Resource Summary Report

Generated by dkNET on Apr 23, 2025

MEGA2

RRID:SCR_009286
Type: Tool

Proper Citation

MEGA2 (RRID:SCR_009286)

Resource Information

URL: http://watson.hgen.pitt.edu/register/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 16,2023. Software application that uses as input a trio of files: 1) a LINKAGE-format locus file modified to contain locus name information; 2) a LINKAGE-format pedigree file; and 3) a map file. Mega2 then takes this trio of input files and, via a menu-driven interface, transforms them into various other file formats, thus greatly facilitating a variety of different analyses. In addition, for many of these options, it also sets up a C-shell script that then can automatically run these analyses (if you are using Mega2 in a Unix environment that supports C-shell scripts). (entry from Genetic Analysis Software)

Abbreviations: MEGA2

Synonyms: a Manipulation Environment for Genetic Analyses

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, unix, (solaris, silicon graphics, osf1, macos x), linux, ms-windows, macos, (x)

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MEGA2

Resource ID: SCR_009286

Alternate IDs: nlx_154471

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250421T053724+0000

Ratings and Alerts

No rating or validation information has been found for MEGA2.

No alerts have been found for MEGA2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 114 mentions in open access literature.

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

Quiat D, et al. (2023) Damaging variants in FOXI3 cause microtia and craniofacial microsomia. Genetics in medicine : official journal of the American College of Medical Genetics, 25(1), 143.

Miles S, et al. (2022) Expanding the family of Mu-class glutathione transferases in the cestode parasite Echinococcus granulosus sensu lato. Gene, 835, 146659.

Jones JL, et al. (2021) A 127?kb truncating deletion of PGRMC1 is a novel cause of X-linked isolated paediatric cataract. European journal of human genetics : EJHG, 29(8), 1206.

Inoue C, et al. (2020) Involvement of MCL1, c-myc, and cyclin D2 protein degradation in ponatinib-induced cytotoxicity against T315I(+) Ph+leukemia cells. Biochemical and biophysical research communications, 525(4), 1074.

Vojinovic D, et al. (2018) Whole-Genome Linkage Scan Combined With Exome Sequencing Identifies Novel Candidate Genes for Carotid Intima-Media Thickness. Frontiers in genetics, 9, 420.

Baron RV, et al. (2018) The Mega2R package: R tools for accessing and processing genetic data in common formats. F1000Research, 7, 1352.

Govil M, et al. (2018) Novel caries loci in children and adults implicated by genome-wide analysis of families. BMC oral health, 18(1), 98.

Woodbury-Smith M, et al. (2017) Combined genome-wide linkage and targeted association analysis of head circumference in autism spectrum disorder families. Journal of neurodevelopmental disorders, 9, 5.

Khan SA, et al. (2017) Rules for resolving Mendelian inconsistencies in nuclear pedigrees typed for two-allele markers. PloS one, 12(3), e0172807.

Pilatti P, et al. (2017) Orbit orientation in didelphid marsupials (Didelphimorphia: Didelphidae). Current zoology, 63(4), 403.

Levine AP, et al. (2016) Genetic Complexity of Crohn's Disease in Two Large Ashkenazi Jewish Families. Gastroenterology, 151(4), 698.

Levine AP, et al. (2015) Combinatorial Conflicting Homozygosity (CCH) analysis enables the rapid identification of shared genomic regions in the presence of multiple phenocopies. BMC genomics, 16(1), 163.

Scholl UI, et al. (2015) Recurrent gain of function mutation in calcium channel CACNA1H causes early-onset hypertension with primary aldosteronism. eLife, 4, e06315.

Trinh BQ, et al. (2015) The homeobox gene DLX4 regulates erythro-megakaryocytic differentiation by stimulating IL-1? and NF-?B signaling. Journal of cell science, 128(16), 3055.

Nyegaard M, et al. (2015) A Novel Locus Harbouring a Functional CD164 Nonsense Mutation Identified in a Large Danish Family with Nonsyndromic Hearing Impairment. PLoS genetics, 11(7), e1005386.

Gorin MB, et al. (2014) Endophenotypes for Age-Related Macular Degeneration: Extending Our Reach into the Preclinical Stages of Disease. Journal of clinical medicine, 3(4), 1335.

Rodríguez-Marí A, et al. (2013) Retinoic acid metabolic genes, meiosis, and gonadal sex differentiation in zebrafish. PloS one, 8(9), e73951.

Hill SY, et al. (2013) Family-based association analysis of alcohol dependence implicates KIAA0040 on Chromosome 1q in multiplex alcohol dependence families. Open journal of genetics, 3(4), 243.

Hersheson J, et al. (2013) Mutations in the autoregulatory domain of ?-tubulin 4a cause hereditary dystonia. Annals of neurology, 73(4), 546.

Yamamoto K, et al. (2013) Functionally deregulated AML1/RUNX1 cooperates with BCR-ABL to induce a blastic phase-like phenotype of chronic myelogenous leukemia in mice. PloS one, 8(9), e74864.