



The NCBI Map Viewer

An online tool to view sequence- and marker-based genome maps in a single display

<http://www.ncbi.nlm.nih.gov/mapview/>

National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

Scope and access

The Map Viewer is the primary graphical display tool for genome maps for eukaryotic organisms. The Map Viewer has the ability to search all maps for markers, display chromosome maps, and zoom in to greater levels of detail for a region of interest. The number and types of available maps vary by organism. Maps are aligned using shared markers and gene names, or the sequence coordinate system. Currently genomes from more than 40 eukaryotic organisms are available through the Map Viewer. The Map Viewer homepage (www.ncbi.nlm.nih.gov/mapview/) is the main gateway for searching and browsing maps of all available genomes. More details on the functions and features of the Map Viewer are available in the on-line help document (www.ncbi.nlm.nih.gov/mapview/static/MapViewHelp.html).



Map Viewer homepage

A target genome can be queried using terms such as gene symbols, marker names, disease names, or sequence accession numbers. The organism search box provides quick access to target organism through a pull-down list (A). Alternatively, available genomes can be browsed through a list of taxonomic groups (B). Clicking the header of a taxonomic group (C) expands the section to show the organisms with available genomic maps, their current build and links to available tools (D). The Tools Legend (E) describes the function of each icon shown on in the Tools column and tools available are Map Viewer search, genome BLAST, clone finder, region-zoom dialog box, and organism-specific genome resource guide. The help document (F) provides more details on Map Viewer.

Scientific name	Common name	Build	Tools
<i>Callithrix jacchus</i>	white-tufted-ear marmoset	Annotation Release 101	Q B
<i>Gorilla gorilla</i>	western gorilla	Annotation Release 100	Q B Cr
<i>Homo sapiens</i>	human	Annotation Release 106	Q B R G
<i>Macaca fascicularis</i>	crab-eating macaque	Annotation Release 100	Q B
<i>Macaca mulatta</i>	rhesus macaque	Build 1.2	Q B R G
<i>Nomascus leucogenys</i>	northern white-cheeked gibbon	Annotation Release 101	Q B
<i>Otolemur garnettii</i>	small-eared galago	Annotation Release 100	Q B
<i>Pan paniscus</i>	pygmy chimpanzee	Annotation Release 100	Q B
<i>Pan troglodytes</i>	chimpanzee	Annotation Release 102	Q B G
<i>Papio anubis</i>	olive baboon	Annotation Release 100	Q B
<i>Pongo abelii</i>	Sumatran orangutan	Annotation Release 101	Q B
<i>Saimiri boliviensis</i>	Bolivian squirrel monkey	Annotation Release 100	Q B

Map Viewer search result

The Map Viewer displays search results in a summary format showing the matches as red tick marks on the ideogram (G). It also provides key information about the genomic assembly being searched (H) and a link to genome BLAST page for sequence-based search (I). The header above the result list displays the complete query used in the search along with the field restrictions and Boolean operators if applicable (J). The number under the chromosome (K) indicates the hits found on that chromosome. Details are displayed in a table view (L) below, providing more details on the type of annotation, map and assembly for each hits. A Quick Filter (M) allows the filtering of hits so only particular feature maps desired is kept. The Advanced Search (N) provides extensive options for framing and refining the search.

Chr	Match	Map element	Type	Maps
4	all matches			
	Homo sapiens huntingtin (HTT), mRNA	NM_002111.6	TRANSCRIPT	RefSeq RNA
	HTT : huntingtin disease protein	HTT	GENE	Genes_seq
17	solute carrier family 6 member 4	SLC6A4	GENE	Genes_seq

Map Viewer Advanced Search Page

Clicking the **Advanced Search** button (A) opens up a limits page with functions to make a search result more specific. It does so through field restrictions for search terms (B), limit of searches to particular chromosomes (C), genomic assemblies (D), as well as annotation types (E) and maps (F). Genomic assemblies can be displayed include the reference assembly derived from GRC assembly, and the alternate assemblies of the complete hydatidiform mole (CMH) and HuRef (J.C. Venter) (D). Map for variations (from dbSNP) can be filtered based on level of heterozygosity, relationship to a nearby gene and available genotype data (G).

Detailed Map Viewer Display

In the search summary page, clicking on chromosome with a red “hit” in the graphical view or a link in the table view opens a detailed interactive display. At the top is an overview indicating the query used, the annotation, and chromosome shown (H). The central portion of the page displays several annotated chromosomal maps whose titles are linked to their description in the help document (I). The feature match on the maps is colored in pink along with a vertical red highlight (J) showing the relative length and location of the feature. The right-most map is the master, “Genes_seq” in this case, showing the most detailed annotation information (K) and a set of links to related records in other NCBI databases (L). Legends for links are given in the insert. The navigational controls in the left sidebar allow for quick customization of the display. The region of the chromosomal maps displayed can be altered using the **Region Shown** (M) dialog if specific coordinates are known, while a zoom in/zoom out feature (N) changes the resolution of the current display at preselected intervals. The red mark in the chromosomal ideogram (O) shows the relative position of the displayed region. At the top of this section, also duplicated in the upper right corner, is a **Maps & Options** button (P) that launches a new window for more detailed customization of the map display.

Customizing the display with Maps & Options

Clicking Maps & Options button opens the control window (shown at right) providing a multitude of options to customize an existing Map Viewer Display. Here pull-down lists allow for displaying maps based on Organism and Assembly (A), when available. The list of available maps for the selected combination of Organism and Assembly is shown in the box below (B). Clicking the “+” sign (C) to the right of a map adds it to the Track Displayed list to the right (D). Conversely, clicking the “-” sign (E) to the right of a map in the Track Displayed list removes it. Clicking and dragging a track up or down the list changes its display position (F). Clicking the “R” icon toggles on or off the ruler display, and a map with ruler on has its icon colored blue (G). Checking the “Show Connections” option (H) will connect the matching features on adjacent maps with grey lines. Clicking the OK button (I) activates the selected changes.

Comparing different assemblies

The Map Viewer is able to display maps from different assemblies in the same browser window for side-by-side comparison. Maps can be selected using the Maps and Options dialog’s Organism and Assembly options. For a limited set of organisms, this can be used to display genomic synteny. The example below shows the syntenic region around the HTT gene regions for mouse, rat, chimpanzee, and human. The relationship between gene loci on adjacent maps are shown by the added grey and red lines (red highlights match from a search, J) activated by the “Show Connections” option (H).

Symbol	Links	E	Cyto	Description
GRK4	OMIM HGNC sv pr dl ev hm sts SNP			best RefSeq 4p16.3 G protein-coupled receptor
HTT-AS	HGNC sv dl ev SNP			best RefSeq 4p16.3 HTT antisense RNA (head
HTT	OMIM HGNC sv pr dl ev hm sts SNP			best RefSeq 4p16.3 huntingtin
MSANTD1	HGNC sv pr dl ev hm SNP			best RefSeq 4p16.3 Myb/SANT-like DNA-bind

Downloading Data and Sequences

Information about features displayed in the Map Viewer window can be viewed in tabular format using the [Data as Table View](#) link (A) in the left sidebar. In display (below), annotations and nucleotide sequences can be downloaded in a number of formats: the [Download All](#) (B) saves all displayed features to a single text file; the [Download Data](#) link in each section (C) saves the data (gene features in this case) for the section. The [Download/View Sequence/Evidence](#) links to a display (D), which provides a venue to save sequence data for the displayed region through the [Save to Disk](#) option (E).

Linking into Map Viewer through genome BLAST

The Map Viewer is integrated with a wide range of NCBI resources. In addition to extensive links associated with each map (p.2), Map Viewer is also linked from records in other NCBI resources such as records in Gene and Nucleotide databases, as well as genome-BLAST results. For example, a human genome-BLAST result page contains links to a customized display in Map Viewer to show matches on annotated chromosomes under a genomic context. Specifically, a summary display is available under the [Human genome view](#) link, which sums up the hits on the ideogram (F). Clicking the chromosome opens the detailed map display (G), where alignments are shown as colored lines next to each map (H). The color of each line acts as an indicator of the alignment score (I).

Map Viewer Home
 Map Viewer Help
 Human Maps Help
 FTP
[Data As Table View](#) (A)
[Maps & Options](#)

Homo sapiens (human) Annotation Release 106 (Current) [BLAST human sequences](#)

Data As Table View (A) [Download All !](#) (B) [Download Data](#) (C)

Genes On Sequence: All Sequence Maps
 Region Displayed: 2,990K-3,410K bp
 Total Genes On Chromosome: 1702 [not localized]
 Genes in Region: 7

start	stop	Symbol	Links	E	Cyto	Description
2963505	3040747	GRK4	+ OMIM HGNC sv pr dl ev hm sts	SNP	best RefSeq 4p16.3	G protein-coupled receptor kinase 4
3063246	3074514	HTT-AS	+ HGNC sv dl ev	SNP	best RefSeq 4p16.3	HTT antisense RNA (head to head)
3074681	3243960	HTT	+ OMIM HGNC sv pr dl ev hm sts	SNP	best RefSeq 4p16.3	huntingtin
3246590	3271738	MSANTD1	+ HGNC sv pr dl ev hm	SNP	best RefSeq 4p16.3	Myb/SANT-like DNA-binding domain containing 1
3292978	3439913	RGS12	+ OMIM			
3312421	3312929	LOC100286945	+ OMIM			
3323926	3324782	RPL7AP29	-			

[Download/View Sequence/Evidence](#) (D)

Homo sapiens (human) (Annotation Release 106)
 Region to retrieve (in chromosome coordinates):
 Chromosome: 4 Strand: plus
 from: 2988980 adjust by: -0K
 to: 3412180 adjust by: +0K [Change Region/Strand](#)
 Sequence Format: FASTA

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

Contig	start	stop	strand
NT_006051.19	2978980	3402180	+

[Display](#) (E) [Save to Disk](#) [View Evidence](#)

Homo sapiens (human) Annotation Release 106 (Current)
 Chromosome: 1 2 3 [4] 5 6 7 8 9 10 11 12
 Query: [BLAST AS6T0SY7015: ref|NM_002111.6](#)

Color key for alignment scores: <40 40-50 50-80 80-200 >=200

Master Map: Contig
 Region Displayed: 3,050K-3,143K bp
[RefSeq](#) [RNA](#) [Genes_seq](#) [Contig](#)

Graphic Summary
 Distribution of 67 Blast Hits on the Query Sequence
 Mouse-over to show define and scores, click to show alignments

Color key for alignment scores: <40 40-50 50-80 80-200 >=200

Homo sapiens (human) genome view
 Annotation Release 106 statistics [Switch to previous build](#)

1 2 3 4 5 6 7 8 9 10 11 12
 Hit 1: 1042..1724
 Hits: 67

Color key for scores: <40 40-50 50-80 80-200 >=200

Related NCBI resources

Gene	www.ncbi.nlm.nih.gov/gene/
Genome	www.ncbi.nlm.nih.gov/genome/
RefSeq	www.ncbi.nlm.nih.gov/RefSeq/
BLAST	blast.ncbi.nlm.nih.gov/