

## Molecular In My Pocket™ ...

# Bioinformatics: Interpretation Databases

Database	Description	Website
<b>Population Databases Exclude Polymorphisms</b>		
Genome Aggregation Database (gnomAD)	A database that aggregates and harmonizes exome and genome sequencing data from a variety of large-scale sequencing projects, and makes summary data available for the wider scientific community. The database includes Exome Aggregation Consortium (ExAC) database.	<a href="https://gnomad.broadinstitute.org/">https://gnomad.broadinstitute.org/</a>
Single Nucleotide Polymorphism Database (dbSNP)	A public archive for genetic variation, include SNPs and short indels from 1000 Genomes (1000g) Project and Exome Variant Server (EVS).	<a href="https://www.ncbi.nlm.nih.gov/snp/">https://www.ncbi.nlm.nih.gov/snp/</a>
<b>Interpretation Databases Determine the Importance of the Variants. Somatic Interpretation ● ; Germline Interpretation ● .</b>		
Catalog of Somatic Mutations in Cancer (COSMIC) ●	A database of somatically acquired mutations found in human cancer.	<a href="https://cancer.sanger.ac.uk/cosmic">https://cancer.sanger.ac.uk/cosmic</a>
cBioPortal for Cancer Genomics ●	A resource for interactive exploration of multidimensional cancer genomics data sets. The database includes Cancer Hotspots and GENIE (requires registration).	<a href="http://www.cbioportal.org/">http://www.cbioportal.org/</a>
ClinVar ● ●	A public archive that aggregates information about genomic variation and its relationship to human health.	<a href="https://www.ncbi.nlm.nih.gov/clinvar/">https://www.ncbi.nlm.nih.gov/clinvar/</a>
Human Gene Mutation Database (HGMD) ●	A comprehensive collection of published germline mutations in nuclear genes that underlie, or are closely associated with, human inherited disease.	<a href="http://www.hgmd.cf.ac.uk/ac/index.php">http://www.hgmd.cf.ac.uk/ac/index.php</a>
My Cancer Genome ●	A precision cancer medicine knowledge resource that contains information on the clinical impact of molecular biomarkers in cancer-related genes, proteins, and other biomarker types on the use of anticancer therapies in cancer.	<a href="https://www.mycancergenome.org/">https://www.mycancergenome.org/</a>
PeCan ● ●	A resource that provides pediatric cancer mutations.	<a href="https://pecan.stjude.cloud/home">https://pecan.stjude.cloud/home</a>
<b>Protein Function Prediction Databases Predict Impact of Variants on Proteins</b>		
Polymorphism Phenotyping v2 (PolyPhen2)	Categorical prediction: D: probably damaging; P: possibly damaging; B: benign	<a href="http://genetics.bwh.harvard.edu/pph2/">http://genetics.bwh.harvard.edu/pph2/</a>
Sorting Intolerant From Tolerant (SIFT)	Categorical prediction: D: deleterious; T: tolerated	<a href="https://sift.bii.a-star.edu.sg/">https://sift.bii.a-star.edu.sg/</a>
<i>Notes: This is not an inclusive list, only the most common databases.</i>		