

Genome Data Viewer Survey

OMB Control Number: 0925-0648 Expiration Date: 05/31/2021

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

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

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 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_16547365)
 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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Genome Data Viewer Survey , write to us

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