Resource Summary Report

Generated by dkNET on Apr 17, 2025

ALLEGRO

RRID:SCR_009116
Type: Tool

Proper Citation

ALLEGRO (RRID:SCR_009116)

Resource Information

URL: http://www.decode.com/software/

Proper Citation: ALLEGRO (RRID:SCR_009116)

Description: Software application that is a faster version of GENEHUNTER and Allegro 1.2 (several degrees of increase of speed, can handle bigger families, up to 50 bits) (entry from Genetic Analysis Software)

Abbreviations: ALLEGRO

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++

Funding:

Resource Name: ALLEGRO

Resource ID: SCR_009116

Alternate IDs: nlx_154217

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063537+0000

Ratings and Alerts

No rating or validation information has been found for ALLEGRO.

No alerts have been found for ALLEGRO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Linker TM, et al. (2024) Neutron scattering and neural-network quantum molecular dynamics investigation of the vibrations of ammonia along the solid-to-liquid transition. Nature communications, 15(1), 3911.

Nawaz H, et al. (2024) Brachyolmia, dental anomalies and short stature (DASS): Phenotype and genotype analyses of Egyptian and Pakistani patients. Heliyon, 10(1), e23688.

Coste A, et al. (2024) Developing an Implicit Solvation Machine Learning Model for Molecular Simulations of Ionic Media. Journal of chemical theory and computation, 20(1), 411.

Frank JT, et al. (2024) A Euclidean transformer for fast and stable machine learned force fields. Nature communications, 15(1), 6539.

Lévêque A, et al. (2024) Levels and Spatial Patterns of Effective Population Sizes in the Southern Damselfly (Coenagrion mercuriale): On the Need to Carefully Interpret Single-Point and Temporal Estimations to Set Conservation Guidelines. Evolutionary applications, 17(12), e70062.

Santos-Beneit F, et al. (2023) Screening Enzymes That Can Depolymerize Commercial Biodegradable Polymers: Heterologous Expression of Fusarium solani Cutinase in Escherichia coli. Microorganisms, 11(2).

Loose TD, et al. (2023) Coarse-Graining with Equivariant Neural Networks: A Path Toward Accurate and Data-Efficient Models. The journal of physical chemistry. B, 127(49), 10564.

Musaelian A, et al. (2023) Learning local equivariant representations for large-scale atomistic dynamics. Nature communications, 14(1), 579.

Rosenbohm A, et al. (2022) Familial Cerebellar Ataxia and Amyotrophic Lateral Sclerosis/Frontotemporal Dementia with DAB1 and C9ORF72 Repeat Expansions: An 18-Year Study. Movement disorders : official journal of the Movement Disorder Society, 37(12), 2427.

Neitzel H, et al. (2022) Transmission ratio distortion of mutations in the master regulator of centriole biogenesis PLK4. Human genetics, 141(11), 1785.

Jaquier N, et al. (2021) Geometry-aware manipulability learning, tracking, and transfer. The International journal of robotics research, 40(2-3), 624.

Sacco G, et al. (2021) How to deal with the consent of adults with cognitive impairment involved in European geriatric living labs? Philosophy, ethics, and humanities in medicine : PEHM, 16(1), 3.

Majmundar AJ, et al. (2021) Recessive NOS1AP variants impair actin remodeling and cause glomerulopathy in humans and mice. Science advances, 7(1).

Spijkers S, et al. (2021) Whole-body MRI versus an [18F]FDG-PET/CT-based reference standard for early response assessment and restaging of paediatric Hodgkin's lymphoma: a prospective multicentre study. European radiology, 31(12), 8925.

Downie ML, et al. (2021) Identification of a Locus on the X Chromosome Linked to Familial Membranous Nephropathy. Kidney international reports, 6(6), 1669.

Ramzan S, et al. (2021) A Novel Missense Mutation in TNNI3K Causes Recessively Inherited Cardiac Conduction Disease in a Consanguineous Pakistani Family. Genes, 12(8).

Zhang H, et al. (2020) Three-Dimensional Printing of Continuous Flax Fiber-Reinforced Thermoplastic Composites by Five-Axis Machine. Materials (Basel, Switzerland), 13(7).

Mol MO, et al. (2020) Clinical and pathologic phenotype of a large family with heterozygous STUB1 mutation. Neurology. Genetics, 6(3), e417.

Sanz-Garcia A, et al. (2020) A Versatile Open-Source Printhead for Low-Cost 3D Microextrusion-Based Bioprinting. Polymers, 12(10).

Mescheriakova JY, et al. (2019) Linkage analysis and whole exome sequencing identify a novel candidate gene in a Dutch multiple sclerosis family. Multiple sclerosis (Houndmills, Basingstoke, England), 25(7), 909.