What is ClinVar?
An NCBI database of variant interpretations.

Variants interpreted by
- Clinical laboratories
- Research groups
- Expert panels and more

Search ClinVar by
- Gene symbols
  HFE or BRCA1
- HGVS expressions
  NM_000410.3:c.277G>C
- rs numbers
  rs28934597
- Protein changes
  p.Gly93Arg
- Disease and phenotype
  Hemochromatosis
- Submitting organization
  children’s national medical center
- PubMed ID or other citations

Key statistics
- Over 273,000 interpreted variants
- From over 670 submitters

Steps to submit your interpretation
1. Go to ClinVar Submission Portal
2. Register your organization
3. Submit your data
   - single variant interpretation
     Use our single submission wizard
   - Batch of variant interpretations
     Fill in our submission spreadsheet template, then upload your file. Learn more at:

To learn more about ClinVar
dbSNP is changing

- New streamlined build system for establishing reference SNPs (RefSNPs, rs)
- New display to report on RefSNPs
- New content available in JSON format via FTP
- Consistent reporting on RefSNPs across products
- New internal representation of RefSNPs as objects
- New Variation Services for comparing and processing variations

Pre-Alph release of new products

Files on FTP site
- VCF files for assemblies GRCh37 and CRCh38
- Full set of RefSNPs in the JSON format

Variation Services
- Web services for comparing, grouping and interconverting sequence variants
  https://www.ncbi.nlm.nih.gov/projects/variation/services/v0/
- A BLOG post with additional details

Spread the news

Please share this with your colleagues, particular those involved in managing the bioinformatics resources and sequence variation data for your group or institutions.

Address your questions or feedback to variation-services@ncbi.nlm.nih.gov