Resource Summary Report

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DECIPHER

RRID:SCR_006552
Type: Tool

Proper Citation

DECIPHER (RRID:SCR_006552)

Resource Information

URL: http://decipher.sanger.ac.uk/

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Description: Interactive database which incorporates a suite of tools designed to aid the interpretation of submicroscopic chromosomal imbalance. Used to enhance clinical diagnosis by retrieving information from bioinformatics resources relevant to the imbalance found in the patient. Contributing to the DECIPHER database is a Consortium, comprising an international community of academic departments of clinical genetics. Each center maintains control of its own patient data (which are password protected within the center""s own DECIPHER project) until patient consent is given to allow anonymous genomic and phenotypic data to become freely viewable within Ensembl and other genome browsers. Once data are shared, consortium members are able to gain access to the patient report and contact each other to discuss patients of mutual interest, thus facilitating the delineation of new microdeletion and microduplication syndromes.

Abbreviations: DECIPHER

Synonyms: Database of Chromosomal Imbalance and Phenotype in Humans using Ensembl Resources, DECIPHER: Database of Chromosomal Imbalance and Phenotype in Humans using Ensembl Resources, Database of Chromosomal Imbalance Phenotype in Humans using Ensembl Resources, Decipher

Resource Type: database, data or information resource

Defining Citation: PMID:19344873

Keywords: chromosomal imbalance, phenotype, chromosome, gene, genome, deletion, duplication, copy number, genotype, polymorphism, FASEB list

Related Condition: Developmental disorder, Microdeletion Syndrome, Overgrowth syndrome, Microduplication syndrome, Deletion syndrome, Duplication syndrome, Wolf-Hirschhorn Syndrome, Williams-Beuren Syndrome, Smith-Magenis Syndrome, Etc

Funding Agency: Wellcome Trust

Availability: Acknowledgement required

Resource Name: DECIPHER

Resource ID: SCR_006552

Alternate IDs: nlx_151653, OMICS_00265

Ratings and Alerts

No rating or validation information has been found for DECIPHER.

No alerts have been found for DECIPHER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1450 mentions in open access literature.

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

Barrenechea Angeles I, et al. (2024) Assigning the unassigned: A signature-based classification of rDNA metabarcodes reveals new deep-sea diversity. PloS one, 19(2), e0298440.

Alkhidir S, et al. (2024) The genetic basis and the diagnostic yield of genetic testing related to nonsyndromic hearing loss in Qatar. Scientific reports, 14(1), 4202.

Zhuang J, et al. (2024) Prenatal diagnosis and molecular cytogenetic characterization of fetuses with central nervous system anomalies using chromosomal microarray analysis: a seven-year single-center retrospective study. Scientific reports, 14(1), 2271.

Anzueto A, et al. (2024) Delphi Consensus on Clinical Applications of GOLD 2023 Recommendations in COPD Management: How Aligned are Recommendations with Clinical

Practice? Pulmonary therapy, 10(1), 69.

Wang Z, et al. (2024) VarCards2: an integrated genetic and clinical database for ACMG-AMP variant-interpretation guidelines in the human whole genome. Nucleic acids research, 52(D1), D1478.

Taillieu E, et al. (2024) The role of Helicobacter suis, Fusobacterium gastrosuis, and the pars oesophageal microbiota in gastric ulceration in slaughter pigs receiving meal or pelleted feed. Veterinary research, 55(1), 15.

Carrillo Heredero AM, et al. (2024) Fecal microbiota characterization of an Italian local horse breed. Frontiers in veterinary science, 11, 1236476.

Hosseini M, et al. (2024) Metformin reduces the clonal fitness of Dnmt3aR878H hematopoietic stem and progenitor cells by reversing their aberrant metabolic and epigenetic state. Research square.

Tanner A, et al. (2024) Genetic analysis of ocular tumour-associated genes using large genomic datasets: insights into selection constraints and variant representation in the population. BMJ open ophthalmology, 9(1).

Bittner MJ, et al. (2024) New chemical and microbial perspectives on vitamin B1 and vitamer dynamics of a coastal system. ISME communications, 4(1), ycad016.

Chaves TF, et al. (2024) A cohort study of neurodevelopmental disorders and/or congenital anomalies using high resolution chromosomal microarrays in southern Brazil highlighting the significance of ASD. Scientific reports, 14(1), 3762.

Devarajalu P, et al. (2024) Gut microbiota of preterm infants in the neonatal intensive care unit: a study from a tertiary care center in northern India. Frontiers in microbiology, 15, 1329926.

T?šický M, et al. (2024) Nearly (?) sterile avian egg in a passerine bird. FEMS microbiology ecology, 100(1).

Deschamps C, et al. (2024) Canine Mucosal Artificial Colon: development of a new colonic in vitro model adapted to dog sizes. Applied microbiology and biotechnology, 108(1), 166.

Ansari M, et al. (2024) Heterozygous loss-of-function SMC3 variants are associated with variable growth and developmental features. HGG advances, 5(2), 100273.

Cheung K, et al. (2024) Whole-mitogenome analysis unveils previously undescribed genetic diversity in cane toads across their invasion trajectory. Ecology and evolution, 14(3), e11115.

Hsieh CC, et al. (2024) Amelioration of the brain structural connectivity is accompanied with changes of gut microbiota in a tuberous sclerosis complex mouse model. Translational psychiatry, 14(1), 68.

Soh WT, et al. (2024) Protein degradation by human 20S proteasomes elucidates the

interplay between peptide hydrolysis and splicing. Nature communications, 15(1), 1147.

Srivastava P, et al. (2024) Neurofibromatosis type 1: Clinical characteristics and mutation spectrum in a North Indian cohort. Heliyon, 10(1), e23685.

Ahmad AR, et al. (2024) Falcon gut microbiota is shaped by diet and enriched in Salmonella. PloS one, 19(1), e0293895.