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".

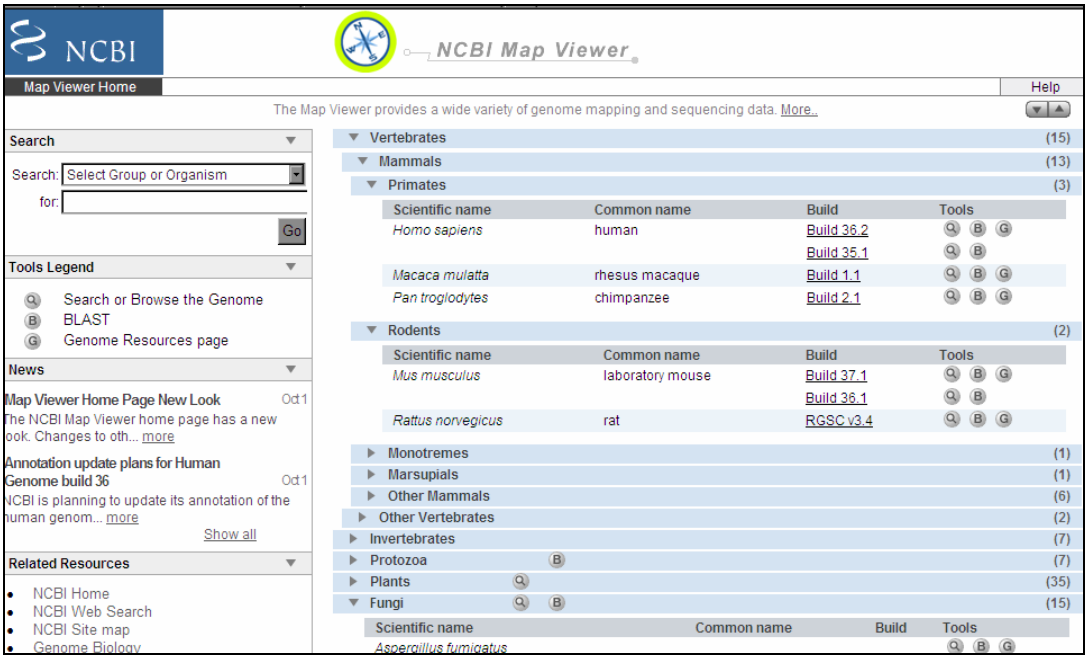
Using the Model Maker (mm), obtain a possible alternatively spliced product and its translated amino acid sequence. Search for similar proteins by using BLAST.

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.

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

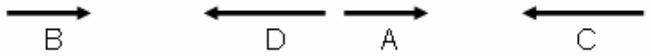
- Locate a human gene
- Download the gene sequence along with its upstream region (for promoter analysis)
- Determine whether the sequence is in draft or finished form
- Find a possible splice variant via Model Maker
- Identify whether variations in the gene are associated with a disease
- Obtain information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

High Throughput Genomic Sequences

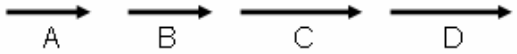
Sequencing of BACs:

Draft:

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



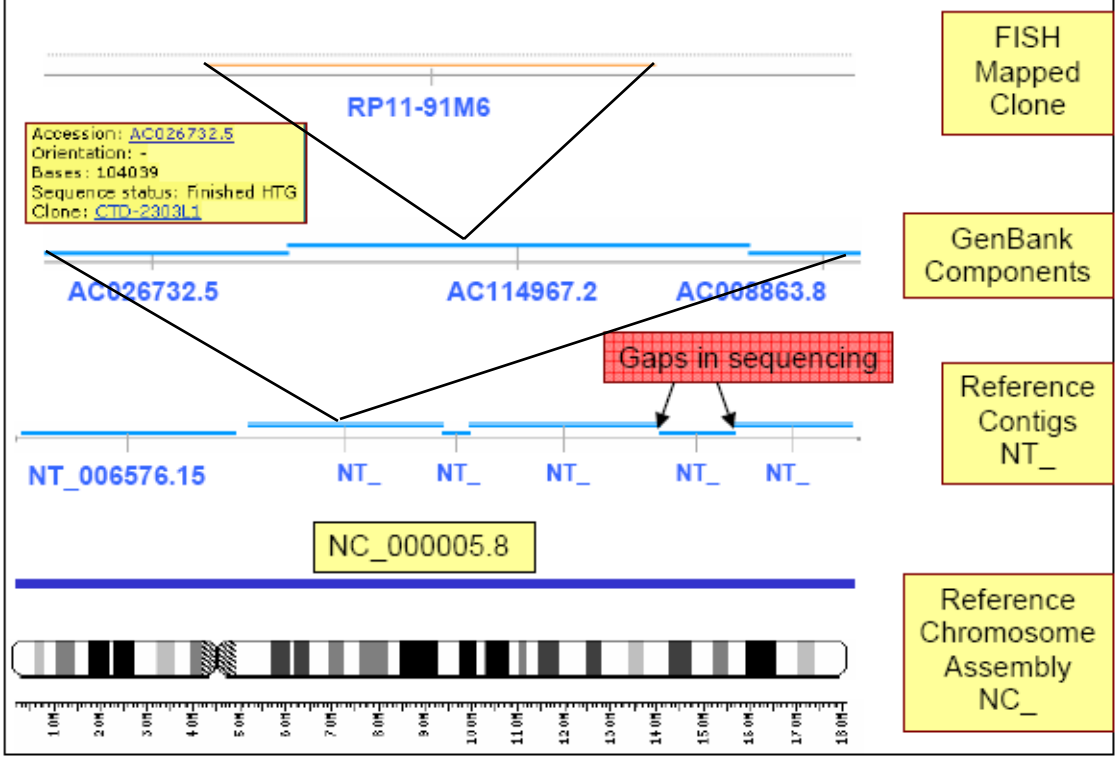
Phase 2 – unfinished, ordered with gaps



Finished:

Phase 3 – high quality finished sequence with no gaps

Genome Assembly Accession Numbers



NCBI

NCBI Map Viewer

Map Viewer Home | Help

The Map Viewer provides a wide variety of genome mapping and sequencing data. More..

Search

Search: Select Group or Organism

for:

Go

Tools Legend

- Search or Browse the Genome
- BLAST
- Genome Resources page

News

Map Viewer Home Page New Look Oct 1

The NCBI Map Viewer home page has a new look. Changes to oth... more

Annotation update plans for Human Genome build 36 Oct 1

NCBI is planning to update its annotation of the human genom... more

Show all

Related Resources

- NCBI Home
- NCBI Web Search
- NCBI Site map
- Genome Biology

▼ Vertebrates			(15)
▼ Mammals			(13)
▼ Primates			(3)
Scientific name	Common name	Build	Tools
Homo sapiens	human	Build 36.2	
		Build 35.1	
Macaca mulatta	rhesus macaque	Build 1.1	
Pan troglodytes	chimpanzee	Build 2.1	
▼ Rodents			(2)
Scientific name	Common name	Build	Tools
Mus musculus	laboratory mouse	Build 37.1	
		Build 36.1	
Rattus norvegicus	rat	RGSC v3.4	
▶ Monotremes			(1)
▶ Marsupials			(1)
▶ Other Mammals			(6)
▶ Other Vertebrates			(2)
▶ Invertebrates			(7)
▶ Protozoa			(7)
▶ Plants			(35)
▼ Fungi			(15)
Scientific name	Common name	Build	Tools
Aspergillus fumigatus			

NCBI

NCBI Map Viewer

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

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

All
reference
CRA_TCAGchr7v2
Celera
DR53
c22_H2
c5_H2
c6_COX
c6_QBL

BLAST search the human genome

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

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.

NCBI

NCBI Map Viewer

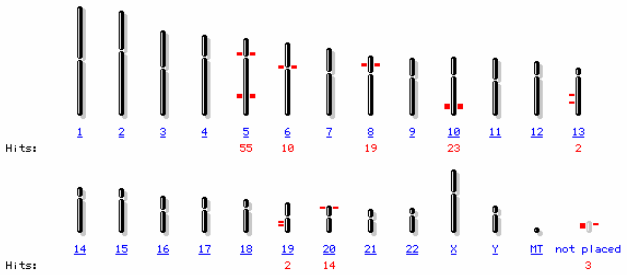
PubMed | Nucleotide | Protein | Genome | Gene | Structure | PopSet | Taxonomy | Help

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

Homo sapiens (human) genome view

Build 36.2 statistics Switch to previous build

BLAST search the human genome



Search results for query "GDNF": 128 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

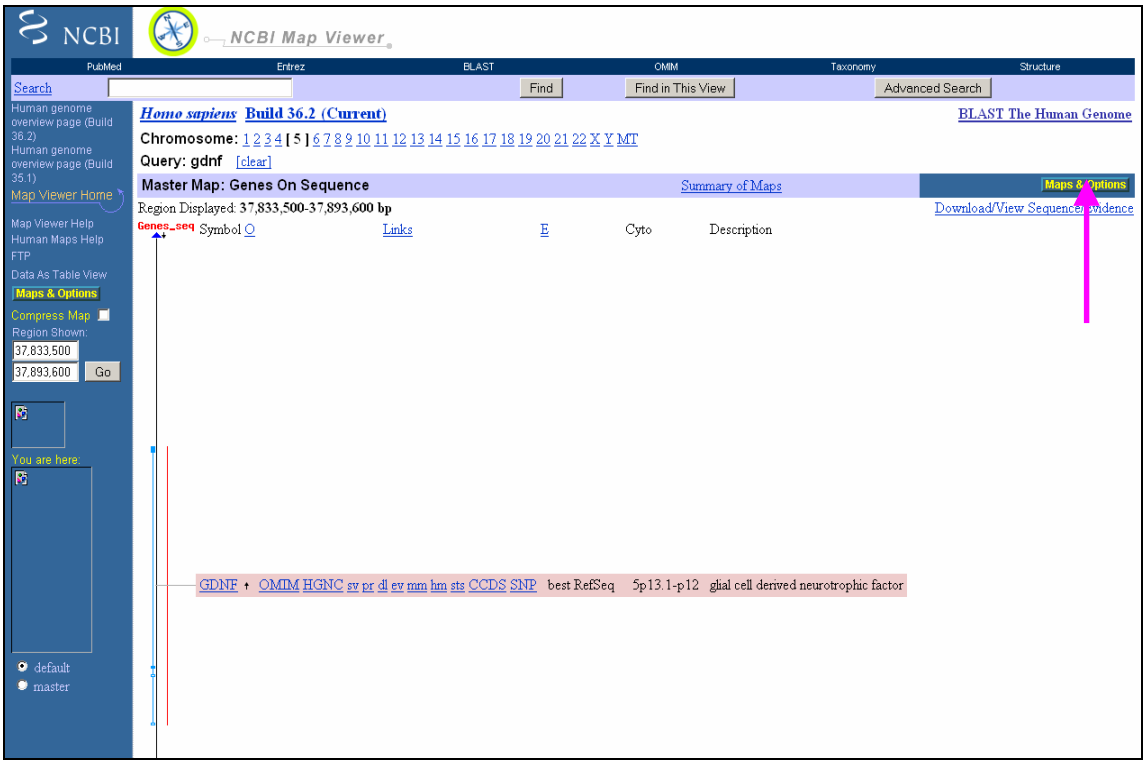
Chr	Assembly	Match	Map element	Type	Maps
5	reference	all matches			
		GDNF family receptor alpha 3	Hs.58042	Hs_EST_Cl	Hs UniG
		tk05a07.x1 NCI_CGAP_Lu24 Homo...**GDNF** FAMILY RECEPTOR ALPHA...	AI887844.1	TRANSCRIPT	Hs RNA
		Rattus norvegicus glial cell...**Gdnf**), mRNA	NM_019139.1	TRANSCRIPT	Rn RNA
		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

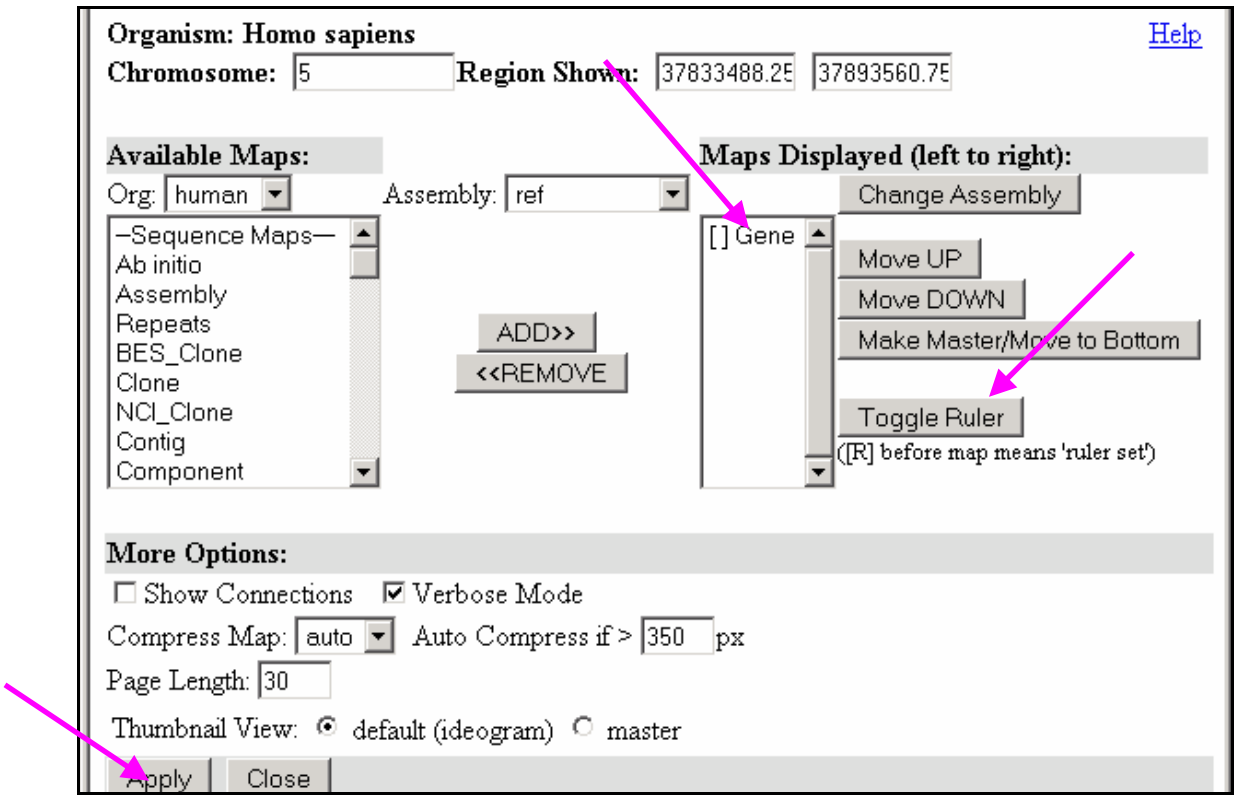
Quick Filter
- [x] Gene
Transcript :
- [ ] all
- [ ] RefSeq
- [ ] STS
- [ ] Unigene

Filter

Search results for query "GDNF AND gene[obj_type]": 14 hits

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


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 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
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
You are here:
default
master


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:
37,833K
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[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 O | Links | E | Cyto | Description

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

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)
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

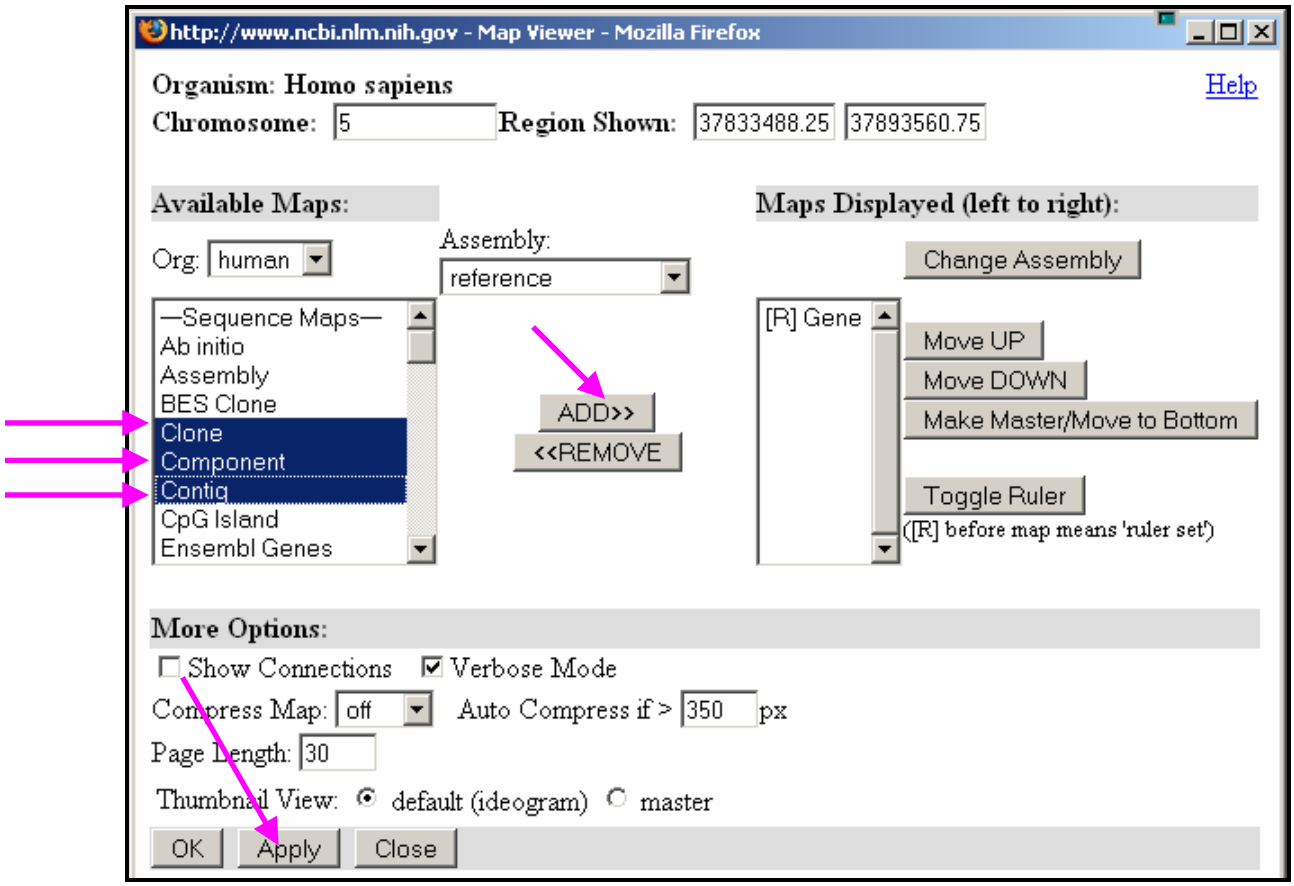
---

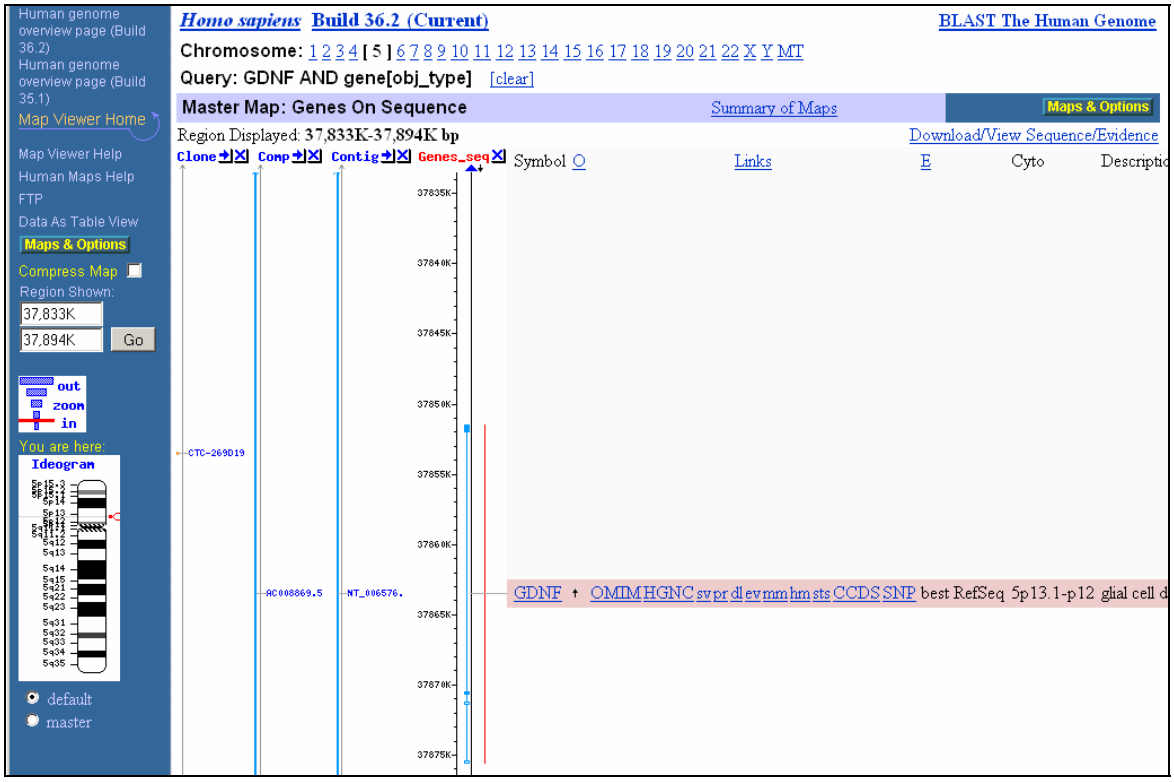
Homo sapiens (Build 36.2)
Region to retrieve (in chromosome coordinates):
Chromosome: 5 Strand: minus
from: 37851510 adjust by: -0K
to: 37875539 adjust by: +0K Change Region/Strand

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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master
Homo sapiens Build 36.2 (Current)
BLAST The Human Genome
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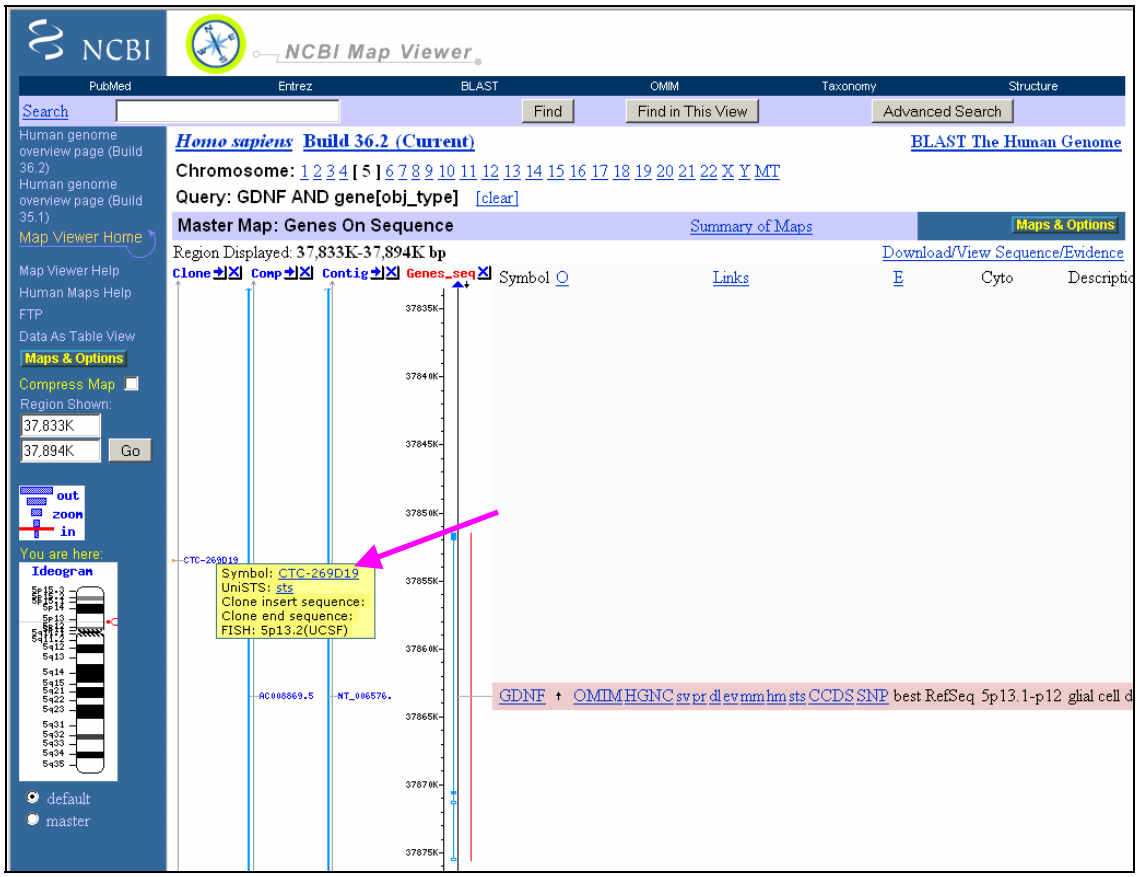
Query: GDNF AND gene[obj_type] [clear]
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 37,833K-37,894K bp
Download/View Sequence/Evidence
Clone
Comp
Contig
Genes_seq
Symbol
Links
Cyto
37835K
37840K
37845K
37850K
37855K
37860K
37865K
37870K
37875K
CTC-269D19
AC008869.5
NT_006576.
GDNF OMIM HGNC 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
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Human genome overview page (Build 36.2)
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37,833K
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You are here:
Ideogram
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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
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Region Displayed: 37,833K-37,894K bp
Download/View Sequence/Evidence
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Comp
Contig
Genes_seq
Symbol O
Links
E
Cyto
Descriptio
37835K
37840K
37845K
37850K
37855K
37860K
37865K
37870K
37875K
CTC-269D19
Symbol: CTC-269D19
UniSTS: sts
Clone insert sequence:
Clone end sequence:
FISH: 5p13.2(UCSF)
AC008869.5
NT_006576.
GDNF OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq 5p13.1-p12 glial cell d

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 from clone library

Name: Research Genetics

Email: libraries@resgen.com

Web: http://www.resgen.com/resources/index.php3

Available as part of clone set HBRC_1.resgen

Name: Research Genetics

Email: libraries@resgen.com

Web: http://www.resgen.com/resources/index.php3

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:

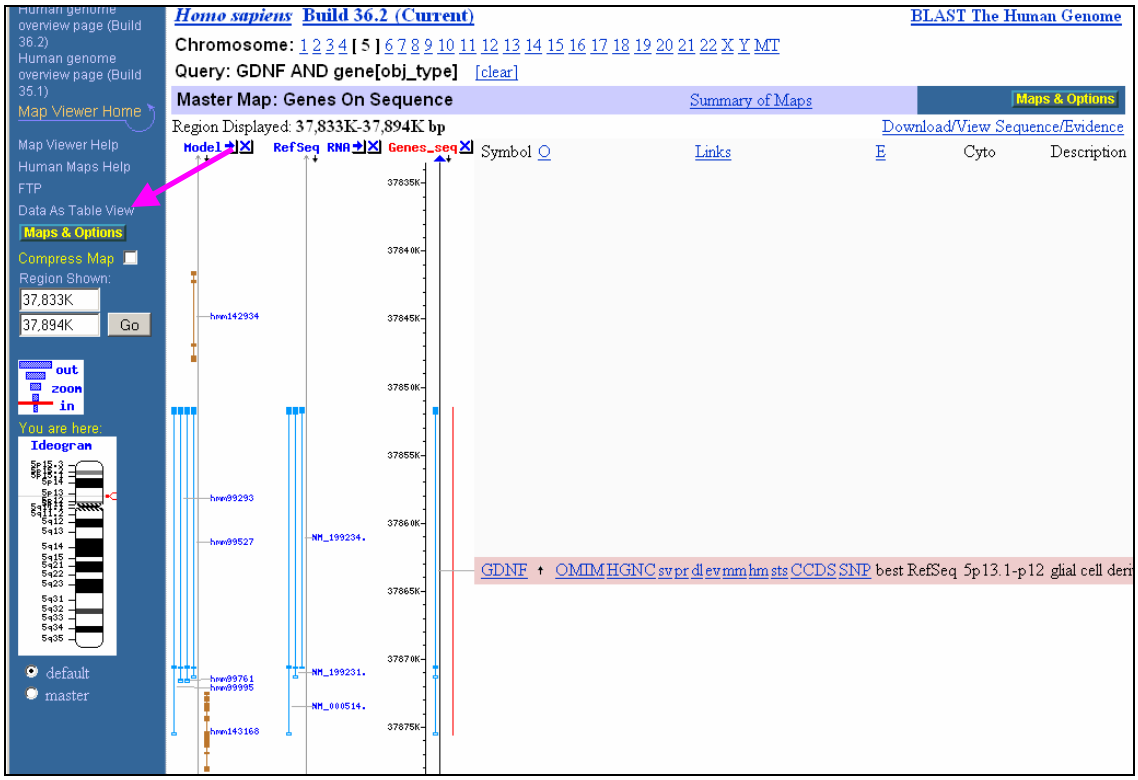
☐ Show Connections ☑ Verbose Mode

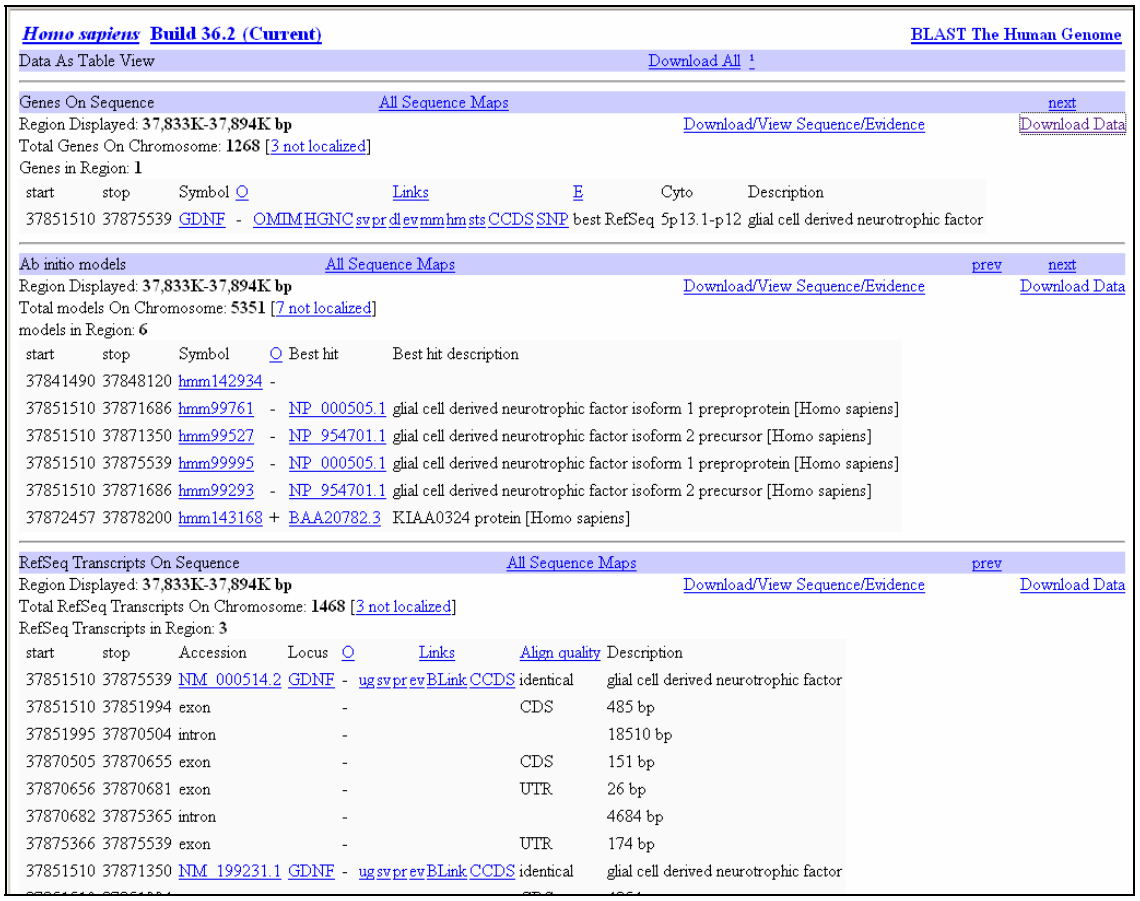
Compress Map: off Auto Compress if > 350 px

Page Length: 30

Thumbnail View: ○ default (ideogram) ○ master

OK Apply Close





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 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: **37,833K-37,894K bp** — Download/View Sequence/Evidence — Download Data

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

models in Region: **6**

start	stop	Symbol	O	Best hit	Best hit description
37841490	37848120	hmm142934	-		
37851510	37871686	hmm99761	-	NP_000505.1	glial cell derived neurotrophic factor isoform 1 preproprotein [Homo sapiens]
37851510	37871350	hmm99527	-	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]
37851510	37871686	hmm99293	-	NP_954701.1	glial cell derived neurotrophic factor isoform 2 precursor [Homo sapiens]
37872457	37878200	hmm143168	+	BAA20782.3	KIAA0324 protein [Homo sapiens]

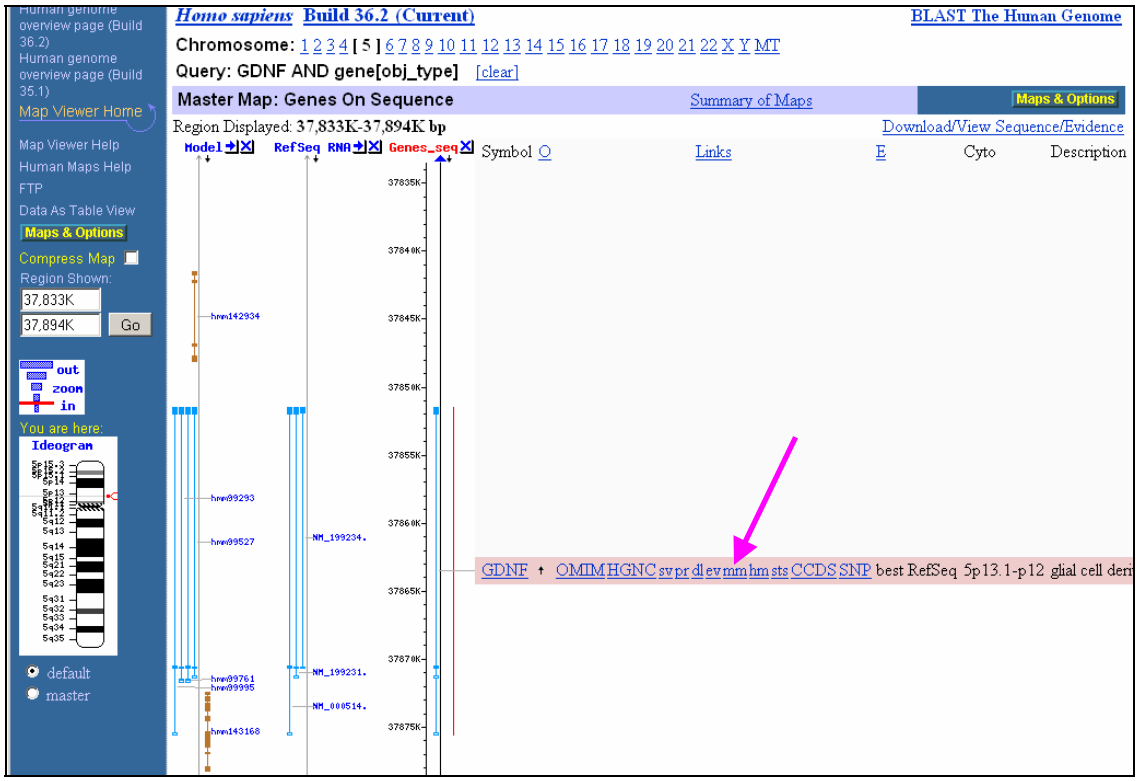
RefSeq Transcripts On Sequence — All Sequence Maps — prev

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	O	Links	Align quality	Description
37851510	37875539	NM_000514.2	GDNF	-	ug sv pr ev BLink CCDS	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	NM_199231.1	GDNF	-	ug sv pr ev BLink CCDS	identical	glial cell derived neurotrophic factor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BLAST The Human Genome
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Maps & Options
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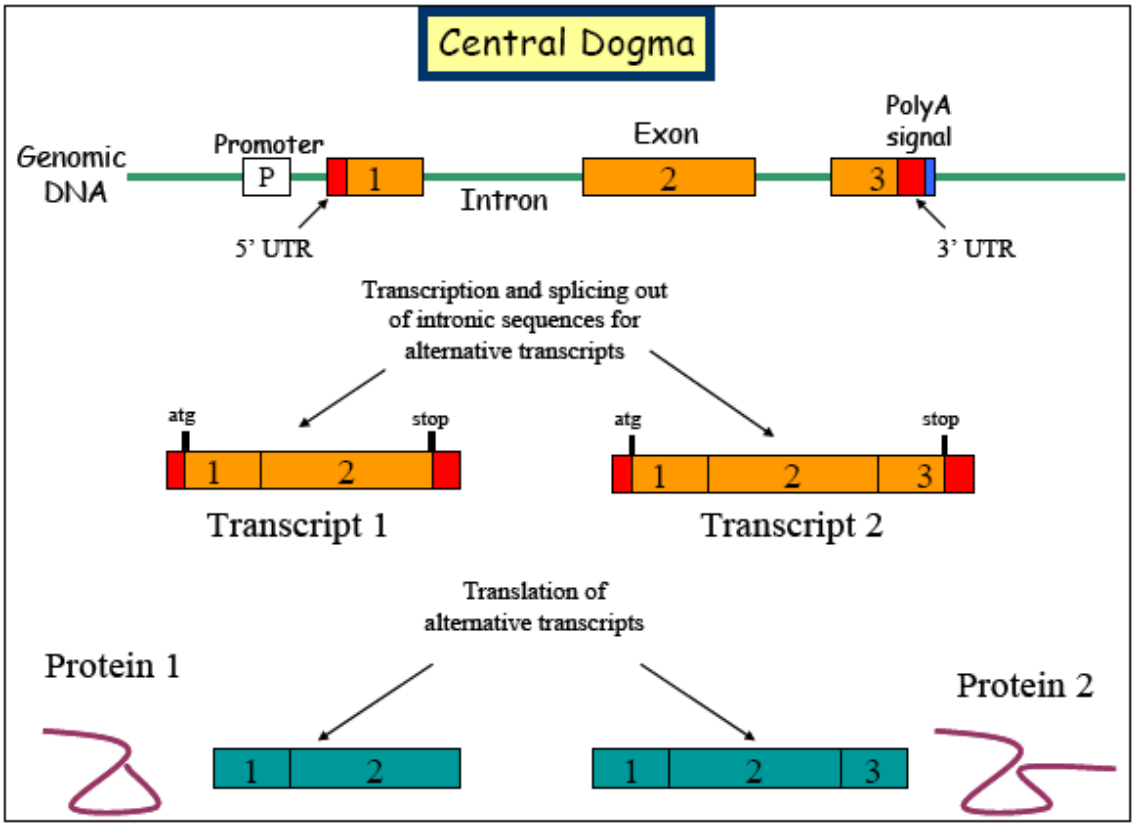
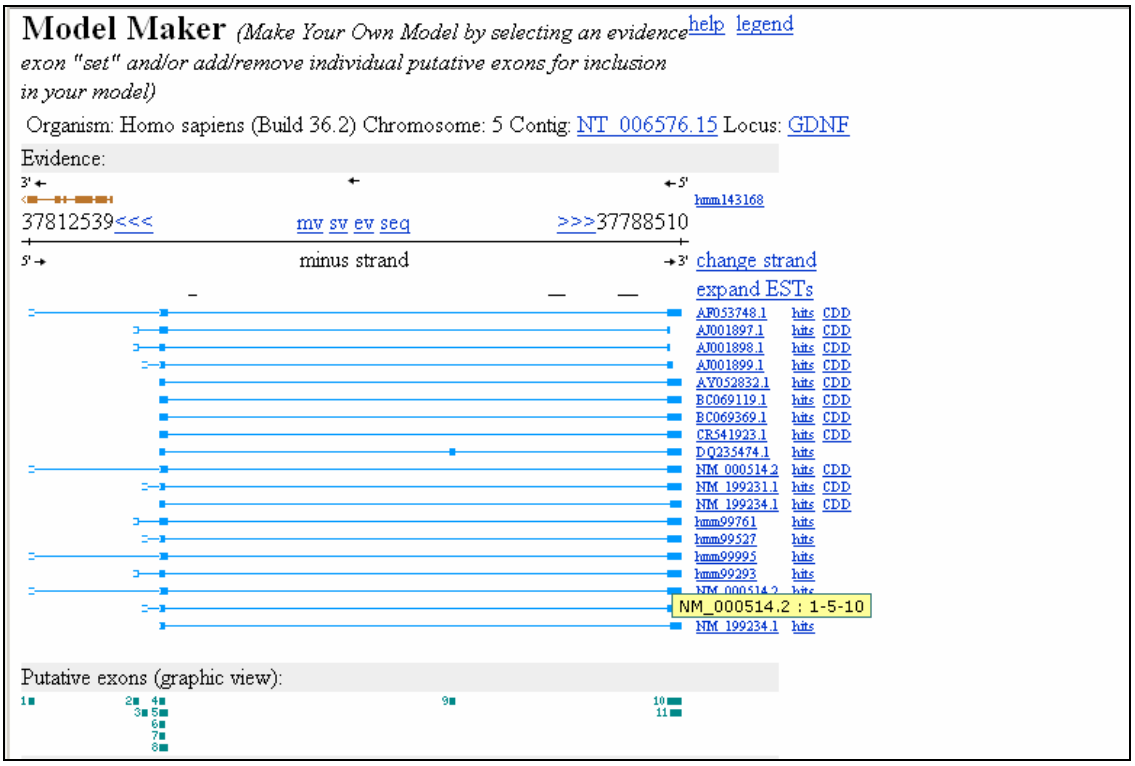
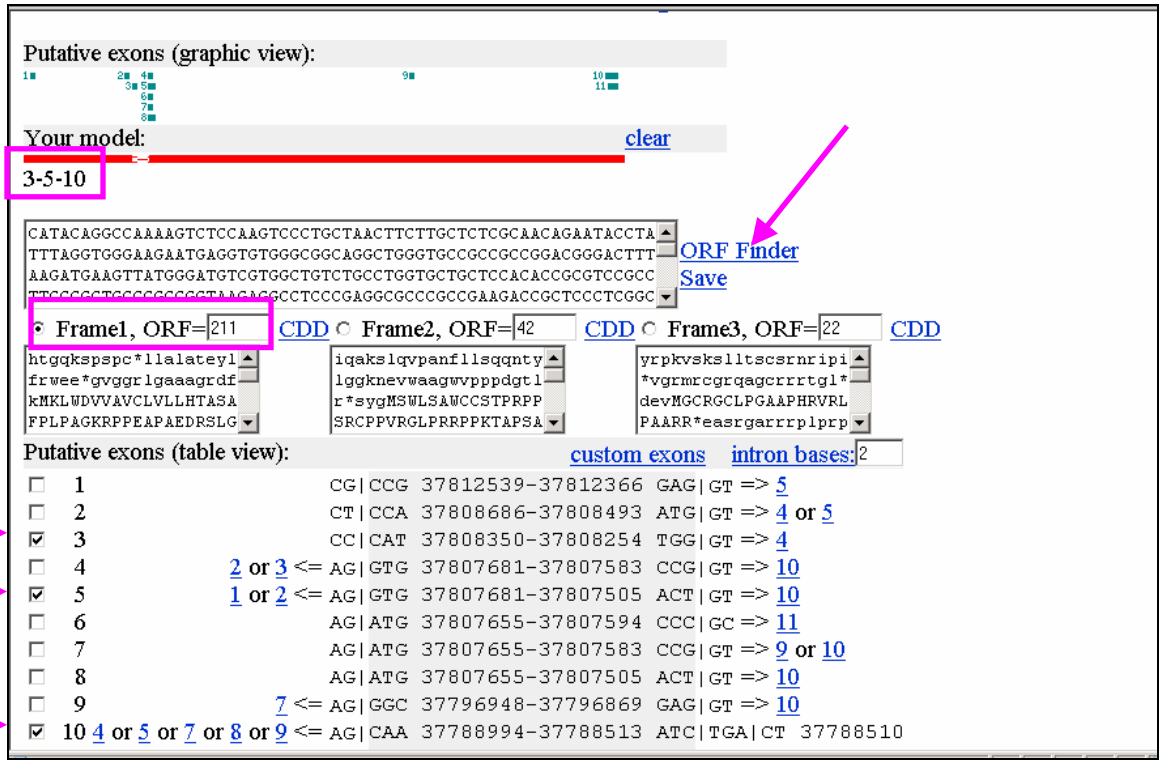
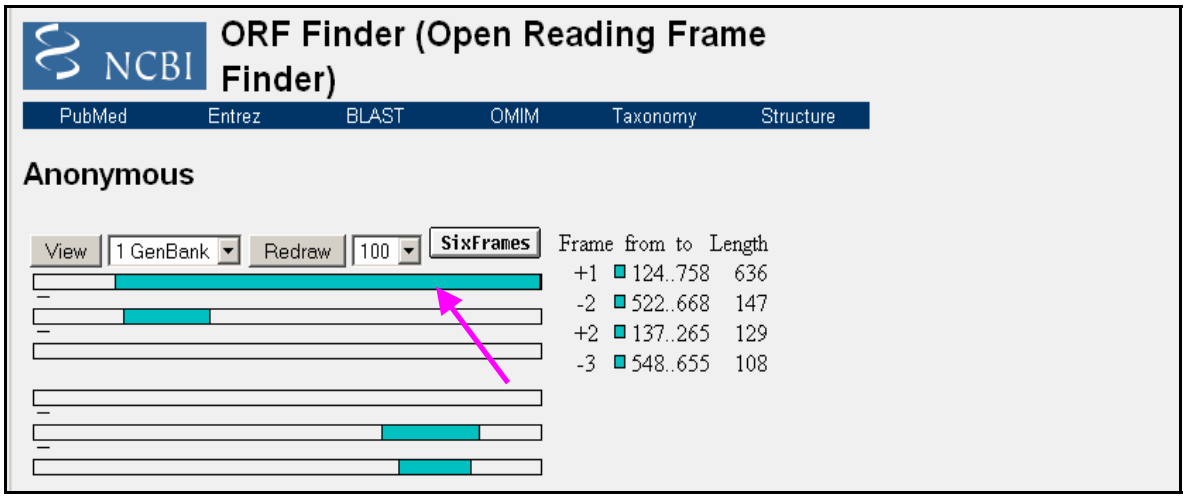
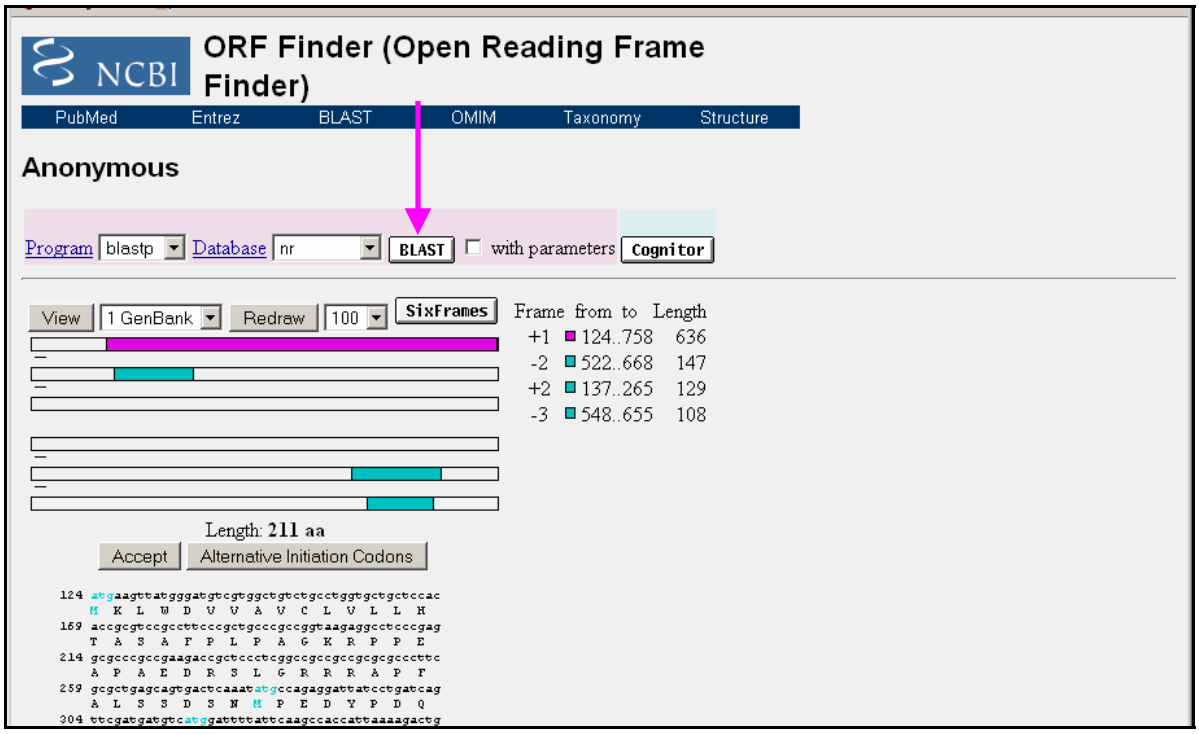
Data As Table View
Compress Map
Region Shown:
37,833K
37,894K
Go
out
zoom
in
You are here:
Ideogram
default
master
Model
RefSeq RNA
Genes_seq
Symbol
Links
Cyto
Description
GDNF OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSeq 5p13.1-p12 glial cell deri

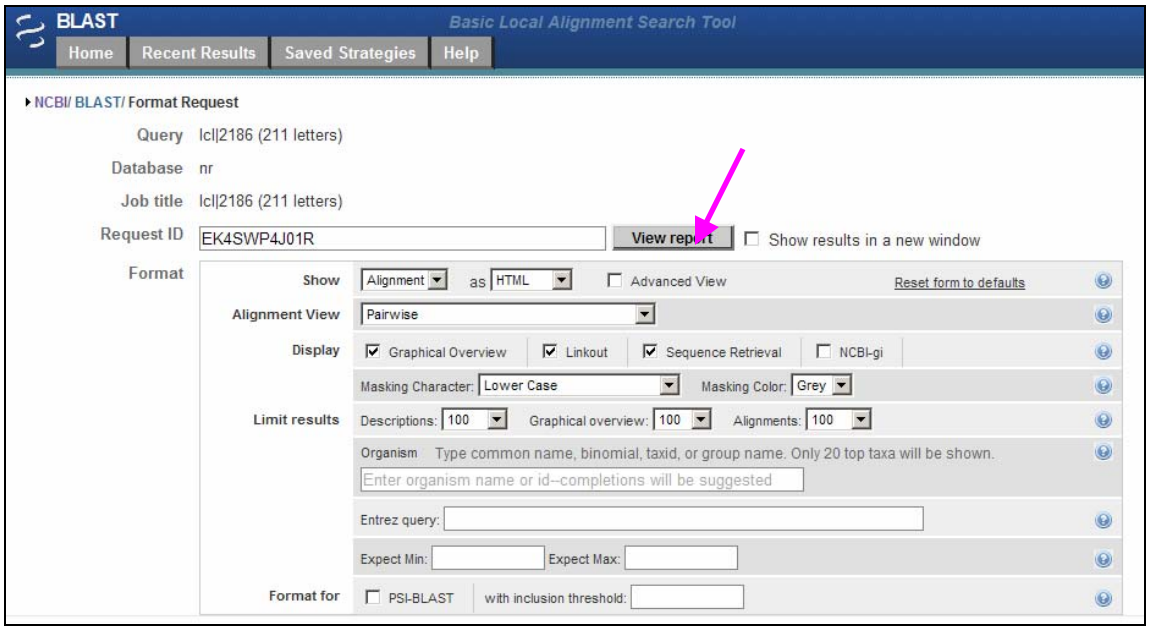

Central Dogma
Genomic DNA
Promoter
P
1
Intron
Exon
2
PolyA signal
3
5' UTR
3' UTR
Transcription and splicing out of intronic sequences for alternative transcripts
atg
stop
1
2
Transcript 1
atg
stop
1
2
3
Transcript 2
Translation of alternative transcripts
Protein 1
1
2
1
2
3
Protein 2

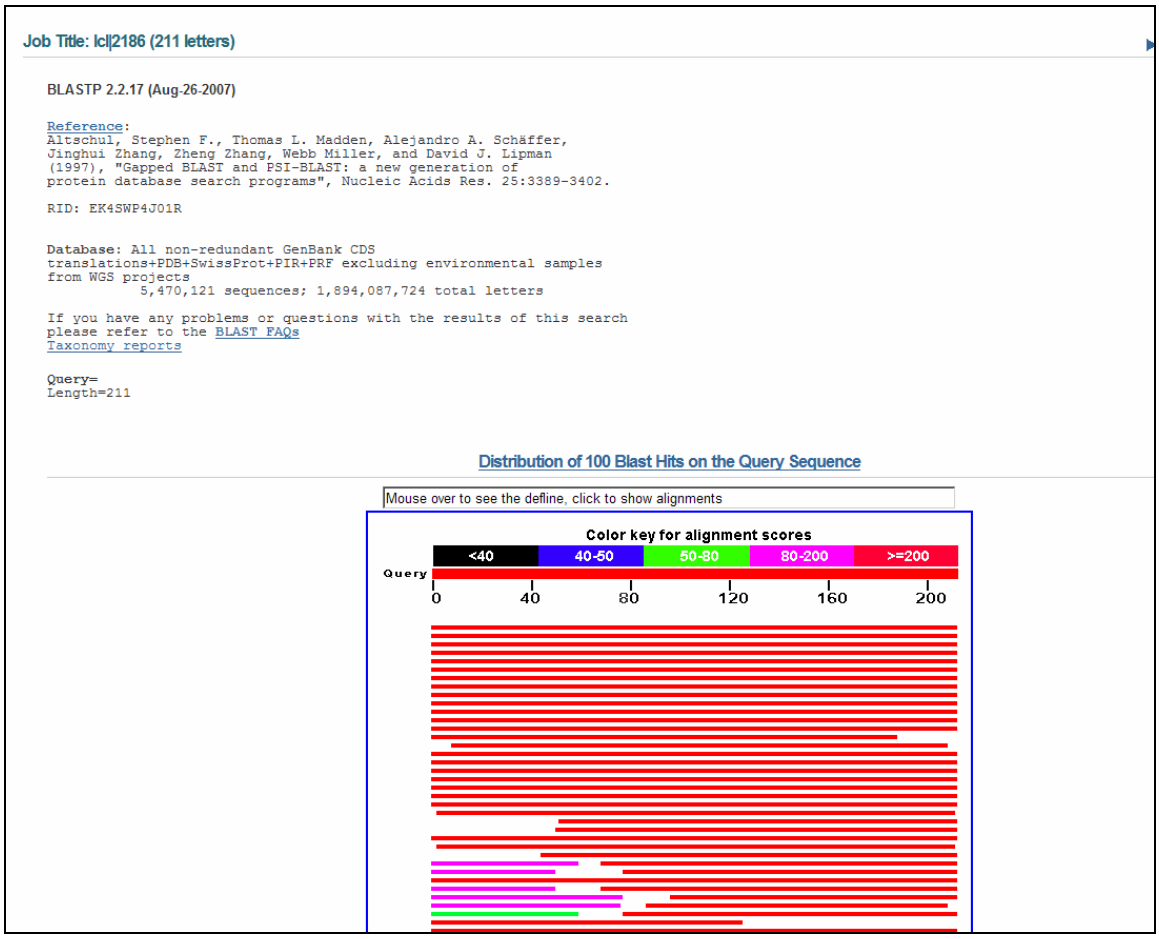

Model Maker (Make Your Own Model by selecting an evidence exon "set" and/or add/remove individual putative exons for inclusion in your model)
help legend
Organism: Homo sapiens (Build 36.2) Chromosome: 5 Contig: NT_006576.15 Locus: GDNF
Evidence:
37812539<<<
mv sv ev seq
>>>37788510
minus strand
change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

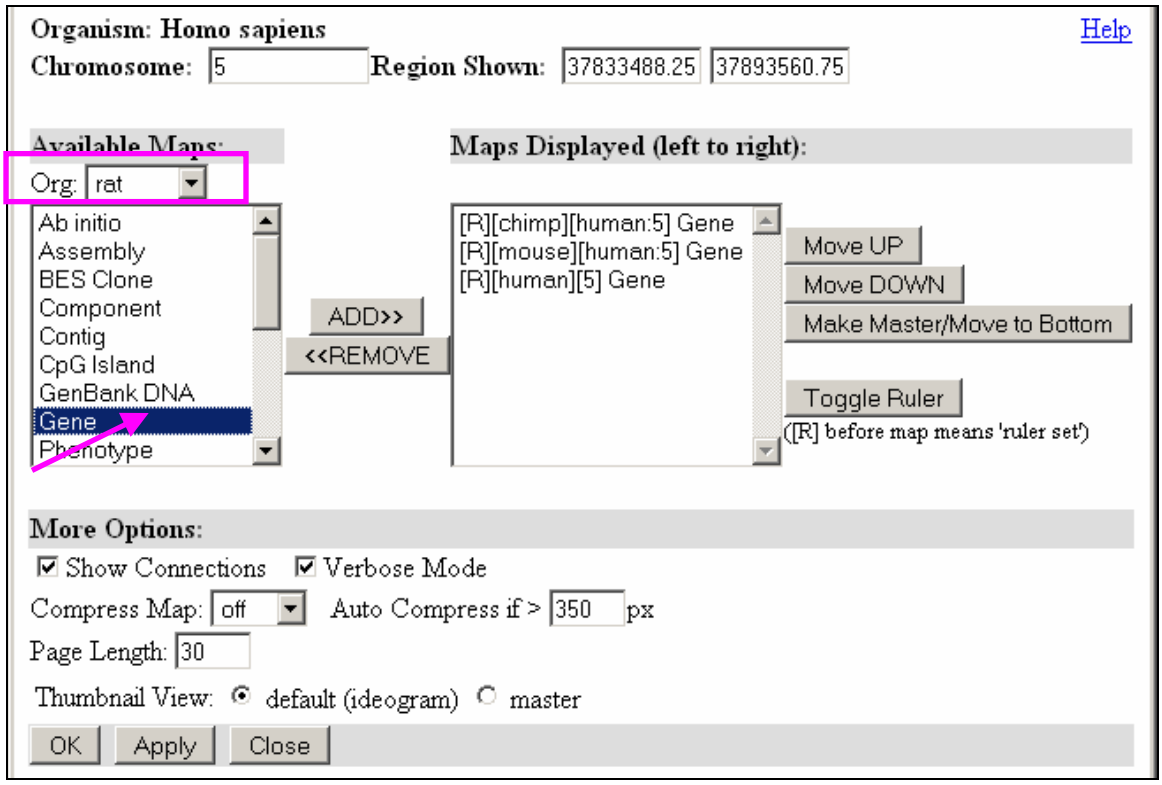

BLAST
Basic Local Alignment Search Tool
Home
Recent Results
Saved Strategies
Help
NCBI/ BLAST/ Format Request
Query lcl|2186 (211 letters)
Database nr
Job title lcl|2186 (211 letters)
Request ID EK4SWP4J01R
View report
Show results in a new window
Format
Show Alignment as HTML
Advanced View
Reset form 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:

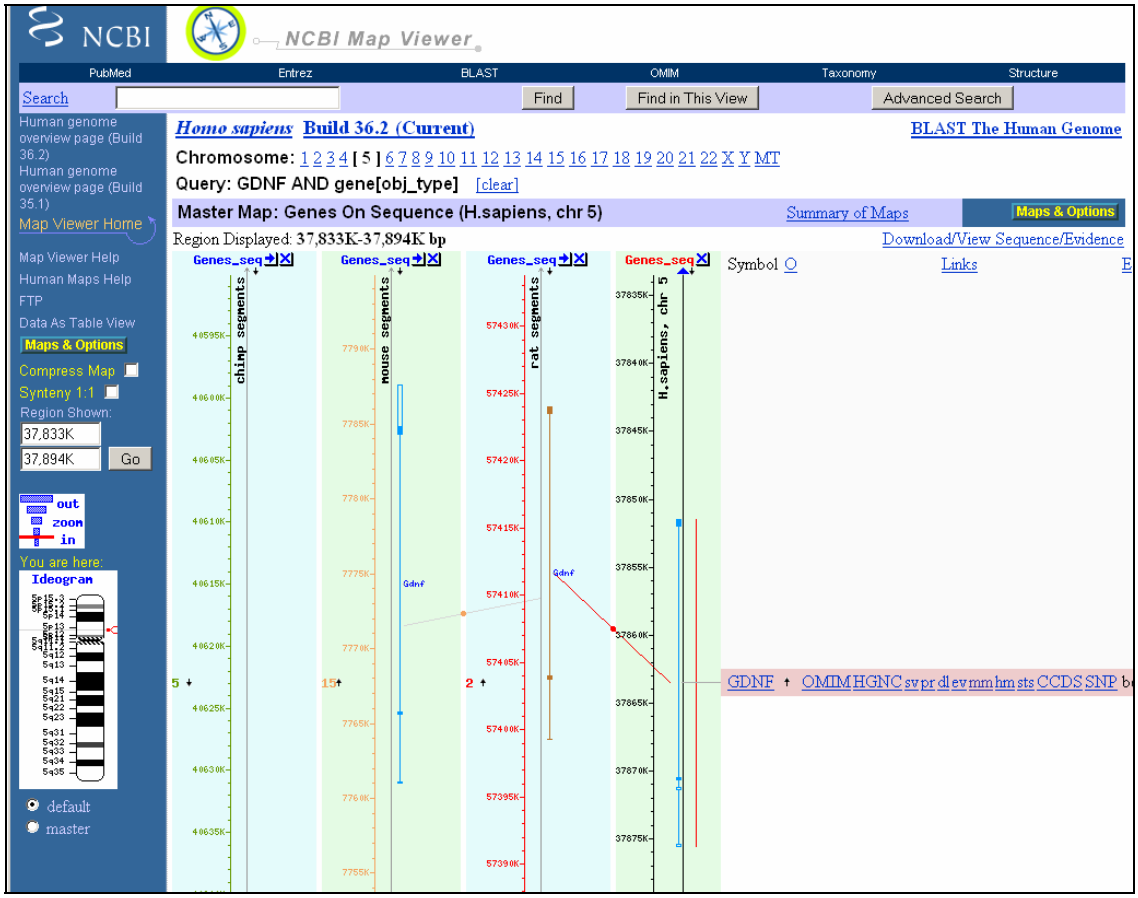

Job Title: lcl|2186 (211 letters)
BLASTP 2.2.17 (Aug-26-2007)
Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
protein database search programs", Nucleic Acids Res. 25:3389-3402.
RID: EK4SWP4J01R
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
from WGS projects
5,470,121 sequences; 1,894,087,724 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 see the defline, 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: rat
Ab initio
Assembly
BES Clone
Component
Contig
CpG Island
GenBank DNA
Gene
Phenotype
ADD>>
<<REMOVE
Maps Displayed (left to right):
[R][chimp][human:5] Gene
[R][mouse][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
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
Synteny 1:1
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 (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
Gdnf
Symbol
Links
GDNF
OMIM HGNC sv pr dl ev mm hm sts CCDS SNP

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 O Links E Cyto Description
37835K
37840K
37845K
37850K
37855K
37860K
37870K
37875K
MHS6
GDNF
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

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
N Nomenclature
R RefSeq
G GenBank
P Protein
U UniGene

LinkOut
HGMD

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 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.