

## NCBI Gene User 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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**1. Which professional category best describes you? Please select only one.**

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

**2. Please pick one category that best describes your organization.**

- College or University  
 Commercial / Industry  
 Non-profit Organization  
 Government  
 Other (please specify)

**3. How often do you use NCBI Gene?**

- Every day  
 A few times a week  
 About once a week  
 A few times a month  
 Once a month  
 Less than once a month

**4. How do you obtain gene-related information from NCBI? Please check all that apply.**

- Gene web pages  
 Gene FTP site  
 NCBI programming utilities APIs (E-Utilities, EDirect)  
 Other (please specify)

**5. Which of the following organism(s) are the focus of your research? Please check all that apply.**

- Human  
 Mouse  
 Mammals other than mouse or human  
 Non-mammalian vertebrates  
 Invertebrates  
 Plants  
 Fungi  
 Protozoa  
 Prokaryotes  
 Viruses

**6. What was the purpose of your visit to Gene today? Please check all that apply.**

- Find general information about a gene  
 Find sequences  
 Use links to other resources (GEO, SNP, ClinVar, etc.)  
 Get information about gene expression  
 Get information about gene / protein function  
 Find publications  
 Other (please specify)

**7. What sections or features of the NCBI Gene page do you use in your work? Please check all that apply.**

- Nomenclature  
 Summary  
 Graphical View/Sequence Viewer  
 Link to Gene sequence and location  
 Expression  
 Interactions and Pathways  
 Orthologs  
 Variation  
 Genomic context  
 Publications  
 RefSeq transcripts and proteins  
 Gene Ontology

**8. What publication information would you like to access from NCBI Gene? Please check all that apply.**

- All publications  
 The most recent publications  
 Selected publications that provide information about gene function  
 GeneRIF summaries of functional information about the gene  
 I don't use any of the publication information in Gene

**9. How do you use the information you obtain from NCBI Gene? Please check all that apply.**

- Experiment/assay design  
 Manuscript preparation  
 Clinical analysis  
 Teaching  
 Generating reports/protocols  
 Other (please specify)

**10. What content do you use from the NCBI Gene FTP files? Please check all that apply.**

- RefSeq-Ensembl matches from gene2ensembl.gz and gene2vega.gz  
 Gene Ontology from gene2go.gz  
 I don't use the Gene FTP site  
 Gene summary information from gene\_info.gz  
 Genome annotation from ASN\_BINARY  
 RefSeq accessions for each gene from gene2refseq.gz  
 RefSeq-UniProtKB matches from gene\_refseq\_uniprotkb\_collab.gz  
 Publications from gene2pubmed.gz  
 Summaries from ASN\_BINARY  
 Orthology data from gene\_orthologs.gz  
 GeneRIF  
 Other

**11. Which of the following additions to NCBI Gene would benefit your research the most? Please check all that apply.**

- Expanded orthology information to include organisms outside the vertebrates  
 Expression data for more organisms  
 Expression data from more tissues/developmental stages  
 Comparison between RefSeq annotation and Ensembl or GenBank  
 Expanded reporting of UniProt accessions (both SwissProt and TrEMBL)  
 Advanced search for expression data  
 Pan-genome analyses  
 Transcript variant-specific expression information  
 Sequence data from multiple strains/breeds/cultivars  
 Other (please specify)

**12. Did you find what you were looking for today?**

- Yes  
 No

**13. How easy was it to find what you were looking for on the NCBI Gene website?**

- Extremely easy  
 Very easy  
 Somewhat easy  
 Not so easy  
 Not at all easy

**14. Please provide any additional suggestions you may have on improving NCBI Gene.**

**15. How likely is it that you would recommend NCBI Gene 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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Please write to us at [info@ncbi.nlm.nih.gov](mailto:info@ncbi.nlm.nih.gov) you'd like to provide additional feedback about NCBI Gene resources.

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