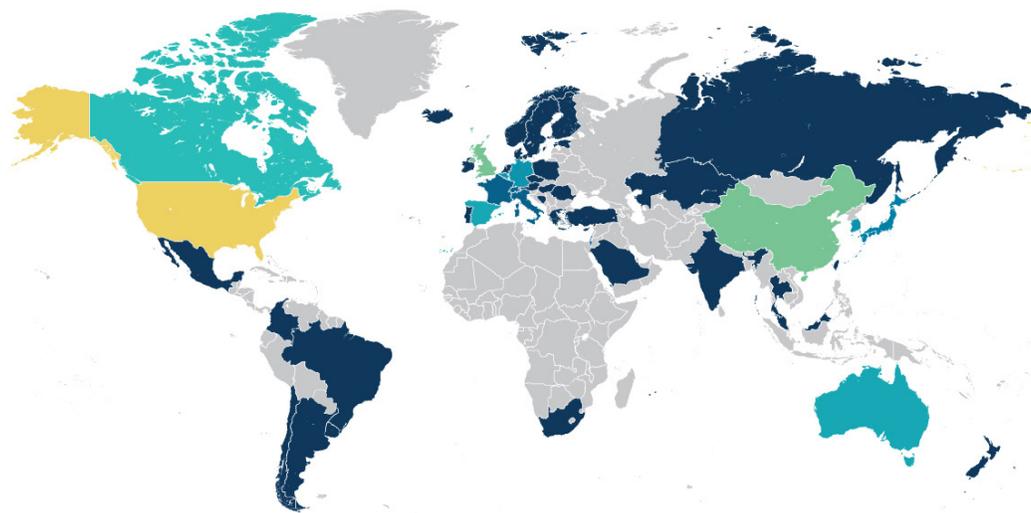


dbGaP



An NIH-sponsored repository for archiving, curating, and distributing information produced by genome-scale studies investigating the interaction of human genotype and phenotype



Approved Data Access Requests By Country



- As of Sept 1, 2019, dbGaP contained data from over 2.2 million research subjects submitted from ~ 1,300 separate research studies.
- Researchers from 52 different countries have been approved for more than 56,000 requests to access the controlled-access data.
- Citation in publications - Over 2,600 PMC articles citing a dbGaP accession

dbGaP study submission steps (NIH funded studies) <https://go.usa.gov/xVPda>

1 Registration

- Contact NIH Program Officer or Genomic Program Administrator (GPA)
- Receive invitation
- Enter study metadata

2 Submission

- Use dbGaP submission guide to upload files
- Work with curators to complete submission
- Get accession number

3 Release

- Approve processed data
- Release study

dbGaP study access steps (for Principal Investigators (PIs)) <http://bit.ly/2kCTGmF>

1 Account Setup

- NIH Intramural researchers – submit permission form to establish data request eligibility in dbGaP
- Other researchers – Get eRA commons user account

2 Access Application

- Complete / revise and submit application to Signing Officer (SO)
- SO certifies application with one or more Data Access Requests (DAR)

3 Approval and Access

- dbGaP Data Access Committee (DAC) reviews and approves application
- dbGaP approved data is provided for download



U.S. National Library of Medicine
National Center for Biotechnology Information



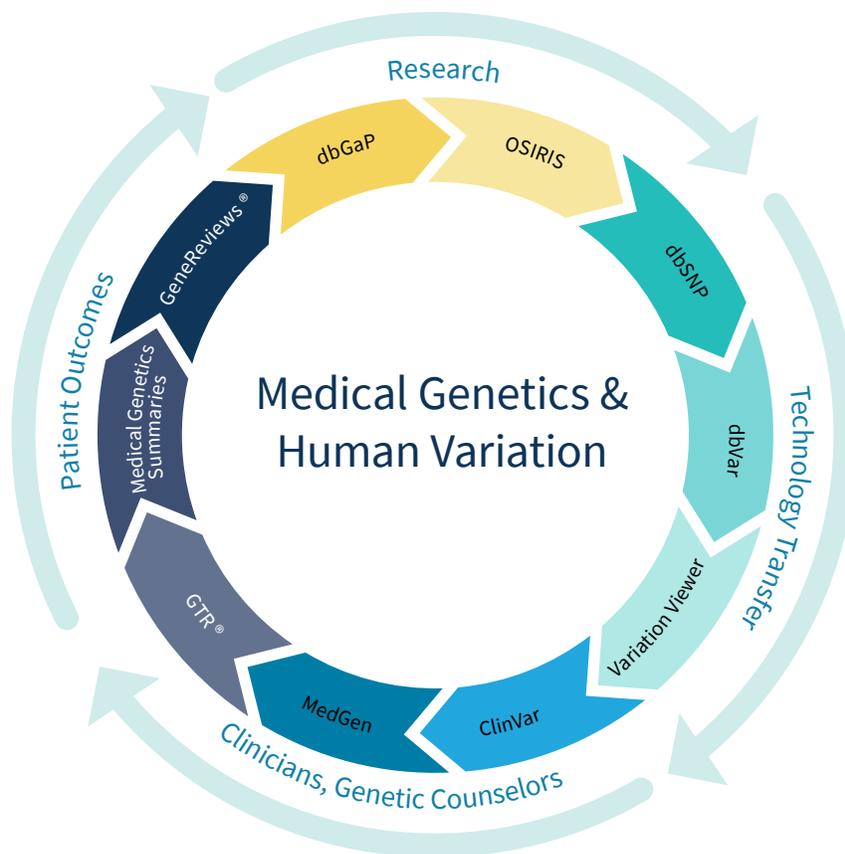
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ClinVar

user-submitted database for information about genomic variation and its relationship to human health.



dbGaP

database for genotype and phenotype research studies.



dbSNP and dbVar

databases of small and large genomic variants including both common variations and clinical mutations.



GTR[®]

provider-submitted database of clinical and research molecular, cytogenetic and biochemical genetic tests and supporting information.



MedGen

aggregates information from and provides access to authoritative medical genetics resources.



Medical Genetics Summaries and GeneReviews[®]

up-to-date, peer-reviewed, medically actionable summaries for heritable diseases and pharmacogenetics.



OSIRIS

Open source short tandem repeat (STR) analysis tool for forensic, clinical and research use.



Variation Viewer

interactive browser for examination of nucleotide variants in a genomic context.