Resource Summary Report

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PolyPhred

RRID:SCR_002337
Type: Tool

Proper Citation

PolyPhred (RRID:SCR_002337)

Resource Information

URL: http://droog.gs.washington.edu/polyphred/

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Description: Software program that compares fluorescence-based sequences across traces obtained from different individuals to identify heterozygous sites for single nucleotide substitutions. Its functions are integrated with the use of three other programs: Phred (Brent Ewing and Phil Green), Phrap (Phil Green), and Consed (David Gordon and Phil Green). PolyPhred identifies potential heterozygotes using the base calls and peak information provided by Phred and the sequence alignments provided by Phrap. Potential heterozygotes identified by PolyPhred are marked for rapid inspection using the Consed tool.

Abbreviations: PolyPhred

Resource Type: software resource

Defining Citation: PMID:17115056, PMID:16493422, PMID:9207020

Keywords: windows, sequence, nucleotide substitution, heterozygote, polymorphic, genotype, single nucleotide polymorphism, fluorescence, single nucleotide substitution, polymorphism, insertion, deletion, indel, bio.tools

Funding:

Availability: Free for academic use, Commercial use requires a license

Resource Name: PolyPhred

Resource ID: SCR_002337

Alternate IDs: biotools:polyphred, OMICS_01815

Alternate URLs: https://bio.tools/polyphred

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250420T014100+0000

Ratings and Alerts

No rating or validation information has been found for PolyPhred.

No alerts have been found for PolyPhred.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 121 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zhu Y, et al. (2024) Two Novel and Two Recurrent Variants of the ADAR1 Gene in Three Chinese Families with Dyschromatosis Symmetrica Hereditaria. Clinical, cosmetic and investigational dermatology, 17, 2373.

Li S, et al. (2024) A monoallelic variant in CCN2 causes an autosomal dominant spondyloepimetaphyseal dysplasia with low bone mass. Bone research, 12(1), 60.

Hop PJ, et al. (2024) Systematic rare variant analyses identify RAB32 as a susceptibility gene for familial Parkinson's disease. Nature genetics, 56(7), 1371.

Mei Y, et al. (2024) Echocardiographic abnormalities and joint hypermobility in Chinese patients with Osteogenesis imperfecta. Orphanet journal of rare diseases, 19(1), 116.

Wang X, et al. (2024) Two Novel and Three Recurrent Mutations in the Mevalonate Pathway Genes in Chinese Patients with Porokeratosis. Clinical, cosmetic and investigational dermatology, 17, 191.

Ren N, et al. (2024) Clinical features, treatment, and follow-up of OPPG and high-bone-mass disorders: LRP5 is a key regulator of bone mass. Osteoporosis international : a journal established as result of cooperation between the European Foundation for Osteoporosis and the National Osteoporosis Foundation of the USA, 35(8), 1395.

Wang PY, et al. (2023) Distilling functional variations for human UGT2B4 upstream region based on selection signals and implications for phenotypes of Neanderthal and Denisovan. Scientific reports, 13(1), 3134.

Ye M, et al. (2023) New Endothelial Corneal Dystrophy in a Chinese Family. Cornea, 42(5), 529.

He J, et al. (2023) Case report: A novel mutation in the EYA1 gene in a child with branchiootic syndrome with secretory otitis media and bilateral vestibular hypofunction. Frontiers in genetics, 14, 1292085.

Tao XH, et al. (2022) Clinical characteristics and identification of a novel TGFB1 variant in three unrelated Chinese families with Camurati-Engelmann disease. Molecular genetics & genomic medicine, 10(5), e1922.

Zhang W, et al. (2022) Identification of a novel CNV at the EYA4 gene in a Chinese family with autosomal dominant nonsyndromic hearing loss. BMC medical genomics, 15(1), 113.

Wu J, et al. (2022) Mutations in exon region of BRCA1-related RING domain 1 gene and risk of breast cancer. Molecular genetics & genomic medicine, 10(3), e1847.

Wang L, et al. (2021) Analysis of genetic variation in human papillomavirus type 16 E1 and E2 in women with cervical infection in Xinjiang, China. BMC medical genomics, 14(1), 268.

Chen J, et al. (2021) Composite pheochromocytoma/paraganglioma-ganglioneuroma: analysis of SDH and ATRX status, and identification of frequent HRAS and BRAF mutations. Endocrine connections, 10(8), 926.

Wu J, et al. (2021) Correlation between ZBRK1/ZNF350 gene polymorphism and breast cancer. BMC medical genomics, 14(1), 7.

Gowans LJJ, et al. (2021) Co-occurrence of orofacial clefts and clubfoot phenotypes in a sub-Saharan African cohort: Whole-exome sequencing implicates multiple syndromes and genes. Molecular genetics & genomic medicine, 9(4), e1655.

Cao L, et al. (2021) Novel missense mutation of SASH1 in a Chinese family with dyschromatosis universalis hereditaria. BMC medical genomics, 14(1), 168.

Suzuki K, et al. (2021) NOD2 Genotypes Affect the Symptoms and Mortality in the Porcine Circovirus 2-Spreading Pig Population. Genes, 12(9).

Pira E, et al. (2021) Polymorphisms at Myostatin Gene (MSTN) and the Associations with Sport Performances in Anglo-Arabian Racehorses. Animals : an open access journal from MDPI, 11(4).

Kujawski S, et al. (2020) Loss of Crb2b-lf leads to anterior segment defects in old zebrafish. Biology open, 9(2).