NCBI Map Viewer Tutorial

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 these exercises, 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 and rat homologs
- Obtain phenotype information

The first exercise includes screenshots of the suggested steps as well as a few introductory slides.

Exercise 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 the Map Viewer link in the footer of the NCBI home page, then selecting the "*Homo sapiens* (human) Build 37.1" 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 RefSeq Transcripts 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".

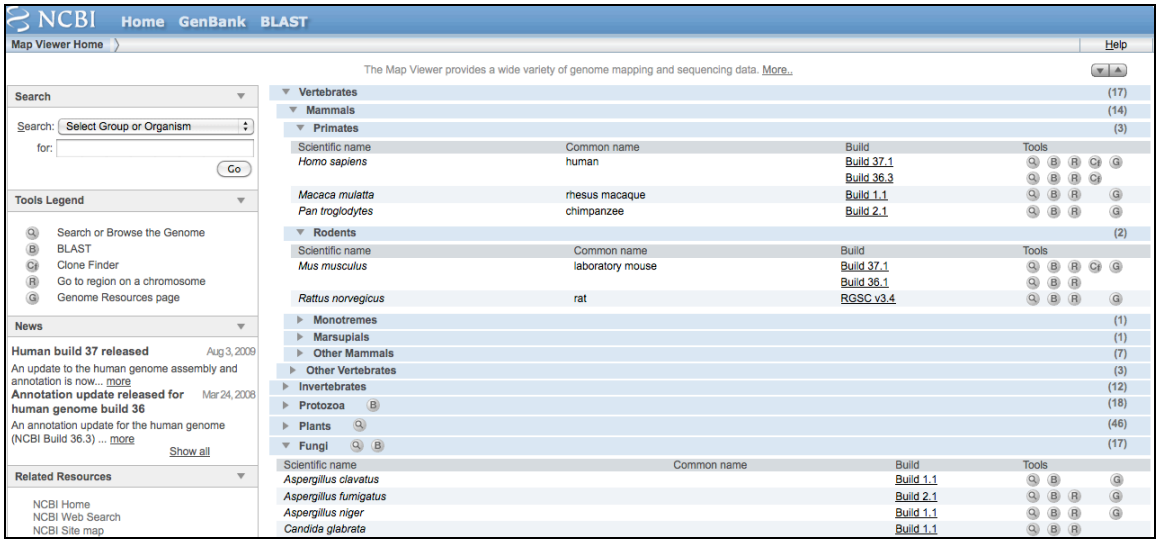
Using the Model Maker (mm), obtain a possible alternatively spliced product and its translated amino acid sequence. Search for similar proteins by using BLAST.

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.

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

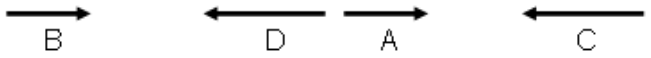
- Locate a human gene
- Download the gene sequence along with its upstream region (for promoter analysis)
- Determine whether the sequence is in draft or finished form
- Find a possible splice variant via Model Maker
- Identify whether variations in the gene are associated with a disease
- Obtain information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

High Throughput Genomic Sequences

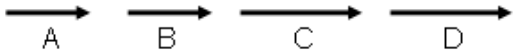
Sequencing of BACs:

Draft:

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



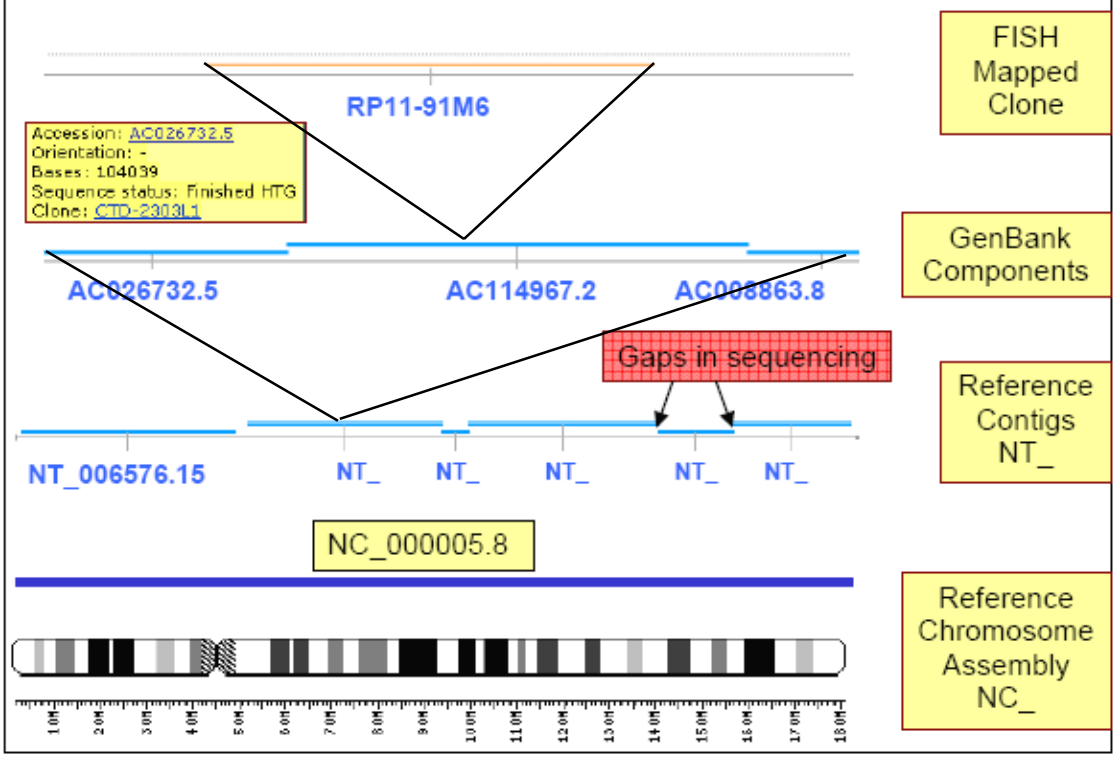
Phase 2 – unfinished, ordered with gaps

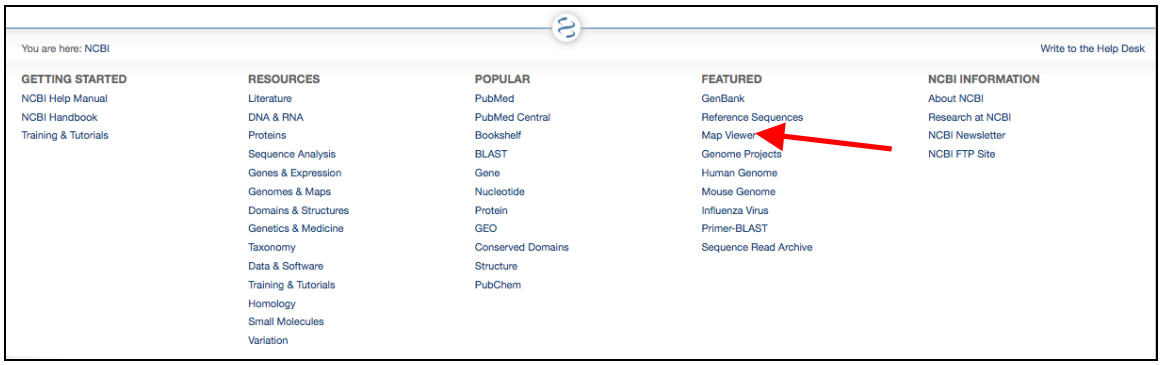


Finished:

Phase 3 – high quality finished sequence with no gaps

Genome Assembly Accession Numbers

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Human Genome
Mouse Genome
Influenza Virus
Primer-BLAST
Sequence Read Archive
NCBI INFORMATION
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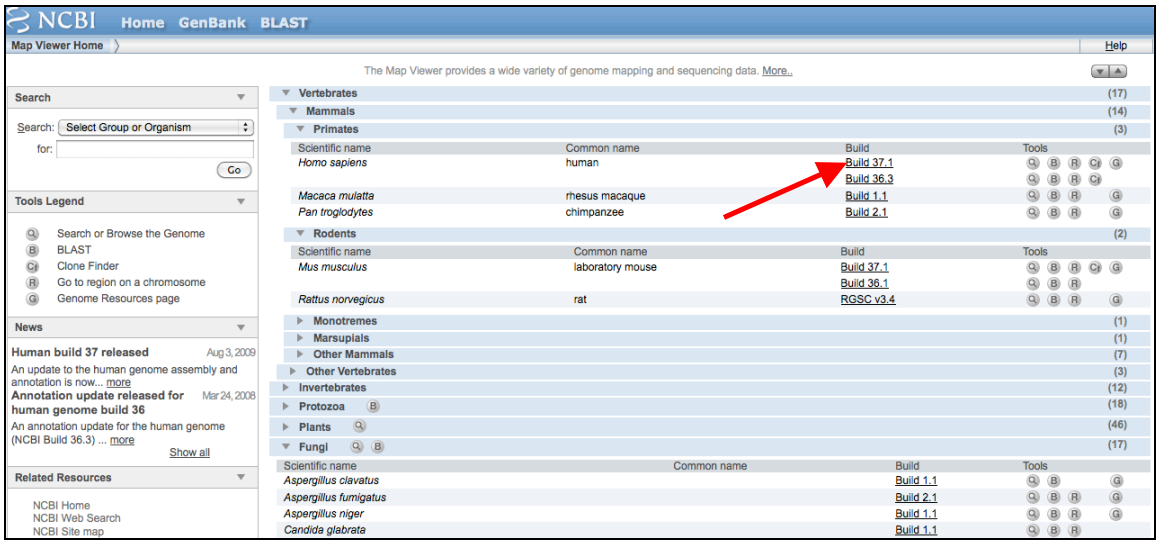
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Map Viewer Home
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The Map Viewer provides a wide variety of genome mapping and sequencing data. More..
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An update to the human genome assembly and annotation is now... more
Annotation update released for human genome build 36 Mar 24, 2008
An annotation update for the human genome (NCBI Build 36.3) ... more
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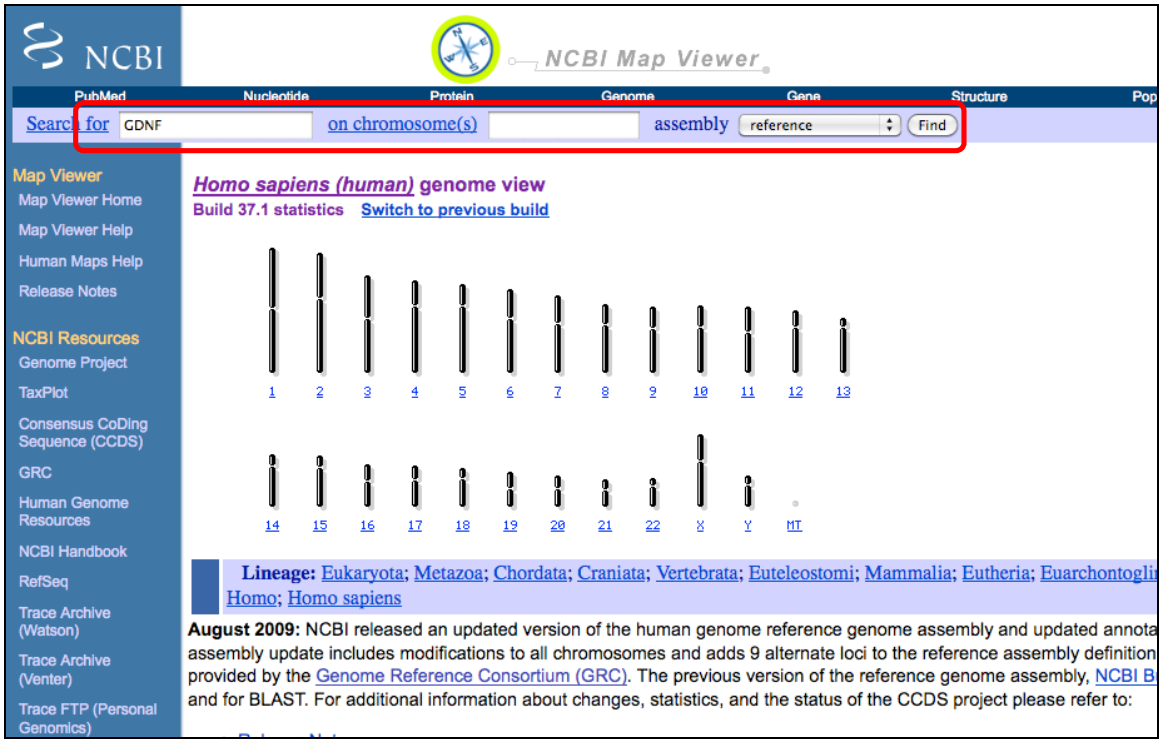
Vertebrates (17)
Mammals (14)
Primates (3)
Scientific name Common name Build Tools
Homo sapiens human Build 37.1
Build 36.3
Macaca mulatta rhesus macaque Build 1.1
Pan troglodytes chimpanzee Build 2.1
Rodents (2)
Mus musculus laboratory mouse Build 37.1
Build 36.1
Rattus norvegicus rat RGSC v3.4
Monotremes (1)
Marsupials (1)
Other Mammals (7)
Other Vertebrates (3)
Invertebrates (12)
Protozoa (18)
Plants (46)
Fungi (17)
Scientific name Common name Build Tools
Aspergillus clavatus Build 1.1
Aspergillus fumigatus Build 2.1
Aspergillus niger Build 1.1
Candida glabrata Build 1.1


NCBI
NCBI Map Viewer
PubMed Nucleotide Protein Genome Gene Structure Pop
Search for GDNF on chromosome(s) assembly reference Find
Map Viewer
Map Viewer Home
Map Viewer Help
Human Maps Help
Release Notes
NCBI Resources
Genome Project
TaxPlot
Consensus CoDing Sequence (CCDS)
GRC
Human Genome Resources
NCBI Handbook
RefSeq
Trace Archive (Watson)
Trace Archive (Venter)
Trace FTP (Personal Genomics)
Homo sapiens (human) genome view
Build 37.1 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; Euarchontogli
Homo; Homo sapiens
August 2009: NCBI released an updated version of the human genome reference genome assembly and updated annota
assembly update includes modifications to all chromosomes and adds 9 alternate loci to the reference assembly definition
provided by the Genome Reference Consortium (GRC). The previous version of the reference genome assembly, NCBI B
and for BLAST. For additional information about changes, statistics, and the status of the CCDS project please refer to:

NCBI

NCBI Map Viewer

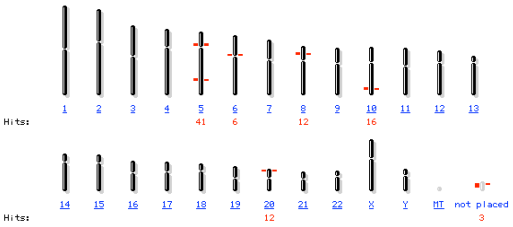
PubMed | Nucleotide | Protein | Genome | Gene | Structure | PopSet | Taxonomy | Help

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

Homo sapiens (human) genome view

Build 37.1 statistics Switch to previous build

BLAST search the human genome



Search results for query "GDNF": 90 hits (assembly **reference**)

Chr	Match	Map element	Type	Maps
5	all matches			
	GDNF family receptor alpha 3	Hs.58042	Hs_EST_Cl	Hs UniG
	ENST00000452487	ENST00000452487	TRANSCRIPT	ensRNA
	ENST00000427982	ENST00000427982	TRANSCRIPT	ensRNA
	ENST00000381826	ENST00000381826	TRANSCRIPT	ensRNA
	ENST00000344622	ENST00000344622	TRANSCRIPT	ensRNA
	ENST00000326524	ENST00000326524	TRANSCRIPT	ensRNA
	Rattus norvegicus **GDNF** family receptor alpha 3 (Gfra3...	NM_053398.1	TRANSCRIPT	Rn RNA
	Rattus norvegicus glial cell...**Gdnf**), mRNA	NM_019139.1	TRANSCRIPT	Rn RNA
	Rattus norvegicus **GDNF** family receptor alpha 3, mRNA...	BC079378.1	TRANSCRIPT	Rn RNA
	Rattus norvegicus neurotrophic...**GDNF** (Gdnf) mRNA, partial...	AF497634.1	TRANSCRIPT	Rn RNA
	Rattus norvegicus brain **GDNF** splice variant 2 mRNA, partial...	AF205714.1	TRANSCRIPT	Rn RNA
	Rattus norvegicus brain **GDNF** splice variant 1 mRNA, partial...	AF205713.1	TRANSCRIPT	Rn RNA

Quick Filter
- ☑ Gene
- Transcript :
  - ☐ all
  - ☐ RefSeq
  - ☐ STS
  - ☐ Unigene

Filter

NCBI

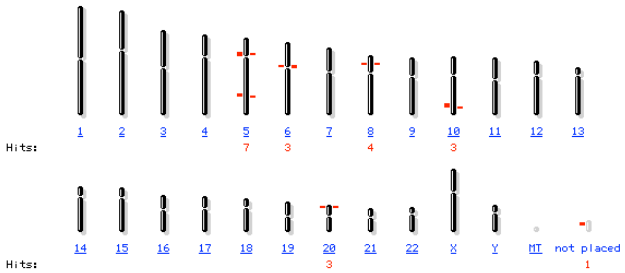
NCBI Map Viewer

PubMed | Nucleotide | Protein | Genome | Gene | Structure | PopSet | Tax

Search for GDNF AND gene[obj_type] on chromosome(s) assembly All Find

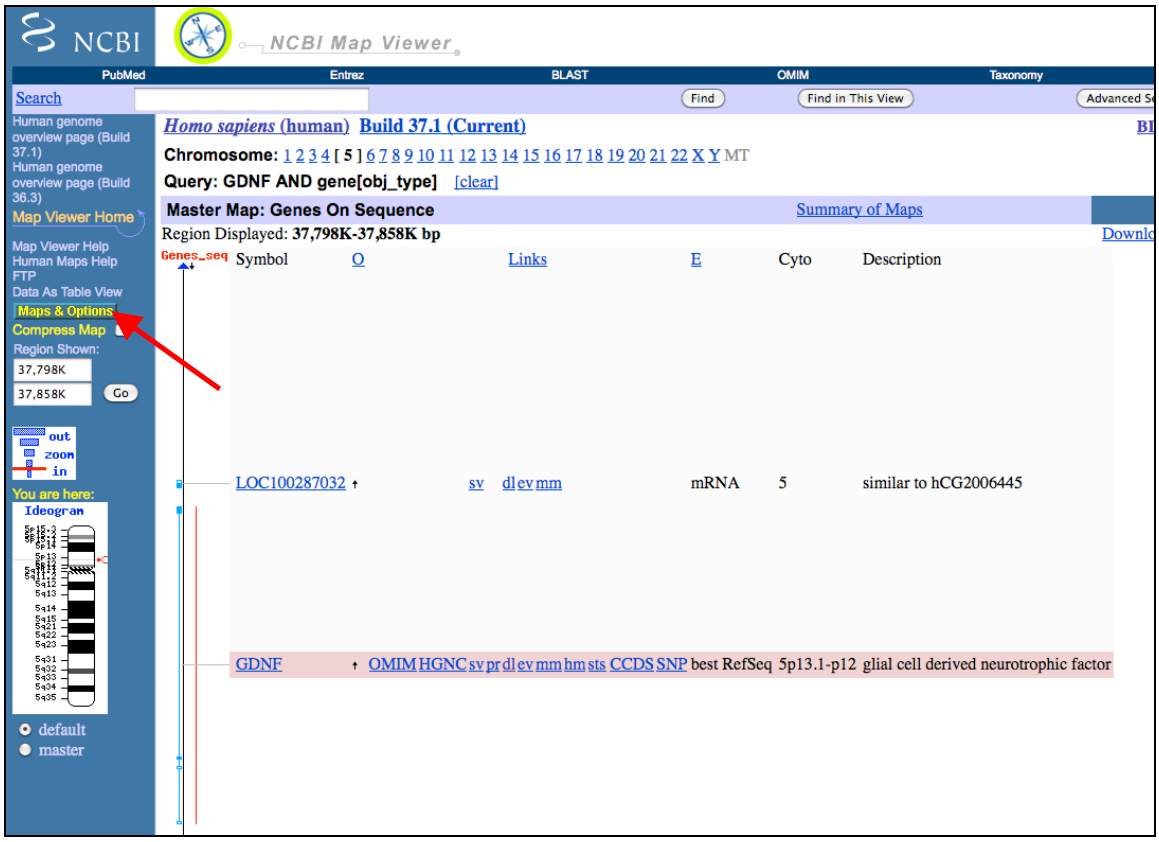
Homo sapiens (human) genome view

Build 37.1 statistics Switch to previous build



Search results for query "GDNF AND gene[obj_type]": 21 hits

Chr	Assembly	Match	Map element	Type	Maps
5	reference	all matches			
		GDNF family receptor alpha 3	GFRA3	GENE	Genes_cyto | Genes_seq
		GDNF : glial cell derived neurotrophic factor	GDNF	GENE	Genes_cyto | Genes_seq
		GDNF : ENSG00000168621	GDNF	GENE	ensGenes
5	Celera	all matches			
		GDNF family receptor alpha 3	GFRA3	GENE	craGenes | Genes_seq
		GDNF : glial cell derived neurotrophic factor	GDNF	GENE	craGenes | Genes_seq
5	HuRef	all matches			
		GDNF family receptor alpha 3	GFRA3	GENE	Genes_seq
		GDNF : glial cell derived neurotrophic factor	GDNF	GENE	Genes_seq
6	reference	**GDNF** family receptor alpha like	GFRAL	GENE	Genes_cyto | Genes_seq
6	Celera	**GDNF** family receptor alpha like	GFRAL	GENE	Genes_seq
6	HuRef	**GDNF** family receptor alpha like	GFRAL	GENE	Genes_seq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NCBI Map Viewer
PubMed
Entrez
BLAST
OMIM
Taxonomy
Search
Find
Find in This View
Human genome overview page (Build 37.1)
Human genome overview page (Build 36.3)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,798K
37,858K
Go
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in
You are here:
Ideogram
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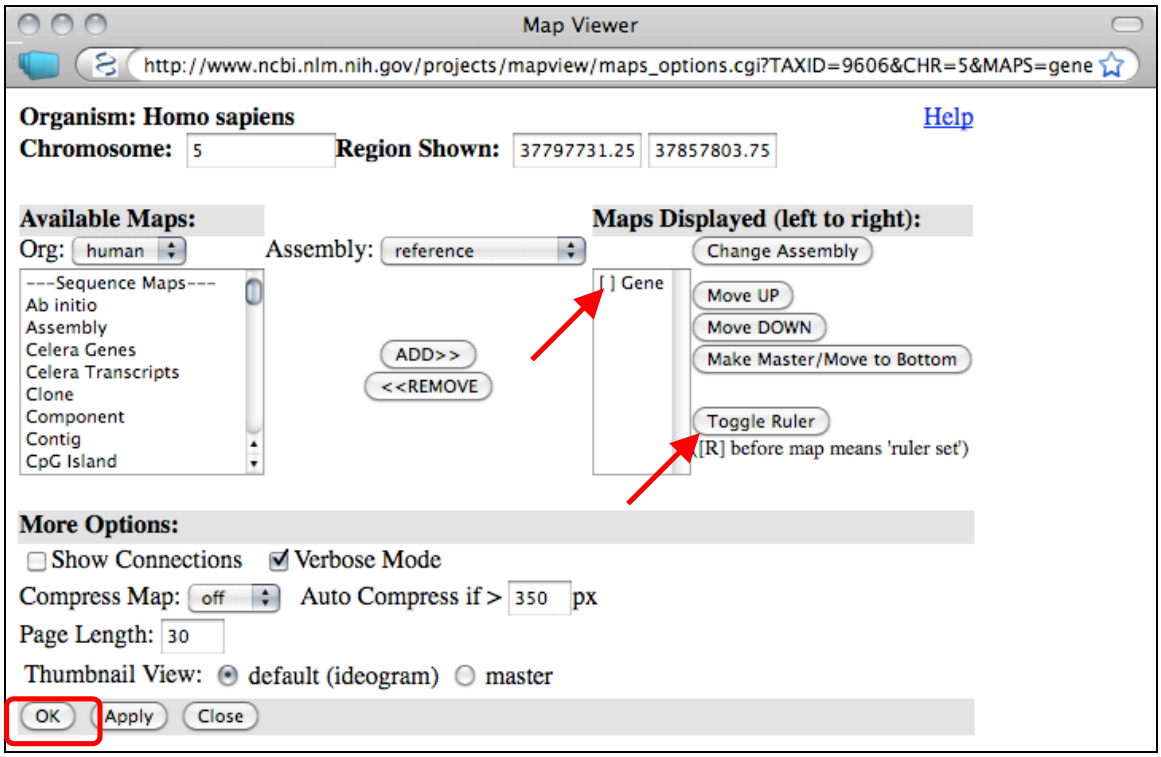
master
Homo sapiens (human) Build 37.1 (Current)
Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT
Query: GDNF AND gene[obj_type] [clear]
Master Map: Genes On Sequence
Summary of Maps
Region Displayed: 37,798K-37,858K bp
Genes_seq
Symbol
O
Links
E
Cyto
Description
LOC100287032
sv
dl ev mm
mRNA
5
similar to hCG2006445
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq
5p13.1-p12
glial cell derived neurotrophic factor


Map Viewer
http://www.ncbi.nlm.nih.gov/projects/mapview/maps_options.cgi?TAXID=9606&CHR=5&MAPS=gene
Organism: Homo sapiens
Help
Chromosome: 5
Region Shown: 37797731.25 37857803.75
Available Maps:
Org: human
Assembly: reference
---Sequence Maps---
Ab initio
Assembly
Celera Genes
Celera Transcripts
Clone
Component
Contig
CpG Island
ADD>>
<<REMOVE
Maps Displayed (left to right):
Change Assembly
[ ] 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

NCBI NCBI Map Viewer

PubMed Entrez BLAST OMIM Taxonomy

Search Find Find in This View Advanced Searc

Human genome overview page (Build 37.1)
Human genome overview page (Build 36.3)
Map Viewer Home
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Human Maps Help
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Data As Table View
Maps & Options
Compress Map
Region Shown:
37,798K
37,858K Go

out
zoom
in

You are here:
Ideogram

default
master

Homo sapiens (human) Build 37.1 (Current) BLA

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

Region Displayed: **37,798K-37,858K bp** Download

Genes_seq	Symbol	O	Links	E	Cyto	Description
37800K, 37805K, 37810K, 37815K, 37820K, 37825K, 37830K, 37835K, 37840K	LOC100287032 ↑	sv	dl ev mm	mRNA	5	similar to hCG2006445
	GDNF ↑	OMIM HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	5p13.1-p12	glial cell derived neurotrophic factor

Homo sapiens (human) (Build 37.1)
Region to retrieve (in chromosome coordinates):
Chromosome: 5 Strand: plus
from: 37815753 adjust by: -0K
to: 37839782 adjust by: +0K Change Region/Strand

Sequence Format: FASTA

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

Contig	start	stop	strand	
NT_006576.16	37805753	37829782	+	Display Save to Disk View Evidence ModelMaker

Homo sapiens (human) (Build 37.1)
Region to retrieve (in chromosome coordinates):
Chromosome: 5 Strand: minus
from: 37815753 adjust by: -0K
to: 37839782 adjust by: +0K Change Region/Strand

Sequence Format: FASTA

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

Contig	start	stop	strand	
NT_006576.16	37805753	37829782	+	Display Save to Disk View Evidence ModelMaker

Organism: Homo sapiens

Help

Chromosome: 5 Region Shown: 37797731.25 37857803.75

Available Maps:

Org: human Assembly: reference

---Sequence Maps---
Ab initio
Assembly
Celera Genes
Celera Transcripts
Clone
Component
Contig
CpG Island

ADD>>
<<REMOVE

Maps Displayed (left to right):

[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: off Auto Compress if > 350 px

Page Length: 30

Thumbnail View: default (ideogram) master

OK Apply Close

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PubMed Entrez BLAST OMIM Taxonomy Structure

Search Find Find in This View Advanced Search

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Human genome overview page (Build 36.3)
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Region Shown:
37,798K
37,858K Go

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Homo sapiens (human) Build 37.1 (Current) BLAST The Hum

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]

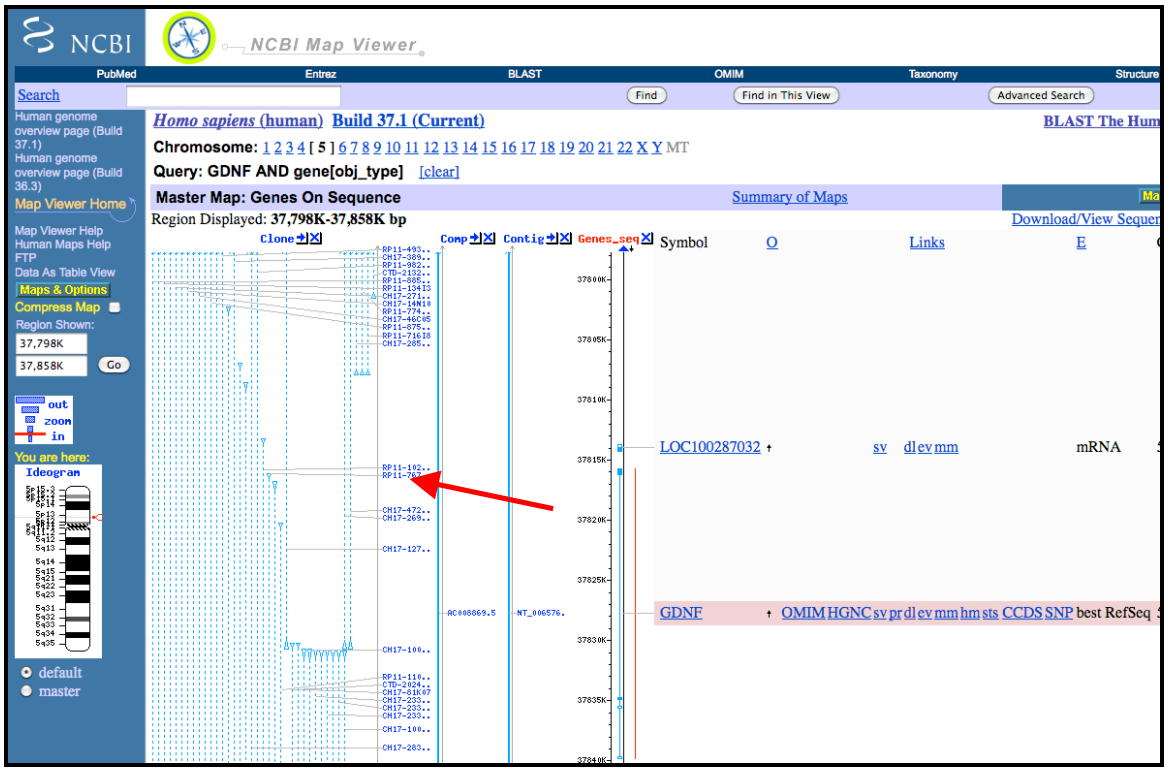
Master Map: Genes On Sequence Summary of Maps

Region Displayed: 37,798K-37,858K bp Download/View Sequer

Clone Comp Contig Genes_seq Symbol O Links E

LOC100287032 sv dl ev mm mRNA

GDNF OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq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Taxonomy
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Find in This View
Advanced Search
Homo sapiens (human) Build 37.1 (Current)
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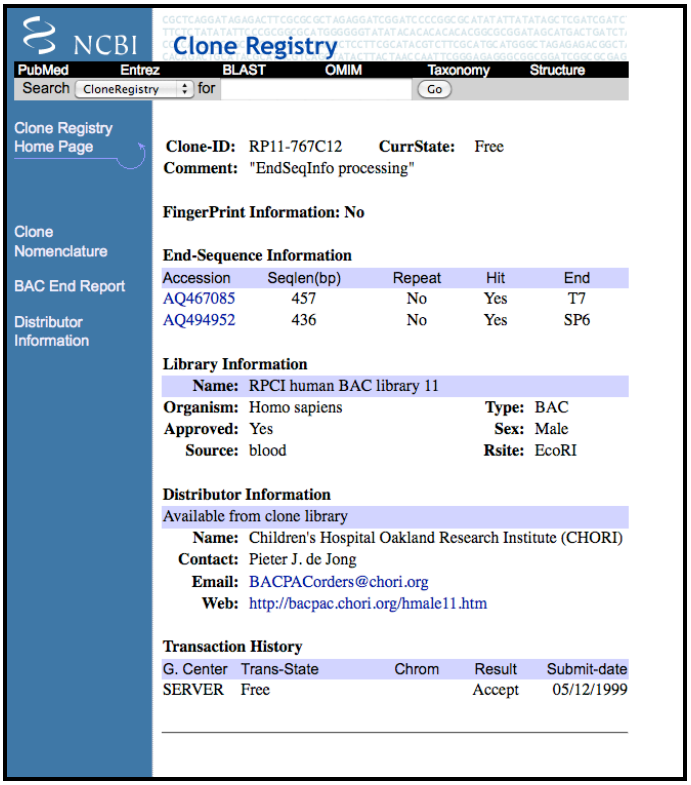
OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq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Structure
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Clone Registry Home Page
Clone Nomenclature
BAC End Report
Distributor Information
Clone-ID: RP11-767C12 CurrState: Free
Comment: "EndSeqInfo processing"
FingerPrint Information: No
End-Sequence Information
Accession Seqlen(bp) Repeat Hit End
AQ467085 457 No Yes T7
AQ494952 436 No Yes SP6
Library Information
Name: RPCI human BAC library 11
Organism: Homo sapiens
Type: BAC
Approved: Yes
Sex: Male
Source: blood
Rsite: EcoRI
Distributor Information
Available from clone library
Name: Children's Hospital Oakland Research Institute (CHORI)
Contact: Pieter J. de Jong
Email: BACPACorders@chori.org
Web: http://bacpac.chori.org/hmale11.htm
Transaction History
G. Center Trans-State Chrom Result Submit-date
SERVER Free Accept 05/12/1999

Organism: Homo sapiens
Help
Chromosome: 5 Region Shown: 37797731.25 37857803.75

Available Maps:
Org: human
Assembly: reference
Ensembl Genes
Ensembl Transcripts
FISH Clone (seq)
GenBank DNA
Gene
Phenotype
RefSeq Transcripts
Repeats
rnaBt
ADD>>
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Homo sapiens (human) Build 37.1 (Current)
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Query: GDNF AND gene[obj_type] [clear]
Master Map: Genes On Sequence
Summary of Maps
Region Displayed: 37,798K-37,858K bp

Symbol	O	Links	E	Cyto	Description
LOC100287032	sv	dl ev mm	mRNA	5	similar to hCG2006445
GDNF	OMIM HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	5p13.1-p12	glial cell derived neurotrophic factor	

Homo sapiens (human) **Build 37.1 (Current)** BLAST The Human Genome

Data As Table View Download All !

Genes On Sequence All Sequence Maps next

Region Displayed: **37,798K-37,858K bp** Download/View Sequence/Evidence Download Data

Total Genes On Chromosome: **1536**

Genes in Region: **2**

start	stop	Symbol	O	Links	E	Cyto	Description
37813681	37814281	LOC100287032	-	sv dl ev mm	mRNA	5	similar to hCG2006445
37815753	37839782	GDNF	-	OMIM HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	5p13.1-p12	glial cell derived neurotrophic factor

Ab initio models All Sequence Maps prev next

Region Displayed: **37,798K-37,858K bp** Download/View Sequence/Evidence Download Data

Total models On Chromosome: **3410**

models in Region: **5**

start	stop	Symbol	O	Best hit	Best hit description
37805733	37812363	hmm1374634	-		
37813681	37814281	hmm1376634	-		
37815753	37835929	hmm12438633	-	NP_000505.1	glial cell derived neurotrophic factor isoform 1 preproprotein [Homo sapiens]
37815753	37839776	hmm12436633	-	NP_000505.1	glial cell derived neurotrophic factor isoform 1 preproprotein [Homo sapiens]
37836700	37845817	hmm1378634	+		

RefSeq Transcripts On Sequence All Sequence Maps prev

Region Displayed: **37,798K-37,858K bp** Download/View Sequence/Evidence Download Data

Total RefSeq Transcripts On Chromosome: **1527**

RefSeq Transcripts in Region: **4**

start	stop	Accession	Locus	O	Links	Align quality	Description
37813681	37814281	XM_002342491.1	LOC100287032	-	sv prev BLink	identical	similar to hCG2006445
37815753	37834898	NM_199234.1	GDNF	-	ug sv prev BLink	identical	glial cell derived neurotrophic factor
37815753	37816100	exon		-		CDS	348 bp
37816101	37834836	intron		-			18736 bp
37834837	37834890	exon		-		CDS	54 bp
37834891	37834898	exon		-		UTR	8 bp
37815753	37835593	NM_199231.1	GDNF	-	ug sv prev BLink CCDS	identical	glial cell derived neurotrophic factor
37815753	37816237	exon		-		CDS	485 bp
37816238	37834825	intron		-			18588 bp

NCBI NCBI Map Viewer

PubMed Entrez BLAST OMIM Taxonomy

Search Find Find in This View Advanced Search

Human genome overview page (Build 37.1)
Human genome overview page (Build 36.3)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,798K
37,858K
Go
out
zoom
in
You are here:
Ideogram
default
master

Homo sapiens (human) **Build 37.1 (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

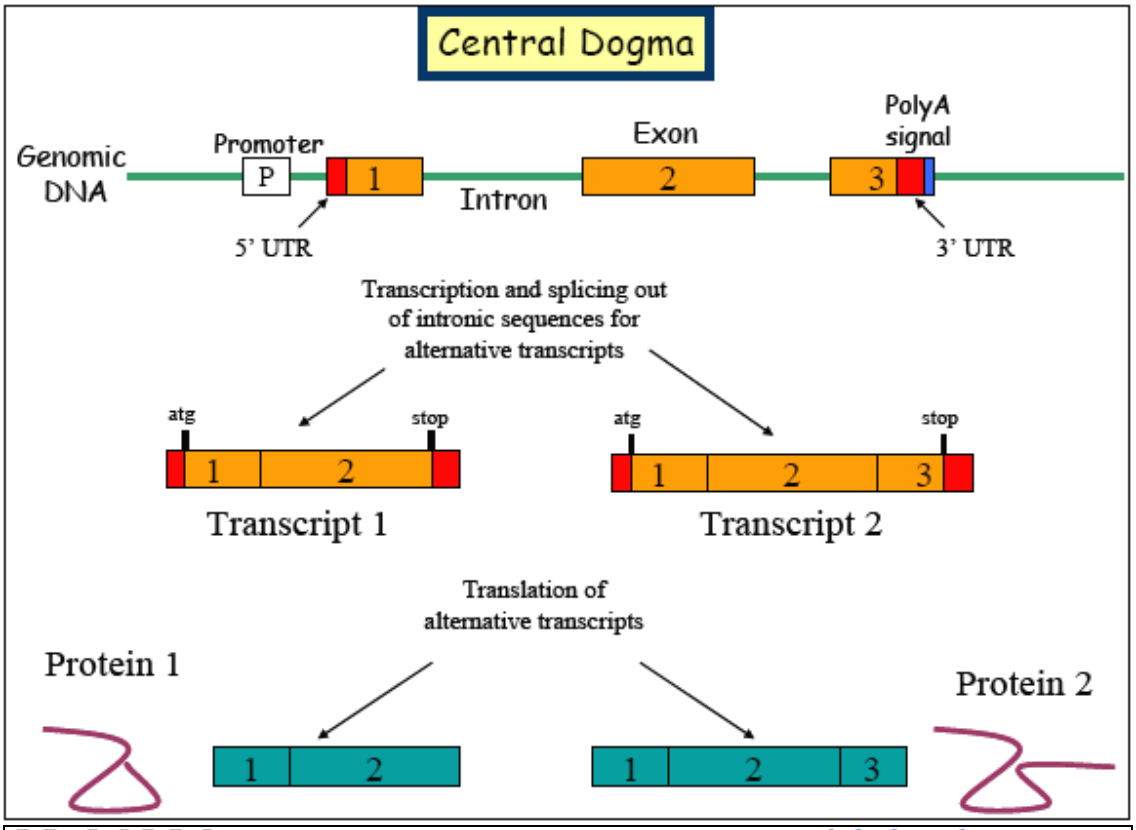
Query: GDNF AND gene[obj_type] [clear]

Master Map: Genes On Sequence Summary of Maps

Region Displayed: **37,798K-37,858K bp**

Model RefSeq RNA Genes_seq

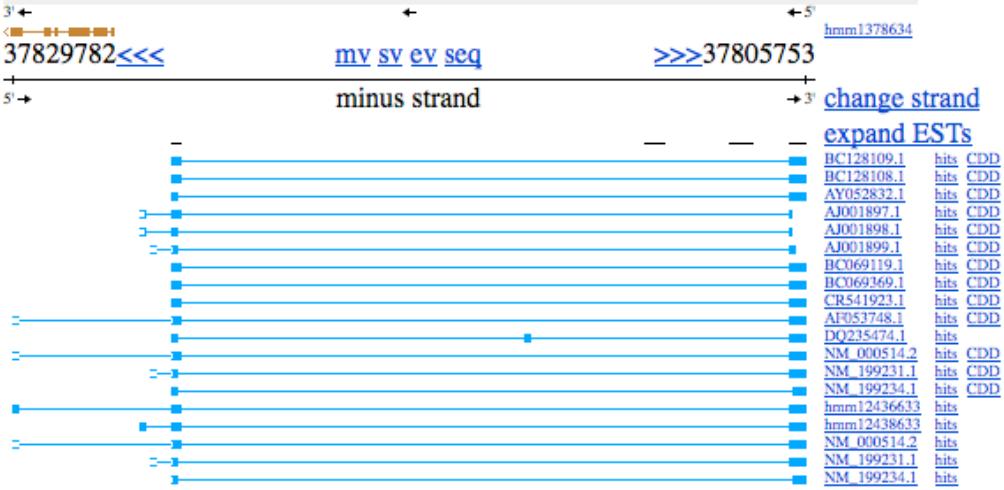
Symbol	O	Links	E	Cyto	Description
LOC100287032	+	sv dl ev mm	mRNA	5	similar to hCG2006445
GDNF	+	OMIM HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	5p13.1-p12	glial cell derived neurotrophic factor



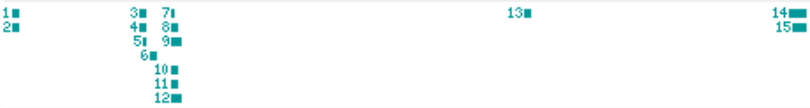
Model Maker *(Make Your Own Model by selecting an evidence exon "set" and/or add/remove individual putative exons for inclusion in your model)* help legend

Organism: Homo sapiens (Build 37.1) Chromosome: 5 Contig: NT_006576.16 Locus: GDNF

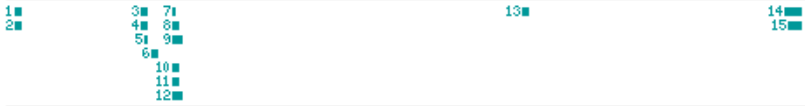
Evidence:



Putative exons (graphic view):



Putative exons (graphic view):



Your model: clear

3-9-14

```
CCAAAGCGTCCGAGACTGGGTACAGTCGTCCAGGCGTGACGGGGGCGCGGGGAGCCAGTG
ACTCCTCTGGGAGGGGAAGGGATTAGGGCCAGAATCTCTCAAAGGTGCAAAAATCCAGTC
AAGAGAGGGTTTTCGGGTATACCACGGAGGATTAAAACTTTCAAGACAAGTGCCGCCGCC
GGACGGGACTTTAAGATGAAGTTATGGGATGTCGTGGCTGTCTGCCTGGTGCTGCTCCAC
ACCGCGTCCGCCTTCCCGCTGCCCGCCGGTAAGAGGCCTCCCGAGGCGCCCGCCGAAGAC
```

ORF Finder
Save

Frame1, ORF= 211 CDD Frame2, ORF= 42 CDD Frame3, ORF= 22 CDD

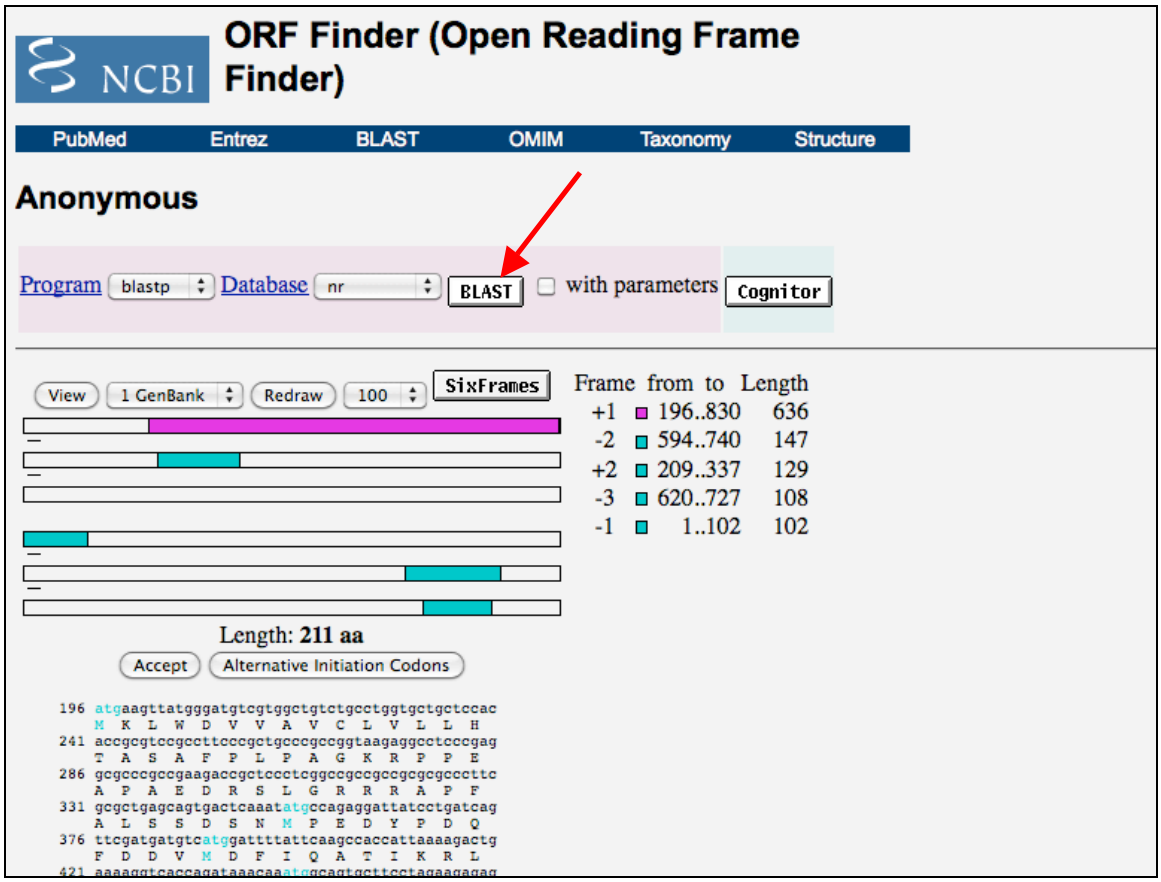
```
pxrprlqtvvqa*rqrqepv
tplqqegirarisqrcknpv
krqfsqiprriktfktsaaa
qrdfkMKLWDVVAVCLVLLH
TASAFPLPAGKRPPEAPAED
```

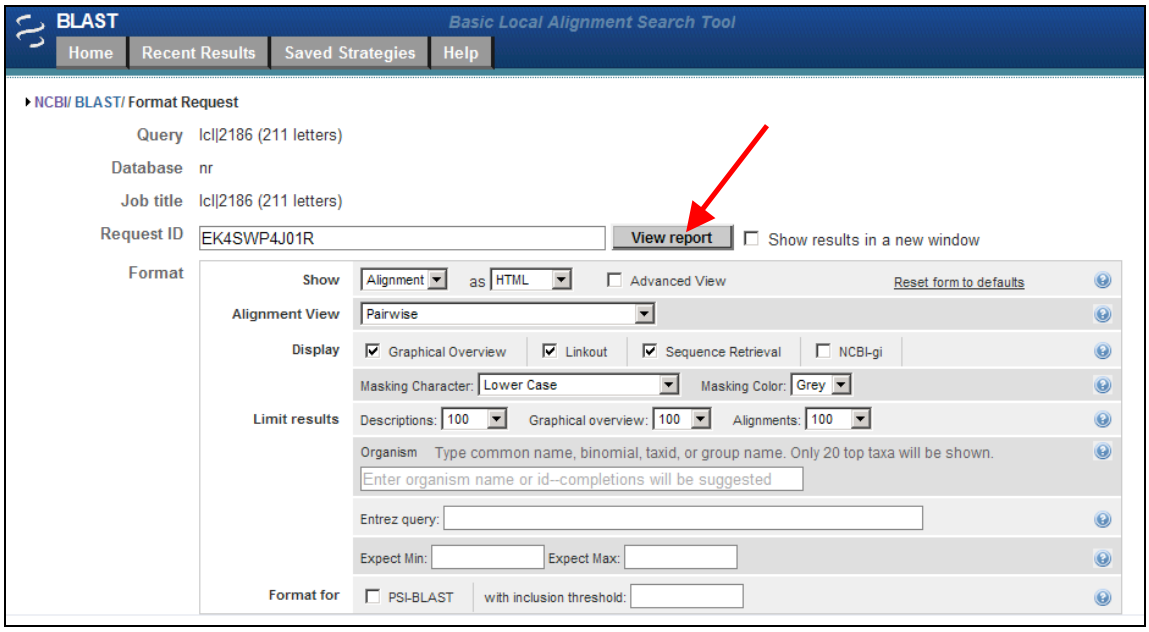
```
qsvrdwvqssrrdqqagsq*
llweqkqlqpeslkqakiqs
reqfrvyhqqlklsrqvppp
dqtlr*syqMSWLSAWCCST
PRPPSRCPPVRGLPRRPPKT
```

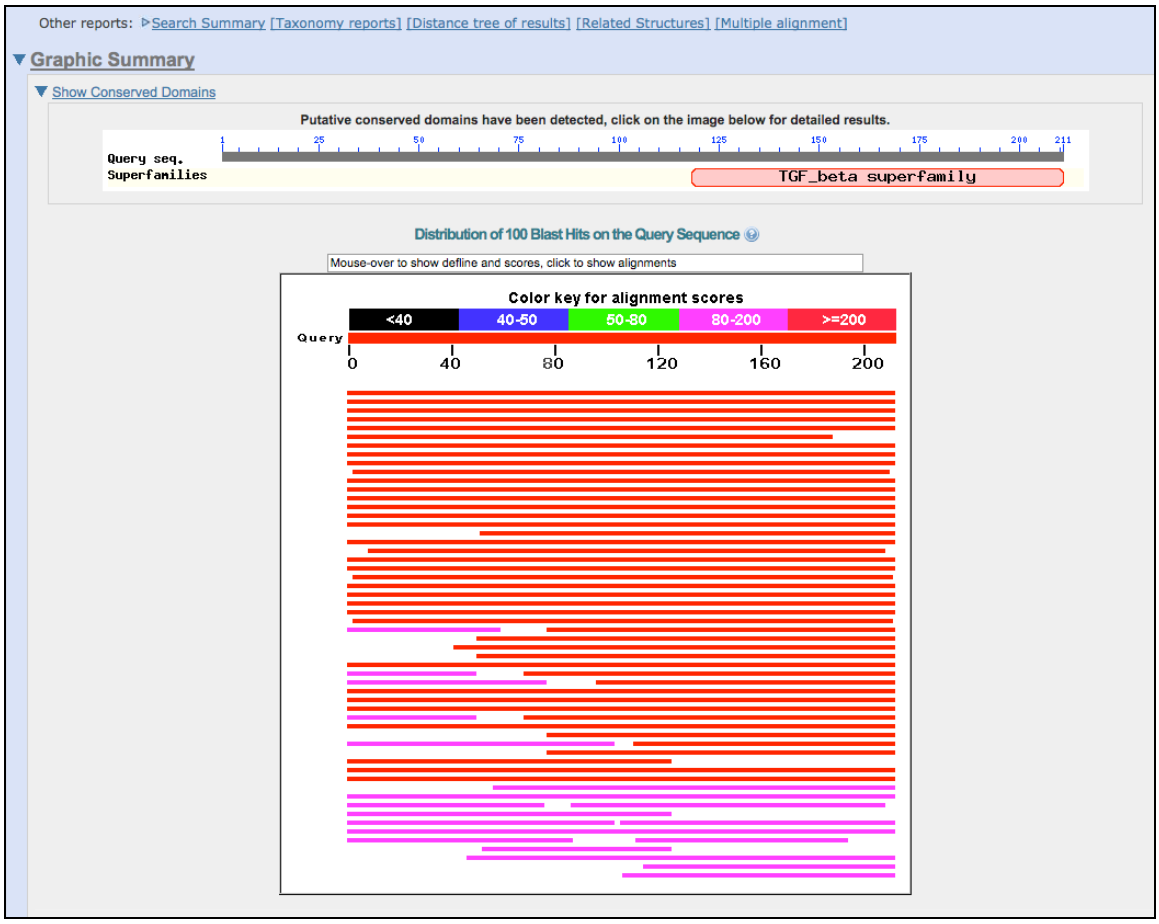
```
kasetqysrpqvtqarqasd
ssqrqrd*qqnlskvqkssq
ervfqytted*nfqdkcrrr
tql*devMGCRGCLPGAAPH
RVRLPAARR*easrqarrrp
```

Putative exons (table view): custom exons intron bases: 2

☐	1			CG	CCG	37829782-37829609	GAG	GT	=> 9
☐	2		2 <=	CT	CCA	37829776-37829609	GAG	GT	=> 2 or 7
☑	3			CT	CCA	37825929-37825761	CAA	AT	=> 4
☐	4		3 <=	CT	CCA	37825929-37825736	ATG	GT	=> 5 or 8 or 9
☐	5		4 <=	AA	ATG	37825760-37825736	ATG	GT	=> 9
☐	6			CC	CAT	37825593-37825497	TGG	GT	=> 8
☐	7		2 <=	AG	GTG	37824924-37824899	AAG	AT	=> 9
☐	8		4 or 6 <=	AG	GTG	37824924-37824826	CCG	GT	=> 14
☑	9		1 or 4 or 5 or 7 <=	AG	GTG	37824924-37824748	ACT	GT	=> 12 or 14
☐	10			AG	ATG	37824898-37824837	CCC	GC	=> 15
☐	11			AG	ATG	37824898-37824826	CCG	GT	=> 13 or 14
☐	12		9 <=	AG	ATG	37824898-37824748	ACT	GT	=> 14
☐	13		11 <=	AG	GGC	37814191-37814112	GAG	GT	=> 14
☑	14	8 or 9 or 11 or 12 or 13 <=		AG	CAA	37806237-37805756	ATC	TGA	CT 37805753
☐	15		10 <=	CA	GCT	37806100-37805753	TGA	CT	


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
+1 196..830 636
-2 594..740 147
+2 209..337 129
-3 620..727 108
-1 1..102 102
Length: 211 aa
Accept
Alternative Initiation Codons
196 atgaagttatgggatgtcgtggctgtctgcctggtgctgctccac
M K L W D V V A V C L V L L H
241 accgcgtccgccttcccgctgcccgccggtaagaggcctcccgag
T A S A F P L P A G K R P P E
286 gcgcccgccgaagaccgctccctcggccgccgccgcgcgcgcccttc
A P A E D R S L G R R R A P F
331 gcgctgagcagtgactcaaatatgccagaggattatcctgatcag
A L S S D S N M P E D Y P D Q
376 ttcgatgatgtcatggattttattcaagccaccattaaaagactg
F D D V M D F I Q A T I K R L


BLAST
Basic Local Alignment Search Tool
Home
Recent Results
Saved Strategies
Help
NCBI/ BLAST/ Format Request
Query lcl|2186 (211 letters)
Database nr
Job title lcl|2186 (211 letters)
Request ID EK4SWP4J01R
View report
Show results in a new window
Format
Show Alignment as HTML
Advanced View
Reset form to defaults
Alignment View Pairwise
Display Graphical Overview Linkout Sequence Retrieval NCBI-gi
Masking Character: Lower Case
Masking Color: Grey
Limit results Descriptions: 100 Graphical overview: 100 Alignments: 100
Organism Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.
Enter organism name or id--completions will be suggested
Entrez query:
Expect Min:
Expect Max:
Format for PSI-BLAST with inclusion threshold:



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    MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ  60
            MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ
Sbjct  18   MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ  77

Query  61   FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL  120
            FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL
Sbjct  78   FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL  137

Query  121  TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR  180
            TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR
Sbjct  138  TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR  197

Query  181  PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI  211
            PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI
Sbjct  198  PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI  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%)

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            MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ
Sbjct  1    MKLWDVVAVCLVLLHTASAFPLPAGKRPPEAPAEDRSLGRRRAPFALSSDSNMPEDYPDQ  60

Query  61   FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL  120
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Sbjct  61   FDDVMDFIQATIKRLKRSPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRGCVL  120

Query  121  TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR  180
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Sbjct  121  TAIHLNVTDLGLGYETKEELIFRYCSGSCDAAETTYDKILKNLSRNRRLVSDKVGQACCR  180

Query  181  PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI  211
            PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI
Sbjct  181  PIAFDDDLSFLDDNLVYHILRKHSAKRCGCI  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]
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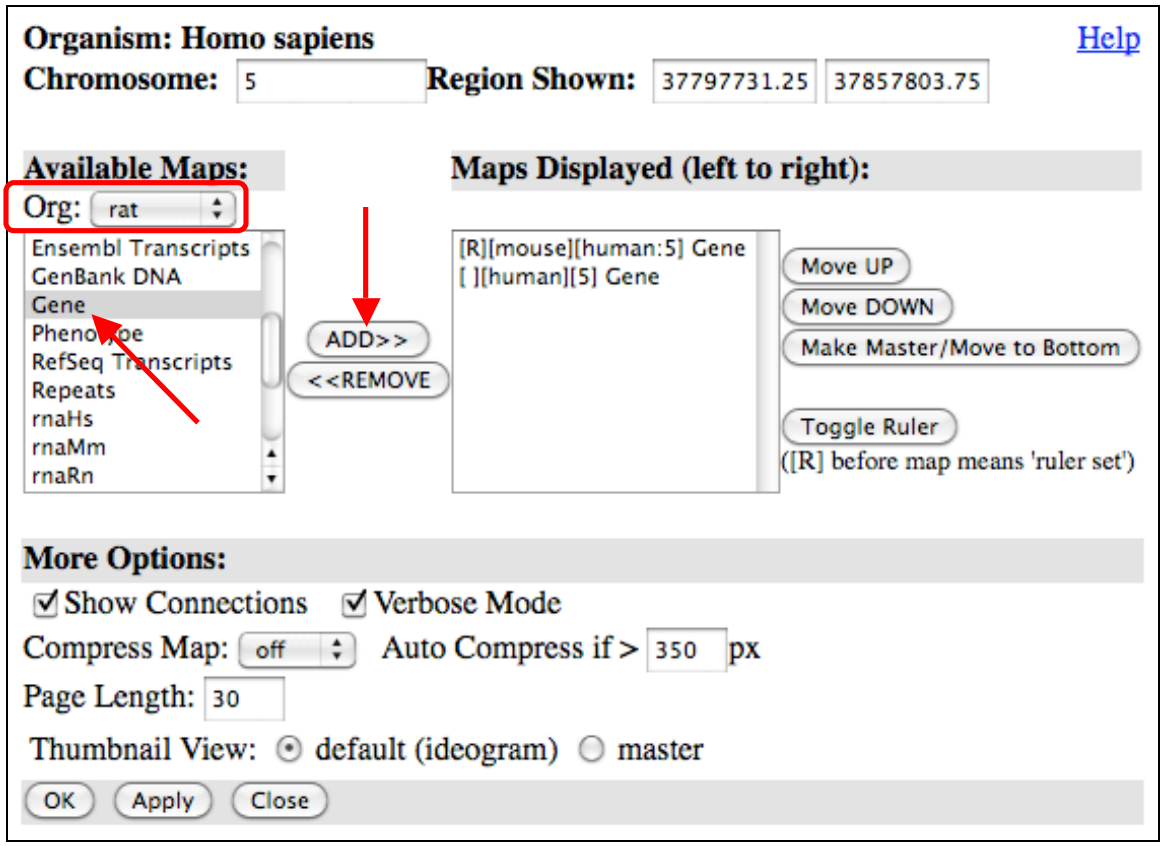

NCBI Map Viewer

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Search | Find | Find in This View

Human genome overview page (Build 37.1)
Human genome overview page (Build 36.3)
Map Viewer Home
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Synteny 1:1
Region Shown:
37,798K
37,858K
Go
out
zoom
in
You are here:
Ideogram
default
master

Homo sapiens (human) Build 37.1 (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] [clear]

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

Region Displayed: 37,798K-37,858K bp

Genes_seq | Genes_seq | Genes_seq

mouse segments | rat segments | H.sapiens, chr 5

Symbol	O	Links	E	Cyto	Description
LOC100287032	sv	dl ev mm	mRNA	5	similar to h
GDNF	OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq			5p13.1-p12	glial cell de

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

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)
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:
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 — Summary of Maps — Maps & Options

Region Displayed: 37,833K-37,894K bp — Download/View Sequence/Evidence

Pheno | Genes_seq | Symbol | Links | E | Cyto | Description

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

MHS6

GDNF ↑ OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq 5p13.1-p12 glial cell derived neurotrophic fact

Symbol: GDNF
Description: glial cell derived neurotrophic factor

NCBI

OMIM
Online Mendelian Inheritance in Man
Johns Hopkins University

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All Databases | PubMed | Nucleotide | Protein | Genome | Structure | PMC | OMIM

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Display Detailed Show 20 Send to

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
GAD
komp
MGI

*600837 — GeneTests, Links

GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR; GDNF

Alternative titles; symbols

HIRSCHSPRUNG DISEASE, SUSCEPTIBILITY TO, 3, INCLUDED; HSCR3, INCLUDED

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

Exercise 2

Search for "PRNP" in the Map Viewer. Access the Human Map Viewer page by clicking on Map Viewer, then selecting the "*Homo sapiens* (human) Build 36" link. 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 RefSeq Transcripts 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.