Resource Summary Report

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TopoSNP

RRID:SCR_005572
Type: Tool

Proper Citation

TopoSNP (RRID:SCR_005572)

Resource Information

URL: http://gila.bioengr.uic.edu/snp/toposnp

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Description: A topographic database for analyzing non-synonymous SNPs (nsSNPs) that can be mapped onto known 3D structures of proteins. These include disease- associated nsSNPs derived from the Online Mendelian Inheritance in Man (OMIM) database and other nsSNPs derived from dbSNP, a resource at the National Center for Biotechnology Information that catalogs SNPs. TopoSNP further classifies each nsSNP site into three categories based on their geometric location: those located in a surface pocket or an interior void of the protein, those on a convex region or a shallow depressed region, and those that are completely buried in the interior of the protein structure. These unique geometric descriptions provide more detailed mapping of nsSNPs to protein structures. It also includes relative entropy of SNPs calculated from multiple sequence alignment as obtained from the Pfam database (a database of protein families and conserved protein motifs) as well as manually adjusted multiple alignments obtained from ClustalW. These structural and conservational data can be useful for studying whether nsSNPs in coding regions are likely to lead to phenotypic changes. TopoSNP includes an interactive structural visualization web interface, as well as downloadable batch data.

Abbreviations: TopoSNP

Synonyms: topographic mapping of Single Nucleotide Polymorphism

Resource Type: database, data or information resource

Defining Citation: PMID:14681472

Keywords: visualization, disease, non-disease, non-synonymous single nucleotide polymorphism, topographic mapping, single nucleotide polymorphism, 3d structure, protein, protein structure, coding region, entropy

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Resource Name: TopoSNP

Resource ID: SCR_005572

Alternate IDs: nif-0000-03570, OMICS_00191

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250412T054950+0000

Ratings and Alerts

No rating or validation information has been found for TopoSNP.

No alerts have been found for TopoSNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Doss CG, et al. (2014) Integrating in silico prediction methods, molecular docking, and molecular dynamics simulation to predict the impact of ALK missense mutations in structural perspective. BioMed research international, 2014, 895831.

Izarzugaza JM, et al. (2012) Interpretation of the consequences of mutations in protein kinases: combined use of bioinformatics and text mining. Frontiers in physiology, 3, 323.

Lee W, et al. (2009) Analytical methods for inferring functional effects of single base pair substitutions in human cancers. Human genetics, 126(4), 481.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.