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.

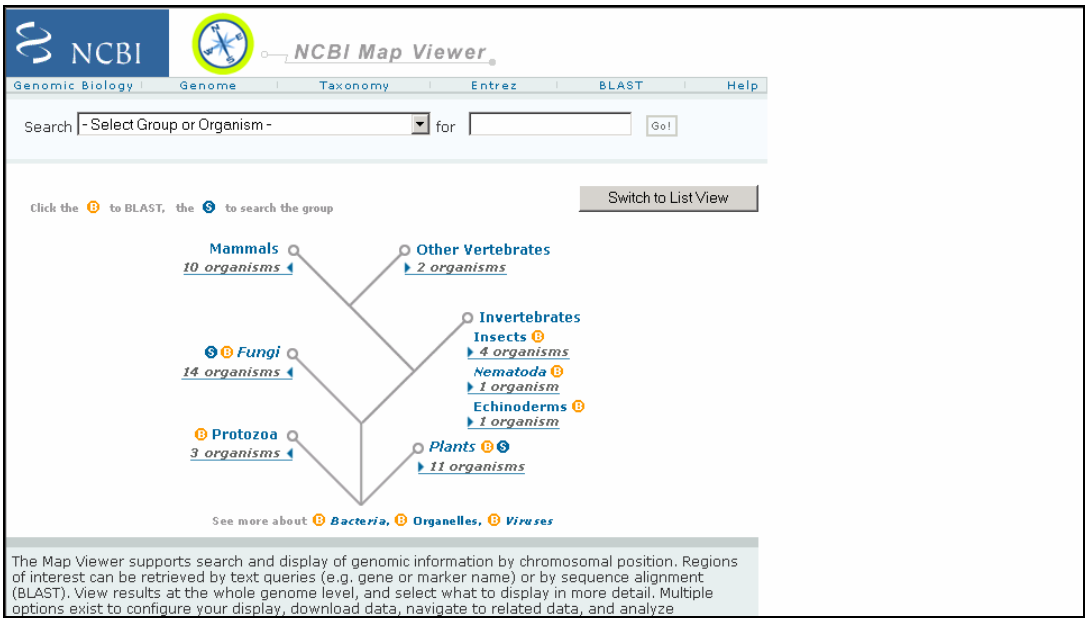
Remove all the maps except Genes_seq and add the Gene maps for mouse, chimp and rat. Are the gene structures in the three organisms similar?
Remove all the maps except the human Gene map, and add the phenotype map. Name the disease with which the GDNF gene is associated. Obtain more information about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

NCBI 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:

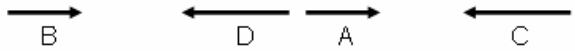
NC_

High Throughput Genomic Sequences

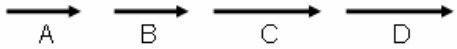
Sequencing of BACs:

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

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

Search results for query "GNDF": No matches found

Query Help

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

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:					53	10		22		25			

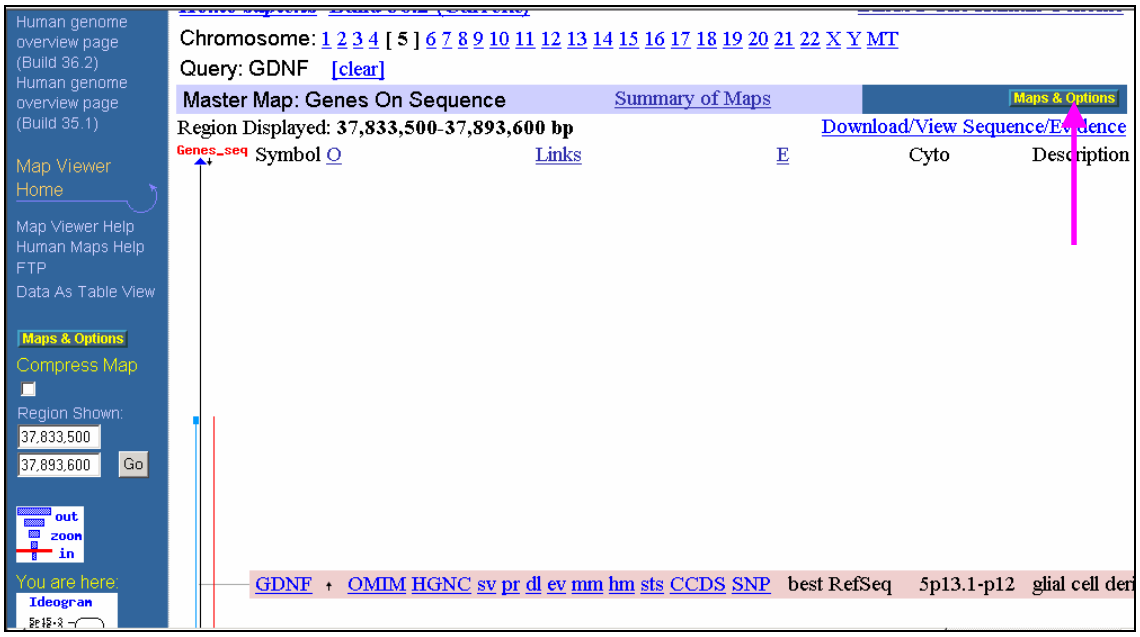
	14	15	16	17	18	19	20	21	22	X	Y	MT	not placed
Hits:							14						3

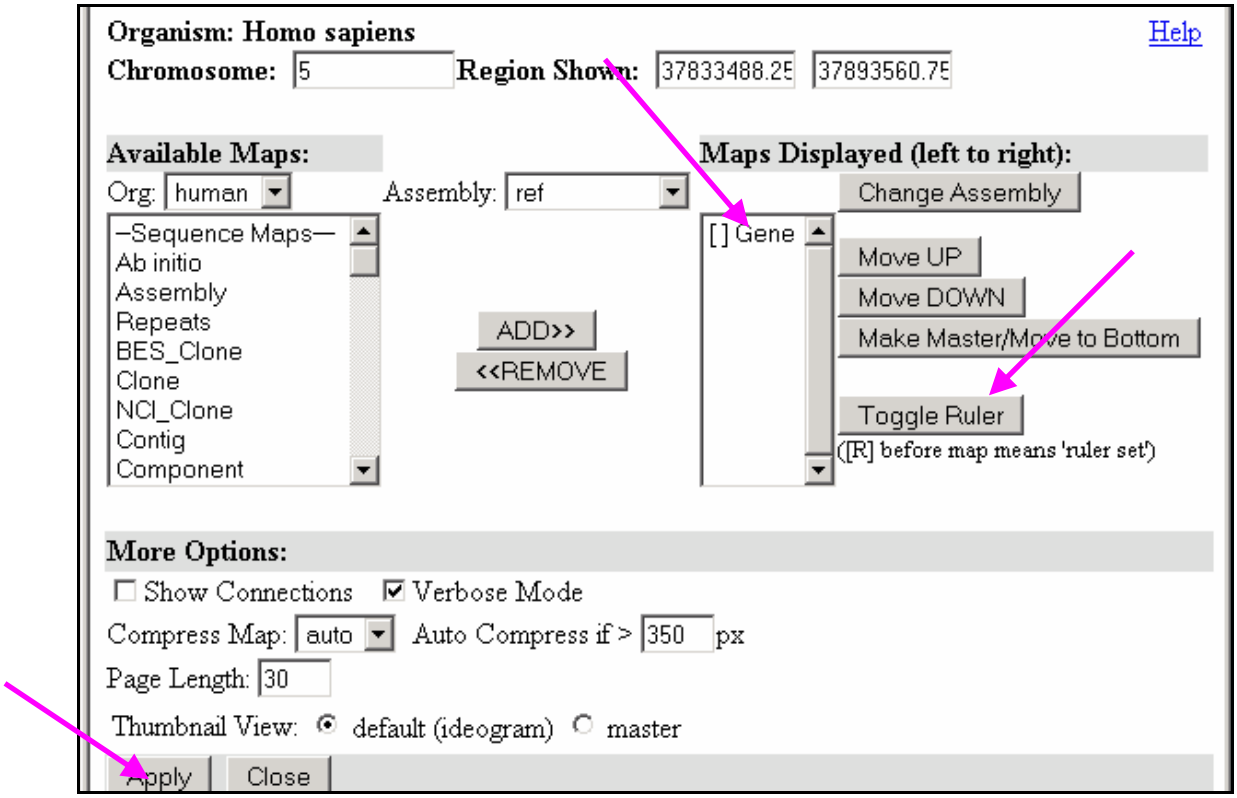
Search results for query "GDNF": 127 hits

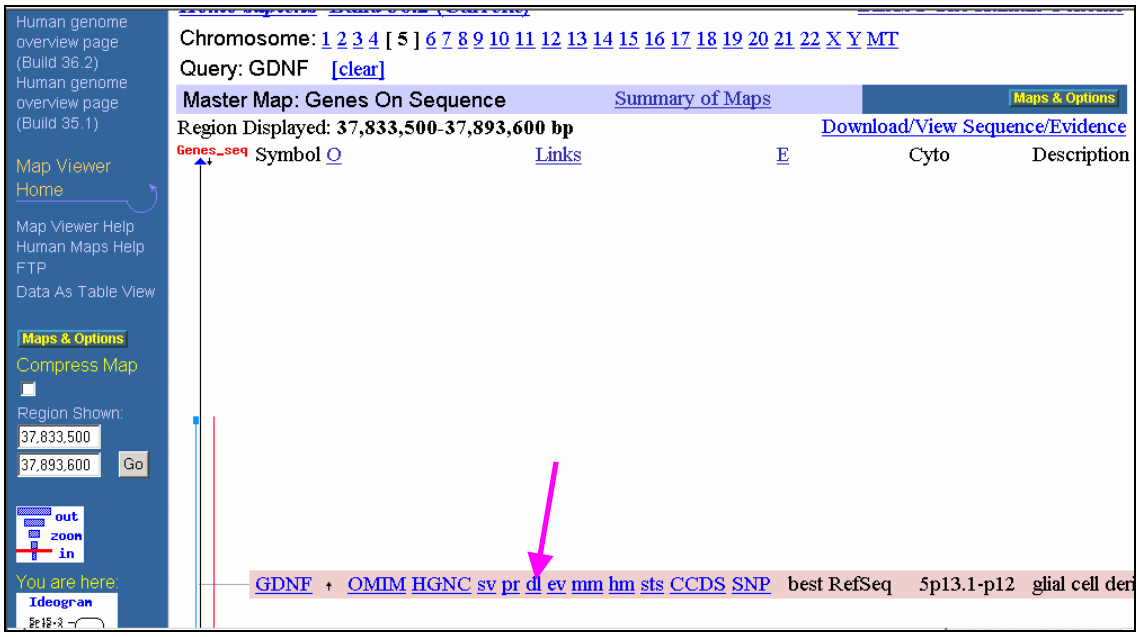
Hits shown: 1 - 100 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT not placed

Filter

Chr	Assembly	Match	Map element	Type	Maps
5	reference	all matches			
		GDNF : glial derived neurotrophic factor	GDNF	GENE	Genes_seq | Genes_cyto
		glial cell line-derived neurotrophic factor receptor alpha-3	GFRA3	GENE	Genes_seq | Genes_cyto
		NM_000514.2	NM_000514.2	TRANSCRIPT	RefSeq RNA | Hs RNA
		GDNF : ENSG00000168621	GDNF	GENE	ensGenes
		Gdnf	Gdnf	STS	STS
		Hirschsprung disease			

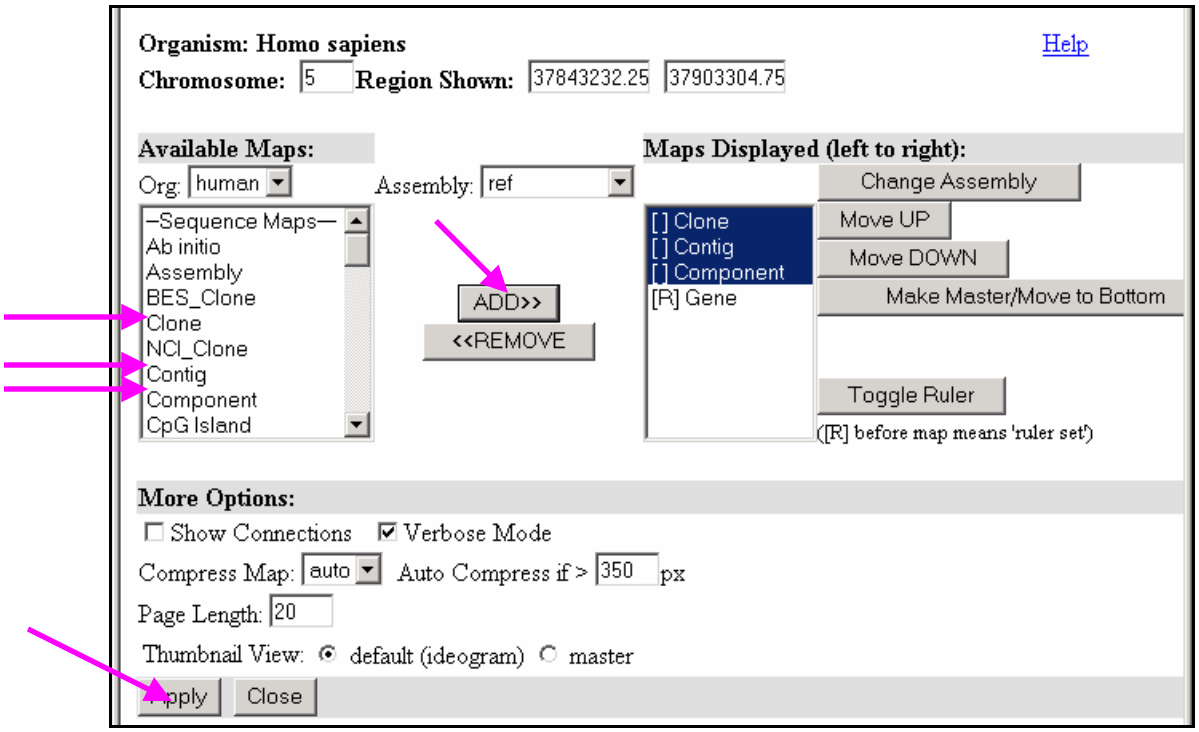

Human genome overview page (Build 36.2)
Human genome overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 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 deri

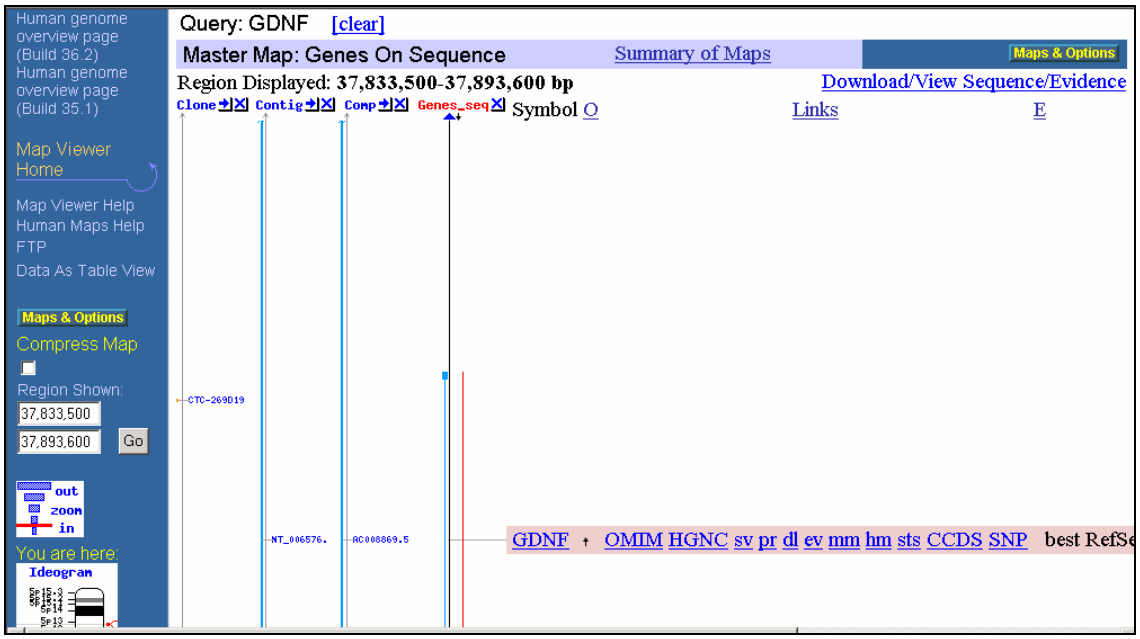

Organism: Homo sapiens
Help
Chromosome: 5
Region Shown: 37833488.25 37893560.75
Available Maps:
Org: human
Assembly: ref
–Sequence Maps–
Ab initio
Assembly
Repeats
BES_Clone
Clone
NCI_Clone
Contig
Component
ADD>>
<<REMOVE
Maps Displayed (left to right):
[ ] Gene
Change Assembly
Move UP
Move DOWN
Make 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

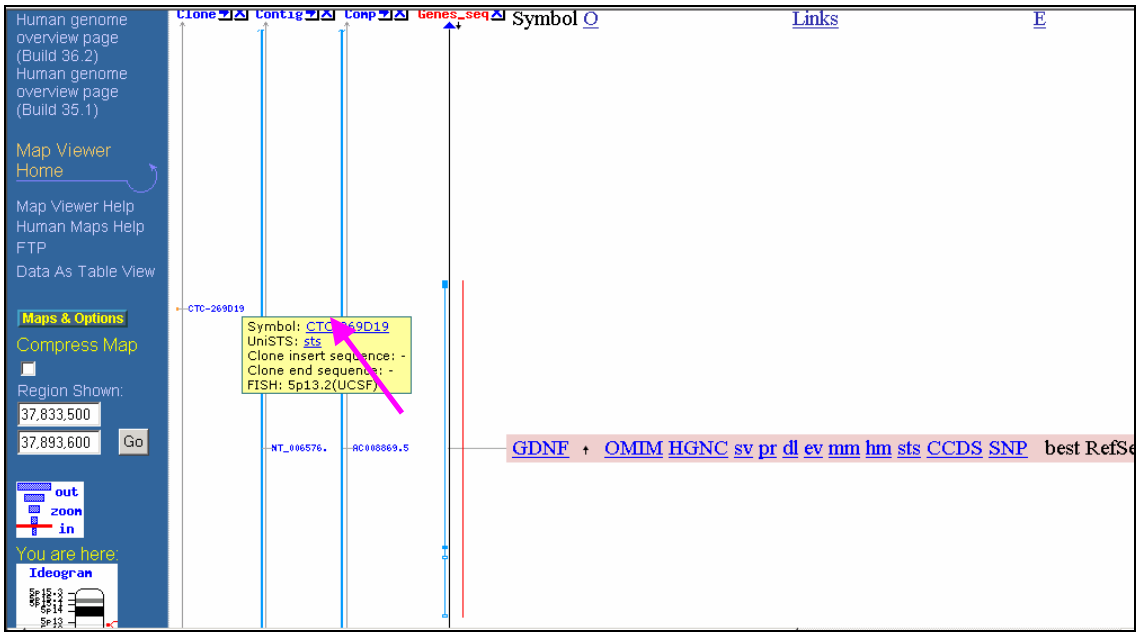

Human genome overview page (Build 36.2)
Human genome overview page (Build 35.1)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
Chromosome: 1 2 3 4 [5] 6 7 8 9 10 11 12 13 14 15 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 deri

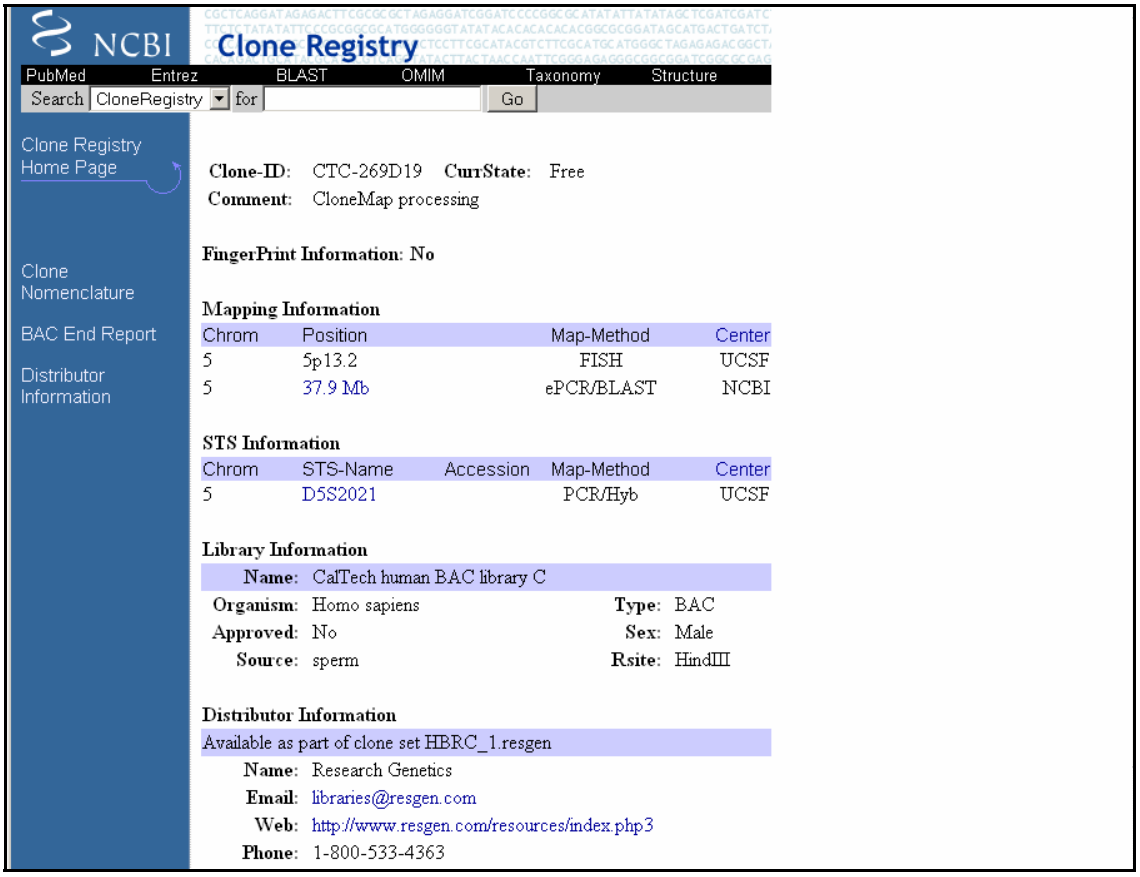
Homo sapiens Genome (build 35.1)
Region to retrieve (in chromosome coordinates):
Chromosome: 5
Strand: plus
from: 37851510
adjust by: -0K
to: 37875539
adjust by: +0K
Change Region/Strand
Sequence Format: FASTA
This chromosome region corresponds to the contig region(s):
Contig start stop strand
NT_006576.15 37788510 37812539 + Display Save to Disk View Evidence ModelMaker

Region to retrieve (in chromosome coordinates):
Chromosome: 5
Strand: minus
from: 37851510
adjust by: -0K
to: 37875539
adjust by: +0K
Change Region/Strand
Sequence Format: FASTA
Reverse Complement of this chromosome region corresponds to the contig region(s):
Contig start stop strand
NT_006576.15 37788510 37812539 - Display Save to Disk View Evidence ModelMaker


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


Human genome overview page (Build 36.2)
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
Query: GDNF [clear]
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
Clone Contig Comp Genes_seq Symbol O
Links
E
CTC-269D19
NT_006576.
AC008869.5
GDNF OMIM HGNC sv pr dl ev mm hm sts CCDS SNP best RefSe


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

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

Query: GDNF [clear]

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

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

Model RefSeq RNA Genes_seq Symbol O Links E

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

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	Descriptio
37851510	37875539	GDNF	-	OMIM	HGNC	sv	pr	dl	ev	mm	hm	sts	CCDS	SNP	best RefSeq	5p13.1-p12	glial cell c

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

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

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

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

Model RefSeq RNA Genes_seq Symbol O Links E

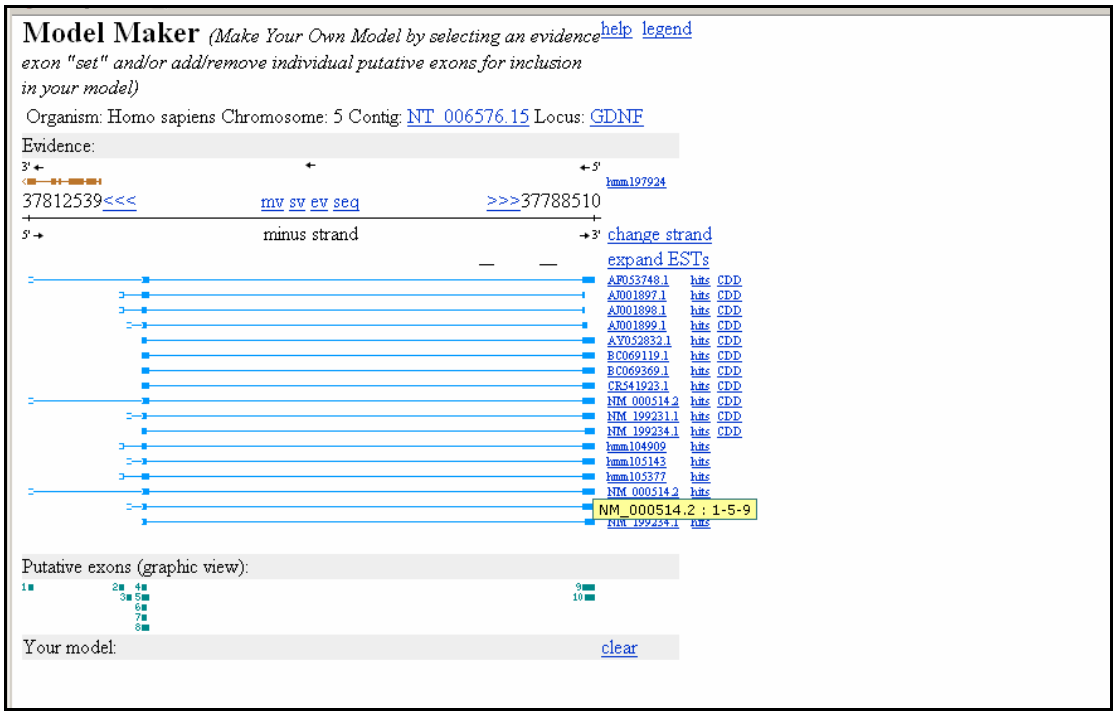
hmm197456

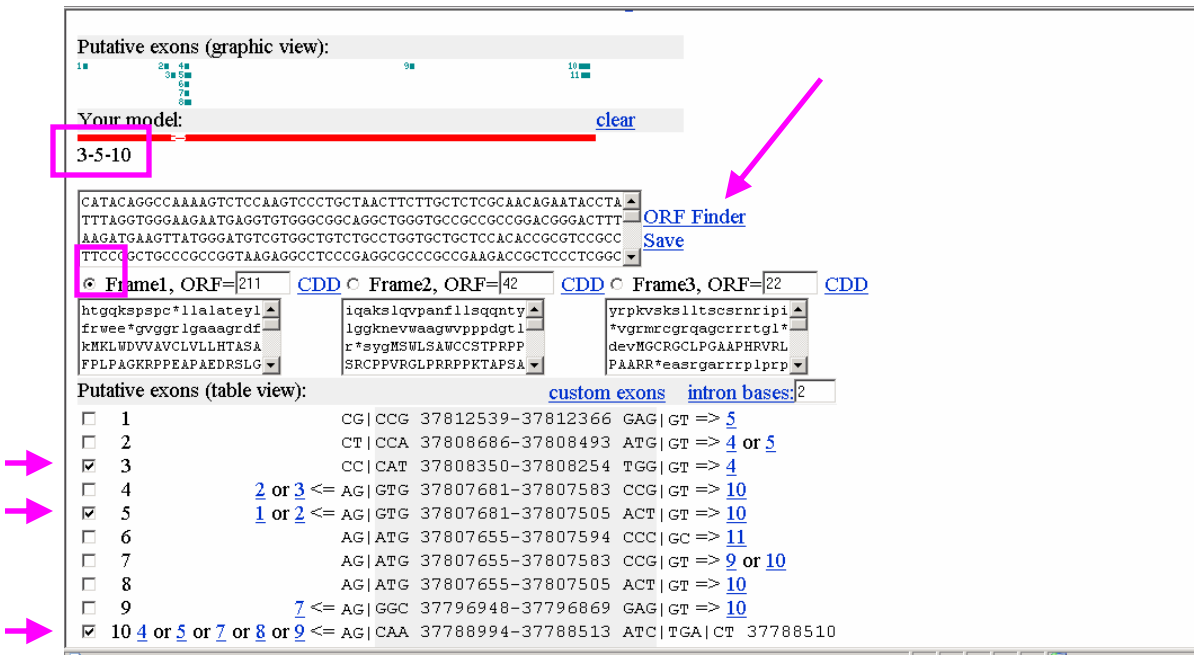
hmm197690 XM_929687. LOC646739 sv dl ev mm mRNA

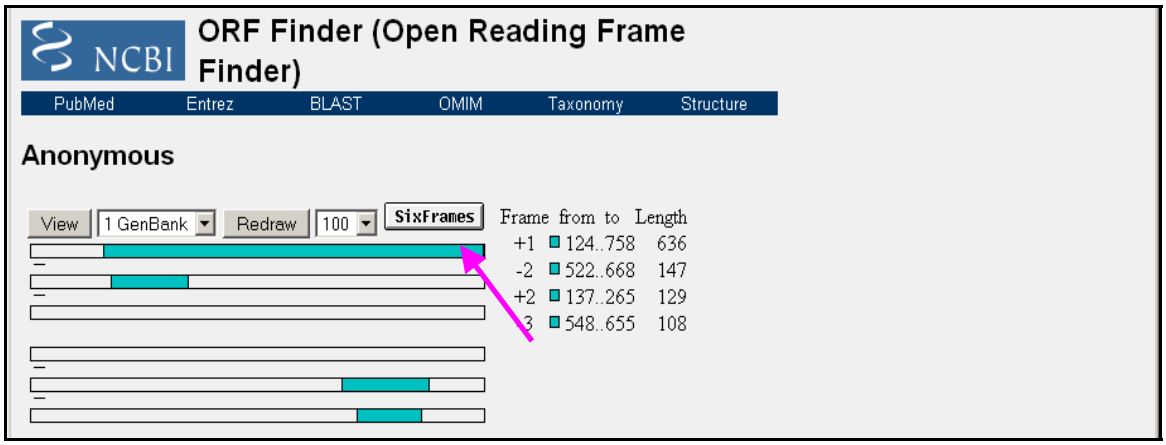
hmm105377

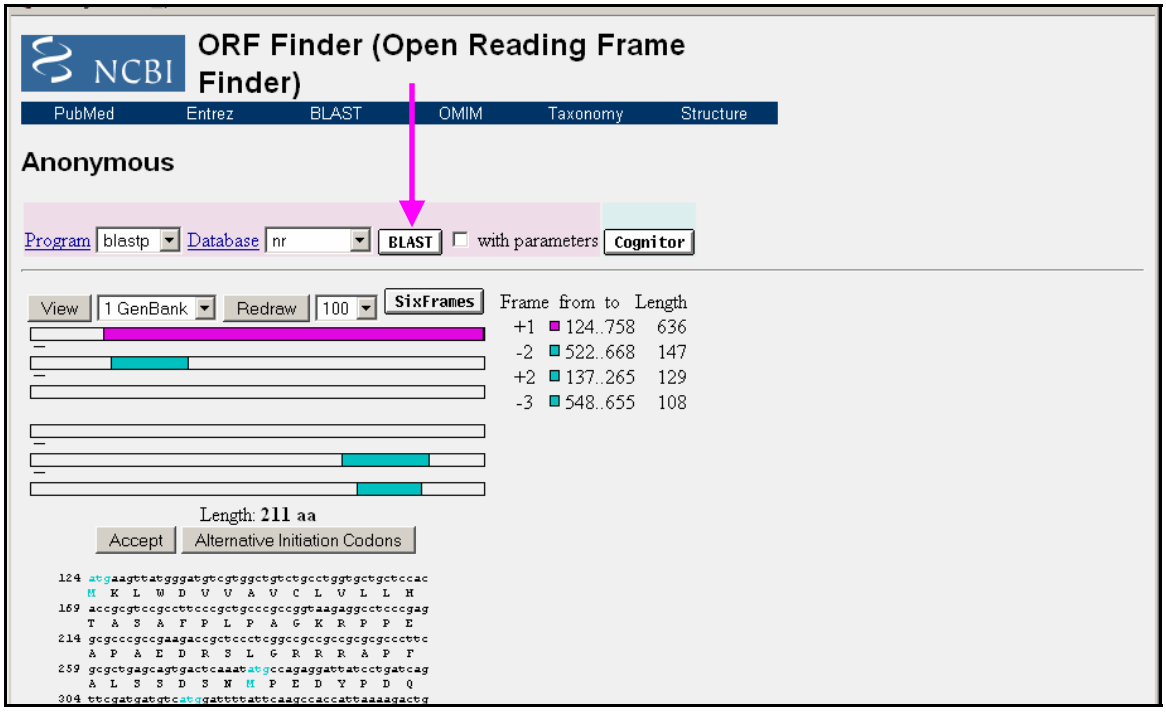
hmm105143 NM_199234.

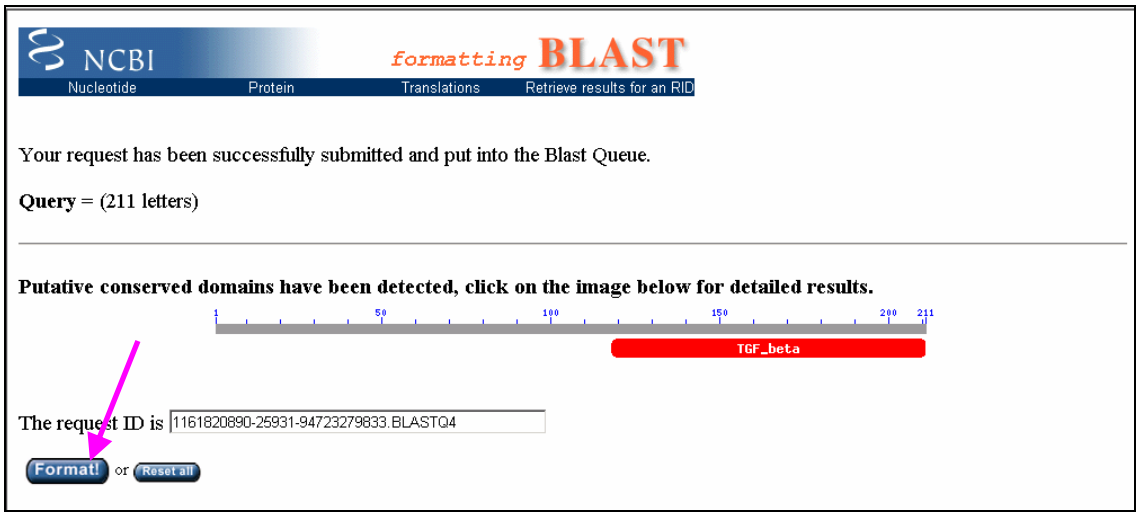
GDNF OMIM HGNC sv pr dl ev mm hm sts CCDS best RefSeq

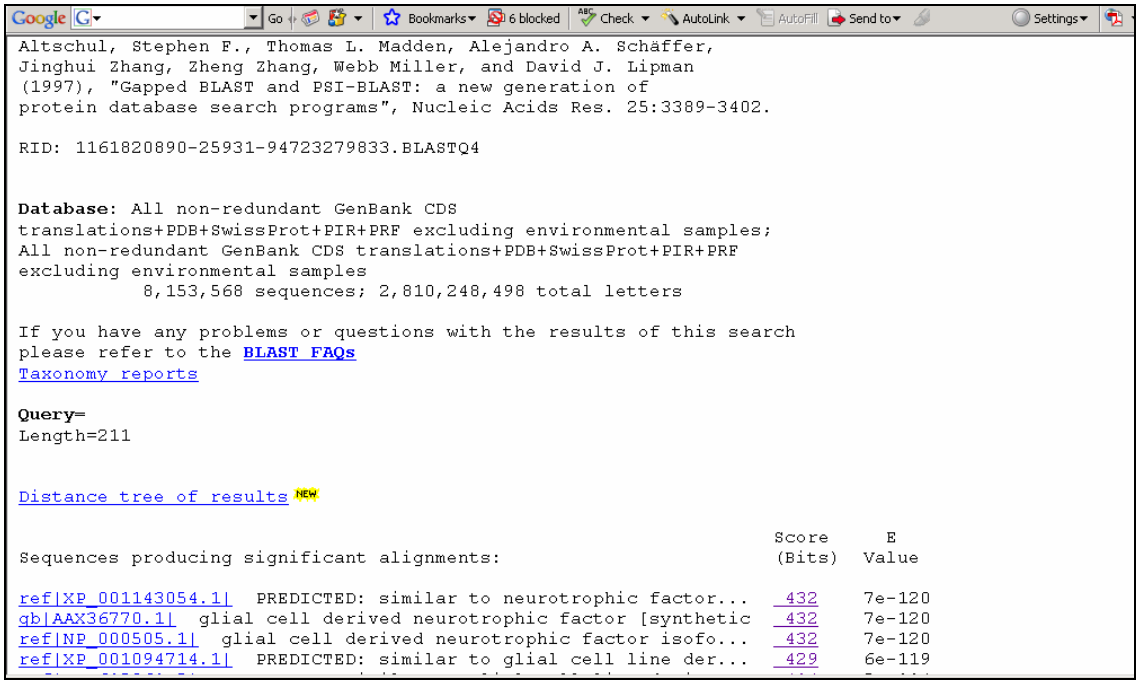

Model Maker (Make Your Own Model by selecting an evidence exon "set" and/or add/remove individual putative exons for inclusion in your model)
help legend
Organism: Homo sapiens Chromosome: 5 Contig: NT_006576.15 Locus: GDNF
Evidence:
37812539<<<
mv sv ev seq
>>>37788510
minus strand
change strand
expand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


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



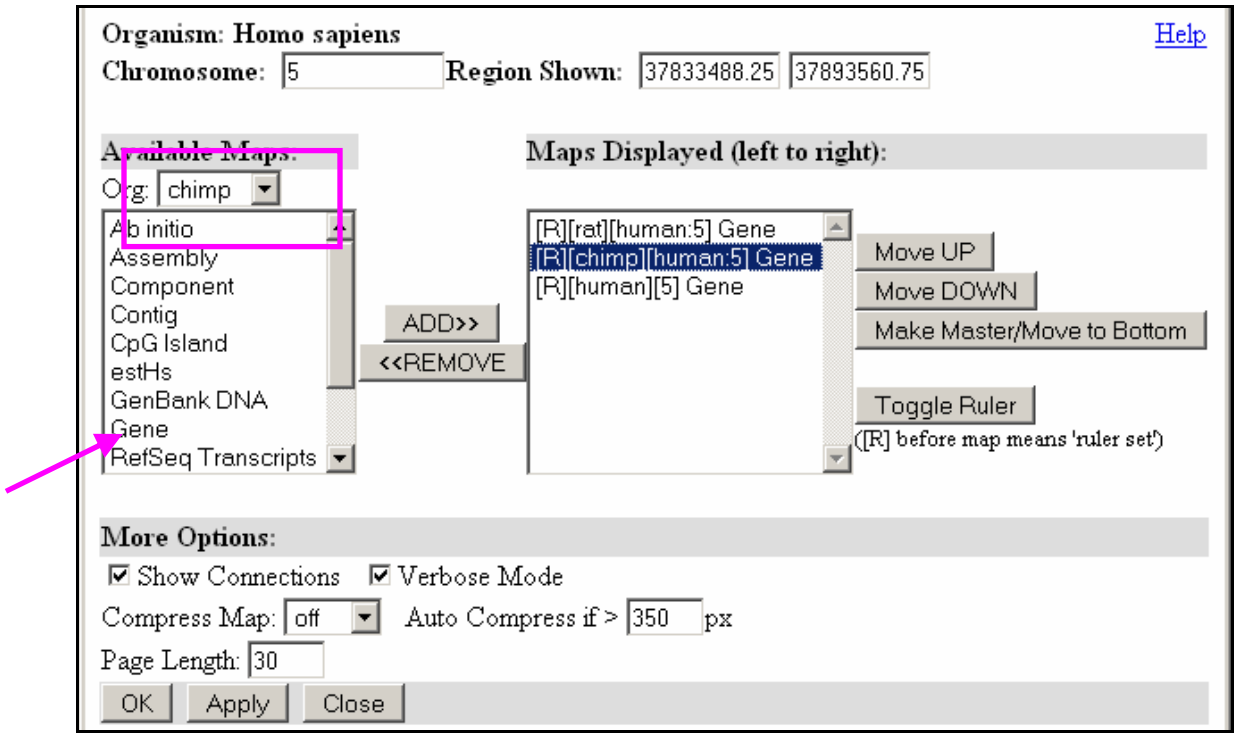


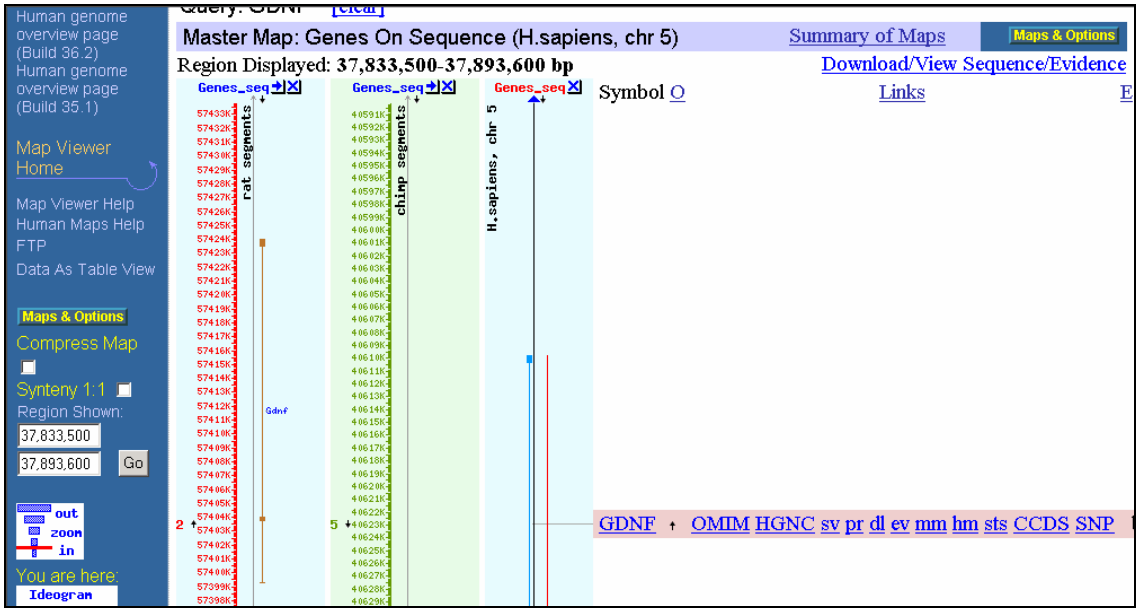
```
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1161820890-25931-94723279833.BLASTQ4


Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples;
All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
excluding environmental samples
           8,153,568 sequences; 2,810,248,498 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


Distance tree of results NEW

                                                                  Score     E
Sequences producing significant alignments:                       (Bits)  Value

ref|XP_001143054.1|  PREDICTED: similar to neurotrophic factor...  432    7e-120
gb|AAX36770.1|  glial cell derived neurotrophic factor [synthetic  432    7e-120
ref|NP_000505.1|  glial cell derived neurotrophic factor isofo...  432    7e-120
ref|XP_001094714.1|  PREDICTED: similar to glial cell line der...  429    6e-119
```

Alignments

```
>ref|XP_001143054.1| PREDICTED: similar to neurotrophic factor isoform 3 [Pan troglodytes]
Length=228

 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  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
```

```
>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


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:
37,833,500
37,893,600
Go
out
zoom
in
You are here:
Ideogram
Master Map: Genes On Sequence (H.sapiens, chr 5)
Summary of Maps
Maps & Options
Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
Genes_seq
rat segments
chimp segments
H.sapiens, chr 5
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

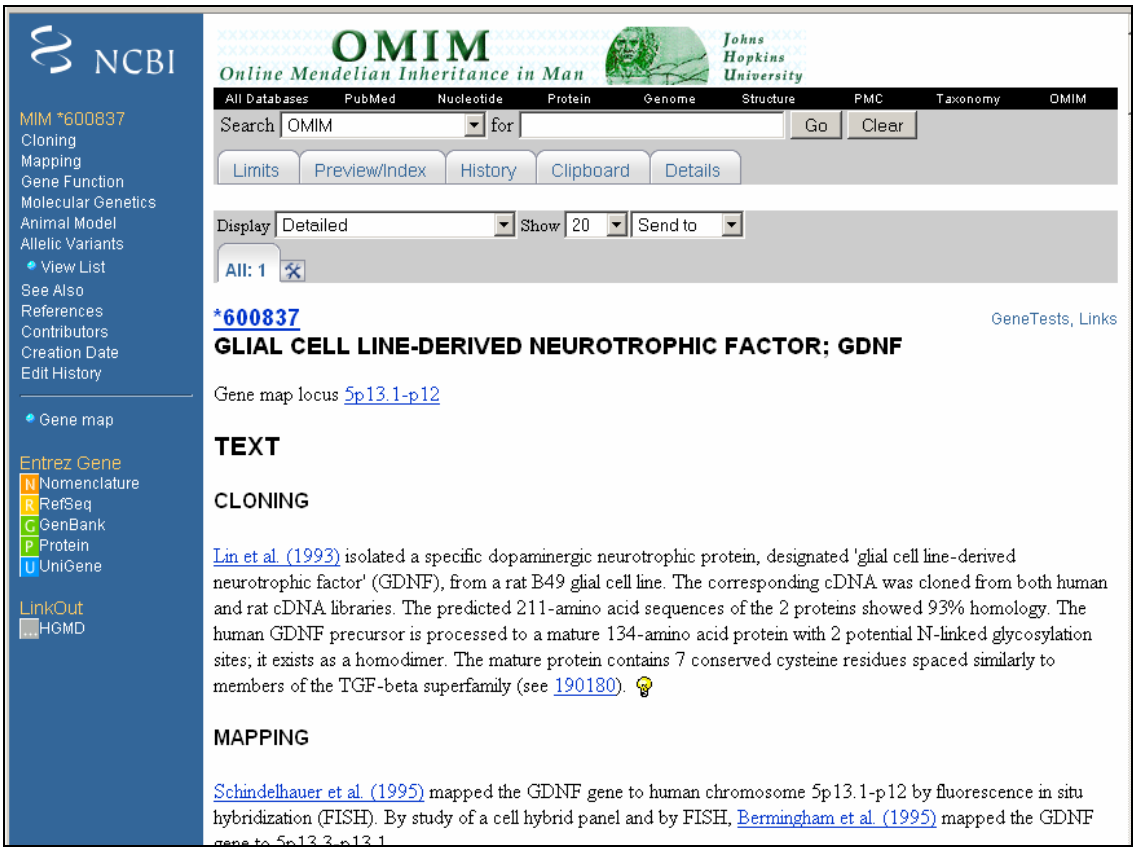
Available Maps:
Org: human
Assembly: reference
GenBank DNA
Gene
NCI Clone
Phenotype
RefSeq Transcripts
Repeats
STS
TCAG Genes
TCAG Transcripts
ADD>>
<<REMOVE

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

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

Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 37,833,500-37,893,600 bp
Download/View Sequence/Evidence
Pheno Genes_seq Symbol O Links E Cyto
LOC646739 sv dl ev mm mRNA 5p13.2
GDNF OMIM HGNC sv pr dl ev mm hm sts CCDS best RefSeq 5p13.1-p12
Symbol: GDNF
Description: al cell derived neurotrophic factor



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.