

Genome Data Viewer Survey

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1. Which professional category best describes you? Please select only one.

- ☐ Bioinformatics Professional
- ☐ Clinical Testing Laboratory Staff
- ☐ Computer Scientist / Software Developer
- ☐ Educator
- ☐ Other (please specify)
- ☐ Health Professional / Clinician
- ☐ Life Science Researcher
- ☐ Student
- ☐ Librarian / Information Specialist

2. Pick one category that best describes your organization

- ☐ College or University
- ☐ Commercial or Industry
- ☐ Non-Profit Organization
- ☐ Government
- ☐ Clinical diagnostics
- ☐ Clinical research
- ☐ Other (please specify)

3. What organisms do you study? Choose as many as apply.

- ☐ Human
- ☐ Mouse
- ☐ Other mammals
- ☐ Other vertebrates
- ☐ Invertebrates
- ☐ Plants
- ☐ Fungi
- ☐ Protozoa
- ☐ Other (please specify)

4. How did you access this Genome Data Viewer (GDV) browser view today?

- ☐ NCBI Gene
- ☐ NCBI Genome
- ☐ NCBI Assembly
- ☐ GDV home page
- ☐ NCBI BLAST
- ☐ Other NCBI page
- ☐ Other non-NCBI page
- ☐ Internet search
- ☐ Saved or shared link
- ☐ Other (please specify)

5. Please tell with us what you would like to do in GDV today.

6. Which other NCBI resources have you used to view a graphical sequence display in recent weeks? Please check all that apply.

- ☐ dbSNP
- ☐ BLAST
- ☐ Nucleotide
- ☐ Variation Viewer
- ☐ Gene
- ☐ Protein
- ☐ Other (please specify)

7. Which other sequence or genome visualization tools do you use on a regular basis? Please check all that apply

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

8. Which of the following features have you used recently in GDV? Please check all that apply.

- ☐ Downloaded a PDF or SVG file of the graphical view
- ☐ Sent sequence to Primer-BLAST or BLAST
- ☐ Downloaded track data (e.g. BED, GFF3, VCF)
- ☐ Viewed BLAST results
- ☐ Set markers
- ☐ Accessed the Sequence Text View
- ☐ Added custom data (e.g. GFF file, remote BAM or VCF, track hub, etc)
- ☐ Obtained information from the tooltips of track features
- ☐ Downloaded sequence (FASTA or GenBank format)
- ☐ None of the above

9. Which of the following biological track data do you find valuable to view in GDV? Please check all that apply.

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

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

- ☐ Yes, I modify the track display
- ☐ 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

11. If you modify the display, do you add custom track data not provided by NCBI? Please check all that apply.

- ☐ Yes, I register a track hub and add tracks found in that hub
- ☐ Yes, I upload my own data tracks (e.g. GFF3, BED, WIG, VCF, etc)
- ☐ Yes, I add non track-hub data hosted remotely (e.g. BAM, tabix VCF, bigBed, etc.)
- ☐ No, I don't add custom data but would like to learn how to do this
- ☐ No, I do not need to add custom data OR I do not need to modify the display

12. What types of data do you download (or would you like to download) from GDV? Please check all that apply.

- ☐ FASTA sequence of data in view or a selected region
- ☐ GenBank flat file (e.g. selected sequence, feature, or sequence in view)
- ☐ Gene annotation in tabular form (e.g. GFF3, BED, CSV)
- ☐ FASTA sequence of a feature in a track (e.g. transcript or protein)
- ☐ SNP annotation in table form (e.g. BED, VCF)
- ☐ Annotation of other data tracks in table form (e.g. CpG Islands in BED)
- ☐ Other (please specify)

13. What types of of genomic features/elements do you search for using the main search box in GDV? Check all that apply.

- ☐ genes or proteins
- ☐ disease/phenotypes
- ☐ assembly components or scaffolds
- ☐ I don't perform searches in GDV
- ☐ structural variation
- ☐ sequence variation
- ☐ I don't need to perform searches in GDV
- ☐ Other (please specify)

14. If you do searches within GDV, which of the following search terms would you expect to be recognized? Check all that apply.

- ☐ RefSeq RNA or protein ID
- ☐ Ensembl gene/RNA/protein ID
- ☐ Gene symbol
- ☐ Non-NCBI locus ID (e.g. SGD ID)
- ☐ Assembly component accession (e.g. AAEX03000278.1, AC211344.3)
- ☐ dbVar ID (e.g. nsv3170325)
- ☐ RefSeq accession for an assembly scaffold (e.g. NW_012132914.1, NC_000011.10)
- ☐ non-RefSeq local scaffold name (e.g. chrUn_15547365)
- ☐ RefSNP ID (e.g. rs268)
- ☐ None of the above
- ☐ I don't need to do searches in the GDV

15. How frequently do you use GDV?

- ☐ Daily
- ☐ Weekly
- ☐ Monthly
- ☐ Occasionally
- ☐ This is my first visit

16. How do you prefer to stay informed on GDV updates that enhance functionality? Check all that apply.

- ☐ NCBI Insights Blog
- ☐ Twitter
- ☐ LinkedIn
- ☐ Facebook
- ☐ Announcements on GDV graphical display/web page
- ☐ Release notes
- ☐ Other (please specify)

17. How would you prefer to learn about GDV's features and functions?

- ☐ Webinars
- ☐ YouTube tutorials
- ☐ Conference workshops
- ☐ Help documentation
- ☐ Other (please specify)

18. How likely is it that you would recommend GDV to a friend or colleague?

Not at all likely

Extremely likely

0	1	2	3	4	5	6	7	8	9	10
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19. Please provide any additional thoughts you would like to share with us about GDV or graphical displays at NCBI.

20. How easy was it to find what you needed using the GDV browser today?

- ☐ Very easy
- ☐ Easy
- ☐ Neither easy nor difficult
- ☐ Difficult
- ☐ Very difficult

Additional comments

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Please write to us at suggest@ncbi.nlm.nih.gov if you would like to provide additional feedback on NCBI's Genome Data Viewer.

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Done