



The Genome Workbench Program

A powerful standalone program designed for genome analysis

<https://www.ncbi.nlm.nih.gov/tools/gbench>

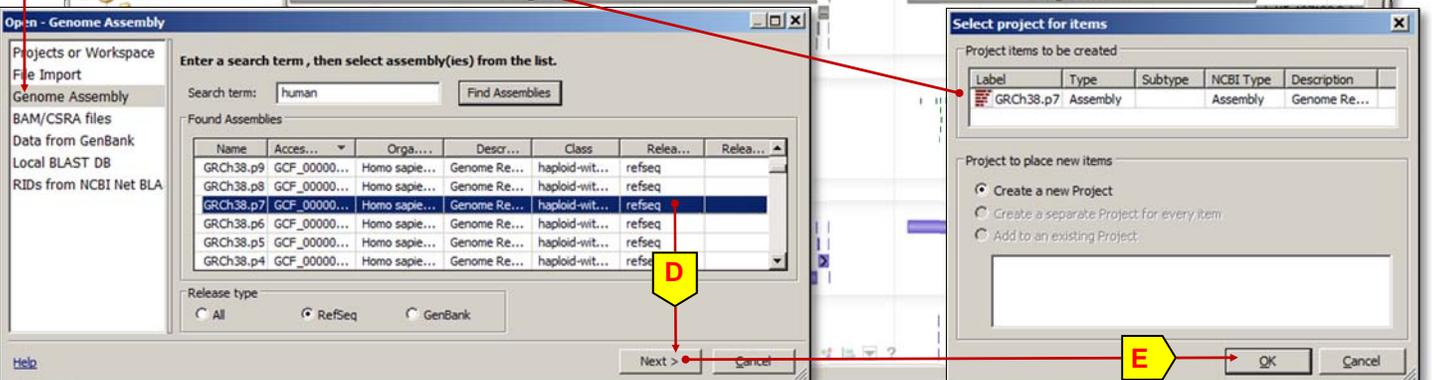
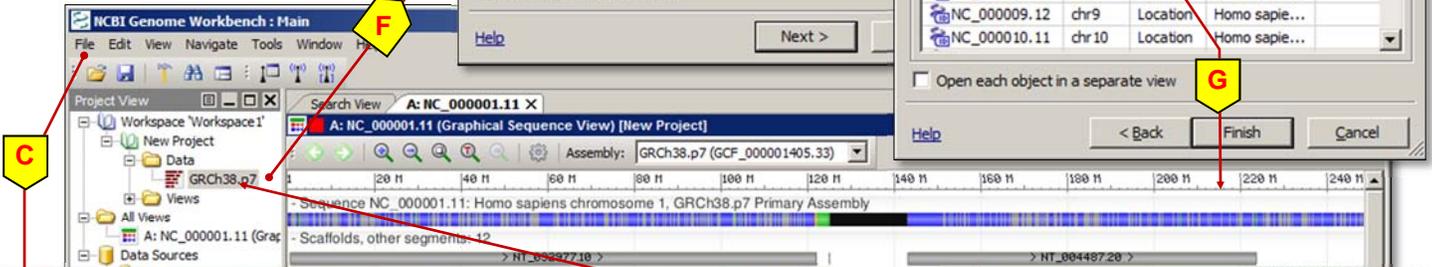
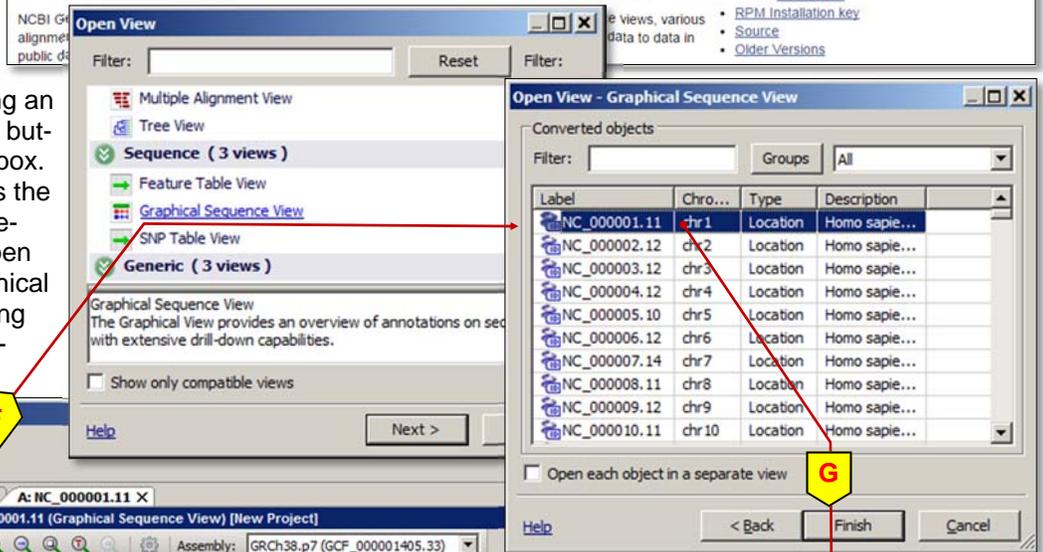
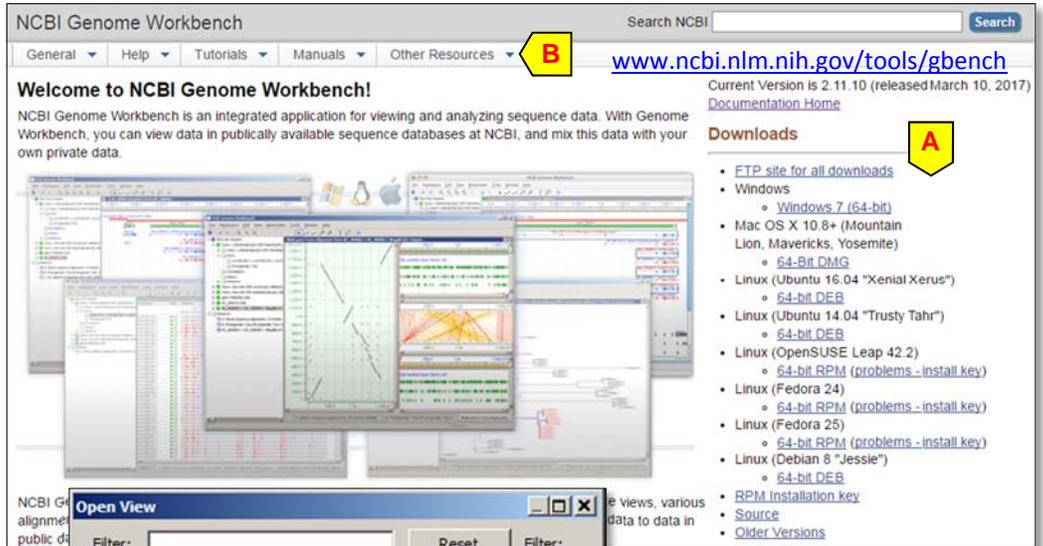
National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

Scope and Access

The Genome Workbench program (GBench) from NCBI is a powerful display and analysis tool for studying biological sequence data. GBench is freely available for download, and runs on most major computing platforms (A). GBench enables access to sequence data publicly available at NCBI as well as the ability to upload private data. Many viewing options in GBench allow data interrogation at all levels, from a graphical overview to single nucleotide resolution. Over 15 different analysis tools, such as BLAST, Splign and Phylogenetic Tree Builder, are built into GBench, making it a powerful software tool for performing sophisticated analysis. Download instructions, help documentation, tutorials and links to video How-To's (B) can be found on the GBench homepage (right). The video tutorials, as part of the NCBI video collection, are directly available on the NCBI YouTube channel (www.youtube.com/ncbinlm/).

Opening a Public Genome Record

A common use of GBench is to graphically display a genomic record and its annotation, which can be done using the "File >> Open" dialog box (C). Highlighting an assembly and clicking the "Next" button (D) opens the project dialog box. Clicking the "OK" button (E) adds the project to the project tree. Double-clicking the project opens the Open View window (F). Clicking "Graphical Sequence View", selecting "chr1" and clicking "Finish" button (G) opens the display.



Searching and Browsing Annotated Features

The “Search View” tab (A) allows for searching with names of genes and other features annotated on the genome. A Feature Search with “IL6R” (B) on the selected chromosome (chr 1) retrieves a single gene. Double-clicking the result adds the feature to the project tree view and updates the graphical display (C) to show details of the retrieved gene. Clicking the arrow (D) in the tools strip activates a menu for customizing tracks shown in that graphical panel. Clicking and dragging across a region in the ruler (E) highlights that region. Right-clicking the highlighted region (F) outside the ruler section allows zooming (G) into that region using the “Zoom” menu option. The “Run Tool ...” option (H) in the right-click menu provides access to tools for analysis of the displayed sequence. Hovering on an object displays its details in a popup (I).

The screenshot illustrates the workflow in NCBI Genome Workbench. At the top, the 'Search View' window (A) shows a search for 'IL6R' (B) on chromosome 1. The results table (C) lists the gene. The main window shows the graphical sequence view (E) with a ruler and tracks. A right-click menu (F) is open over a region, showing options like 'Zoom' (G) and 'Run Tool...' (H). A popup (I) shows details for the gene NP_001193795.1, including its location, length, and various links.

Search	Type	Subtype	NCBI Type	Description	Location	Strand	Accession	Context
IL6R	Feature	Gene	Seq-feat	Gene Featu...	154405193...	+	NC_000001...	A: NC_000...

Search View

Search Tool: Feature Search Start Stop Range Filter Form

Search Context: A: NC_000001.11 (Graphical Sequence View...) Search Type: Regular Expression

Feature Types: Gene CDS, RNA, All... Search Expression: IL6R

Search completed at 1 items.

NCBI Genome Workbench: Main

File Edit View Navigate Tools Window Help

Project View: Workspace 'Workspace 1', Data, Views, All Views, Data Sources, GenBank, Local BLAST, NCBI Net BLAST

Search View: A: NC_000001.11 X

Assembly: GRCh38.p7 (GCF_000001405.33)

Sequence NC_000001.11: Homo sapiens chromosome 1, GRCh38.p7 Primary Assembly

Scaffolds, other segments: 1

Genes, Subtracks: 1 on, 17 off

NCBI genes, 4 gene models shown

IL6R

NP_000... NP_000... NM_18... NP_852... NM_0... NP_001... XM_01...

Tools: AC, Back, Forward, Feature: Previous Splice, Feature: Next Splice, Flip Strands, Interval Rendering Options..., Load Default Tracks, Collapse All Tracks, Expand All Tracks, Show All Tracks

Right-click menu: Open New View... (Ctrl+N), Run Tool... (Ctrl+T), Export..., Ruler, Zoom (Zoom In, Zoom Out, Zoom All, Zoom to Selection, Zoom to Sequence), Go to Sequence Position/Ra..., Back, Forward, Feature: Previous Splice, Feature: Next Splice, Flip Strands, Interval Rendering Options..., Load Default Tracks, Collapse All Tracks, Expand All Tracks, Show All Tracks

Popup (I):

NP_001193795.1

CDS: NP_001193795.1

Title: interleukin-6 receptor subunit alpha isoform 3 precursor

Comment: isoform 3 precursor is encoded by transcript variant 3

Location: 154,405,630..154,437,544

[Length]

Span: 31,915

Placed: 1,059

Product: 352

[Positional Info]

Position: 154,437,516

Sequence: GGTCAAG[C]AATCCTCC

Product Position: 344

Product sequence: AVQSQLTATSASVWVQ[A]ILPPQPPK

[Links & Tools]

View CCDS: [CCDS72927.1](#)

View GeneID: [3570 \(IL6R\)](#), [3570 \(IL6R\)](#)

View HGNC: [6019](#)

View HPRD: [01000](#)

View MIM: [147880](#)

BLAST Genomic: [NC_000001.11 \(154,405,630..154,437,544\)](#)

BLAST Protein: [NP_001193795.1](#)

BLINK Results: [NP_001193795.1](#)

FASTA View: [NC_000001.11 \(154,405,630..154,437,544\)](#), [NP_001193795.1](#)

GenBank View: [NC_000001.11 \(154,405,630..154,437,544\)](#), [NP_001193795.1](#)

Graphical View: [NP_001193795.1](#)

Searching selected sub-sequences with BLAST

Right-clicking a highlighted feature (A) and selecting "Run Tool" (B) in the menu activates the Run Tool widget. Selecting the "Blast" option (C) allows a BLAST search using the sequence as a query against the selected database (D). An Entrez query, such as "*human [orgn] AND biomol_mrna[prop]*" (E), helps restrict the search to a specific subset of sequences in the database. Additional databases are available by clicking the folder icon (F). Follow the dialog boxes to add the search to the project (G).

The Project View displays a successfully completed BLAST search as a new node (H). Double-clicking the node followed by "Multiple Alignment View" menu selection (I) displays the search result in a new panel (J).

Clicking the "+" and "-" signs (K) toggles on and off the annotated features to the right. Options in the right-click menu allow the examination of the alignment at the sequence level in selected color scheme (L).

