Graphical Sequence Display Survey

We want to improve NCBI's products and services. We would like to learn more about how this site helps you with your work, and what we can do better. Please click "next" below to get started.

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Next

Graphical Sequence Display Survey

1. Which professional category best describes you?

- Student
- Life Science Researcher
- Technician
- Bioinformatics Professional
- Educator
- Librarian / Information Specialist
- Computer Scientist / Software Developer
- Other (please specify)

2. Which of the following categories best describes your organization?

- University or College
- Non-profit organization
- Clinical diagnostics
- Clinical research
- Commercial/Industry
- Government
- Other (please specify)

3. Which organism(s) do you study? Please check all that apply.

- human
- mouse
- other mammals
- other vertebrates
- invertebrates
- plants
- fungi
- protozoa
- prokaryotes
- viruses
- Other (please specify)

4. Which NCBI resources have you used to look at a graphical sequence display? Please check all that apply.

- Gene
- dbSNP
- Genome Data Viewer (GDV)
- Variation Viewer
- BLAST
- Nucleotide
- Protein
- Other (please specify)

5. Which other sequence or genome browsers have you used? Please check all that apply.

- UCSC Genome Browser
- I don't use any other sequence or genome browsers
- Model organism database browser
- Ensembl Browser
- Other (please specify)

6. Which of the following biological data tracks are helpful to your analyses? Please check all that apply.

- Comparative genomics (PhyloCSF, phyloP, phastCons, assembly alignments)
- Sequence features (Six-frame translation, RepeatMasker, G+C content, etc)
- Epigenomic data (CpG islands, H3K4me3, etc)
- Assembly support (tiling path, components, segmental duplications, etc)
- Expression support (RNA-seq, CAGE, polyA-seq, peptide data, etc)
- Clinical (dbSNP, ClinVar, dbVar, etc)
- Gene annotation (NCBI annotation, Ensembl annotation, CCDS, etc)
- Other (please specify)

7. Do you typically modify the default tracks in the graphical sequence display?

- Yes, I modify the track display. (Please comment below.)
- No, I use the default because it meets my needs
- No, but I want to learn how to do this

If **Yes**, please tell us how you modify the display.

8. Many genes have extensive alternative splicing resulting in numerous transcript variants. Which filtering options would you like for the Gene annotation track? Please check all that apply.

- Show only protein-coding RefSeqs (hide NR_/XR_)
- Show only the transcript variant that I choose, hide all others
- Show only known/curated RefSeqs (hide XM_/XR_)
- Show only transcript variants that contain the same splice structure and biotype as an Ensembl transcript variant
- Show only a representative "Select" RefSeq
- I would always want to see all RefSeq transcript variants
- Other (please specify)

9. Which RefSeq transcript splice variants would you like to see by default in the NCBI Gene Annotation track?

- Protein-coding RefSeq transcript variants only, hide non-coding transcript variants
- Known/curated RefSeq transcript variants only, hide models
- All RefSeq known/curated and model transcript variants
- A single representative "Select" RefSeq transcript variant for every gene
- Other (please specify)

10. The human dbSNP All Data track is dense, with SNP features located every few nucleotides. What subsets of the dbSNP All Data track would be helpful to your work? Please check all that apply.

- I don't work with human SNP data
- Variants with pre-calculated MAF (minor allele frequency), e.g. >0.01
- Variants with MAF in a range determined by me
- Variants that have a ClinVar database record
- Variants that result in a non-synonymous change in the coding sequence
- Variants cited in PubMed publications
- Variants in the GWAS catalog
- Variants that are suspect or false-positive
- Variants that are somatic
- I would always want to see all known variation in a genomic region
- Other (please specify)

11. Which of the following functions or tools available within the NCBI graphical display are of high value to you? Please check all that apply.

- "Find:" function
- Primer design
- Set markers
- Sequence download (FASTA or GenBank format)
- Sequence text view
- Printable display (PDF)
- BLAST
- None of the above
- Other (please specify)

12. What types of searches would you like NCBI to support in the graphical display? Please check all that apply.

- I don't need to search in the graphical display
- Gene symbol
- Gene full name
- Protein name
- RNA or protein accession
- Locus tag
- Nucleotide sequence (e.g. FASTA)
- SNP ID (e.g. rs111)
- dbVar ID (e.g. nsv317035)
- Disease name
- Other (please specify)

13. What information would you find valuable to download from the graphical display? Please check all that apply.

- RefSeq transcript sequence
- RefSeq protein sequence
- Genomic sequence of a selected range
- Genomic sequence of a pre-calculated range for a gene
- Annotation displayed in a user-specified range
- I do not want to download information from the graphical display
- Other (please specify)

14. If we provided keyboard shortcuts for browsing the graphical sequence display, would you use them?

- Yes
- Maybe/Occasionally
- No

15. How likely is it that you would recommend the graphical sequnece display to a friend or colleague?

Not at all likely — Extremely likely

0	1	2	3	4	5	6	7	8	9	10

16. Please provide any additional comments or suggestions you have about the graphical sequence display.

17. Did you find what you were looking for today?

- Yes
- No

18. How easy was it to find what you needed using the graphical sequence display today?

- Very easy
- Somewhat easy
- Somewhat difficult
- Very difficult

Please contact us at info@ncbi.nlm.nih.gov if you'd like to provide additional feedback about the graphical display.

Prev Done