Resource Summary Report

Generated by NIF on May 16, 2025

Consensus CDS

RRID:SCR_006729
Type: Tool

Proper Citation

Consensus CDS (RRID:SCR_006729)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/CCDS/

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Description: Database (anonymous FTP) resulting from a collaborative effort to identify a core set of human and mouse protein coding regions that are consistently annotated and of high quality. The long term goal is to support convergence towards a standard set of gene annotations. Collaborators are EBI, NCBI, UCSC, WTSI and the initial results are also available from the participants"" genome browser Web sites. In addition, CCDS identifiers are indicated on the relevant NCBI RefSeq and Entrez Gene records and in Map Viewer displays of RNA (RefSeq) and Gene annotations on the reference assembly.

Abbreviations: CCDS

Synonyms: CCDS Database, NCBI Consensus CDS protein set, NCBI CCDS Database

Resource Type: data or information resource, database

Defining Citation: PMID:24217909, PMID:22434842, PMID:19498102

Keywords: human genome sequence, human protein, mouse genome sequence, mouse protein, protein coding region, gene, genome sequence, genome, sequence, gene annotation, protein, gold standard

Funding:

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

Resource Name: Consensus CDS

Resource ID: SCR_006729

Alternate IDs: nif-0000-02645, OMICS_01535

Alternate URLs: http://www.ncbi.nlm.nih.gov/CCDS/CcdsBrowse.cgi

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250507T060439+0000

Ratings and Alerts

No rating or validation information has been found for Consensus CDS.

No alerts have been found for Consensus CDS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 217 mentions in open access literature.

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

Hofmann AL, et al. (2025) Development and application of a clinical core data set for deep brain stimulation in Parkinson's disease, dystonia or tremor: from data collection to data exchange and data sharing. Neurological research and practice, 7(1), 5.

Waduge P, et al. (2025) Feasibility of Ex Vivo Ligandomics. Biomolecules, 15(1).

Cone AS, et al. (2024) CD81 fusion alters SARS-CoV-2 Spike trafficking. mBio, 15(9), e0192224.

Gong B, et al. (2024) Targeted DNA-seq and RNA-seq of Reference Samples with Short-read and Long-read Sequencing. Scientific data, 11(1), 892.

O'Brien H, et al. (2024) A modular protein language modelling approach to immunogenicity prediction. PLoS computational biology, 20(11), e1012511.

Du N, et al. (2024) Identification of a Novel Homozygous Mutation in MTMR2 Gene Causes Very Rare Charcot-Marie-Tooth Disease Type 4B1. The application of clinical genetics, 17, 71.

Pottinger TD, et al. (2024) Rare variant analyses validate known ALS genes in a multi-ethnic

population and identifies ANTXR2 as a candidate in PLS. BMC genomics, 25(1), 651.

Shan M, et al. (2024) Multi-omics analyses reveal bacteria and catalase associated with keloid disease. EBioMedicine, 99, 104904.

Pérez-Serra A, et al. (2024) Implementing a New Algorithm for Reinterpretation of Ambiguous Variants in Genetic Dilated Cardiomyopathy. International journal of molecular sciences, 25(7).

Tabet DR, et al. (2024) Benchmarking computational variant effect predictors by their ability to infer human traits. Genome biology, 25(1), 172.

Abolhassani A, et al. (2024) Clinical application of next generation sequencing for Mendelian disease diagnosis in the Iranian population. NPJ genomic medicine, 9(1), 12.

Burren OS, et al. (2024) Genetic architecture of telomere length in 462,666 UK Biobank whole-genome sequences. Nature genetics, 56(9), 1832.

Deguchi E, et al. (2024) Low-affinity ligands of the epidermal growth factor receptor are long-range signal transmitters in collective cell migration of epithelial cells. Cell reports, 43(11), 114986.

Mao B, et al. (2024) Identification and functional characterization of a novel heterozygous splice?site mutation in the calpain 3 gene causes rare autosomal dominant limb?girdle muscular dystrophy. Experimental and therapeutic medicine, 27(3), 97.

Sajan SA, et al. (2024) De novo variants in GABRA4 are associated with a neurological phenotype including developmental delay, behavioral abnormalities and epilepsy. European journal of human genetics : EJHG, 32(8), 912.

Kim CY, et al. (2024) Advancing the early detection of canine cognitive dysfunction syndrome with machine learning-enhanced blood-based biomarkers. Frontiers in veterinary science, 11, 1390296.

Zhang X, et al. (2024) Loss of heterozygosity of CYP2D6 enhances the sensitivity of hepatocellular carcinomas to talazoparib. EBioMedicine, 109, 105368.

Kaneda Y, et al. (2024) FBXO24 deletion causes abnormal accumulation of membraneless electron-dense granules in sperm flagella and male infertility. eLife, 13.

Zahraeifard S, et al. (2024) Loss of tumor suppressors promotes inflammatory tumor microenvironment and enhances LAG3+T cell mediated immune suppression. Nature communications, 15(1), 5873.

Franchi A, et al. (2024) The Preferential Use of Subcutaneous Arteries (SCIA-SB and SIEA) in Abdominal-based Autologous Breast Reconstruction with a Modified Flap Design. Plastic and reconstructive surgery. Global open, 12(10), e6252.