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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 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](mailto:suggest@ncbi.nlm.nih.gov) if you would like to provide additional feedback on NCBI's Genome Data Viewer.

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Done