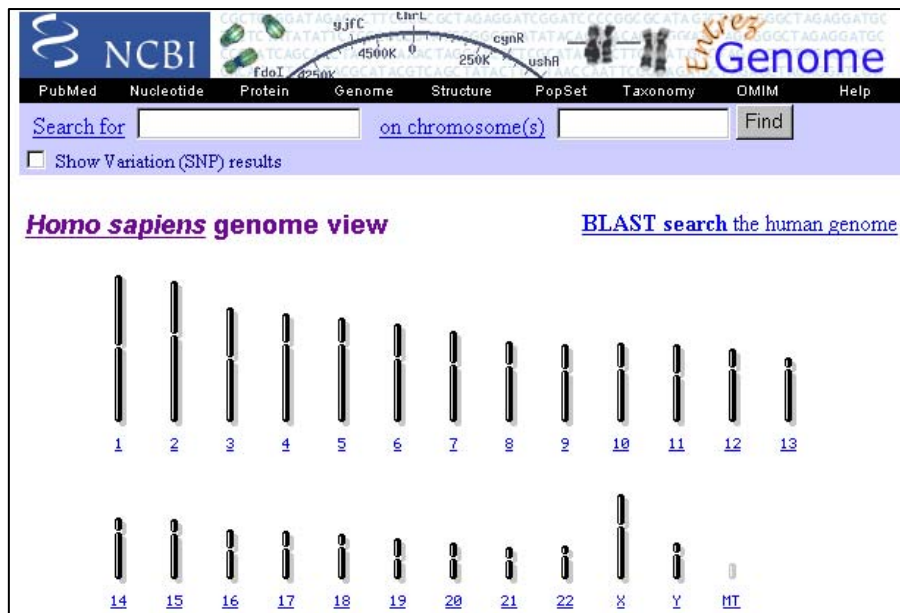


Map Viewer

http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/hum_srch?chr=hum_chr.inf&query

The National Center for Biotechnology Information's Map Viewer provides a graphical view of the human genome, the *Drosophila* genome and the mouse genome. The available sequence data is integrated with cytogenetic, genetic, physical, and radiation hybrid maps and can display the locations of genes, markers and tagged sites, polymorphisms, and disease-related loci within the sequence. Both genes and markers of interest can be found by searching against the whole genome or a single chromosome. Results are shown both graphically, as tick marks on the ideogram, and in a tabular format. The tabular view includes links to the chromosome graphical view. Alternatively, you can browse a chromosome by clicking on a chromosome link on the entry page graphic:



Searching the Map Viewer

The search bar near the top of the page allows you to enter a search term. The chromosome number search field is optional. Search terms include:

- gene symbol
- gene name
- marker name
- aliases for marker name
- text word (e.g, *actin*) or phrase (e.g., *cell adhesion*)

Note: Boolean operators (AND, OR) are not yet accepted.

IMPORTANT: All text words or phrases should be entered surrounded by asterisks. This will retrieve records with the term(s) in any position within a phrase. If asterisks are placed only at the **ends of a phrase** (e.g., **cell adhesion**), the system will only retrieve records in which the terms are adjacent to each other. You can also place an asterisk **between the terms** (e.g., **cell*adhesion**) in order to retrieve records that contain both terms adjacent to, or apart from, each other. The NCBI plans to upgrade the searching function in the future so that the use of asterisks is no longer required and Boolean operators can be used.

Terms can be entered in their full spelling or using the following truncation and wildcard strategies:

- 1. Full Spelling** - will retrieve records that have an exact character string match
- 2. Truncation using asterisk (*) as a wildcard** - An asterisk can be used to represent any number of characters; use the asterisk to represent multiple additional letters.
- 3. Truncation using question mark (?) as a wildcard** - A question mark represents any single character; use the question mark if only **one** letter is missing.
- 4. Using both question mark (?) and asterisk (*)** - These can be used in combination.

The **Chromosome Number** search field is optional:

- **no chromosome number** -
If no chromosome number is specified, all of the chromosomes for that organism are searched, as well as the genomic sequences that have not yet been placed onto a chromosome.
- **single chromosome number** -
To limit search results to a single chromosome, just enter that chromosome number into the "On Chromosome(s)" text box. Use **upper case letters for X and Y** chromosomes.
- **multiple chromosomes** -
To search multiple chromosomes, separate the chromosome numbers by commas (e.g., 1,3,Y)
- **range of chromosome numbers** -
Use the dash to represent a range of numbers (e.g., 3-5 searches chromosomes 3, 4, and 5).
To search chromosome *n* and higher, use a dash (e.g., 2- searches chromosomes 2, 3, 4...Y).

Examples of questions that can be answered with the Entrez Map Viewer:

- Where does a particular gene exist within the genome of an organism? What are some flanking markers?
- Which genes exist on a chromosome, and in what order do they appear?
- Show the genes that exist in region R of the chromosome. Show me the corresponding sequence data for that region.
- Display the region of a chromosome between points A and B. Show both the cytogenetic and sequence map for that region, aligned to each other based on markers that have been placed on both maps.
- What is the distance between two genes? (Note: scale depends on the type of map on which those genes have been placed.)
- I know the cytogenetic location of a gene. What is the corresponding physical location?

Example: Search for genes related to Parkinson's Disease using search term *Parkinson*:

The screenshot shows the NCBI Entrez Genome search interface. The search term is '*Parkinson*' and the results are displayed as a 'Homo sapiens genome view' with a list of 14 hits. The hits table is as follows:

Chr	Match	Map element	Type	Maps
2	Parkinson disease, type 3	Parkinson disease, type 3	mim	Morbid
2	Parkinson disease (autosomal d	PARK3	locus	Genes cyto
4	Parkinson disease, familial, 1	Parkinson disease, familial, 1	mim	Morbid
4	Parkinson disease, type 1, 601	Parkinson disease, type 1, 601	mim	Morbid
4	Parkinson disease (autosomal d	PARK4	locus	Genes cyto
6	Parkinson disease, juvenile, t	Parkinson disease, juvenile, t	mim	Morbid
6	Parkinson disease (autosomal r	PARK2	locus	Genes cyto Genes seq
17	Parkinsonism-dementia with pal	Parkinsonism-dementia with pal	mim	Morbid
17	Dementia, frontotemporal, with	Dementia, frontotemporal, with	mim	Morbid
18	Parkinson disease, susceptibil	Parkinson disease, susceptibil	mim	Morbid
22	Parkinsonism, susceptibility t	Parkinsonism, susceptibility t	mim	Morbid
X	Dystonia-3, torsion, with park	Dystonia-3, torsion, with park	mim	Morbid
X	Waisman parkinsonism-mental re	Waisman parkinsonism-mental re	mim	Morbid
X	dystonia 3 (with Parkinsonism)	DYT3	locus	Genes cyto

The identified genes are shown graphically by the red lines on the genome. A tabular list is also provided that lists the chromosome, match title, map element, and types of maps available for each gene. Click on the map element name or the red mark on the genome view to see the full Map View.

The MapViewer shows the location of the identified gene on a floating chromosome ideograph on the left side of the screen. A more detailed listing of genes in the location is provided with the targeted gene highlighted in color. This list does not necessarily show all of the genes in the specific location, depending on how many are there and how large the region of the chromosome is. Clicking on the red line on the diagram will allow you to zoom in or out.

Homo sapiens Map View

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

Query: *Parkinson* [clear]

Master: Genes On Cytogenetic Map [Display settings]

Total Genes On Chromosome: 882
Region Displayed: 2p13.3
Genes Labeled: 20 Total Genes in Region: 373

Genes_cyto	symbol	links	cyto.
	ARHB		2pter-p12 ras homolog gene family, member B
	PELI1		2p13.3 pellino (Drosophila) homolog 1
	DOK1		2p13 docking protein 1, 62kD (downstream of tyrosine kinase 1)
	ANXA4		2p13 annexin A4
	EGR4		2p13 early growth response 4
	PEE1		2p13 preeclampsia/eclampsia 1
	DCTN1		2p13 dynactin 1 (p150, Glued (Drosophila) homolog)
	AUP1		2p13 ancient ubiquitous protein 1
	ALMS1		2p13 Alstrom syndrome 1
	NBC4		2p13 sodium bicarbonate transporter 4

Zoom menu options: Recenter, Zoom in x2, Zoom in x4, Zoom in x8

Clicking on the gene symbol, in this example 'Park3', will show the corresponding LocusLink record for that gene including links to a variety of other databases.

LocusLink

Search: LocusLink [Display: Brief] Organism: All [Go] [Clear]

ABCDEFGHIJKLMNOPQRSTUVWXYZ

PARK3: Parkinson disease (autosomal dominant, Lewy-body) 3

Locus Information [Submit GeneRIF for PARK3]

LocusID: 5072
Type: gene with protein product, function known or inferred
Alias: Parkinson disease, dominant Lewy-body, 3
OMIM: [602404](#)
Phenotype: [Parkinson disease, type 3](#)

Map Information [?]

Chromosome:	2	mv
Cytogenetic:	2p13	RefSeq

Additional Web Resources [?]

[GeneCard for PARK3](#)

Use the 'Maps and Options' link to alter your option and to view multiple maps simultaneously.

FTP
Data As Table View
Maps&Options

Master Map: Genes On Cytogenetic
Total Genes On Chromosome: **1144**
Region Displayed: **14q24.1-14q31.1**
Genes Labeled: **20** Total Genes in Region: **213**

Maps & Options

Chromosome: Region Shown:

Available Maps:
 --Sequence Maps---
 Clone
 Contig
 Component
 CpG Island
 dbSNP haplotype
 Fosmid
 GenBank_DNA
 Gene

ADD>> <<REMOVE

Maps Displayed (left to right):
 Gene_Cytogenetic

Move UP
Move DOWN
Make Master/Move to Botto
Toggle Ruler
([R] before map means 'ruler set')

Several different maps may be displayed simultaneously. The master map is shown at the right edge of the display along with its details and descriptive text. The identity of the master map can be easily changed using Maps and Options dialog box. Another way to change the Master Map is to click on the right-arrow above the map of interest in the chromosome display. That will move the map to the right side of the window, where the corresponding text will also be displayed.

A wide variety of maps are available including sequence maps (clone, contig, GenBank, STS), cytogenetic maps (FISH, Morbid, Mitelman), genetic linkage maps (Genethon), radiation hybrid maps, and others. More detailed information on the available maps for the human genome can be found at: <http://www.ncbi.nlm.nih.gov/mapview/static/humansearch.html>.

Please note that the maps vary in terms of scale and unit. Not all maps will align properly although they can all be viewed simultaneously.

Links from the Gene (genes_seq) Map

HIF1A	+	sv	ev	hm	seq	mm	C	14q21-q24	hyp
ZFP36L1	+	sv	ev	hm	seq	mm	C	14q22-q24	zin
PSEN1	+	sv	ev	hm	seq	mm	C	14q24.3	pre
FLJ39091	+	sv	ev	-	seq	mm	C	14q24.1	zin

The genes_seq map shows the positions of sequence-based position of genes that have been annotated on the genomic contigs. This includes known and putative genes placed as a result of alignments of mRNAs to the contigs. When the genes_seq map is the master map, there is a particularly useful set of links provided for each identified gene.

- sv - sequence viewer - displays the genomic sequence at the base-pair level including notation of exons, variation sites, and translations
- ev - evidence viewer – displays the evidence used to prove the existence and structure of the gene
- hm - Human-Mouse homology map - displays a synteny map of human and mouse genes
- seq - view/download sequence data from a chromosome region
- mm - Model Maker – allows the manipulation of the evidence for the exon/intron structure of the gene