The Graphical Sequence Viewer

Graphical presentation of sequence data
National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

Scope and Access
The Sequence Viewer (SV) from NCBI is a free, web-based tool for graphical display and analysis of genomic, mRNA, and protein sequences. It is a flexible interface that combines a bird’s eye view of a complete chromosome with a detailed interrogation at a single nucleotide resolution. You can access this display from individual records in Nucleotide, Protein, Gene, Genome, SNP, dbGaP, dbVar and Clone databases, and from various tools such as BLAST and Primer BLAST. You can also import and render custom data in different formats into SV. For more details see the SV help document linked on the project’s homepage at https://www.ncbi.nlm.nih.gov/projects/sviewer/

Activating an SV Display Through the Graphics Link
A common use of SV is to display a large genome. For example, you can retrieve the human chromosome 1 record from the Nucleotide database by its accession number NC_000001, and display it graphically in SV by selecting Graphics under the Display Settings menu (A) or simply by clicking the Graphics link (B) at the top of the record.

SV Display: the Overview Panel
The top-most panel of the Graphics page represents chromosome 1 in its entirety (C) with its ruler showing the genomic coordinates. You can search for Genes and other annotated features using the “Search” option in the “Tools” dropdown menu (D), where the example searches for the IL6R (E) gene. Click the “IL6R” gene (F) to zoom in to that feature for more detailed examination (p. 2).
SV Display: the Graphical Panel

The graphical panel below the overview shows the details of the IL6R gene, with its genomic range shown in the ruler at the top of the panel (A). Click the green Gene bar to see details in the expanded section, which depicts exons as vertical lines/boxes (B) linked by introns (as thin lines, C). Arrows (D) in the display indicates the gene orientation. Mouse over a displayed item, such as a specific transcript variant (E), to see additional details.

SV Display: Manipulation

You can right click on the ruler or any white space to activate a menu (F) to manipulate an SV display. Using the “Set New Marker At Position” option (G), you can add a marker (such as “TStop_Variant3”). The marker context menu enables single-click zoom to sequence at that location (H). This contrasts to the “ATG” icon click (I), which zooms to the center of the current display. Use the zoom slider (J) to zoom in and out incrementally. Pan the display to surrounding regions by holding the left mouse button and dragging the image horizontally, or by using the arrows at the top (K). Click the “Tracks” button (L) to access available tracks through categories listed under the “Tracks” tab, or locate specific ones using the “Search tracks” function in a dialog box (M). Embedded SV displays from records in other NCBI database, such as records from the Gene database, provides NCBI recommended track sets in a cascading menu under Tracks (not shown). You can also save your track setting to My NCBI for reference and easy access.
Examining a Specific Region at Single Nucleotide Resolution

A marker placed at a position of interest (A) enables ready access to sequences through the “Zoom to Sequence At Marker” option in the marker menu (B, activated upon hovering). The zoomed-in display shows the CDS stop for the transcript variant 3 of the ILR6R gene (C).

With the protein track displayed, this display reveals the protein translation at the C-terminus of IL6R transcript variant 3 (D). Select “Reveal in Sequence View” option from the marker menu (E) to open a floating sequence panel. Use the pull-down menu to select variant 3 (F) to see the color-coded sequences for this variant: purple for untranslated region (UTR, G), pink for coding region (H), and green for intron (I). This display preserves the marker positions by highlighting the bases with boxes in the same color as the markers (J). See annotation of other transcript variants by selecting them from the pull-down menu (K).
Additional Displays and Functions

Using the “Tracks” dialog box (A), you can also upload custom data from external sources into a Sequence Viewer display, such as a BLAST result using the assigned Request ID (B) or data file from other sources in various formats (C).

The Sequence Viewer also provides the capability to perform different tasks, such as:

- Set the origin of the sequence to the start of the coding region, using the “Set Sequence Origin At Position” option (D), useful in getting coordinates in HGVS format.
- Flip the orientation to obtain the reverse complement strand of the double-stranded DNA for genes annotated on the reverse strand of the genomic sequence.
- Display alignments and other features annotated on the genome (under Alignments, E).
- Customize tracks displayed using the “Tracks” to add SNP and other variation related tracks (F).
- Right-click on an annotated feature to activate a set of cascading menus for additional views and BLAST analysis (not shown).

Genome Data Viewer (GDV), a new genome browser built on SV with streamlined custom data upload function, is available. A factsheet on GDV is listed and linked from the factsheet readme at: http://bit.ly/ncbi_factsheets.