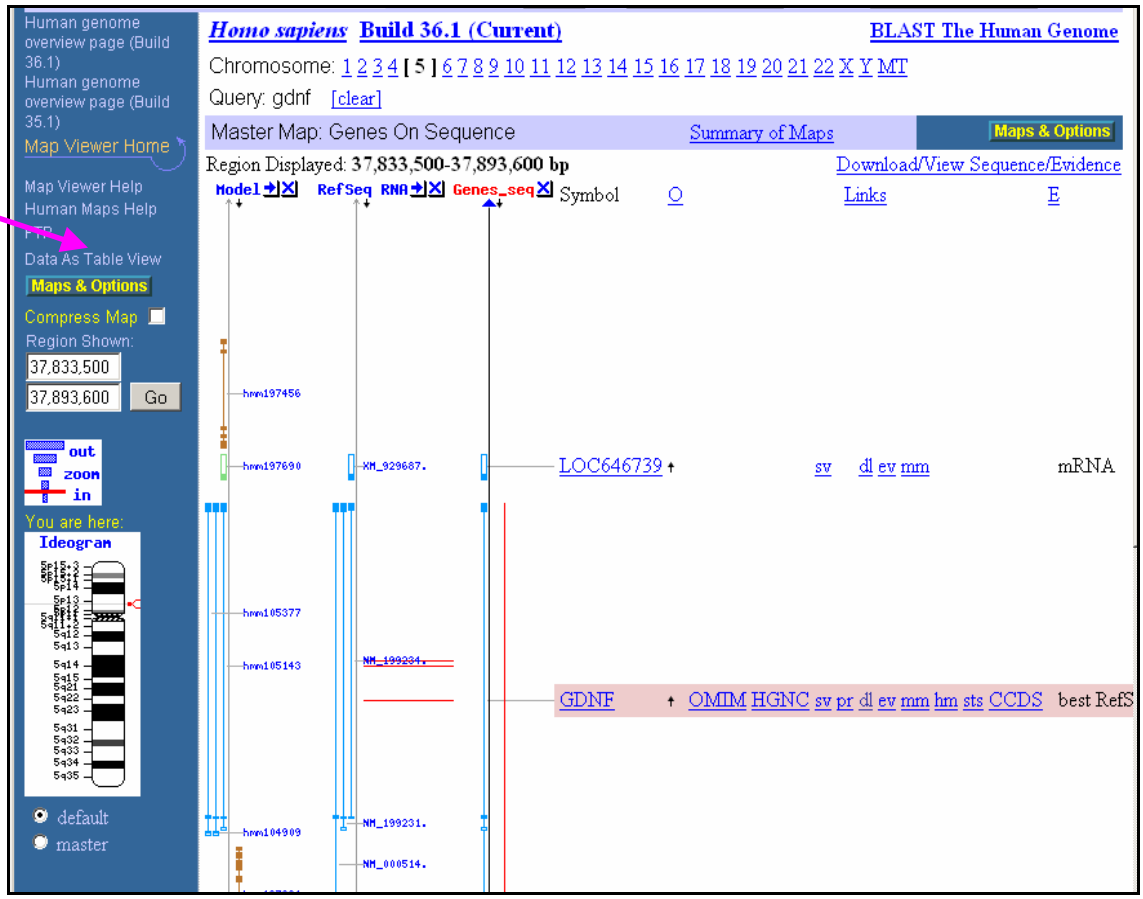
Library Information

Name: CalTech human BAC library C
Organism: Homo sapiens **Type:** BAC
Approved: No **Sex:** Male
Source: sperm **Rsite:** HindIII

Distributor Information

Available as part of clone set HBRC_1.resgen
Name: Research Genetics
Email: libraries@resgen.com
Web: http://www.resgen.com/resources/index.php3
Phone: 1-800-533-4363


http://www.ncbi.nlm.nih.gov - Map Viewer - Mozilla Firefox
Organism: Homo sapiens
Help
Chromosome: 5
Region Shown: 37833488.25 37893560.75
Available Maps:
Org: human
Assembly:
reference
estSsc
GenBank DNA
Gene
NCI Clone
Phenotype
RefSeq Transcripts
Repeats
STS
TCAG Genes
ADD>>
<<REMOVE
Maps Displayed (left to right):
Change Assembly
[ ] Ab initio
[ ] RefSeq Transcripts
[ ] Gene
Move UP
Move DOWN
Make Master/Move to Bottom
Toggle Ruler
([R] before map means 'ruler set')
More Options:
Show Connections
Verbose Mode
Compress Map: off
Auto Compress if > 350 px
Page Length: 30
Thumbnail View: default (ideogram) master
OK
Apply
Close


Human genome overview page (Build 36.1)
Human genome overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
default
master
Homo sapiens Build 36.1 (Current)
BLAST The Human Genome
Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT
Query: gdnf [clear]
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
Model
RefSeq RNA
Genes_seq
Symbol
O
Links
E
hmm197456
hmm197690
XM_929687.
LOC646739
sv
dl ev mm
mRNA
hmm105377
hmm105143
NM_199234.
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS
best RefS
hmm104909
NM_199231.
NM_000514.

Homo sapiens **Build 36.1 (Current)** **BLAST The Human Genome**

Data As Table View Download All [1]

Genes On Sequence All Sequence Maps next

Region Displayed: **37,833,500-37,893,600 bp** Download/View Sequence/Evidence Download Data

Total Genes On Chromosome: **1281** [4 not localized]

Genes in Region: **2**

start	stop	Symbol	O			Links								E	Cyto	Description
37848536	37850038	LOC646739	-			sv		dl	ev	mm				mRNA	5p13.2	hypothetical prote
37848536	37849693	exon	-	UTR	1158 bp											
37849694	37850038	exon	-	CDS	345 bp											
37851510	37875539	GDNF	-	OMIM	HGNC	sv	pr	dl	ev	mm	hm	sts	CCDS	best RefSeq	5p13.1-p12	glial cell derived r
37851510	37851857	exon	-	CDS	348 bp											
37851510	37851994	exon	-	CDS	485 bp											
37851995	37870504	intron			18510 bp											
37870505	37870655	exon	-	CDS	151 bp											
37870583	37870655	exon	-	CDS	73 bp											
37870594	37870647	exon	-	CDS	54 bp											
37870648	37870655	exon	-	UTR	8 bp											
37870656	37870681	exon	-	UTR	26 bp											
37870682	37871253	intron			572 bp											
37871254	37871350	exon	-	UTR	97 bp											
37871351	37875365	intron			4015 bp											
37875366	37875539	exon	-	UTR	174 bp											

Ab initio models All Sequence Maps prev next

Region Displayed: **37,833,500-37,893,600 bp** Download/View Sequence/Evidence Download Data

Total models On Chromosome: **6386** [12 not localized]

models in Region: **6**

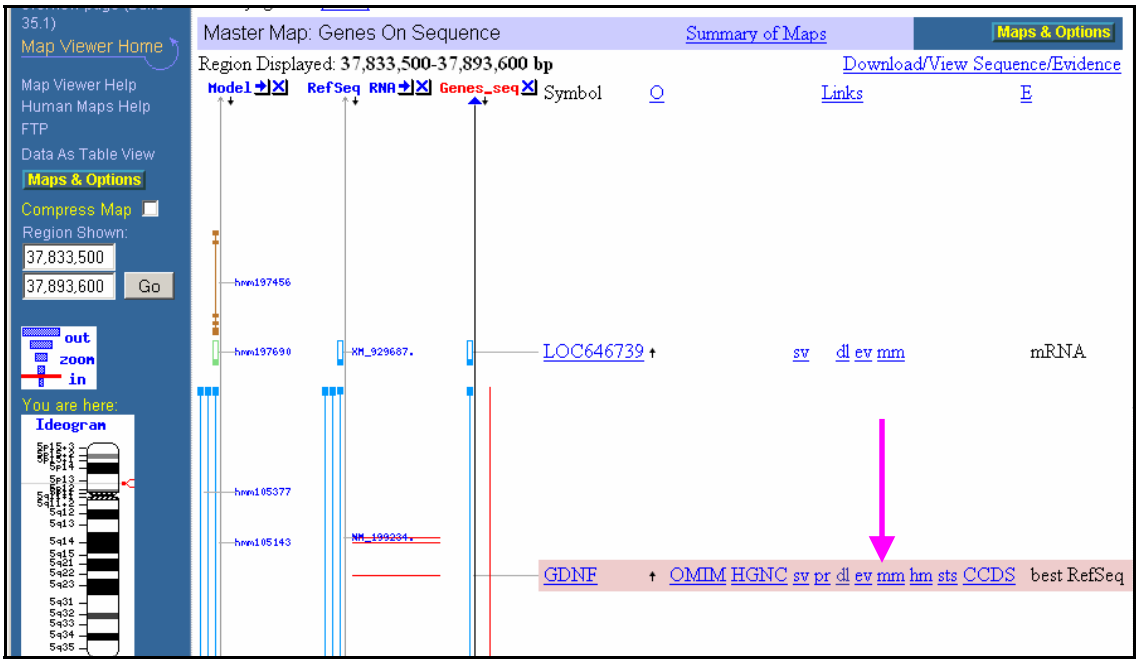
start	stop	Symbol	O	Best hit	Best hit description
37841490	37848120	hmm197456	-		
37848536	37850038	hmm197690	-	AAH08580.1	Unknown (protein for IMAGE:4179986) [Homo sapiens]
37851510	37871344	hmm105143	-	AAL11017.1	glial cell-derived neurotrophic factor isoform [Homo sapiens]
37851510	37871680	hmm104909	-	AAL11017.1	glial cell-derived neurotrophic factor isoform [Homo sapiens]
37851510	37871680	hmm105377	-	NP_000505.1	glial cell derived neurotrophic factor isoform 1 preproprotein [Homo sapiens]
37872457	37878200	hmm197924	+	BAA83714.1	RNA binding protein [Homo sapiens]

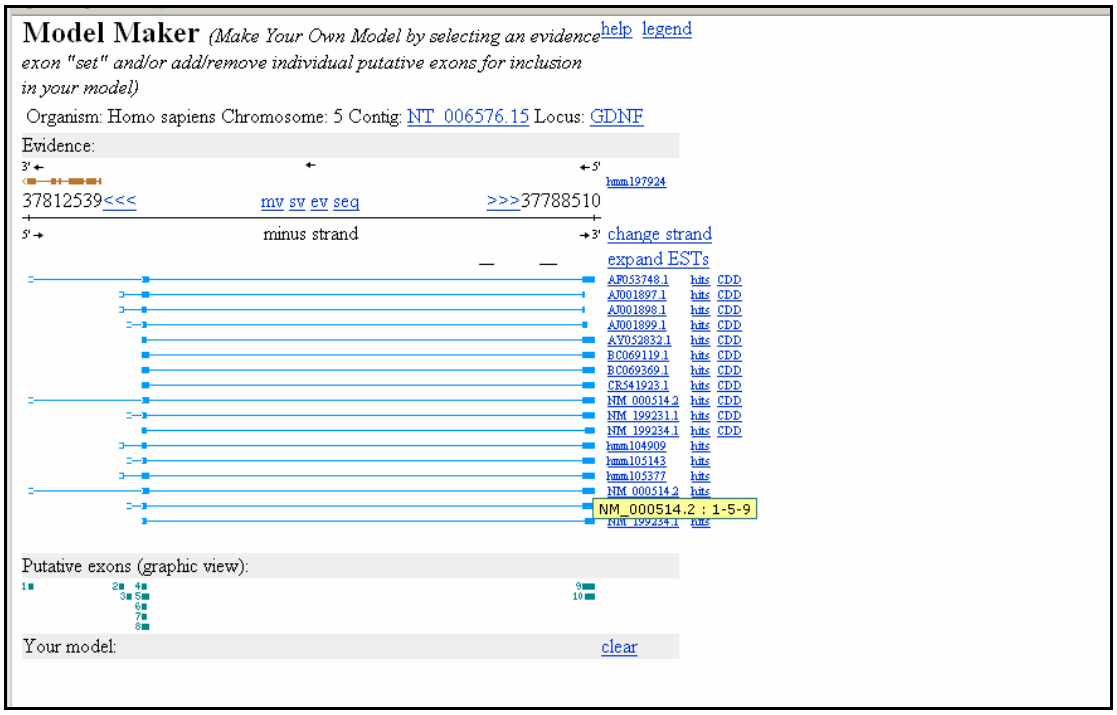
RefSeq Transcripts On Sequence All Sequence Maps prev

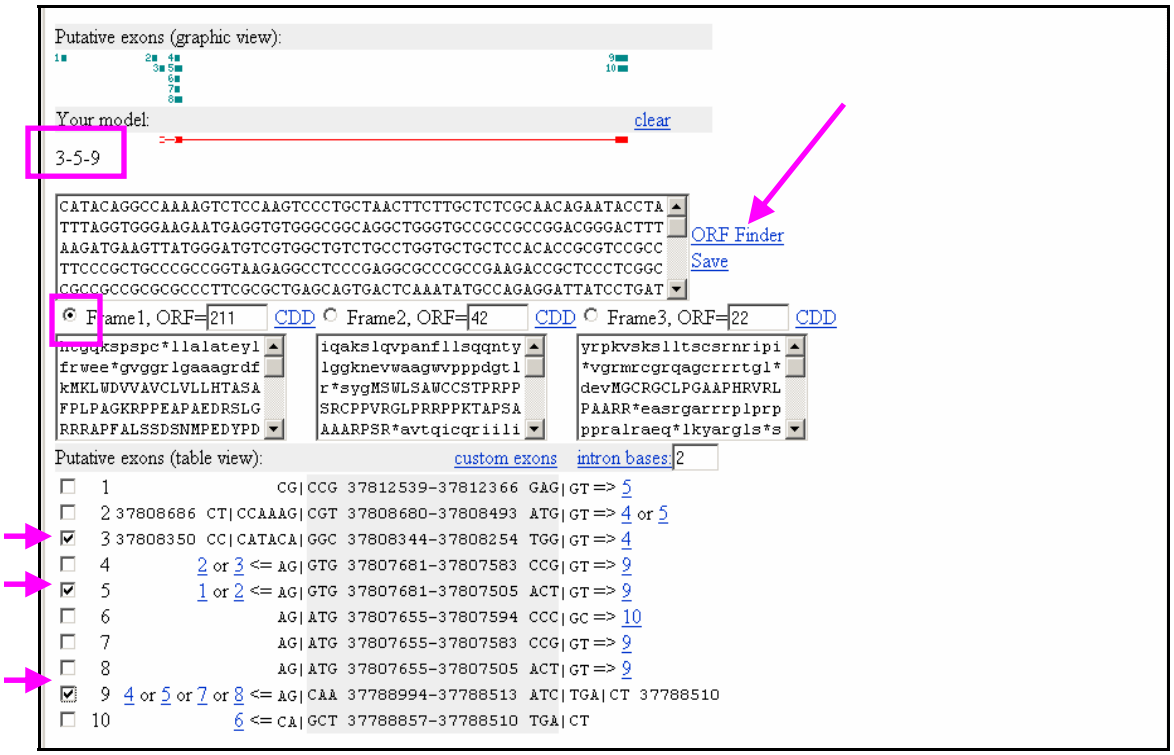
Region Displayed: **37,833,500-37,893,600 bp** Download/View Sequence/Evidence Download Data

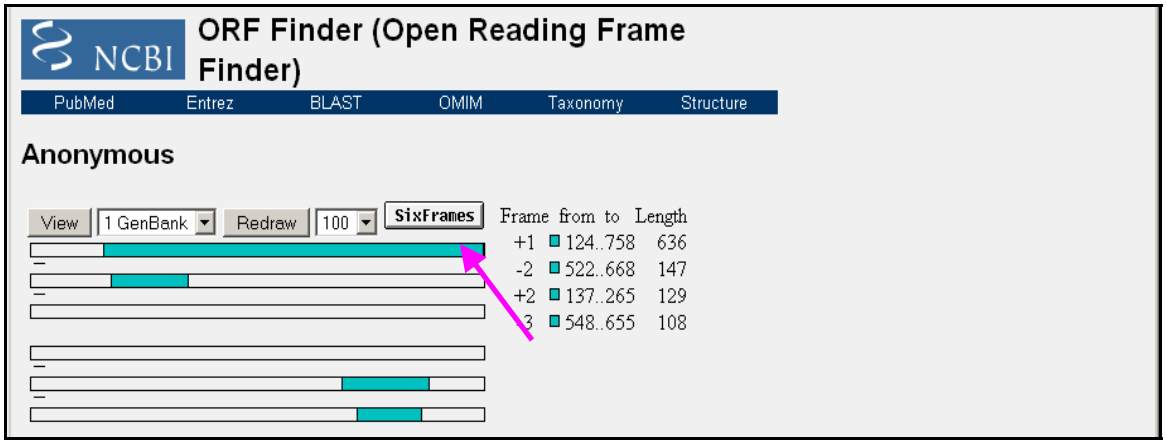
Total RefSeq Transcripts On Chromosome: **1509** [10 not localized]

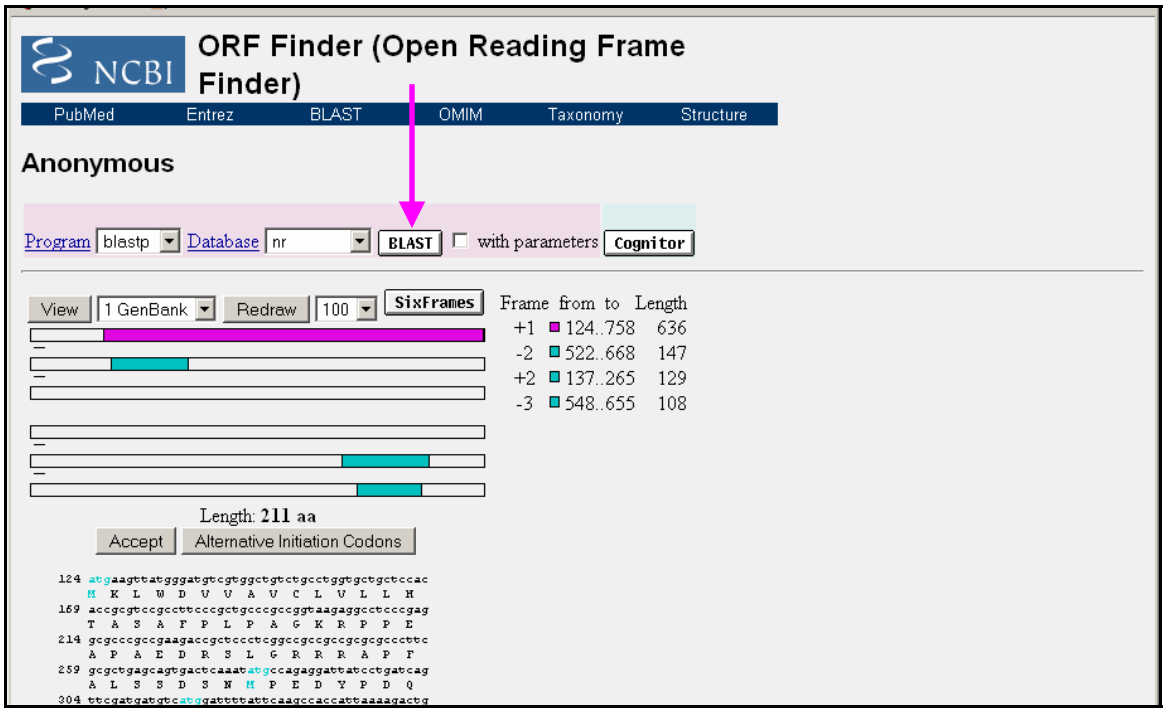
RefSeq Transcripts in Region: **4**

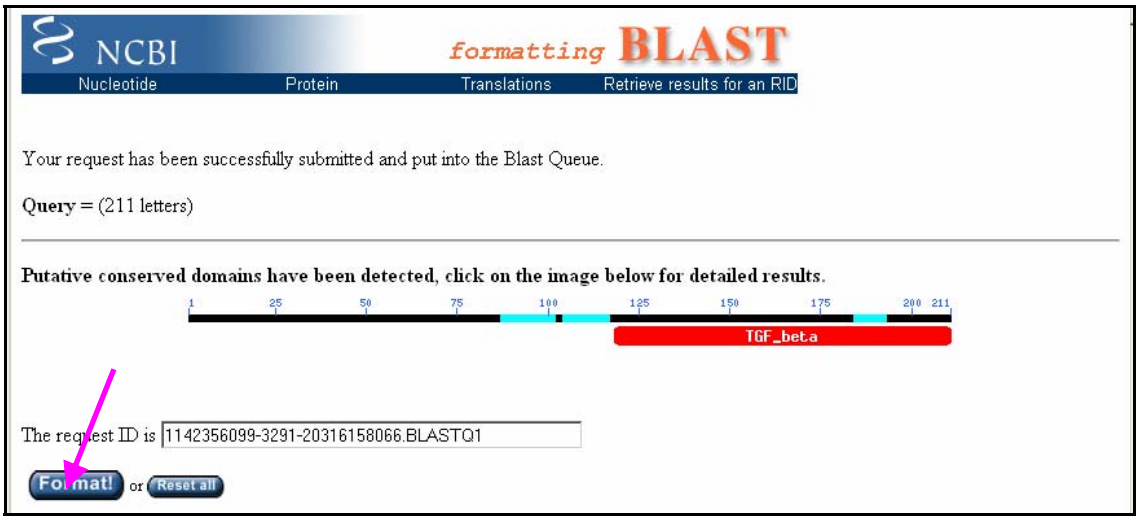

Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
Model
RefSeq RNA
Genes_seq
Symbol
O
Links
E
hmm197456
hmm197690
NM_929687.
LOC646739
sv
dl ev mm
mRNA
hmm105377
hmm105143
NM_199234.
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS
best RefSeq


Model Maker (Make Your Own Model by selecting an evidence exon "set" and/or add/remove individual putative exons for inclusion in your model)
help legend
Organism: Homo sapiens Chromosome: 5 Contig: NT_006576.15 Locus: GDNF
Evidence:
hmm197924
37812539<<<
mv sv ev seq
>>>37788510
minus strand
change strand
expand ESTs
AF053748.1
AJ001897.1
AJ001898.1
AJ001899.1
AY052832.1
BC069119.1
BC069369.1
CR541923.1
NM_000514.2
NM_199231.1
NM_199234.1
hmm104909
hmm105143
hmm105377
NM_000514.2 : 1-5-9
Putative exons (graphic view):
Your model:
clear


Putative exons (graphic view):
Your model:
clear
3-5-9
ORF Finder
Save
Frame1, ORF= 211 CDD
Frame2, ORF= 42 CDD
Frame3, ORF= 22 CDD
Putative exons (table view):
custom exons
intron bases: 2
1 CG|CCG 37812539-37812366 GAG|GT => 5
2 37808686 CT|CCAAAG|CGT 37808680-37808493 ATG|GT => 4 or 5
3 37808350 CC|CATACA|GGC 37808344-37808254 TGG|GT => 4
4 2 or 3 <= AG|GTG 37807681-37807583 CCG|GT => 9
5 1 or 2 <= AG|GTG 37807681-37807505 ACT|GT => 9
6 AG|ATG 37807655-37807594 CCC|GC => 10
7 AG|ATG 37807655-37807583 CCG|GT => 9
8 AG|ATG 37807655-37807505 ACT|GT => 9
9 4 or 5 or 7 or 8 <= AG|CAA 37788994-37788513 ATC|TGA|CT 37788510
10 6 <= CA|GCT 37788857-37788510 TGA|CT


NCBI
ORF Finder (Open Reading Frame Finder)
PubMed Entrez BLAST OMIM Taxonomy Structure
Anonymous
View
1 GenBank
Redraw
100
SixFrames
Frame from to Length
+1 124..758 636
-2 522..668 147
+2 137..265 129
-3 548..655 108


NCBI
ORF Finder (Open Reading Frame Finder)
PubMed
Entrez
BLAST
OMIM
Taxonomy
Structure
Anonymous
Program
blastp
Database
nr
BLAST
with parameters
Cognitor
View
1 GenBank
Redraw
100
SixFrames
Frame from to Length
+1 124..758 636
-2 522..668 147
+2 137..265 129
-3 548..655 108
Length: 211 aa
Accept
Alternative Initiation Codons


NCBI
formatting BLAST
Nucleotide
Protein
Translations
Retrieve results for an RID
Your request has been successfully submitted and put into the Blast Queue.
Query = (211 letters)
Putative conserved domains have been detected, click on the image below for detailed results.
TGF_beta
The request ID is 1142356099-3291-20316158066.BLASTQ1
Format!
or
Reset all

NCBI **results of BLAST**

BLASTP 2.2.14 [May-07-2006]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1149537081-22408-39186213083.BLASTQ1

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples;
All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
excluding environmental samples
7,317,850 sequences; 2,514,302,182 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**
Taxonomy reports

Query=
Length=211

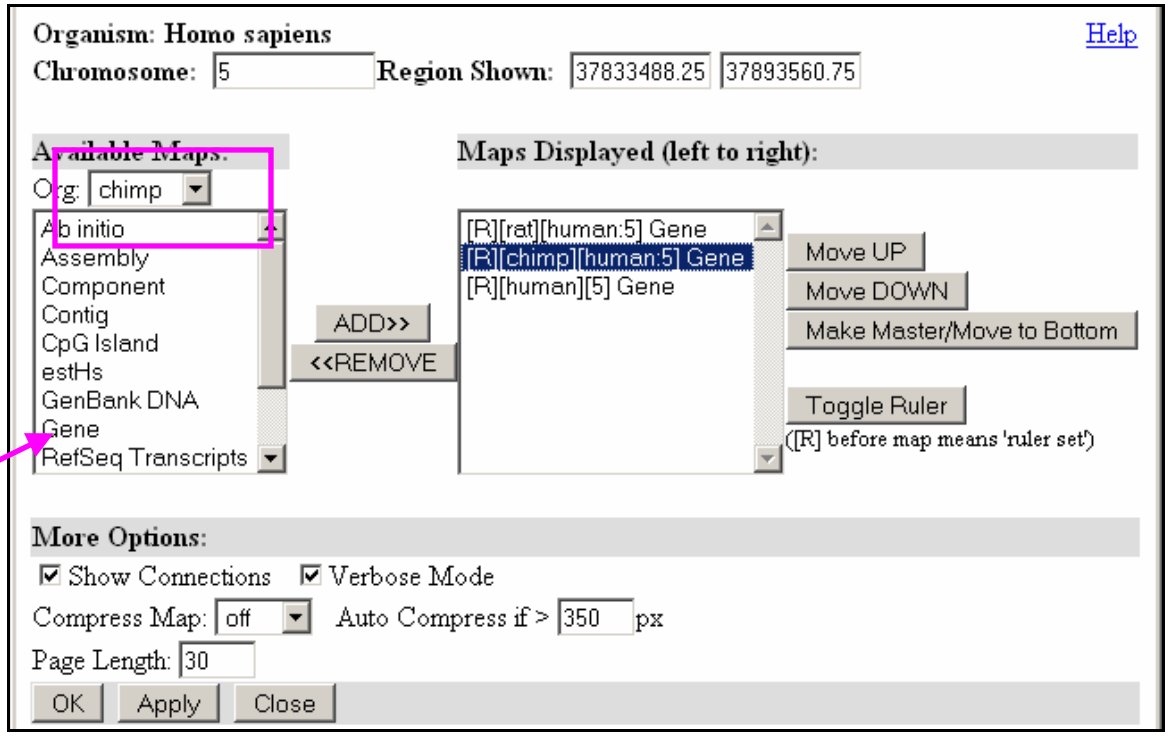
Tree view NEW

Sequences producing significant alignments:	Score (Bits)	E Value
ref|XP_526944.1| PREDICTED: similar to glial cell derived neu...	432	6e-120
gb|AAX36770.1| glial cell derived neurotrophic factor [synthetic	432	6e-120

Alignments

```
>ref|XP_526944.1| PREDICTED: similar to glial cell derived neurotrophic factor
isoform 1 preproprotein; astrocyte-derived trophic factor; glial
cell line derived neurotrophic factor [Pan troglodytes]
 gb|AAH69369.1| Glial cell derived neurotrophic factor, isoform 1 preproprotein
[Homo sapiens]
 gb|AAH69119.1| Glial cell derived neurotrophic factor, isoform 1 preproprotein
[Homo sapiens]
 ref|NP_000505.1| glial cell derived neurotrophic factor isoform 1 preproprotein
[Homo sapiens]
 emb|CAG46721.1| GDNF [Homo sapiens]
 sp|P39905|GDNF_HUMAN Glial cell line-derived neurotrophic factor precursor (Astrocyte-derived
trophic factor 1) (ATF-1)
 gb|AAA67910.1| neurotrophic factor
Length=211

 Score =  432 bits (1112),  Expect = 6e-120
 Identities = 211/211 (100%), Positives = 211/211 (100%), Gaps = 0/211 (0%)

Query  1    MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ  60
           MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ
Sbjct  1    MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ  60

Query  61   FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL  120
           FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL
Sbjct  61   FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL  120

Query  121  TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR  180
           TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR
Sbjct  121  TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR  180

Query  181  PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI  211
           PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI
Sbjct  181  PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI  211
```

```
>gb|AAL11017.1| glial cell-derived neurotrophic factor isoform [Homo sapiens]
 ref|NP_954701.1| glial cell derived neurotrophic factor isoform 2 precursor [Homo
sapiens]
 gb|AAB33493.1| astrocyte-derived trophic factor 1, ATF-1 [human, caudate, Peptide,
185 aa]
Length=185

 Score =  365 bits (938),  Expect = 1e-99
 Identities = 184/211 (87%), Positives = 185/211 (87%), Gaps = 26/211 (12%)

Query  1    MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ  60
            MKLWDVVAVCLVLLHTASAFPLPA                          +NMPEDYPDQ
Sbjct  1    MKLWDVVAVCLVLLHTASAFPLPA--------------------------ANMPEDYPDQ  34

Query  61   FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL  120
            FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL
Sbjct  35   FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL  94

Query  121  TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR  180
            TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR
Sbjct  95   TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR  154

Query  181  PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI  211
            PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI
Sbjct  155  PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI  185
```



Human genome overview page (Build 36.1)
Human genome overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Synteny 1:1
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
default
master

Homo sapiens **Build 36.1 (Current)** BLAST The Human Genome

Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

Query: GDNF [clear]

Master Map: Genes On Sequence (H.sapiens, chr 5) Summary of Maps Maps & Options

Region Displayed: **37,833,500-37,893,600 bp** Download/View Sequence/Evidence

Genes_seq rat segments | Genes_seq chimp segments | Genes_seq H.sapiens, chr 5 | Symbol O Links

LOC646739 sv pr dl ev mm

GDNF OMIM HGNC sv pr dl ev mm hm sts CCD

Organism: Homo sapiens Help

Chromosome: 5 **Region Shown:** 37833488.25 37893560.75

Available Maps:

Org: human

Assembly: reference

GenBank DNA
Gene
NCI Clone
Phenotype
RefSeq Transcripts
Repeats
STS
TCAG Genes
TCAG Transcripts

ADD>>
<<REMOVE

Maps Displayed (left to right):

Change Assembly

[ ] Phenotype
[R] Gene

Move UP
Move DOWN
Make Master/Move to Bottom
Toggle Ruler
([R] before map means 'ruler set')

More Options:

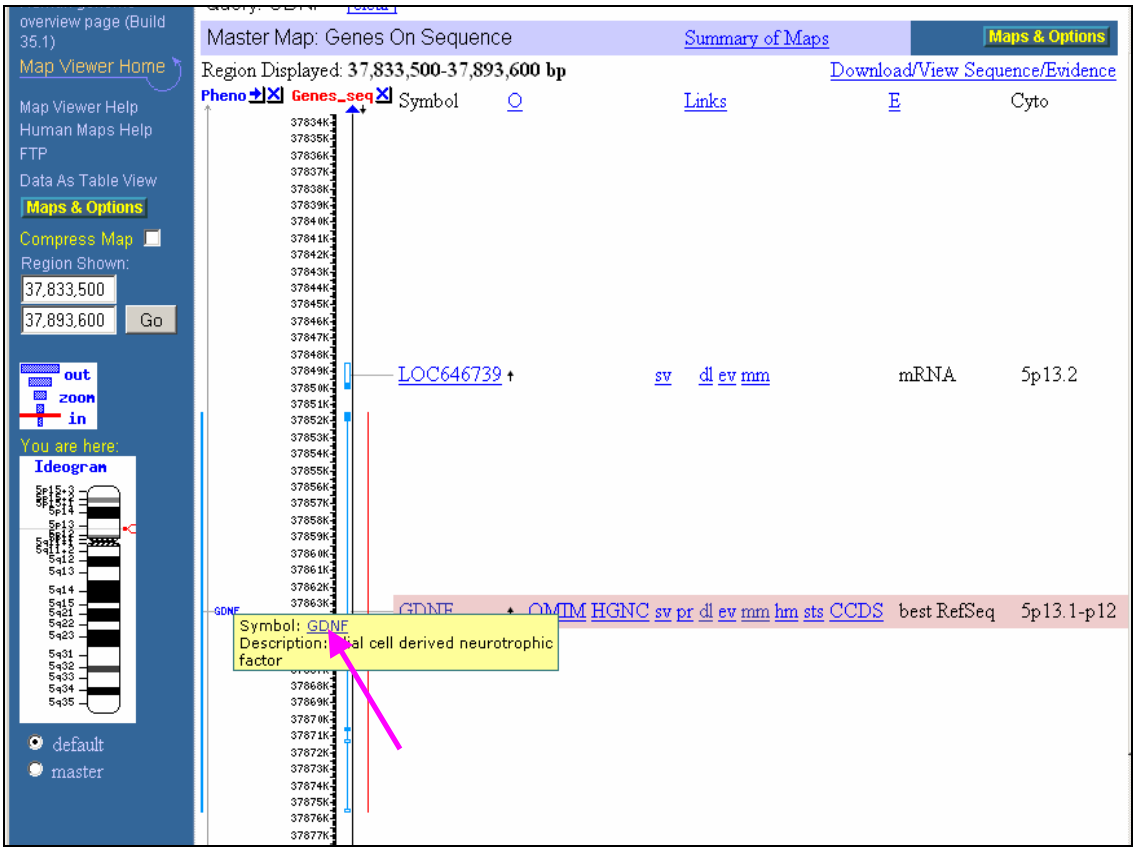
☐ Show Connections ☑ Verbose Mode

Compress Map: off Auto Compress if > 350 px

Page Length: 30

Thumbnail View: default (ideogram) master

OK Apply Close


overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
default
master
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
Pheno
Genes_seq
Symbol
O
Links
E
Cyto
LOC646739
sv
dl ev mm
mRNA
5p13.2
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS
best RefSeq
5p13.1-p12
Symbol: GDNF
Description: al cell derived neurotrophic factor

NCBI
OMIM
Online Mendelian Inheritance in Man
Johns Hopkins University
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
PMC
Taxonomy
OMIM
Search OMIM for
Go
Clear
Limits
Preview/Index
History
Clipboard
Details
Display Detailed
Show 20
Send to
All: 1
MIM *600837
Cloning
Mapping
Gene Function
Molecular Genetics
Animal Model
Allelic Variants
View List
See Also
References
Contributors
Creation Date
Edit History
Gene map
Entrez Gene
Nomenclature
RefSeq
GenBank
Protein
UniGene
LinkOut
HGMD
*600837
GeneTests, Links
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR; GDNF
Gene map locus 5p13.1-p12
TEXT
CLONING
Lin et al. (1993) isolated a specific dopaminergic neurotrophic protein, designated 'glial cell line-derived neurotrophic factor' (GDNF), from a rat B49 glial cell line. The corresponding cDNA was cloned from both human and rat cDNA libraries. The predicted 211-amino acid sequences of the 2 proteins showed 93% homology. The human GDNF precursor is processed to a mature 134-amino acid protein with 2 potential N-linked glycosylation sites; it exists as a homodimer. The mature protein contains 7 conserved cysteine residues spaced similarly to members of the TGF-beta superfamily (see 190180).
MAPPING
Schindelhauer et al. (1995) mapped the GDNF gene to human chromosome 5p13.1-p12 by fluorescence in situ hybridization (FISH). By study of a cell hybrid panel and by FISH, Bermingham et al. (1995) mapped the GDNF

Problem 2

Search for "PRNP" in the Map Viewer. Access the Human Map Viewer page by clicking on Map Viewer and enter PRNP as a search term.

Name the chromosome on which this gene is located. Click on the Genes_seq map link of the map element PRNP in the reference assembly.
What is the map that is displayed? Turn on the ruler line for the map through the Maps & Options link. What are the nucleotide locations for the gene on the chromosome? What is the orientation of the gene on the chromosome?

Download the gene sequence by using the "dl" link. (Change the strand, if necessary). In order to search for promoter elements, you may also download 5000 nucleotides of upstream sequence by adjusting the locations for the upstream 5000 nucleotides.

Add the Clone, Component and Contig maps for this region. Name the contig and GenBank accession numbers for the sequence covering this region. Are the sequences in the finished form? Is there a clone mapped to this region? If so, how can you order it?

Remove all the maps except Genes_seq and add the Ab initio (model) and Transcript (RNA) maps. Does the gene prediction match the current gene annotation? How many alternatively spliced transcripts have been annotated for the gene? Display the current data as "Data As Table View".

Using the Model Maker (mm), obtain a possible alternatively spliced product and its translated amino acid sequence. Search for similar proteins by using BLAST.

Remove all the maps except Genes_seq and add the Gene maps for mouse, chimp and rat. Are the gene structures in the three organisms similar?
Remove all the maps except the human Gene map, and add the phenotype map. Name the disease with which the PRNP gene is associated. Obtain more information about the disease by linking to the corresponding OMIM record.