Resource Summary Report

Generated by dkNET on Apr 27, 2025

ALFRED

RRID:SCR_001730
Type: Tool

Proper Citation

ALFRED (RRID:SCR_001730)

Resource Information

URL: http://alfred.med.yale.edu

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Description: A public curated compilation of allele frequency data on anthropologically defined human population samples linked to the molecular genetics-human genome databases. Only data on well defined population samples that are large enough to yield reasonably accurate frequencies and for polymorphisms sufficiently defined to be replicable can be included in ALFRED. Researchers wishing to have their data entered into ALFRED should contact them. Initially, ALFRED contained primarily data generated in the laboratories of K.K. and J.R. Kidd in the Department of Genetics at Yale, including extensive unpublished data. Data from the published literature are being entered into ALFRED in a systematic way, with a focus on polymorphisms studied in many different populations. ALFRED is distinct from such databases as dbSNP, which catalogs sequence variation. ALFRED's focus is on allele frequencies in diverse anthropologically defined populations. It is not a compendium of human DNA polymorphisms but of frequencies of selected polymorphisms with an emphasis on those that have been studied in multiple populations. All of the data in ALFRED are considered to be in the public domain and available for use in research and teaching. ALFRED provides easy searching options including versatile "Keyword search" and also has numerous summary tables providing quick overviews of contents by chromosome, population, average heterozygosity, Fst and others, all available under various tabs from the ALFRED homepage.

Abbreviations: ALFRED

Synonyms: The ALlele FREquency Database, ALlele FREquency Database

Resource Type: service resource, storage service resource, data or information resource, data repository, database

Defining Citation: PMID:19325849, PMID:11125124, PMID:12209575

Keywords: allele frequency, dna polymorphism, haplotype, high throughput, genome, population, sample, education, polymorphism, allele, chromosome, heterozygosity, fst, loci, pathway, genetics, FASEB list

Funding: NIGMS P01GM 57672

Availability: Public, The community can contribute to this resource

Resource Name: ALFRED

Resource ID: SCR_001730

Alternate IDs: nif-0000-02541

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250426T055457+0000

Ratings and Alerts

No rating or validation information has been found for ALFRED.

No alerts have been found for ALFRED.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 70 mentions in open access literature.

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

Chalvatzaki G, et al. (2023) Learning to reason over scene graphs: a case study of finetuning GPT-2 into a robot language model for grounded task planning. Frontiers in robotics and AI, 10, 1221739.

Kidd KK, et al. (2022) A multipurpose panel of microhaplotypes for use with STR markers in casework. Forensic science international. Genetics, 60, 102729.

Kidd KK, et al. (2022) State of the Art for Microhaplotypes. Genes, 13(8).

Kidd KK, et al. (2022) North Asian population relationships in a global context. Scientific reports, 12(1), 7214.

Priest SJ, et al. (2021) Factors enforcing the species boundary between the human pathogens Cryptococcus neoformans and Cryptococcus deneoformans. PLoS genetics, 17(1), e1008871.

Wabnegger A, et al. (2021) The association between the belief in coronavirus conspiracy theories, miracles, and the susceptibility to conjunction fallacy. Applied cognitive psychology, 35(5), 1344.

Ziadi W, et al. (2021) STAT3 polymorphisms in North Africa and its implication in breast cancer. Molecular genetics & genomic medicine, 9(8), e1744.

Staadig A, et al. (2021) Evaluation of microhaplotypes in forensic kinship analysis from a Swedish population perspective. International journal of legal medicine, 135(4), 1151.

Sarangarajan R, et al. (2021) Ethnic Prevalence of Angiotensin-Converting Enzyme Deletion (D) Polymorphism and COVID-19 Risk: Rationale for Use of Angiotensin-Converting Enzyme Inhibitors/Angiotensin Receptor Blockers. Journal of racial and ethnic health disparities, 8(4), 973.

Fu C, et al. (2021) Dynamic genome plasticity during unisexual reproduction in the human fungal pathogen Cryptococcus deneoformans. PLoS genetics, 17(11), e1009935.

Sánchez-Corrales L, et al. (2021) Phylogenomic analysis and Mycobacterium tuberculosis antibiotic resistance prediction by whole-genome sequencing from clinical isolates of Caldas, Colombia. PloS one, 16(10), e0258402.

Sadlowski H, et al. (2021) Diagnosis of Taenia solium infections based on "mail order" RNA-sequencing of single tapeworm egg isolates from stool samples. PLoS neglected tropical diseases, 15(12), e0009787.

Li M, et al. (2021) Alu retrotransposons and COVID-19 susceptibility and morbidity. Human genomics, 15(1), 2.

Iwanowicz DD, et al. (2020) An updated genetic marker for detection of Lake Sinai Virus and metagenetic applications. PeerJ, 8, e9424.

Kidd KK, et al. (2020) The distinctive geographic patterns of common pigmentation variants at the OCA2 gene. Scientific reports, 10(1), 15433.

Jones P, et al. (2020) Distribution of variants in multiple vitamin D-related loci (DHCR7/NADSYN1, GC, CYP2R1, CYP11A1, CYP24A1, VDR, RXR? and RXR?) vary between European, East-Asian and Sub-Saharan African-ancestry populations. Genes & nutrition, 15(1), 5.

Wein T, et al. (2019) The Effect of Population Bottleneck Size and Selective Regime on Genetic Diversity and Evolvability in Bacteria. Genome biology and evolution, 11(11), 3283.

Boussetta S, et al. (2019) Usefulness of COMT gene polymorphisms in North African populations. Gene, 696, 186.

Pakstis AJ, et al. (2019) Population relationships based on 170 ancestry SNPs from the combined Kidd and Seldin panels. Scientific reports, 9(1), 18874.

Pakstis AJ, et al. (2019) Genetic relationships of European, Mediterranean, and SW Asian populations using a panel of 55 AISNPs. European journal of human genetics : EJHG, 27(12), 1885.