Resource Summary Report

Generated by dkNET on Apr 29, 2025

Project HOPE

RRID:SCR_005141
Type: Tool

Proper Citation

Project HOPE (RRID:SCR_005141)

Resource Information

URL: http://www.cmbi.ru.nl/hope/home

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Description: An easy-to-use webserver that analyses the structural effects of your mutation of interest. The server allows you to submit a protein sequence and the mutation. Project HOPE will then collect and combine available information from a series of webservers and databases and will produce a mutation report complete with results, figures and animations. Where available Project HOPE will use the 3D structure of the protein but the server can also build a homology model if necessary. Other information sources include the Uniprot database and a series of DAS prediction servers.

Abbreviations: HOPE

Synonyms: Have yOur Protein Explained, GSITIC

Resource Type: source code, service resource, production service resource, data analysis service, analysis service resource, software resource

Defining Citation: PMID:21059217

Keywords: protein structure, mutation

Related Condition: Inheritable disease

Funding:

Availability: Acknowledgement requested

Resource Name: Project HOPE

Resource ID: SCR_005141

Alternate IDs: OMICS_00130

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250429T054957+0000

Ratings and Alerts

No rating or validation information has been found for Project HOPE.

No alerts have been found for Project HOPE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Tanshee RR, et al. (2024) A comprehensive in silico investigation into the pathogenic SNPs in the RTEL1 gene and their biological consequences. PloS one, 19(9), e0309713.

Ajith A, et al. (2023) In silico screening of non-synonymous SNPs in human TUFT1 gene. Journal, genetic engineering & biotechnology, 21(1), 95.

Ou L, et al. (2019) Genotype-phenotype correlation of gangliosidosis mutations using in silico tools and homology modeling. Molecular genetics and metabolism reports, 20, 100495.

Ahmed A, et al. (2019) A longitudinal study of neurocognition and behavior in patients with Hurler-Scheie syndrome heterozygous for the L238Q mutation. Molecular genetics and metabolism reports, 20, 100484.

Islam MJ, et al. (2019) Prediction of Deleterious Non-synonymous SNPs of Human STK11 Gene by Combining Algorithms, Molecular Docking, and Molecular Dynamics Simulation. Scientific reports, 9(1), 16426.

Jayaraman M, et al. (2019) Structural insight into conformational dynamics of non-active site mutations in KasA: A Mycobacterium tuberculosis target protein. Gene, 720, 144082.

Ou L, et al. (2017) Phenotype prediction for mucopolysaccharidosis type I by in silico analysis. Orphanet journal of rare diseases, 12(1), 125.

Nailwal M, et al. (2017) Computational Analysis of High Risk Missense Variant in Human UTY Gene: A Candidate Gene of AZFa Sub-region. Journal of reproduction & infertility, 18(3), 298.

Awan FM, et al. (2017) Mutation-Structure-Function Relationship Based Integrated Strategy Reveals the Potential Impact of Deleterious Missense Mutations in Autophagy Related Proteins on Hepatocellular Carcinoma (HCC): A Comprehensive Informatics Approach. International journal of molecular sciences, 18(1).

Martin-Fernandez L, et al. (2017) Next generation sequencing to dissect the genetic architecture of KNG1 and F11 loci using factor XI levels as an intermediate phenotype of thrombosis. PloS one, 12(4), e0176301.

Alipoor B, et al. (2016) A Bioinformatics Approach to Prioritize Single Nucleotide Polymorphisms in TLRs Signaling Pathway Genes. International journal of molecular and cellular medicine, 5(2), 65.

Akhoundi F, et al. (2016) In silico analysis of deleterious single nucleotide polymorphisms in human BUB1 mitotic checkpoint serine/threonine kinase B gene. Meta gene, 9, 142.

Kinnersley B, et al. (2016) Search for new loci and low-frequency variants influencing glioma risk by exome-array analysis. European journal of human genetics : EJHG, 24(5), 717.

Hu H, et al. (2016) X-exome sequencing of 405 unresolved families identifies seven novel intellectual disability genes. Molecular psychiatry, 21(1), 133.

Hempel A, et al. (2016) Deletions and de novo mutations of SOX11 are associated with a neurodevelopmental disorder with features of Coffin-Siris syndrome. Journal of medical genetics, 53(3), 152.

Martin-Fernandez L, et al. (2016) The Unravelling of the Genetic Architecture of Plasminogen Deficiency and its Relation to Thrombotic Disease. Scientific reports, 6, 39255.

Sujitha SP, et al. (2016) DNA Repair Gene (XRCC1) Polymorphism (Arg399Gln) Associated with Schizophrenia in South Indian Population: A Genotypic and Molecular Dynamics Study. PloS one, 11(1), e0147348.

Kalaiarasan P, et al. (2015) In silico screening, genotyping, molecular dynamics simulation and activity studies of SNPs in pyruvate kinase M2. PloS one, 10(3), e0120469.

Maria M, et al. (2015) Homozygosity mapping and targeted sanger sequencing reveal genetic defects underlying inherited retinal disease in families from pakistan. PloS one, 10(3), e0119806.

Vulto-van Silfhout AT, et al. (2014) Mutations affecting the SAND domain of DEAF1 cause intellectual disability with severe speech impairment and behavioral problems. American

journal of human genetics, 94(5), 649.