

Tool	Type	Summary	User input			Online?	Download?
			Sequence	Alignment	Other		
Align-GVGD	Sequence/evolutionary conservation	Characterises biochemical properties of substitutions	✓	Optional	Alignment depth options	✓	✗
BONGO	Protein structure-based	Protein structure internal interactions mapped and compared using graph theory. <b>NOT CURRENTLY WORKING</b>	✗	✗	PDB code	✓	✗
CanPredict	Supervised-learning (RF)	Uses a random forest algorithm trained on classification from SIFT, Pfam-based scores and gene ontology	✓	✗	Protein accession/ID	✓	✗
Hansa	Supervised-learning (SVM)	Uses a support vector machine combining position-specific, protein structure and amino acid property	✓	✗	NA	✓	✗
LS-SNP/PDB	Protein structure-based	Features of protein structure used to highlight biological importance of variants	✗	✗	Protein ID/dbSNP ID/PDB code/KEGG pathway	✓	✗
MAPP	Sequence/evolutionary conservation	Predictions based on physicochemical variation	✗	✓	Phylogenetic tree required	✗	✓
MutationAssessor	Sequence/evolutionary conservation	Partitioned alignment identifies functionally important positions	✗	✗	Protein accession/ID	✓	✗
MutationTaster	Supervised-learning (Bayes classifier)	Predictions based on multiple sources combined with a naive Bayes classifier	✗	✗	Transcript ID	✓	✓
MutPred	Supervised-learning (RF)	MutPred uses a random forest algorithm based on the probabilities of gain or loss of properties relating to many features of protein structure and function	✓	✗	NA	✓	✗
nsSNPAnalyzer	Supervised-learning (RF)	Uses a random forest algorithm based on sequence alignment and protein structure information	✓	✗	NA	✓	✓
PANTHER	Sequence/evolutionary conservation	Homology to HMM alignments of protein families identifies important positions	✓	✗	NA	✓	✓
Parepro	Supervised-learning (SVM)	Uses a support vector machine combining position-specific information and amino acid differences	✗	✓	NA	✗	✓
PhD-SNP	Supervised-learning (SVM)	Uses a combination of support vector machines trained on sequence and evolutionary information	✓	✗	SVM options	✓	✓
PMut	Supervised-learning (NN)	Neural network method trained on disease-associated and neutral mutations	✓	Optional	NN options	✓	✗
PolyPhen	Protein sequence and structure-based	Empirical cutoffs of a number of sequence and structural properties. <b>NO LONGER SUPPORTED OR MAINTAINED</b>	✓	✗	Protein accession/ID	✓	✗
PolyPhen-2	Protein sequence and structure-based	Sequence and structural information combined in a Bayesian approach	✓	Optional in download version	Protein accession/ID	✓	✗
SIFT	Sequence/evolutionary conservation	Calculates normalised probability of substitution given sequence homology	✓	Optional	Other optional available	✓	✓
SNAP	Supervised-learning (NN)	Neural network method trained on protein structural features	✓	✗	Other advanced options	✓	✗
SNPeffect	Protein sequence and structure-based	A database for phenotyping SNPs using molecular characterisation and annotation	✓	✗	Can submit PDB file, PDB ID or UniProt ID	✓	✗
SNPs&GO	Machine-learning (SVM)	Uses a support vector machine combining PANTHER, sequence profile and gene ontology scores	✓	✗	SVM and GO options	✓	✗