

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 you'd like to provide additional feedback about NCBI Gene resources.

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