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**

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 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.

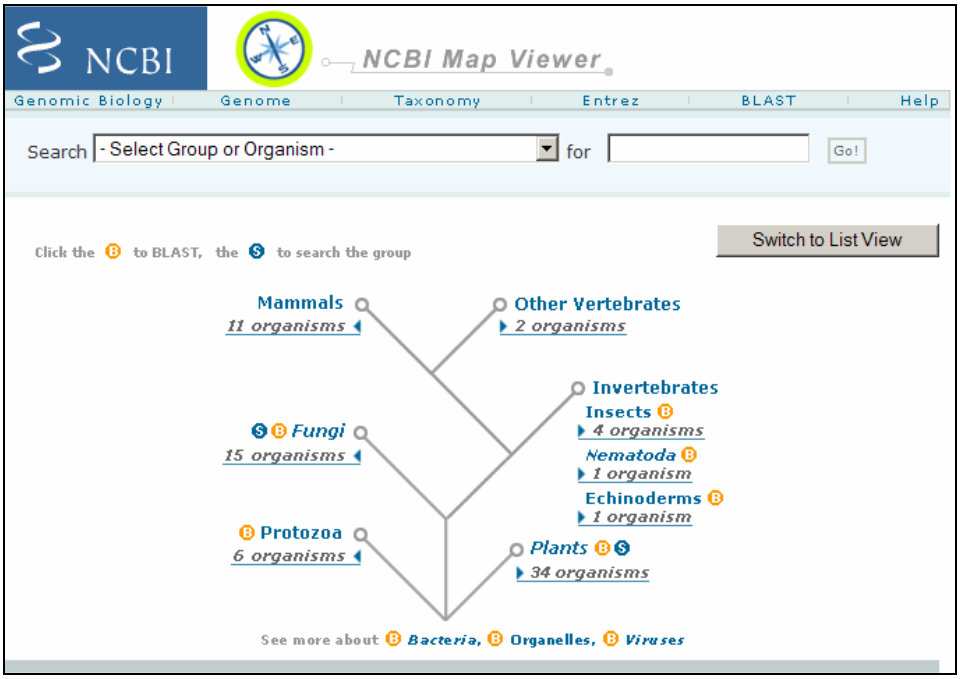
NCBI

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:

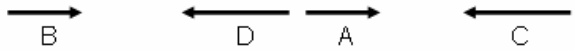
NC_

High Throughput Genomic Sequences

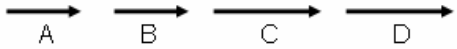
Sequencing of BACs:

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

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)

Organism Data in GenBank
- EST
- Genomic
- mRNA
- Protein
- WGS

Homo sapiens (human) genome view

BLAST search the human genome

Build 36.2 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; Haplorrhini; Catarrhini; Hominidae; Homo; Homo sapiens

September 2006: NCBI released an annotation update for the human genome (NCBI Build 36.2); this update does not change the genome assembly. The previous version of the genome assembly, NCBI Build 35.1, can still be accessed for Map Viewer display and for BLAST. For additional information about changes, statistics, and the status of the CCDS project please refer to:

- Release Notes
- Statistics
- CCDS Project

The NCBI Map Viewer provides graphical displays of features on the human genome sequence assembly as well as cytogenetic, genetic, physical, and radiation hybrid maps. Extensive documentation is provided to describe the resource features and methods used, tutorials, and statistics.

Map features that can be seen along the sequence include genes, transcripts, NCBI contigs (the 'Contig' map), the BAC tiling path (the 'Component' map), STSs, FISH mapped clones, ESTs and transcripts from several different organisms, Gnomon predicted gene models, and more.

http://www.ncbi.nlm.nih.gov/mapview/map_search.cgi?taxid=9606&query=gdnf&qchr=&strain=All&advsrch=off

Homo sapiens (human) genome view

BLAST search the human genome

Build 36.2 statistics Switch to previous build

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

Hits: 55 10 19 23

14 15 16 17 18 19 20 21 22 X Y MT not placed

Hits: 14 3

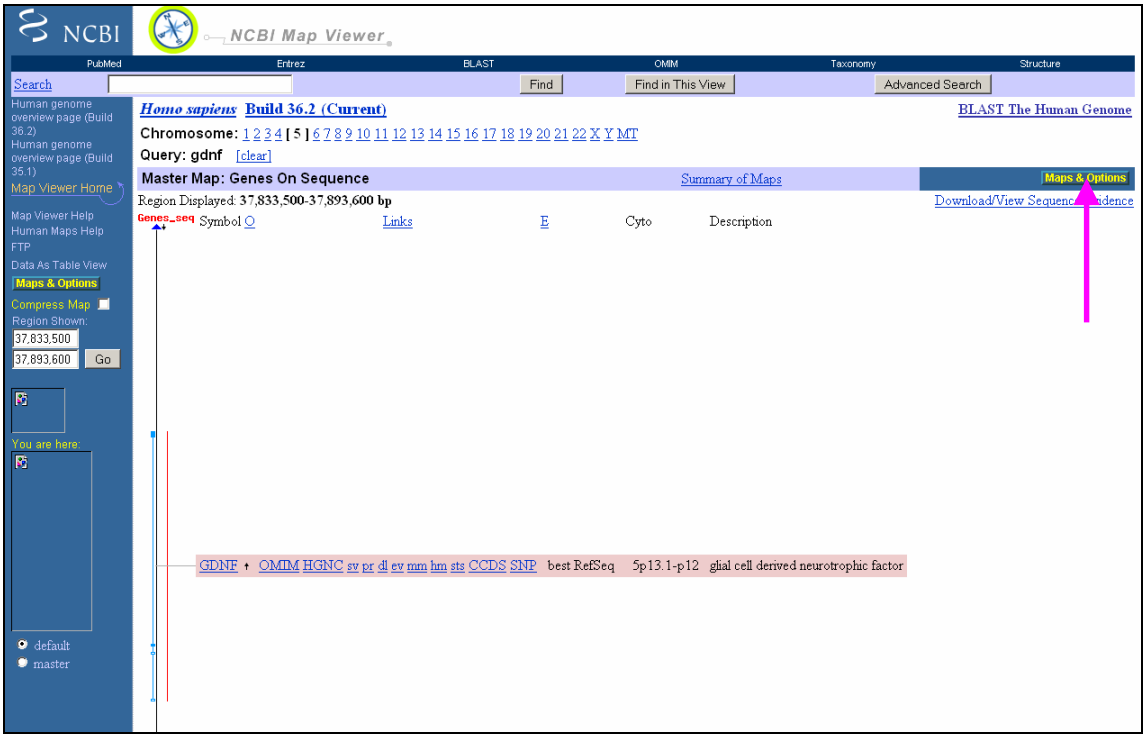
Search results for query "gdnf": 124 hits

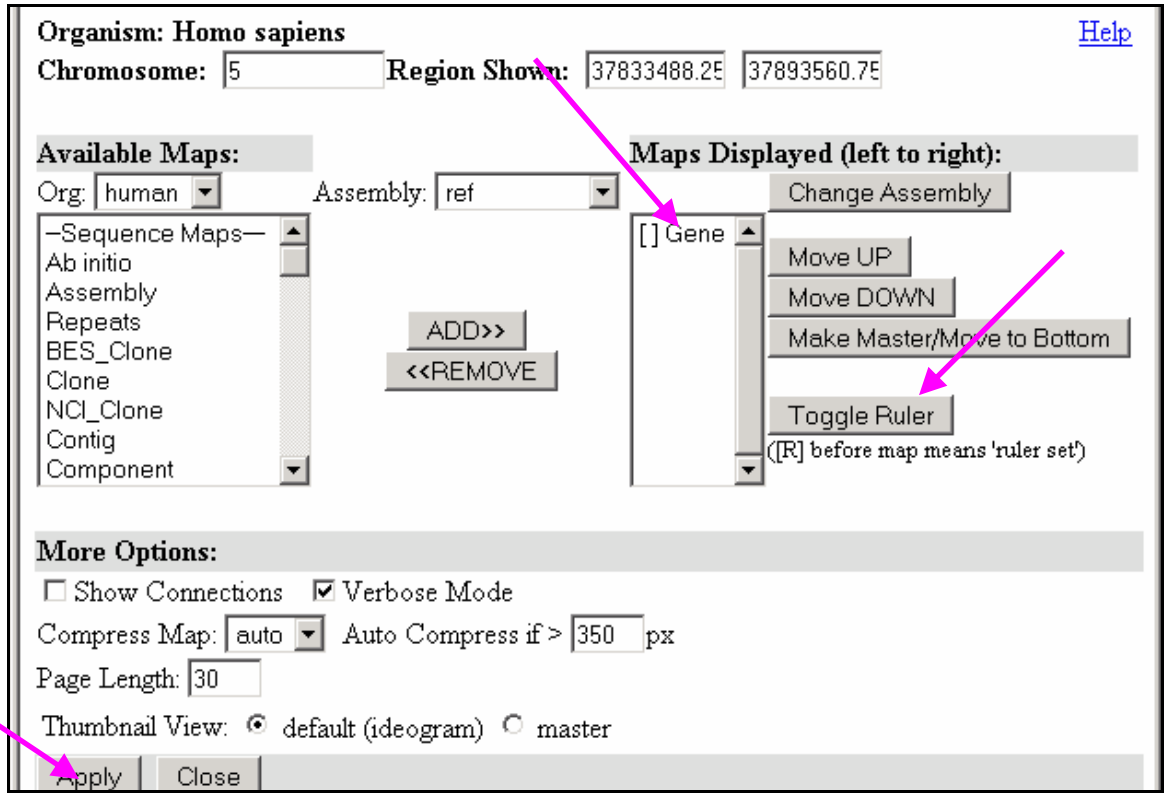
Hits shown: 1 - 100 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT not placed

Chr	Assembly	Match	Map element	Type	Maps
5	reference	all matches			
		GDNF family receptor alpha 3	Hs.58042	Hs_EST_Cl	Hs UniG
		tk05a07.x1 NCI_CGAP_Lu24 Homo...**GDNF** FAMILY RECEPTOR ALPHA...	AI887844.1	TRANSCRIPT	Hs RNA
		Rattus norvegicus glial cell...**Gdnf**), mRNA	NM_019139.1	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
		Mus musculus glial derived...**GDNF**) mRNA, 3_UTR, partial...	U66196.1	TRANSCRIPT	Mm RNA
		Mus musculus glial cell line...**Gdnf**), mRNA	NM_010275.1	TRANSCRIPT	Mm RNA
		Mus musculus **GDNF** mRNA for glial cell line-derived neurotrophic...	D49921.1	TRANSCRIPT	Mm RNA
		Mus musculus **GDNF** family receptor alpha 3 mRNA, complete...	AF051766.1	TRANSCRIPT	Mm RNA
		Homo sapiens glial cell derived...**GDNF**), transcript variant...	NM_199234.1	TRANSCRIPT	RefSeq RNA | Hs RNA
		Homo sapiens glial cell derived...**GDNF**), transcript variant...	NM_199231.1	TRANSCRIPT	RefSeq RNA | Hs RNA
		Homo sapiens **GDNF** family receptor alpha 3 (GFRA3), mRNA	NM_001496.3	TRANSCRIPT	RefSeq RNA | Hs RNA
		Homo sapiens glial cell derived...**GDNF**), transcript variant...	NM_000514.2	TRANSCRIPT	RefSeq RNA | Hs RNA
		Homo sapiens full open reading...**GDNF**, glial cell derived...	CR541923.1	TRANSCRIPT	Hs RNA
		Homo sapiens **GDNF** family receptor alpha 3, mRNA (cDNA...	BC037951.1	TRANSCRIPT	Hs RNA
		Homo sapiens glial cell-derived...**GDNF**) mRNA, complete...	AY052832.1	TRANSCRIPT	Hs RNA
		Homo sapiens mRNA for alternative...**GDNF**, HFK2	AJ001899.1	TRANSCRIPT	Hs RNA
		Homo sapiens mRNA for alternative...**GDNF**, HFK4	AJ001898.1	TRANSCRIPT	Hs RNA
		Homo sapiens mRNA for alternative...**GDNF**, HFK3	AJ001897.1	TRANSCRIPT	Hs RNA
		Homo sapiens glial cell line...**GDNF**) mRNA, partial cds	AF053748.1	TRANSCRIPT	Hs RNA
		Homo sapiens **GDNF** family receptor alpha 3 (GFRA3) mRNA...	AF051767.1	TRANSCRIPT	Hs RNA
		Hirschsprung disease, _id_142623_/id__name_142623_/name_; Central...	Hirschsprung disease, 142623;	Marker	Morbid
		glial cell line-derived neurotrophic factor receptor alpha-3	GFRA3	Gene	Genes_cyto | Genes_seq
		GDNF : glial derived neurotrophic factor	GDNF	Gene	Genes_cyto | Genes_seq
		GDNF : glial cell derived neurotrophic factor	GDNF	PHENOTYPE	Pheno
		Gdnf	Gdnf	STS	STS

Quick Filter
- Gene
- Transcript
- STS
- Unigene

Filter


NCBI
NCBI Map Viewer
PubMed
Entrez
BLAST
OMIM
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_seq Symbol O
Links
E
Cyto
Description
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
You are here:
default
master
GDNF + OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq 5p13.1-p12 glial cell derived neurotrophic factor


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 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:
37,833,500
37,893,600 Go
out
zoom
in
You are here:
Ideogram

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_seq | Symbol O | Links | E | Cyto | Description

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

Homo sapiens (Build 36.2)
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 (Build 36.2)
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

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

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

ADD>>
<<REMOVE

Maps Displayed (left to right):

Change Assembly

[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

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:
37,828,300
37,895,800
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 [clear]

Master Map: Genes On Sequence

Summary of Maps

Maps & Options

Region Displayed: 37,828,300-37,895,800 bp

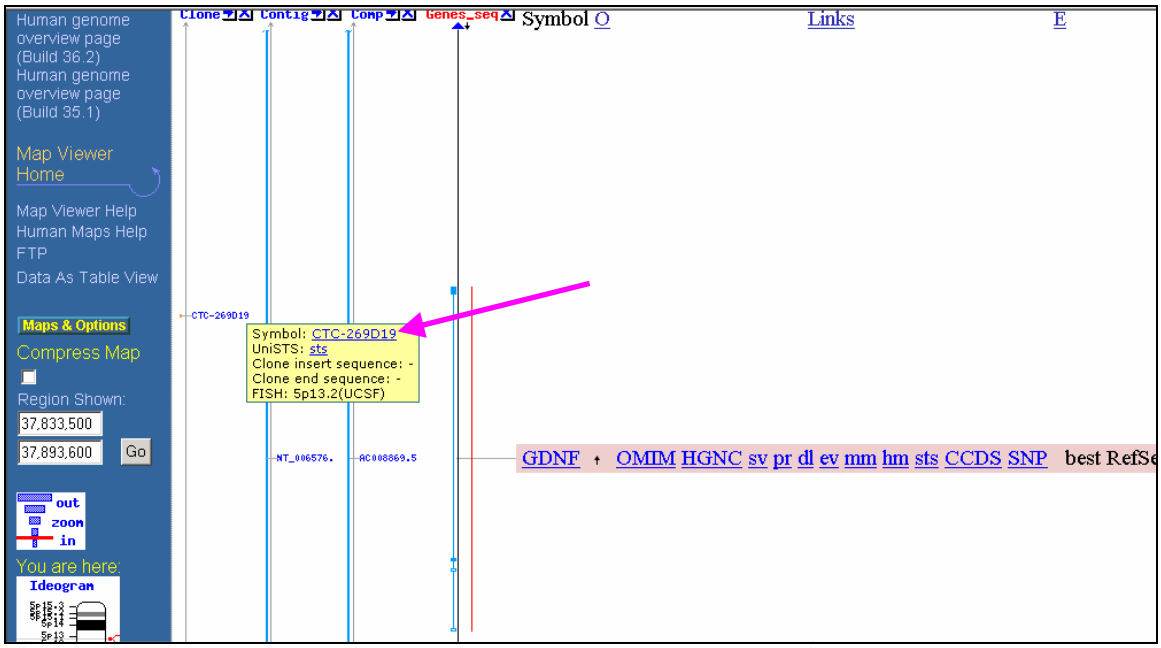
Download/View Sequence/Evidence

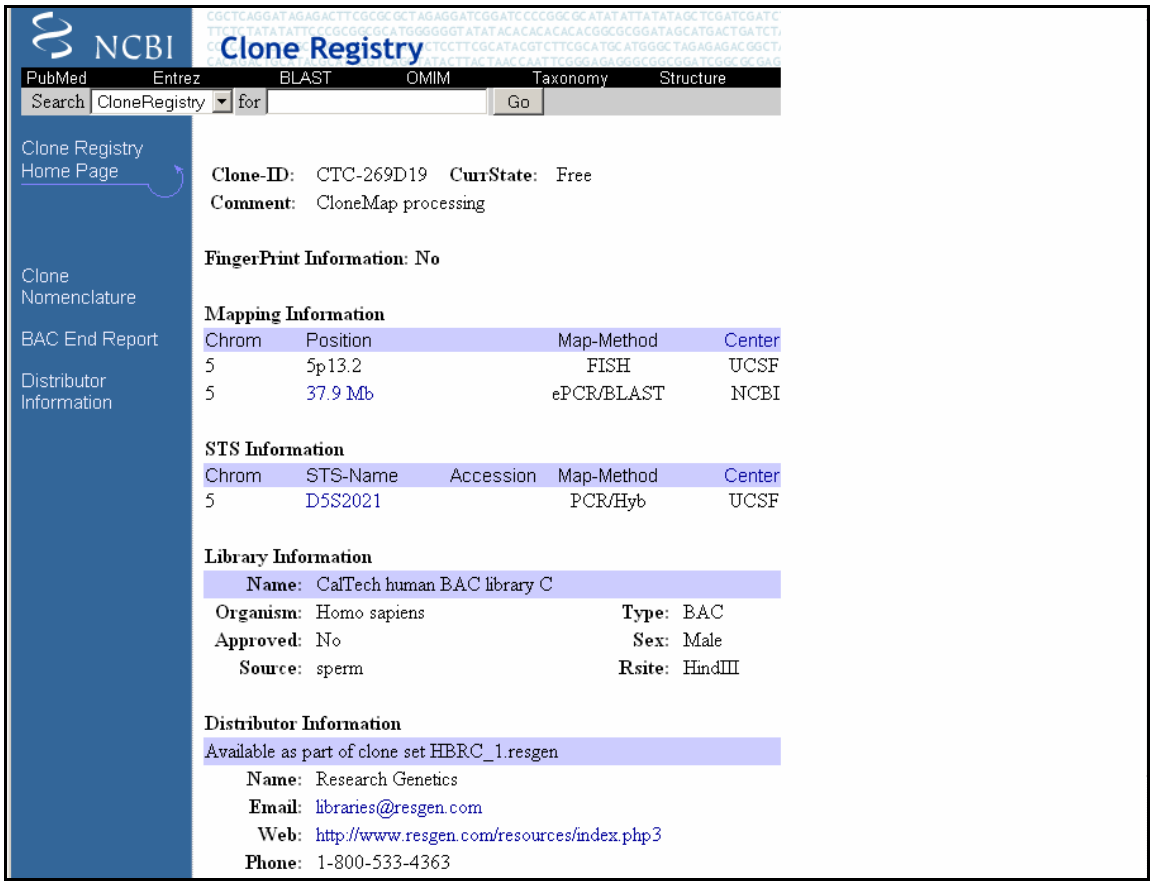
Clone Contig Comp Genes_seq Symbol O Links E Cyto Description

CTC-269D19

NT_006576. AC008869.5

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


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:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
Clone
Contig
Comp
Genes_seq
Symbol
Links
CTC-269D19
Symbol: CTC-269D19
UniSTS: sts
Clone insert sequence: -
Clone end sequence: -
FISH: 5p13.2(UCSF)
NT_006576.
AC008869.5
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS SNP
best RefSe


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

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:
37,828,300
37,895,800 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 [clear]

Master Map: Genes On Sequence

Summary of Maps

Maps & Options

Region Displayed: 37,828,300-37,895,800 bp

Download/View Sequence/Evidence

Model RefSeq RNA Genes_seq Symbol O Links E Cyto Description

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

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

Total Genes On Chromosome: **1268** [3 not localized]

Genes in Region: **1**

start	stop	Symbol O	Links	E	Cyto	Description
37851510	37875539	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: **37,833,500-37,893,600 bp** Download/View Sequence/Evidence Download Data

Total models On Chromosome: **5351** [7 not localized]

models in Region: **6**

start	stop	Symbol	O	Best hit	Best hit description
37841490	37848120	hmm142934	-		
37851510	37871350	hmm99527	-	NP_954701.1	glial cell derived neurotrophic factor isoform 2 precursor [Homo sapiens]
37851510	37871686	hmm99761	-	NP_000505.1	glial cell derived neurotrophic factor isoform 1 preproprotein [Homo sapiens]
37851510	37871686	hmm99293	-	NP_954701.1	glial cell derived neurotrophic factor isoform 2 precursor [Homo sapiens]
37851510	37875539	hmm99995	-	NP_000505.1	glial cell derived neurotrophic factor isoform 1 preproprotein [Homo sapiens]
37872457	37878200	hmm143168	+	BAA20782.3	KIAA0324 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: **1468** [3 not localized]

RefSeq Transcripts in Region: **3**

start	stop	Accession	Locus	O		Links	Align quality	Description
37851510	37870655	NM_199234.1	GDNF	-	ug	sv pr ev BLink	identical	glial cell derived neurotrophic factor
37851510	37851857	exon	-	CDS	348 bp			
37851858	37870593	intron			18736 bp			
37870594	37870647	exon	-	CDS	54 bp			
37870648	37870655	exon	-	UTR	8 bp			
37851510	37871350	NM_199231.1	GDNF	-	ug	sv pr ev BLink CCDS	identical	glial cell derived neurotrophic factor
37851510	37851994	exon	-	CDS	485 bp			
37851995	37870582	intron			18588 bp			
37870583	37870655	exon	-	CDS	73 bp			
37870656	37870681	exon	-	UTR	26 bp			
37870682	37871253	intron			572 bp			
37871254	37871350	exon	-	UTR	97 bp			
37851510	37875539	NM_000514.2	GDNF	-	ug	sv pr ev BLink CCDS	identical	glial cell derived neurotrophic factor
37851510	37851994	exon		CDS	485 bp			

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:
37,828,300
37,895,800
Go

out
zoom
in

You are here:
Ideogram
default

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]

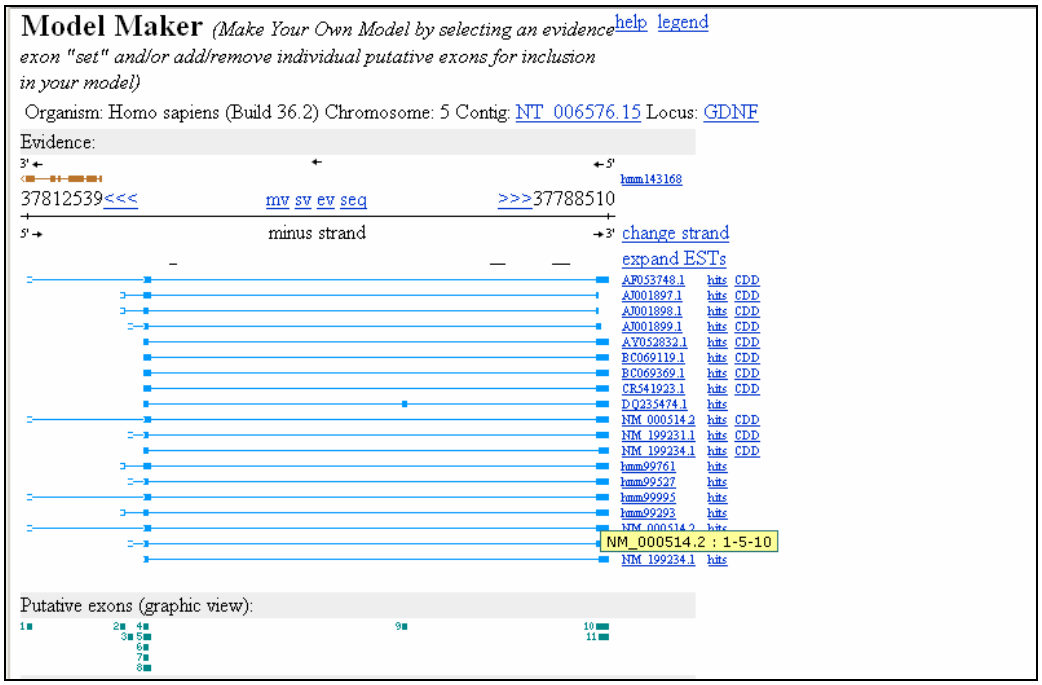
Master Map: Genes On Sequence Summary of Maps Maps & Options

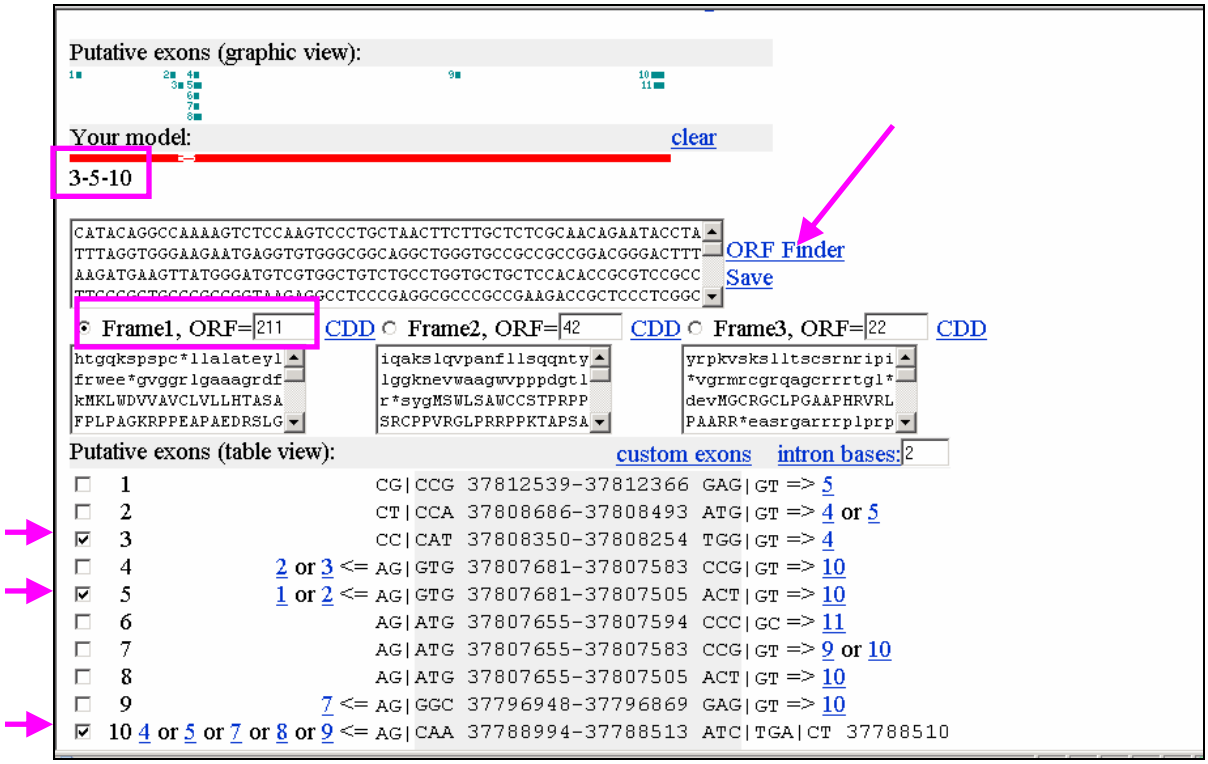
Region Displayed: **37,828,300-37,895,800 bp** Download/View Sequence/Evidence

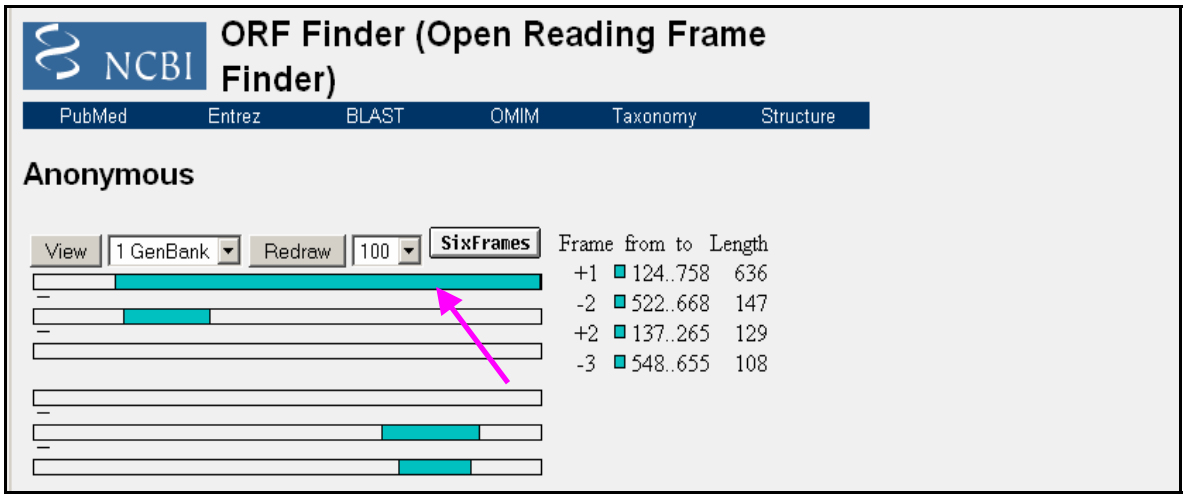
Model RefSeq RNA Genes_seq Symbol O Links E Cyto Description

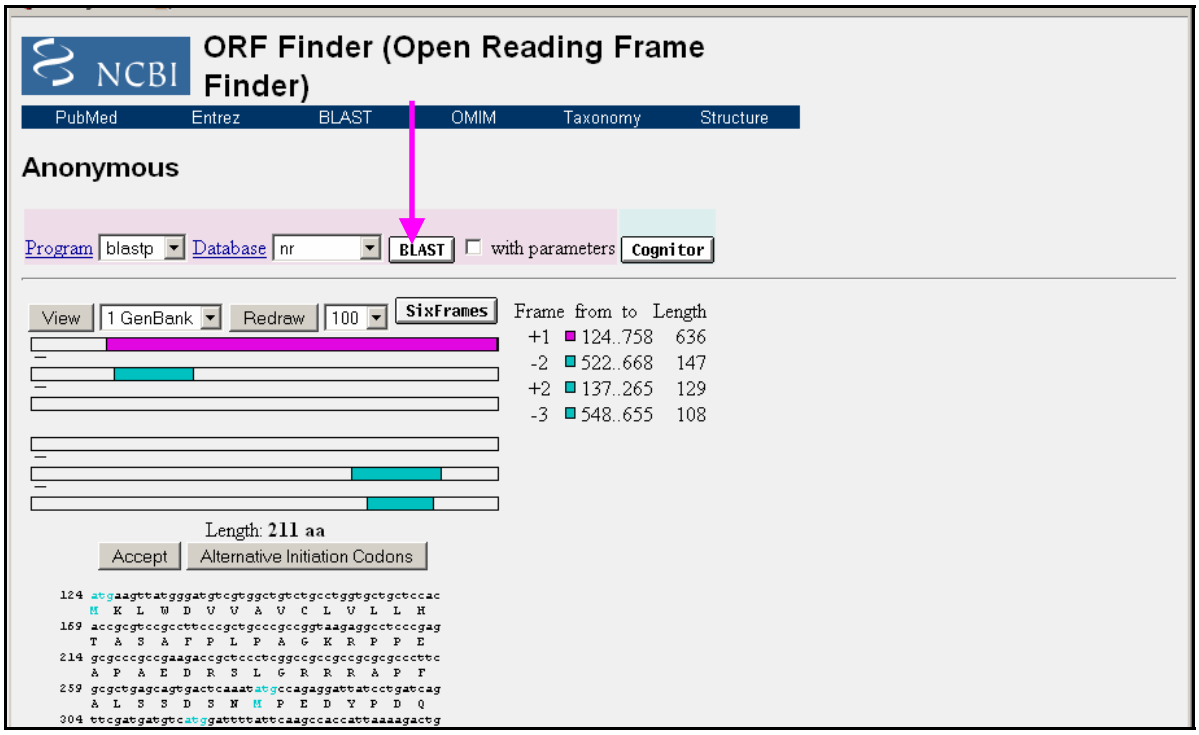
hmm142934
hmm99293
hmm99527
hmm99761
hmm99995
NM_199234.
NM_199231.
NM_000514.

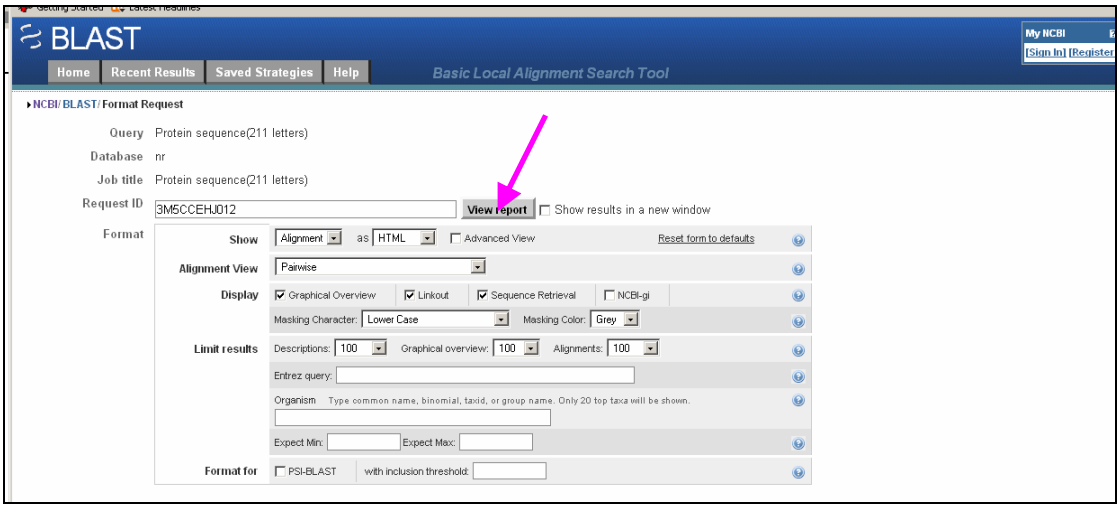
GDNF + OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq 5p13.1-p12 glial cell derived neurotrophic factor

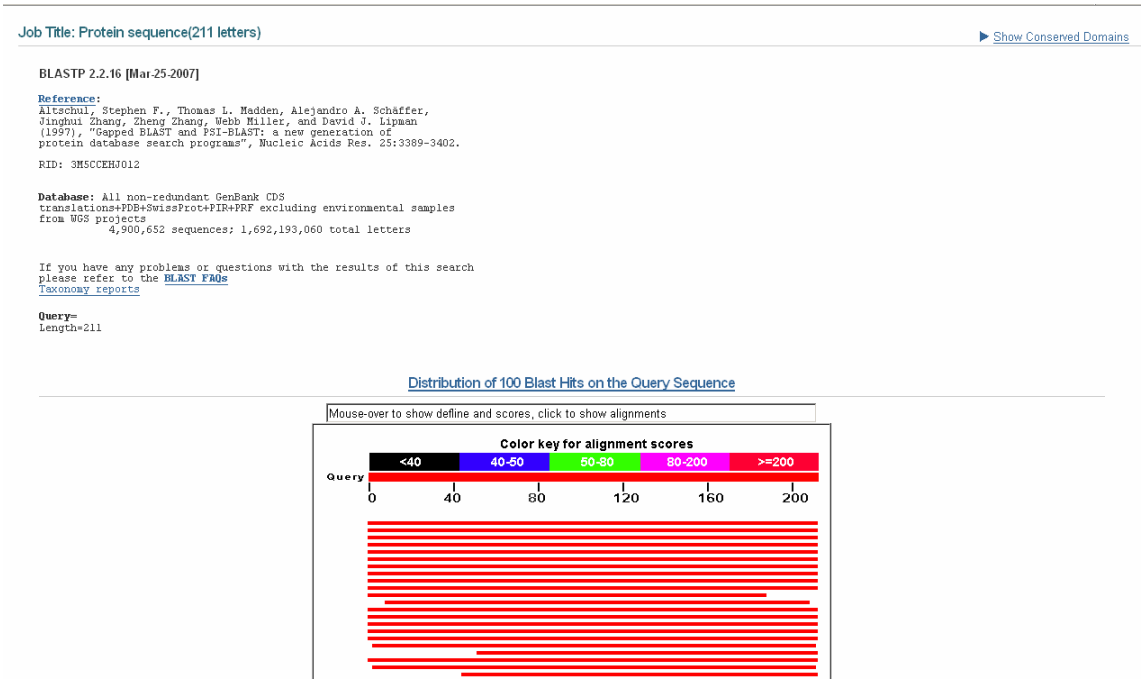

Model Maker (Make Your Own Model by selecting an evidence exon "set" and/or add/remove individual putative exons for inclusion in your model)
help legend
Organism: Homo sapiens (Build 36.2) Chromosome: 5 Contig: NT_006576.15 Locus: GDNF
Evidence:
37812539<<<
mv sv ev seq
>>>37788510
minus strand
change strand
expand ESTs
NM_000514.2 : 1-5-10
Putative exons (graphic view):


Putative exons (graphic view):
Your model:
clear
3-5-10
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 CT|CCA 37808686-37808493 ATG|GT => 4 or 5
3 CC|CAT 37808350-37808254 TGG|GT => 4
4 2 or 3 <= AG|GTG 37807681-37807583 CCG|GT => 10
5 1 or 2 <= AG|GTG 37807681-37807505 ACT|GT => 10
6 AG|ATG 37807655-37807594 CCC|GC => 11
7 AG|ATG 37807655-37807583 CCG|GT => 9 or 10
8 AG|ATG 37807655-37807505 ACT|GT => 10
9 7 <= AG|GGC 37796948-37796869 GAG|GT => 10
10 4 or 5 or 7 or 8 or 9 <= AG|CAA 37788994-37788513 ATC|TGA|CT 37788510


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

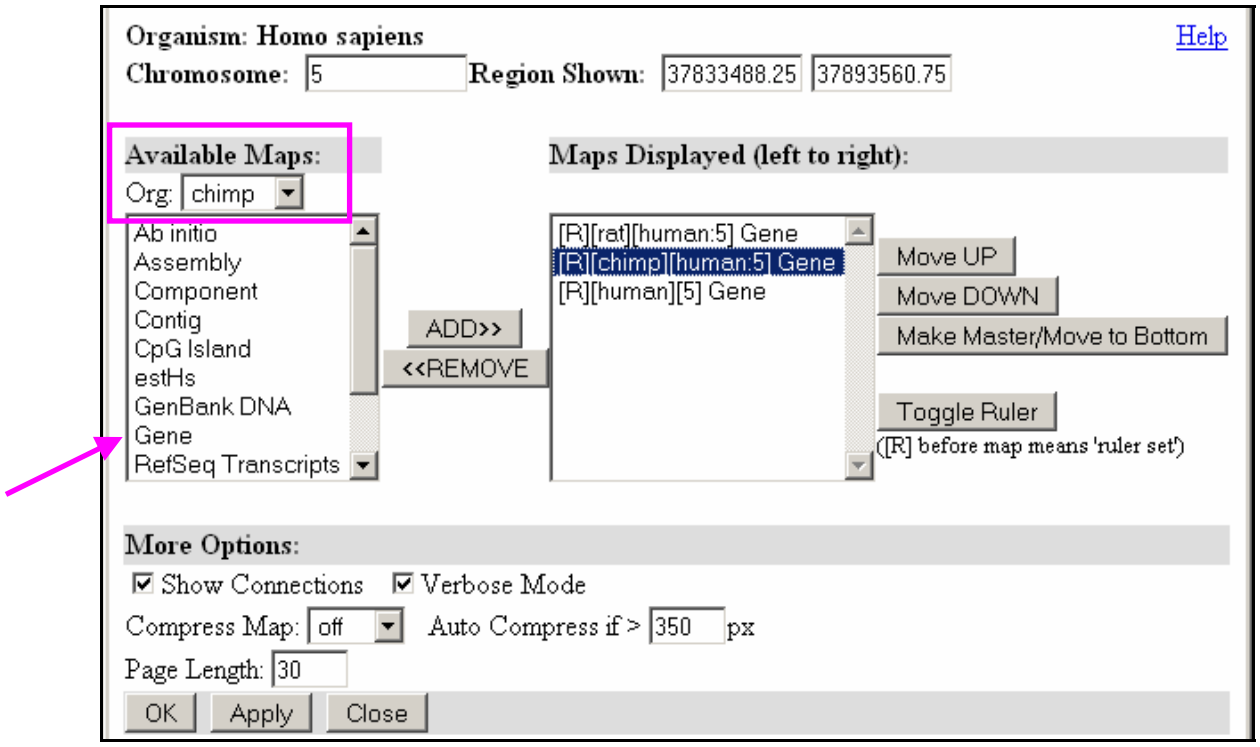

BLAST
Home
Recent Results
Saved Strategies
Help
Basic Local Alignment Search Tool
My NCBI
[Sign In] [Register
NCBI/ BLAST/ Format Request
Query Protein sequence(211 letters)
Database nr
Job title Protein sequence(211 letters)
Request ID 3M5CCEHJ012
View report
Show results in a new window
Format
Show 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
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:

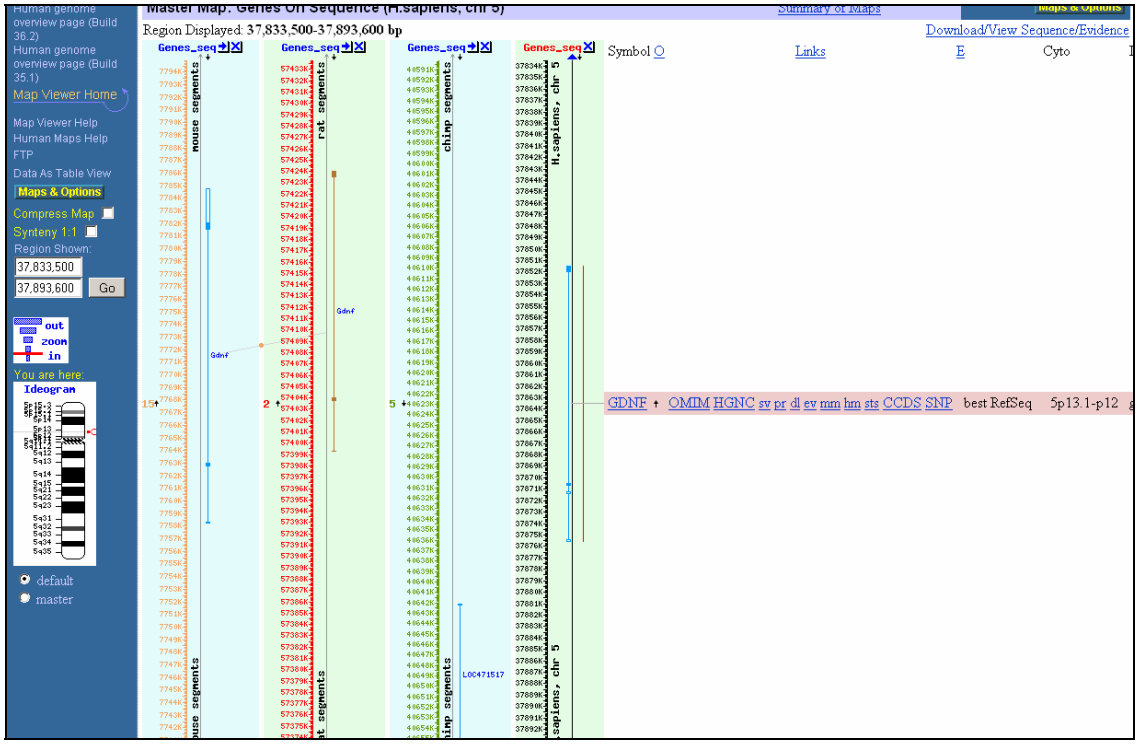

Job Title: Protein sequence(211 letters)
Show Conserved Domains
BLASTP 2.2.16 [Mar-25-2007]
Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
protein database search programs", Nucleic Acids Res. 25:3389-3402.
RID: 3M5CCEHJ012
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF 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
Mouse-over to show defline and scores, click to show alignments
Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
0
40
80
120
160
200

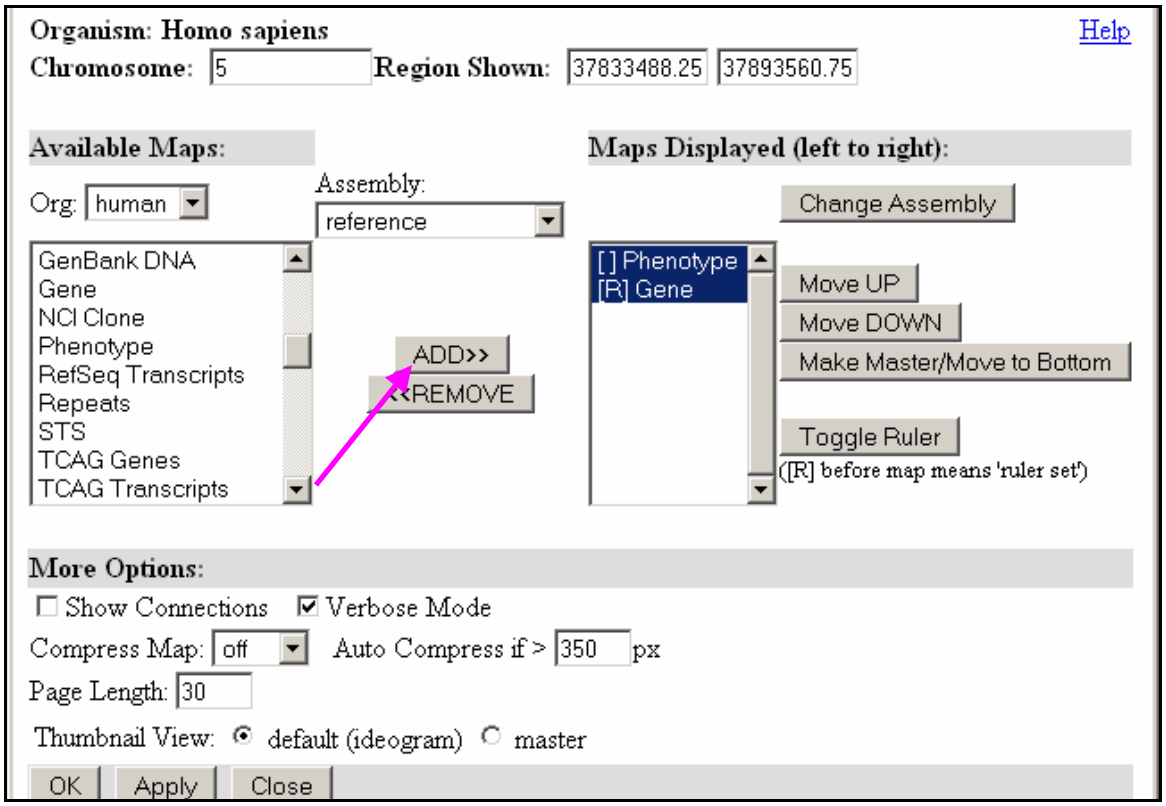
Alignments

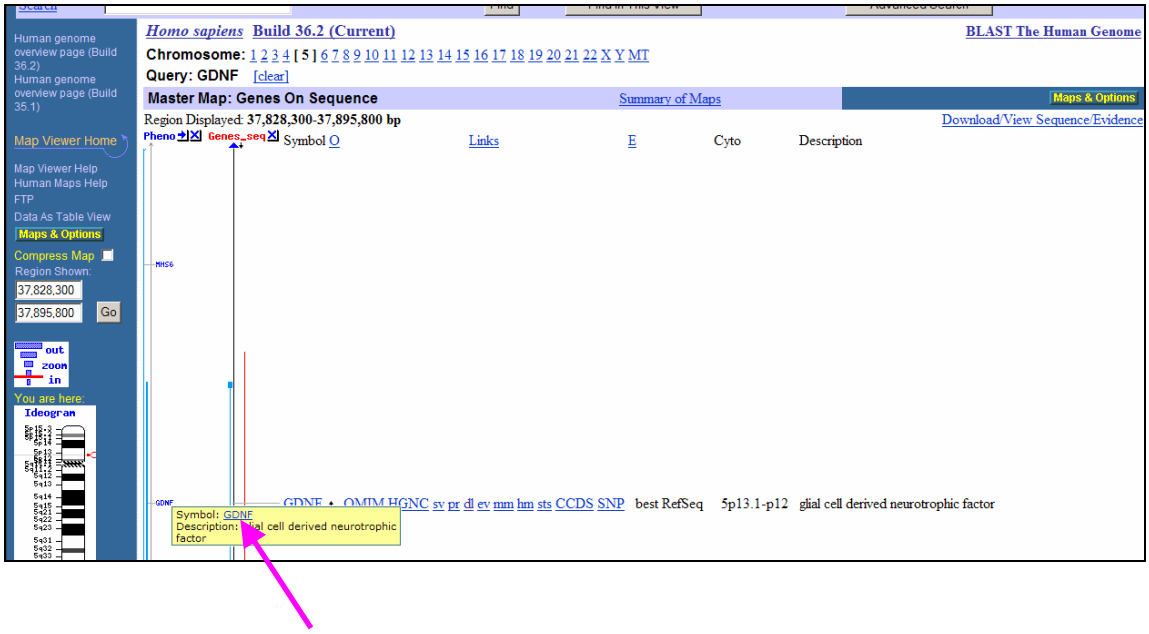
```
>ref|XP_001143054.1| PREDICTED: similar to neurotrophic factor isoform 3 [Pan troglodytes]
 gb|EAW55964.1| glial cell derived neurotrophic factor, isoform CRA_b [Homo sapiens]
Length=228

 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%)

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


>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: 5
Region Shown: 37833488.25 37893560.75
Available Maps:
Org: chimp
Ab initio
Assembly
Component
Contig
CpG Island
estHs
GenBank DNA
Gene
RefSeq Transcripts
ADD>>
<<REMOVE
Maps Displayed (left to right):
[R][rat][human:5] Gene
[R][chimp][human:5] Gene
[R][human][5] 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
OK
Apply
Close


Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
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
Genes_seq
mouse segments
rat segments
chimp segments
H.sapiens, chr 5
Symbol
Links
Cyto
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS SNP
best RefSeq
5p13.1-p12


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


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: 37,828,300-37,895,800 bp
Download/View Sequence/Evidence
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Compress Map
Region Shown:
37,828,300
37,895,800
Go
You are here:
Ideogram
Symbol
Links
Cyto
Description
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS SNP
best RefSeq
5p13.1-p12
glial cell derived neurotrophic factor
Symbol: GDNF

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

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

GeneTests, Links

***600837**

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 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.