

## 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>

Course developed by Medha Bhagwat (bhagwat@ncbi.nlm.nih.gov)

## 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](#). Further, access the current human genome assembly by selecting the "*Homo sapiens* (human) Build 36" link. Enter GDNF as a search term and click on the "Find" button. Filter your search result for gene maps by checking the "Gene" box in the "Quick Filter" menu.

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.

The screenshot shows the NCBI Map Viewer interface. At the top, there is a navigation bar with links for Genomic Biology, Genome, Taxonomy, Entrez, BLAST, and Help. Below this is a search bar with a dropdown menu set to "- Select Group or Organism -" and a "Go!" button. A message below the search bar reads: "Click the **B** to BLAST, the **S** to search the group". To the right of this message is a "Switch to List View" button. The main content area displays a taxonomic tree with the following categories and organism counts:

- Mammals: 11 organisms
- Other Vertebrates: 2 organisms
- Fungi: 15 organisms
- Protozoa: 6 organisms
- Invertebrates
  - Insects: 4 organisms
  - Nematoda: 1 organism
  - Echinoderms: 1 organism
- Plants: 34 organisms

At the bottom, there is a link to "See more about Bacteria, Organelles, Viruses".



NCBI Map Viewer

- Locate a human gene
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- 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

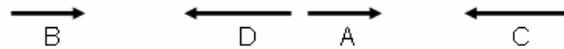
## High Throughput Genomic Sequences

Sequencing of BACs:

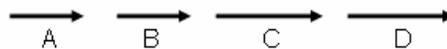
Draft:

Phase 0 – single/few pass reads of a single clone

Phase 1 – unfinished, unordered BACs with gaps



Phase 2 – unfinished, ordered with gaps

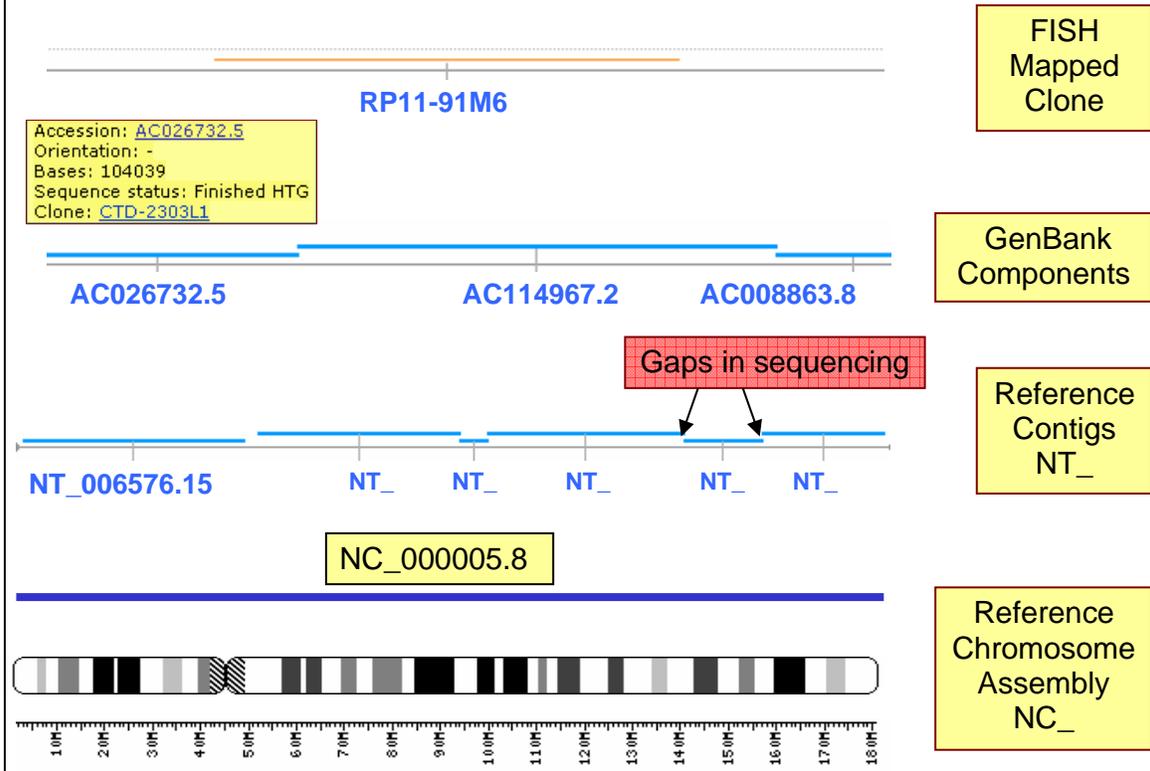


Finished:

Phase 3 – high quality finished sequence with no gaps



# Genome Assembly Accession Numbers



**Vertebrates**

**Mammals**

- [BLAST](#) *Bos taurus* (cow) Build 3.1
- [BLAST](#) *Bos taurus* (cow) Build 2.1
- [BLAST](#) *Canis familiaris* (dog)
- [BLAST](#) *Equus caballus* (domestic horse)
- [BLAST](#) *Felis catus* (cat)
- [BLAST](#) *Homo sapiens* (human) Build 36
- [BLAST](#) *Homo sapiens* (human) Build 35
- [BLAST](#) *Macaca mulatta* (rhesus macaque)
- [BLAST](#) *Monodelphis domestica* (gray short-tailed opossum)
- [BLAST](#) *Mus musculus* (mouse) Build 37
- [BLAST](#) *Mus musculus* (mouse) Build 36
- [BLAST](#) *Ornithorhynchus anatinus* (platypus)
- [BLAST](#) *Ovis aries* (sheep)
- [BLAST](#) *Pan troglodytes* (chimpanzee)
- [BLAST](#) *Rattus norvegicus* (rat)
- [BLAST](#) *Sus scrofa* (pig)

**Other Vertebrates**

- [BLAST](#) *Danio rerio* (zebrafish)
- [BLAST](#) *Gallus gallus* (chicken)

**Invertebrates**

**Insects**

- [BLAST](#) *Anopheles gambiae* (mosquito)
- [BLAST](#) *Apis mellifera* (honey bee) Amel\_4.0
- [BLAST](#) *Apis mellifera* (honey bee) Amel\_3.0

**Metazoa**

- [BLAST](#) *Amoeba proteus*
- [BLAST](#) *Dictyostelium discoideum*
- [BLAST](#) *Paramecium tetraurelia*
- [BLAST](#) *Trichoplax adhaesiva*

**Eukaryotes**

- [BLAST](#) *Arabidopsis thaliana*
- [BLAST](#) *Candida albicans*
- [BLAST](#) *Drosophila melanogaster*
- [BLAST](#) *Escherichia coli*
- [BLAST](#) *Homo sapiens*
- [BLAST](#) *Mus musculus*
- [BLAST](#) *Rattus norvegicus*
- [BLAST](#) *Saccharomyces cerevisiae*
- [BLAST](#) *Sus scrofa*
- [BLAST](#) *Xenopus laevis*



Search results for query "GDNF AND gene[obj\_type]": 14 hits

Chr	Assembly	Match	Map element	Type	Maps
5	reference	<a href="#">all matches</a>			
		glial cell line-derived neurotrophic factor receptor alpha-3	<a href="#">GFRA3</a>	Gene	<a href="#">Genes cyto</a>   <a href="#">Genes seq</a>
		GDNF : glial derived neurotrophic factor	<a href="#">GDNF</a>	Gene	<a href="#">Genes cyto</a>   <a href="#">Genes seq</a>
5	Celera	GDNF : ENSG00000168621	<a href="#">GDNF</a>	GENE	<a href="#">ensGenes</a>
5	reference	<a href="#">all matches</a>			
		glial cell line-derived neurotrophic factor receptor alpha-3	<a href="#">GFRA3</a>	GENE	<a href="#">Genes seq</a>
		GDNF : glial derived neurotrophic factor	<a href="#">GDNF</a>	GENE	<a href="#">Genes seq</a>
6	reference	IVFI9356	<a href="#">GFRAL</a>	Gene	<a href="#">Genes cyto</a>   <a href="#">Genes seq</a>
6	Celera	IVFI9356	<a href="#">GFRAL</a>	GENE	<a href="#">Genes seq</a>
8	reference	<a href="#">all matches</a>			
		similar to GDNF family receptor alpha 2	<a href="#">LOC727724</a>	Gene	<a href="#">Genes cyto</a>   <a href="#">Genes seq</a>
		neurturin receptor alpha	<a href="#">GFRA2</a>	Gene	<a href="#">Genes cyto</a>   <a href="#">Genes seq</a>
8	Celera	neurturin receptor alpha	<a href="#">GFRA2</a>	GENE	<a href="#">Genes seq</a>
10	reference	TGF-beta related neurotrophic factor receptor 1	<a href="#">GFRA1</a>	Gene	<a href="#">Genes cyto</a>   <a href="#">Genes seq</a>
10	Celera	TGF-beta related neurotrophic factor receptor 1	<a href="#">GFRA1</a>	GENE	<a href="#">Genes seq</a>
20	reference	persephin receptor	<a href="#">GFRA4</a>	Gene	<a href="#">Genes cyto</a>   <a href="#">Genes seq</a>
	Celera	persephin receptor	<a href="#">GFRA4</a>	GENE	<a href="#">Genes seq</a>

NCBI  **NCBI Map Viewer**

PubMed Entrez BLAST OMM Taxonomy Structure

Search  Find Find in This View Advanced Search

**Homo sapiens Build 36.2 (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	Symbol	Links	E	Cyto	Description
<a href="#">GDNF</a>	<a href="#">OMIM</a> <a href="#">HGNC</a> <a href="#">sv</a> <a href="#">pr</a> <a href="#">dl</a> <a href="#">ev</a> <a href="#">nm</a> <a href="#">hm</a> <a href="#">stg</a> <a href="#">CCDS</a> <a href="#">SNP</a>	<a href="#">best RefSeq</a>	5p13.1-p12	glial cell derived neurotrophic factor	

default  
 master

**Organism: Homo sapiens** [Help](#)

**Chromosome:** 5 **Region Shown:** 37833488.2E 37893560.7E

**Available Maps:** Org: human Assembly: ref Change Assembly

- Sequence Maps-
- Ab initio
- Assembly
- Repeats
- BES\_Clone
- Clone
- NCL\_Clone
- Contig
- Component

**Maps Displayed (left to right):** [ ] Gene

ADD>> <<REMOVE

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 36.2) [BLAST The Human Genome](#)

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: 37,833K 37,894K Go

out zoom in

You are here:

**Homo sapiens Build 36.2 (Current)**

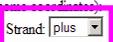
Chromosome: 1 2 3 4 [ 5 ] 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

Query: GDNF[gene name] [clear]

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

Region Displayed: 37,833K-37,894K bp [Download/View Sequence/Evidence](#)

Genes_seq	Symbol	Links	E	Cyto	Description
	GDNF	†	OMIMHGNC sv pr di ev mm hm sts CCDS SNP	best RefSeq	5p13.1-p12 glial cell derived neurotrophic factor

*Homo sapiens* (Build 36.2)  
 Region to retrieve (in chromosome coordinates):  
 Chromosome:  Strand:    
 from:  adjust by:   
 to:  adjust by:   

Sequence Format:

---

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](#)

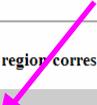
*Homo sapiens* (Build 36.2)  
 Region to retrieve (in chromosome coordinates):  
 Chromosome:  Strand:   
 from:  adjust by:   
 to:  adjust by:

Sequence Format:

---

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](#)

http://www.ncbi.nlm.nih.gov - Map Viewer - Mozilla Firefox

Organism: **Homo sapiens** [Help](#)

Chromosome:  Region Shown:

**Available Maps:**

Org:  Assembly:

- Sequence Maps—
- Ab initio
- Assembly
- BES Clone
- Clone
- Component
- Contig**
- CpG Island
- Ensembl Genes

**Maps Displayed (left to right):**

[R] Gene

([R] before map means 'ruler set')

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**More Options:**

Show Connections  Verbose Mode

Compress Map:  Auto Compress if >  px

Page Length:

Thumbnail View:  default (ideogram)  master

Human genome overview page (Build 36.2) | [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: 37,833K - 37,894K |  |  |  |  | You are here: **Ideogram** |  default |  master

**Homo sapiens Build 36.2 (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 AND gene[obj\_type] |

Master Map: Genes On Sequence | [Summary of Maps](#) | **Maps & Options**

Region Displayed: 37,833K-37,894K bp | [Download/View Sequence/Evidence](#)

[Clone](#) | [Comp](#) | [Contig](#) | [Genes\\_seq](#) | Symbol | [Links](#) | [E](#) | Cyto | Description

CTC-269D19

AC068869.5

NT\_046576

GDNF + OMIMHGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq 5p13.1-p12 glial cell d

NCBI | **NCBI Map Viewer**

PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure

|  |  |

Human genome overview page (Build 36.2) | [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: 37,833K - 37,894K |  |  |  |  | You are here: **Ideogram** |  default |  master

**Homo sapiens Build 36.2 (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 AND gene[obj\_type] |

Master Map: Genes On Sequence | [Summary of Maps](#) | **Maps & Options**

Region Displayed: 37,833K-37,894K bp | [Download/View Sequence/Evidence](#)

[Clone](#) | [Comp](#) | [Contig](#) | [Genes\\_seq](#) | Symbol | [Links](#) | [E](#) | Cyto | Description

CTC-269D19

AC068869.5

NT\_046576

GDNF + OMIMHGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq 5p13.1-p12 glial cell d

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


CGCTCAGGATAGAGACTTCGGCGCTAGAGGATCGGATCCCGGCATATATTATATAGCTCGATCGATC  
TTCTTTATATATTTCGGCGCGATGGGGGGTATATACACACACACACGGCGCGGATAGCATGACTGATCT  
CTCTTCGCATACGCTCTCGCATGCGATGGCGTAGAGAGACGGCT  
CTACTTATTAATTAATTCGGCGCGATGGGGCGATTCGGCGCGAT

[PubMed](#)   [Entrez](#)   [BLAST](#)   [OMIM](#)   [Taxonomy](#)   [Structure](#)

Search  for

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**

<b>Name:</b> CalTech human BAC library C	
<b>Organism:</b> Homo sapiens	<b>Type:</b> BAC
<b>Approved:</b> No	<b>Sex:</b> Male
<b>Source:</b> sperm	<b>Rsite:</b> HindIII

**Distributor Information**

Available from clone library

<b>Name:</b> Research Genetics
<b>Email:</b> <a href="mailto:libraries@resgen.com">libraries@resgen.com</a>
<b>Web:</b> <a href="http://www.resgen.com/resources/index.php3">http://www.resgen.com/resources/index.php3</a>

Available as part of clone set HBRC\_1.resgen

<b>Name:</b> Research Genetics
<b>Email:</b> <a href="mailto:libraries@resgen.com">libraries@resgen.com</a>
<b>Web:</b> <a href="http://www.resgen.com/resources/index.php3">http://www.resgen.com/resources/index.php3</a>

http://www.ncbi.nlm.nih.gov - Map Viewer - Mozilla Firefox

Organism: **Homo sapiens** [Help](#)

Chromosome:  Region Shown:

**Available Maps:**      **Maps Displayed (left to right):**

Org:  Assembly:

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

Ab initio  
 RefSeq Transcripts  
 Gene

([R] before map means 'ruler set')

**More Options:**

Show Connections     Verbose Mode

Compress Map:  Auto Compress if >  px

Page Length:

Thumbnail View:  default (ideogram)     master

Human genome overview page (Build 36.2) [BLAST The Human Genome](#)

[Homo sapiens Build 36.2 \(Current\)](#)

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 AND gene[obj\_type]**

**Master Map: Genes On Sequence**      [Summary of Maps](#)      [Maps & Options](#)

Region Displayed: 37,833K-37,894K bp

Model  RefSeq  RNO  Genes\_seq  Symbol  Links  E  Cyto  Description

37835K  
37840K  
37845K  
37850K  
37855K  
37860K  
37865K  
37870K  
37875K

[hene142934](#)  
[hene09293](#)  
[hene09527](#)  
[NH\\_199234](#)  
[hene09761](#)  
[hene09995](#)  
[NH\\_199231](#)  
[NH\\_000514](#)  
[hene143166](#)

**GDNF** + [OMIM](#) [HGNC](#) [sv](#) [pr](#) [dl](#) [ev](#) [mm](#) [hm](#) [sts](#) [CCDS](#) [SNP](#) best RefSeq 5p13.1-p12 glial cell deriv

**Map Viewer Home**

Map Viewer Help  
Human Maps Help  
FTP  
Data As Table View  
[Maps & Options](#)  
Compress Map   
Region Shown:

**You are here:**  
**Ideogram**

default  
 master

**Homo sapiens Build 36.2 (Current)** [BLAST The Human Genome](#)

Data As Table View [Download All 1](#)

---

**Genes On Sequence** [All Sequence Maps](#) [next](#)

Region Displayed: 37,833K-37,894K bp [Download/View Sequence/Evidence](#) [Download Data](#)

Total Genes On Chromosome: 1268 [\[3 not localized\]](#)

Genes in Region: 1

start	stop	Symbol	Links	E	Cyto	Description
37851510	37875539	<a href="#">GDNF</a>	- <a href="#">OMIMHGNC</a> <a href="#">svpr</a> <a href="#">dl</a> <a href="#">ev</a> <a href="#">mm</a> <a href="#">hm</a> <a href="#">sts</a> <a href="#">CCDS</a> <a href="#">SNP</a>			best RefSeq 5p13.1-p12 glial cell derived neurotrophic factor

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**Ab initio models** [All Sequence Maps](#) [prev](#) [next](#)

Region Displayed: 37,833K-37,894K bp [Download/View Sequence/Evidence](#) [Download Data](#)

Total models On Chromosome: 5351 [\[7 not localized\]](#)

models in Region: 6

start	stop	Symbol	Best hit	Best hit description
37841490	37848120	<a href="#">hmm142934</a>	-	
37851510	37871686	<a href="#">hmm99761</a>	- <a href="#">NP_000505.1</a>	glial cell derived neurotrophic factor isoform 1 preproprotein [Homo sapiens]
37851510	37871350	<a href="#">hmm99527</a>	- <a href="#">NP_954701.1</a>	glial cell derived neurotrophic factor isoform 2 precursor [Homo sapiens]
37851510	37875539	<a href="#">hmm99995</a>	- <a href="#">NP_000505.1</a>	glial cell derived neurotrophic factor isoform 1 preproprotein [Homo sapiens]
37851510	37871686	<a href="#">hmm99293</a>	- <a href="#">NP_954701.1</a>	glial cell derived neurotrophic factor isoform 2 precursor [Homo sapiens]
37872457	37878200	<a href="#">hmm143168</a>	+ <a href="#">BAA20782.3</a>	KIAA0324 protein [Homo sapiens]

---

**RefSeq Transcripts On Sequence** [All Sequence Maps](#) [prev](#)

Region Displayed: 37,833K-37,894K bp [Download/View Sequence/Evidence](#) [Download Data](#)

Total RefSeq Transcripts On Chromosome: 1468 [\[3 not localized\]](#)

RefSeq Transcripts in Region: 3

start	stop	Accession	Locus	Links	Align quality	Description
37851510	37875539	<a href="#">NM_000514.2</a>	<a href="#">GDNF</a>	- <a href="#">ug</a> <a href="#">svpr</a> <a href="#">ev</a> <a href="#">BLink</a> <a href="#">CCDS</a>	identical	glial cell derived neurotrophic factor
37851510	37851994	exon	-	-	CDS	485 bp
37851995	37870504	intron	-	-	-	18510 bp
37870505	37870655	exon	-	-	CDS	151 bp
37870656	37870681	exon	-	-	UTR	26 bp
37870682	37875365	intron	-	-	-	4684 bp
37875366	37875539	exon	-	-	UTR	174 bp
37851510	37871350	<a href="#">NM_199231.1</a>	<a href="#">GDNF</a>	- <a href="#">ug</a> <a href="#">svpr</a> <a href="#">ev</a> <a href="#">BLink</a> <a href="#">CCDS</a>	identical	glial cell derived neurotrophic factor

**Homo sapiens Build 36.2 (Current)** [BLAST The Human Genome](#)

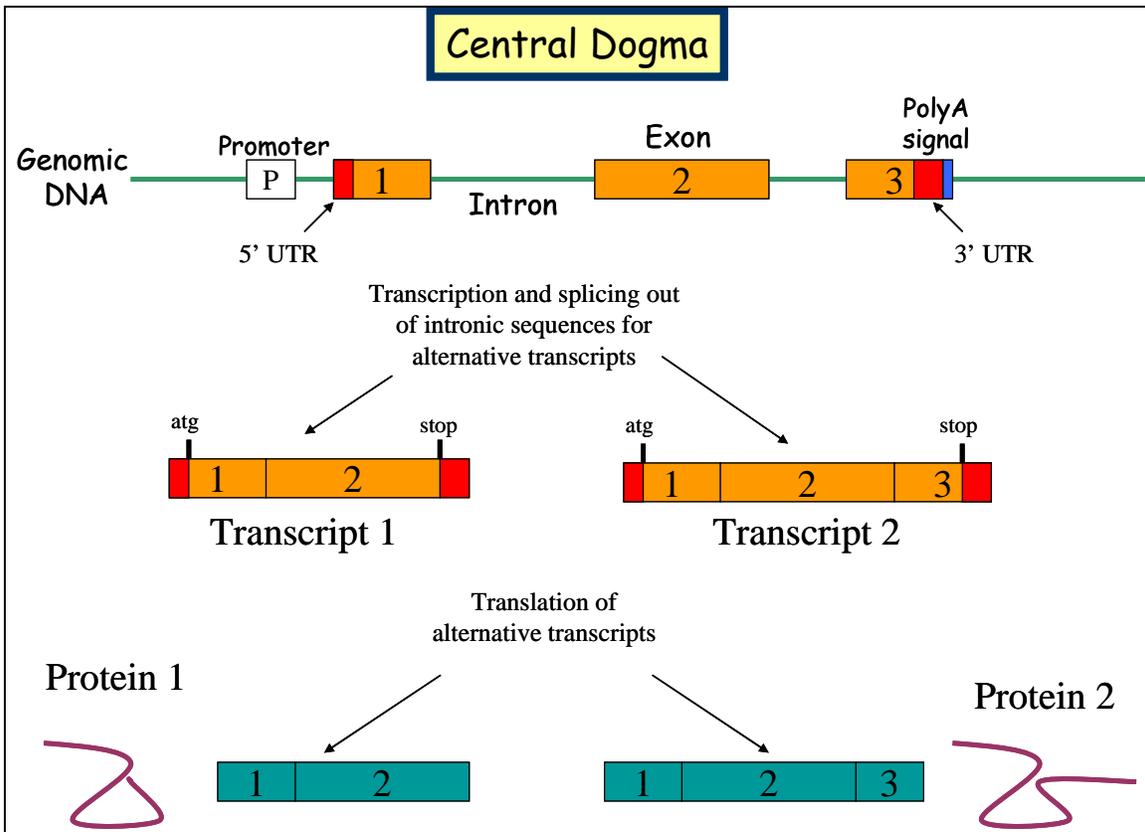
Chromosome: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) [20](#) [21](#) [22](#) [X](#) [Y](#) [MT](#)

Query: [GDNF](#) AND [gene\[obj\\_type\]](#) [\[clear\]](#)

**Master Map: Genes On Sequence** [Summary of Maps](#) [Maps & Options](#)

Region Displayed: 37,833K-37,894K bp [Download/View Sequence/Evidence](#)

Model	RefSeq	RNM	Genes_seq	Symbol	Links	E	Cyto	Description
								<a href="#">GDNF</a> + <a href="#">OMIMHGNC</a> <a href="#">svpr</a> <a href="#">dl</a> <a href="#">ev</a> <a href="#">mm</a> <a href="#">hm</a> <a href="#">sts</a> <a href="#">CCDS</a> <a href="#">SNP</a> best RefSeq 5p13.1-p12 glial cell der



**Model Maker** (Make Your Own Model by selecting an evidence [help](#) [legend](#)  
 exon "set" and/or add/remove individual putative exons for inclusion  
 in your model)

Organism: Homo sapiens (Build 36.2) Chromosome: 5 Contig: [NT\\_006576.15](#) Locus: [GDNF](#)

Evidence:

3' ← 37812539 <<< [mv sv ev seq](#) >>> 37788510 ← 5' [1mm143168](#)

5' → minus strand → 3' change strand

expand ESTs

AF053748.1	hits	CDD
AJ001897.1	hits	CDD
AJ001898.1	hits	CDD
AJ001899.1	hits	CDD
AY052832.1	hits	CDD
BC069119.1	hits	CDD
BC069369.1	hits	CDD
CR541923.1	hits	CDD
DQ235474.1	hits	
NM_000514.2	hits	CDD
NM_199231.1	hits	CDD
NM_199234.1	hits	CDD
1mm09761	hits	
1mm09527	hits	
1mm09995	hits	
1mm09293	hits	
1mm000514.2	hits	
NM_000514.2 : 1-5-10	hits	
NM_199234.1	hits	

Putative exons (graphic view):

Putative exons (graphic view):

Your model:  [clear](#)

**3-5-10**

CATACAGGCCAAAAGTCTCCAAGTCCCTGCTAACTTCTTGTCTCGCAACAGAATACCTA  
 TTTAGGTGGGAAGAATGAGGTGTGGGCGGCAGGCTGGGTGCCGCGCGGACGGGACTTT  
 AAGATGAAGTTATGGGATGTCTGGCTGTCTGCCTGGTGTCTCCACACCGCGTCCGGC  
 TTCGGCTCCCGCGGCTAAGAGGCTCCCGAGGCGCCGCGGAAGACCGCTCCCTCGGC

[ORF Finder](#) [Save](#)

Frame1, ORF= [CDD](#)
 Frame2, ORF= [CDD](#)
 Frame3, ORF= [CDD](#)

Putative exons (table view): [custom exons](#) [intron bases:](#)

Exon	Start	End	Start Codon	Stop Codon	Length
<input type="checkbox"/> 1	CG CCG	37812539-37812366	GAG GT =>	<a href="#">5</a>	
<input type="checkbox"/> 2	CT CCA	37808686-37808493	ATG GT =>	<a href="#">4 or 5</a>	
<input checked="" type="checkbox"/> 3	CC CAT	37808350-37808254	TGG GT =>	<a href="#">4</a>	
<input type="checkbox"/> 4	<a href="#">2 or 3</a> <= AG GTG	37807681-37807583	CCG GT =>	<a href="#">10</a>	
<input checked="" type="checkbox"/> 5	<a href="#">1 or 2</a> <= AG GTG	37807681-37807505	ACT GT =>	<a href="#">10</a>	
<input type="checkbox"/> 6	AG ATG	37807655-37807594	CCC GC =>	<a href="#">11</a>	
<input type="checkbox"/> 7	AG ATG	37807655-37807583	CCG GT =>	<a href="#">9 or 10</a>	
<input type="checkbox"/> 8	AG ATG	37807655-37807505	ACT GT =>	<a href="#">10</a>	
<input type="checkbox"/> 9	<a href="#">7</a> <= AG GGC	37796948-37796869	GAG GT =>	<a href="#">10</a>	
<input checked="" type="checkbox"/> 10	<a href="#">4 or 5 or 7 or 8 or 9</a> <= AG CAA	37788994-37788513	ATC TGA CT	37788510	

**ORF Finder (Open Reading Frame Finder)**

PubMed Entrez BLAST OMIM Taxonomy Structure

Anonymous

View     Frame from to Length

Frame	Start	End	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** OMLM Taxonomy Structure

Anonymous

Program  Database  **BLAST**  with parameters

View  Redraw  **SixFrames** Frame from to Length

Frame	from	to	Length
+1	124..758	636	
-2	522..668	147	
+2	137..265	129	
-3	548..655	108	

Length: 211 aa

```

124 atgaaagtatgggatgtcgtggctgtcgtcgtggtgctccac
M K L W D V V A V C L V L L H
169 accgcgtccgcttcccgctgccgcggtaagaggctcccgag
T A S A F P L P A G K R P P E
214 ggcgcccgaaagaccgctccctggcgcgcgcgcgccttc
A P A E D R S L G R R R A P F
259 gcgtgagcagtgactcaaatatgccagaggattatcctgatcag
A L S S D S N H P E D Y P D Q
304 ttcgatgatgtcattgattttattcaagccaccattaaaagactg
  
```

**BLAST** My NCBI [Sign In] [Register]

Home Recent Results Saved Strategies Help Basic Local Alignment Search Tool

NCBI/BLAST/Format Request

Query Protein sequence(211 letters)

Database nr

Job title Protein sequence(211 letters)

Request ID    Show results in a new window

Format

Show  as   Advanced View

Alignment View

Display  Graphical Overview  Linkout  Sequence Retrieval  NCBI-gi

Masking Character:  Masking Color:

Limit results Descriptions:  Graphical overview:  Alignments:

Entrez query:

Organism  Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.

Expect Min:  Expect Max:

Format for  PSI-BLAST with inclusion threshold:

BLASTP 2.2.16 [Mar-25-2007]

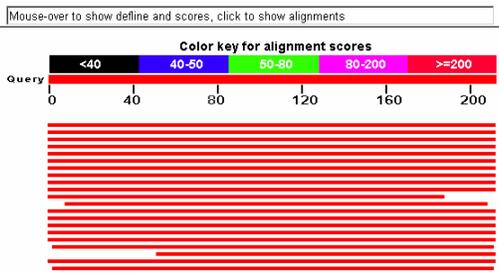
**Reference:**  
 Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,  
 Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman  
 (1990), "Gapped BLAST and PSI-BLAST: a new generation of  
 protein database search programs", *Nucleic Acids Res.* 18:3399-3402.  
 PMID: 3333333

**Database:** All non-redundant GenBank CDS  
 translations+DB+SwissProt+PIR+TrEMBL excluding environmental samples  
 from WGS projects  
 4,900,652 sequences; 1,692,193,060 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

[Distribution of 100 Blast Hits on the Query Sequence](#)



**Alignments**

>[ref|XP\\_001143054.1](#) PREDICTED: similar to neurotrophic factor isoform 3 [Pan troglodytes]  
[gb|EAW55964.1](#) glial cell derived neurotrophic factor, isoform CRA\_b [Homo sapiens]  
 Length=228

Score = 432 bits (1112), Expect = 4e-120  
 Identities = 211/211 (100%), Positives = 211/211 (100%), Gaps = 0/211 (0%)

```

Query 1  MKLWDVVAVCLVLLHTASAFPLPAGKRPEEAPAE DRSLGRRRAPFALSSDSNMPEDYPDQ 60
          MKLWDVVAVCLVLLHTASAFPLPAGKRPEEAPAE DRSLGRRRAPFALSSDSNMPEDYPDQ
Sbjct 18  MKLWDVVAVCLVLLHTASAFPLPAGKRPEEAPAE DRSLGRRRAPFALSSDSNMPEDYPDQ 77

Query 61  FDDVMDFIQATIKRLK RSPDKQMAVLP RRERNRQAAAA NPENSRGKGRRGQRGKNRGCVL 120
          FDDVMDFIQATIKRLK RSPDKQMAVLP RRERNRQAAAA NPENSRGKGRRGQRGKNRGCVL
Sbjct 78  FDDVMDFIQATIKRLK RSPDKQMAVLP RRERNRQAAAA NPENSRGKGRRGQRGKNRGCVL 137

Query 121 TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRLVSDKVGQACCR 180
          TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRLVSDKVGQACCR
Sbjct 138 TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRLVSDKVGQACCR 197

Query 181 PIAFDDDSLFLDDNLVYHILRKHS AKRCGCI 211
          PIAFDDDSLFLDDNLVYHILRKHS AKRCGCI
Sbjct 198 PIAFDDDSLFLDDNLVYHILRKHS AKRCGCI 228
    
```

```

>gb|AAX36770.1| glial cell derived neurotrophic factor [synthetic construct]
Length=212

Score = 432 bits (1112), Expect = 7e-120
Identities = 211/211 (100%), Positives = 211/211 (100%), Gaps = 0/211 (0%)

Query 1 MKLWDVVAVCLVLLHTASAFPLPAGKRPPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ 60
        MKLWDVVAVCLVLLHTASAFPLPAGKRPPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ
Sbjct 1 MKLWDVVAVCLVLLHTASAFPLPAGKRPPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ 60

Query 61 FDDVMDFIQATIKRLKRS PDKQMAVLP RRERNRQAAAANPENS RGKRRGQRGKNRGCVL 120
        FDDVMDFIQATIKRLKRS PDKQMAVLP RRERNRQAAAANPENS RGKRRGQRGKNRGCVL
Sbjct 61 FDDVMDFIQATIKRLKRS PDKQMAVLP RRERNRQAAAANPENS RGKRRGQRGKNRGCVL 120

Query 121 TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR 180
        TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR
Sbjct 121 TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR 180

Query 181 PIAFDDDL SFLDDNLVYHILRKHS AKRCGCI 211
        PIAFDDDL SFLDDNLVYHILRKHS AKRCGCI
Sbjct 181 PIAFDDDL SFLDDNLVYHILRKHS AKRCGCI 211

>ref|NP_000505.1| glial cell derived neurotrophic factor isoform 1 preproprotein
[Homo sapiens]
ref|XP_526944.1| PREDICTED: glial cell derived neurotrophic factor isoform 4 [Pan
troglodytes]

```

Organism: **Homo sapiens** [Help](#)

Chromosome:  Region Shown:

Available Maps: Maps Displayed (left to right):

Org:

- Ab initio
- Assembly
- BES Clone
- Component
- Contig
- CpG Island
- GenBank DNA
- Gene**
- Phenotype

([R] before map means 'ruler set')

**More Options:**

Show Connections  Verbose Mode

Compress Map:  Auto Compress if >  px

Page Length:

Thumbnail View:  default (ideogram)  master

NCBI  NCBI Map Viewer

PubMed Entrez BLAST OMM Taxonomy Structure

Search  Find Find in This View Advanced Search

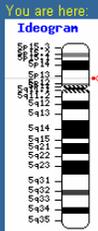
Human genome overview page (Build 36.2) [BLAST The Human Genome](#)

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:   Go

out  zoom  in

You are here:  Ideogram

default  master

**Homo sapiens Build 36.2 (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 AND gene[obj\_type] [\[clear\]](#)

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

Region Displayed: 37,833K-37,894K bp [Download/View Sequence/Evidence](#)

Genes\_seq chImp segments mouse segments rat segments H.sapiens chr 5 Symbol [Links](#)

46595K 46600K 46605K 46610K 46615K 46620K 46625K 46630K 46635K

7730K 7735K 7740K 7745K 7750K 7755K 7760K 7765K 7770K 7775K 7780K 7785K 7790K

57430K 57435K 57440K 57445K 57450K 57455K 57460K 57465K 57470K 57475K 57480K 57485K 57490K 57495K 57500K

37835K 37840K 37845K 37850K 37855K 37860K 37865K 37870K 37875K

GDNF + OMIM HGNC sv pr dl ev mm hm sts CCDS SNP b

Organism: **Homo sapiens** [Help](#)

Chromosome:  Region Shown:

Available Maps: Org:  Assembly:  [Change Assembly](#)

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

[ADD>>](#)  
[<<REMOVE](#)

[ ] 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:  Auto Compress if >  px  
Page Length:   
Thumbnail View:  default (ideogram)  master

[OK](#) [Apply](#) [Close](#)



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 OMIM dbSNP: 0 OMIM UniSTS: 0

**\*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 gene to 5p13.3-p13.1.

**GENE FUNCTION**

[Lin et al. \(1993\)](#) found that recombinant human GDNF specifically promoted the survival and differentiation of dopaminergic neurons in rat embryonic midbrain cell cultures. GDNF also enhanced high-affinity uptake of dopamine in these cells. No effect of GDNF was seen on GABAergic or serotonergic neurons or astrocytes. [Schaar et al. \(1993\)](#) identified Gdnf transcripts in the substantia nigra and in type 1 astrocytes of rat basal forebrain. Recombinant GDNF promoted the survival and differentiation of dopaminergic neurons in embryonic midbrain cultures and promoted their uptake of dopamine. 🗨

[Oppenheim et al. \(1995\)](#) showed that recombinant human GDNF could rescue avian motor neurons from programmed cell death. In vivo, GDNF rescued avian and murine spinal motor neurons from death caused by axotomy. [Beck et al. \(1995\)](#) used GDNF to prevent loss of tyrosine hydroxylase (TH, [191290](#))-expressing neurons in the substantia nigra of adult rat brains after transfection of their axons within the medial forebrain bundle. [Tomac et al. \(1995\)](#) showed that GDNF injected over the substantia nigra or in the striatum of mice could protect cells from the effects of the neurotoxin MPTP in vivo, suggesting a possible use in the treatment

## Problem 2

Search for "PRNP" in the Map Viewer. Access the Human Map Viewer page by clicking on [Map Viewer](#). Further, access the current human genome assembly by selecting the "*Homo sapiens* (human) Build 36" link. Enter PRNP as a search term and click on the "Find" button. Filter your search result for gene maps by checking the "Gene" box in the "Quick Filter" menu.

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.