Resource Summary Report

Generated by T1D on Aug 1, 2026

DECIPHER

RRID:SCR_006552
Type: Tool

Proper Citation

DECIPHER (RRID:SCR_006552)

Resource Information

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

Proper Citation: DECIPHER (RRID:SCR_006552)

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: data or information resource, database

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: Wellcome Trust WT077008

Availability: Acknowledgement required

Resource Name: DECIPHER

Resource ID: SCR_006552

Alternate IDs: nlx_151653, OMICS_00265

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260729T044136+0000

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 1797 mentions in open access literature.

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

Ye H, et al. (2026) Associations between gut microbiota and personality traits: insights from a captive common marmoset (Callithrix jacchus) colony. Microbiology spectrum, 14(1), e0044325.

Liu X, et al. (2025) Increasing Stemness Drives Prostate Cancer Progression, Plasticity, Therapy Resistance and Poor Patient Survival. bioRxiv : the preprint server for biology.

Arbesfeld JA, et al. (2025) Mapping MAVE data for use in human genomics applications. Genome biology, 26(1), 179.

Kalanithy JC, et al. (2025) TFAP2E is implicated in central nervous system, orofacial and maxillofacial anomalies. Journal of medical genetics, 62(2), 126.

Castera L, et al. (2025) A European Survey to Identify Challenges in the Management of Metabolic Dysfunction-Associated Steatotic Liver Disease. Liver international : official journal of the International Association for the Study of the Liver, 45(2), e16224.

Rodriguez-Cruz UE, et al. (2025) Running against the clock: exploring microbial diversity in an extremely endangered microbial oasis in the Chihuahuan Desert. FEMS microbiology ecology, 101(5).

Jiang M, et al. (2025) Sequential prenatal diagnosis of fetal skeletal dysplasia: A cohort study. Acta obstetricia et gynecologica Scandinavica, 104(5), 860.

Ogawa C, et al. (2025) Diversity of Subgroup of Fibrobacter succinogenes in the Rumen and Feces of Cattle and Sheep. Animal science journal = Nihon chikusan Gakkaiho, 96(1), e70043.

Bennett AJ, et al. (2025) Molecular epidemiology of Eimeria spp. parasites and the faecal microbiome of Indiana bats (Myotis sodalis): a non-invasive, multiplex metabarcode survey of an endangered species. Microbial genomics, 11(2).

Pan P, et al. (2025) The Genetics of 241 Fetuses With Talipes Equinovarus: A 8-Year Monocentric Retrospective Study. Molecular genetics & genomic medicine, 13(2), e70076.

Francioli D, et al. (2025) Microbial inoculants modulate the rhizosphere microbiome, alleviate plant stress responses, and enhance maize growth at field scale. Genome biology, 26(1), 148.

Kim GJ, et al. (2025) Exome sequencing of patients with syndromic tall stature reveals four novel candidate genes. Endocrine connections, 14(7).

Xia CR, et al. (2025) DECIPHER for learning disentangled cellular embeddings in large-scale heterogeneous spatial omics data. Nature communications, 16(1), 7991.

Sudhakar DV, et al. (2025) Exome sequencing uncovers promising candidate genes for foetal structural malformations. The Indian journal of medical research, 161(5), 510.

Liu SY, et al. (2025) Potential role of SLC6A3 in neurodevelopmental impairments associated with corpus callosum abnormalities: insights from CNV analysis and clinical phenotyping. Molecular cytogenetics, 18(1), 21.

Pattaroni C, et al. (2025) Bacterial communities co-develop with respiratory immunity early in life, linking dysbiosis to systemic monocyte signature and wheezing. Science advances, 11(42), eadw1410.

Li W, et al. (2025) Assessing the clinical application value of SNP-array in fetal central nervous system malformations. Human genomics, 19(1), 137.

Su YP, et al. (2025) Development of a long-read high-throughput chromatin conformation capture method for evaluating both cis and trans interactions between integrated Hepatitis B Virus and host genomes. bioRxiv : the preprint server for biology.

Sun R, et al. (2025) A recurrent ABCC2 c.2439 + 5G > A variant disturbs mRNA splicing and causes Dubin-Johnson syndrome. BMC medical genomics, 18(1), 118.

Shumeri E, et al. (2025) Digenesis in Charcot-Marie-Tooth Disease: Impact of Combined Mutations in the MFN2 and GDAP1 Genes. Journal of the peripheral nervous system : JPNS, 30(3), e70044.