Resource Summary Report

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OMIA - Online Mendelian Inheritance in Animals

RRID:SCR_006436
Type: Tool

Proper Citation

OMIA - Online Mendelian Inheritance in Animals (RRID:SCR_006436)

Resource Information

URL: http://omia.angis.org.au/

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Description: Describes phenotype relationships with between breeds and genes. Catalogue/compendium of inherited disorders, other (single-locus) traits, and genes in 245 animal species. Database of genes, inherited disorders and traits in animal species other than human, mouse, and rats. Database contains textual information and references, as well as links to relevant records from OMIM, PubMed and Gene.

Abbreviations: OMIA

Synonyms: Online Mendelian Inheritance in Animals

Resource Type: database, data or information resource

Defining Citation: PMID:16381939, PMID:12520001, PMID:9638822

Keywords: gene, inherited disorder, trait, disorder, genetic disorder, animal model, human disorder, homologue, phenotype, comparative biology, genotype, gold standard, FASEB list

Related Condition: Genetic disorder

Funding: H.G. Slater Foundation ;
Australian Commonwealth ;
International Livestock Centre for Africa ;
Food and Agriculture Organization of the United Nations ;
American Humane Association

Availability: Free, Acknowledgement requested, The community can contribute to this

resource, Non-commercial, Commercial with permission, Copyrighted

Resource Name: OMIA - Online Mendelian Inheritance in Animals

Resource ID: SCR_006436

Alternate IDs: nif-0000-03215

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250412T055054+0000

Ratings and Alerts

No rating or validation information has been found for OMIA - Online Mendelian Inheritance in Animals.

No alerts have been found for OMIA - Online Mendelian Inheritance in Animals.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Yang M, et al. (2024) Diagnostic Utility of Whole Genome Sequencing After Negative Karyotyping/Chromosomal Microarray in Infants Born With Multiple Congenital Anomalies. Journal of Korean medical science, 39(36), e250.

Wu L, et al. (2024) Potential mechanism of Luoshi Neiyi prescription in endometriosis based on serum pharmacochemistry and network pharmacology. Frontiers in pharmacology, 15, 1395160.

Xie L, et al. (2024) Exploring the mechanisms underlying effects of bisphenol a on cardiovascular disease by network toxicology and molecular docking. Heliyon, 10(10), e31473.

Guang B, et al. (2023) Dissection of action mechanisms of Zuogui Pill in the treatment of liver cancer based on machine learning and network pharmacology: A review. Medicine, 102(42), e35628.

Felker SA, et al. (2023) Poison exon annotations improve the yield of clinically relevant variants in genomic diagnostic testing. bioRxiv : the preprint server for biology.

Sadler B, et al. (2022) Whole-exome analysis of adolescents with low VWF and heavy menstrual bleeding identifies novel genetic associations. Blood advances, 6(2), 420.

Xiao G, et al. (2021) Prenatal diagnosis of a 4.5-Mb deletion at chromosome 4q35.1q35.2: Case report and literature review. Molecular cytogenetics, 14(1), 53.

Zhu N, et al. (2020) Targets of Vitamin C With Therapeutic Potential for Cardiovascular Disease and Underlying Mechanisms: A Study of Network Pharmacology. Frontiers in pharmacology, 11, 591337.

Gao J, et al. (2020) Genomic Characteristics and Selection Signatures in Indigenous Chongming White Goat (Capra hircus). Frontiers in genetics, 11, 901.

Shickh S, et al. (2019) Health outcomes, utility and costs of returning incidental results from genomic sequencing in a Canadian cancer population: protocol for a mixed-methods randomised controlled trial. BMJ open, 9(10), e031092.

Corbi-Botto CM, et al. (2019) Genomic structural diversity in Criollo Argentino horses: Analysis of copy number variations. Gene, 695, 26.

Li W, et al. (2019) A start codon mutation of the TSPAN12 gene in Chinese families causes clinical heterogeneous familial exudative vitreoretinopathy. Molecular genetics & genomic medicine, 7(10), e00948.

Osei-Amponsah R, et al. (2019) Genetic Selection for Thermotolerance in Ruminants. Animals : an open access journal from MDPI, 9(11).

Holden LA, et al. (2018) Assembly and Analysis of Unmapped Genome Sequence Reads Reveal Novel Sequence and Variation in Dogs. Scientific reports, 8(1), 10862.

Mesbah-Uddin M, et al. (2018) Genome-wide mapping of large deletions and their population-genetic properties in dairy cattle. DNA research : an international journal for rapid publication of reports on genes and genomes, 25(1), 49.

Donner J, et al. (2018) Frequency and distribution of 152 genetic disease variants in over 100,000 mixed breed and purebred dogs. PLoS genetics, 14(4), e1007361.

Reinartz S, et al. (2017) Germline mutation within COL2A1 associated with lethal chondrodysplasia in a polled Holstein family. BMC genomics, 18(1), 762.

Mauri N, et al. (2017) A SINE Insertion in ATP1B2 in Belgian Shepherd Dogs Affected by Spongy Degeneration with Cerebellar Ataxia (SDCA2). G3 (Bethesda, Md.), 7(8), 2729.

Huang X, et al. (2017) Next-generation sequencing reveals a novel NDP gene mutation in a Chinese family with Norrie disease. Indian journal of ophthalmology, 65(11), 1161.

Di Dona F, et al. (2016) Congenital deformity of the distal extremities in three dogs. Open veterinary journal, 6(3), 228.