

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## MEGA2

RRID:SCR\_009286

Type: Tool

### Proper Citation

MEGA2 (RRID:SCR\_009286)

### Resource Information

**URL:** <http://watson.hgen.pitt.edu/register/>

**Proper Citation:** MEGA2 (RRID:SCR\_009286)

**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 application, software resource

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

**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:** 20260905T133249+0000

### Ratings and Alerts

No rating or validation information has been found for MEGA2.

No alerts have been found for MEGA2.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 114 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [Kravitz](#).

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 $\beta$  and NF- $\kappa$ B signaling. *Journal of cell science*, 128(16), 3055.

Nyegaard M, et al. (2015) A Novel Locus Harboring 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.

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.

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

Hersheson J, et al. (2013) Mutations in the autoregulatory domain of  $\beta$ -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.