

## NCBI 2018 Population Frequency 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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Public reporting burden for this collection of information is estimated to average 4 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a current valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to NIH Project Clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA (0925-0648). Do not return the completed form to this address.

Next



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

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

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

- College or University
  Research Institute  
 Commercial / Industry
  Government  
 Non-profit Organization
  Hospital/health care organization  
 Other (please specify)

**3. Which of these is the most frequent kind of search you perform for a variant with allele frequency information?**

- Using a variant genomic or sequence position or region  
 Using a gene name or symbol  
 Using an HGVS name  
 Using a dbSNP Reference SNP (rs) ID  
 Using a disease or phenotype name/description  
 Other (please specify)

**4. How many variants do typically want to search or retrieve?**

- 1-100  
 100-1,000  
 1000-1,000,000  
 > 1,000,000

**5. How often do you perform searches for variants at the NCBI site?**

- Daily  
 Weekly  
 Monthly  
 Yearly

**6. How would you like to filter your results? Please check all that apply.**

- By allele frequency  
 Ethnicity  
 Continent of origin (Asia, Africa, Europe, North America etc.)  
 Functional consequences (Missense, Nonsense, Frame shift)  
 Variant type (Single Nucleotide Variation, Deletion, etc)  
 ClinVar clinical significance  
 Variants cited in publications  
 Other (please specify)

**7. Are you interested in frequency aggregated by asserted/reported ethnic population?**

- Yes  
 No  
 No preference

**8. Are you interested frequency aggregated by computed population (PCA, GRAF, etc.) based on genotype?**

- Yes  
 No  
 No preference

**9. How do you use allele frequency data? Please check all that apply.**

- Classify or prioritize variants for research  
 Identify cancer or disease-causing variants  
 Identify ancestry markers  
 Clinical interpretation  
 Variant quality control or validation  
 Other (please specify)

**10. Are global allele frequencies useful to you?**

- Yes  
 No

**11. How likely is it that you would recommend NCBI variation resources 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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**12. If there was one thing you could change about NCBI variation resources, what would it be?**

Prev

Next

**We welcome your input! Please contact us at [suggest@ncbi.nlm.nih.gov](mailto:suggest@ncbi.nlm.nih.gov) if you would like to provide additional feedback about NCBI variation resources and populationfrequency data.**

Prev

Done