Resource Summary Report

Generated by T1D on Jul 31, 2026

AutoMap

RRID:SCR_013095
Type: Tool

Proper Citation

AutoMap (RRID:SCR_013095)

Resource Information

URL: http://sourceforge.net/projects/ligmap/files/

Proper Citation: AutoMap (RRID:SCR_013095)

Description: A tool for structural biology and drug design.

Abbreviations: AutoMap

Resource Type: software resource

Resource Name: AutoMap

Resource ID: SCR_013095

Alternate IDs: OMICS_01596

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260725T190744+0000

Ratings and Alerts

No rating or validation information has been found for AutoMap.

No alerts have been found for AutoMap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 92 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Han H, et al. (2025) Exome sequencing of 18,994 ethnically diverse patients with suspected rare Mendelian disorders. NPJ genomic medicine, 10(1), 6.

Walker-Milne NL, et al. (2025) A novel use of Stereo Baited Remote Underwater Video and Drop-Down Video for biodiversity and marine landscape mapping and prediction. PloS one, 20(4), e0319355.

Cauti FM, et al. (2025) Ventricular Duration Map Area as a Valuable and Effective Target for VT Ablation End Point in Ischemic Cardiomyopathy: The VEDUM FREEDOM Study. Circulation. Arrhythmia and electrophysiology, 18(11), e013867.

Corral-Serrano JC, et al. (2025) A novel recurrent ARL3 variant c.209G > A p.(Gly70Glu) causes variable non-syndromic dominant retinal dystrophy with defective lipidated protein transport in human retinal stem cell models. Human molecular genetics, 34(9), 821.

Rashid A, et al. (2025) Exome sequencing identifies a homozygous splice site variant in RP1 as the underlying cause of autosomal recessive retinitis pigmentosa in a Pakistani family. Annals of medicine, 57(1), 2470953.

Lee H, et al. (2025) A Korean Patient With Leber Congenital Amaurosis and a Homozygous RPE65 Variant Originating From a Paternal Uniparental Isodisomy. Molecular genetics & genomic medicine, 13(1), e70060.

Huang YS, et al. (2025) High-density mapping in catheter ablation for atrial fibrillation in Asia Pacific region: An observational study. Journal of arrhythmia, 41(1), e13168.

Neupane A, et al. (2025) Genetic improvement of FHB and DON resistance by combining the Fhb1 gene with additional resistance QTL in winter wheat population. The plant genome, 18(3), e70084.

Ahmad R, et al. (2025) Identification of a Novel GRM1 Frameshift Variant in Two Pakistani Families Broadens the Genetic Landscape of Ultra-Rare Spinocerebellar Ataxia Type 13. Cerebellum (London, England), 24(5), 145.

Shravya MS, et al. (2025) Biallelic Variant, c.644-13_644-9del in UNC50 Is Associated With Congenital Myasthenia Syndrome. American journal of medical genetics. Part A, 197(8), e64086.

Nadeali Z, et al. (2025) Investigating TSHR gene variants in consanguineous families: novel insights into variable expression in familial congenital hypothyroidism. Frontiers in endocrinology, 16, 1559281.

Watson CM, et al. (2025) AgileMultiIdeogram: Rapid Identification and Visualization of Autozygous Regions Using Illumina Short-Read Sequencing Data. Biology, 14(6).

Kumar KB, et al. (2025) Spatial synchronization of river floods growing beyond the basin boundaries in Peninsular India. Scientific reports, 15(1), 18160.

Ecker C, et al. (2025) Transcriptomic decoding of surface-based imaging phenotypes and its application to pharmacotranscriptomics. Nature communications, 16(1), 6727.

Ghorbani M, et al. (2025) Near-complete Middle Eastern genomes refine autozygosity and enhance disease-causing and population-specific variant discovery. Nature genetics, 57(5), 1119.

Morán-Ordóñez A, et al. (2025) A spatial planning approach for the identification of critical habitat for threatened species. Conservation biology : the journal of the Society for Conservation Biology, 39(4), e70022.

Ahmad R, et al. (2025) QARS1 associated developmental epileptic encephalopathy: first report of a rare homozygous missense variant from Pakistan causing nonepileptic phenotype in a family of seven patients and a comprehensive review of the literature. Molecular biology reports, 52(1), 528.

Ahmad R, et al. (2025) Rare autosomal recessive hereditary sensory and autonomic neuropathy type VI in a Pakistani family caused by a novel DST variant. Neurological sciences : official journal of the Italian Neurological Society and of the Italian Society of Clinical Neurophysiology, 46(12), 6815.

Resende RT, et al. (2025) GIS-based G × E modeling of maize hybrids through enviromic markers engineering. The New phytologist, 245(1), 102.

Kakar N, et al. (2025) Further evidence of biallelic NAV3 variants associated with recessive neurodevelopmental disorder with dysmorphism, developmental delay, intellectual disability, and behavioral abnormalities. Human genetics, 144(1), 55.