Human Population Frequency Data Survey

We want to improve NCBI's products and services. We would like to learn more about how you use genotype or allele frequency data in 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 2 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.

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If you currently use allele or genotype frequency data please help us to improve the related NCBI product(s) by taking this survey.

1. Which professional categories best describe you? Please select only one.

- ○ Bioinformatics professional
- ○ Educator
- ○ Genetic Counselor
- ○ Librarian / Information Specialist
- ○ Life Science Researcher
- ○ Medical Geneticist
- ○ Other health care professional
- ○ Student
- ○ Technician
- ○ Computer Scientist / Software Developer
- ○ Other (please specify)

2. What is your institutional affiliation?

3. Where do you currently obtain allele/genotype frequency data? Please check all that apply.

- ☐ 1000 Genomes Project
- ☐ GO-ESP
- ☐ gnomAD
- ☐ dbSNP
- ☐ ExAC
- ☐ TOPMED
- ☐ HapMap
- ☐ Alfred
- ☐ Other (please specify)

4. What method would you prefer to use to access frequency data?

- ○ Web pages
- ○ FTP download
- ○ API
- ○ Other (please specify)

5. How easy was it to find what you were looking for on our website?

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

6. 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

7. May we contact you to get additional feedback?

- ○ Yes
- ○ No

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8. Please enter your email address below.

Prev Done