Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

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

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: 20260904T000217+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 242 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Zou XZ, et al. (2026) Phenome-wide analysis of copy number variants in 470,727 UK Biobank genomes. Nature, 652(8110), 675.

Hoffmann M, et al. (2026) How Genomic and Structural Context Could Shape JAK-STAT Variant Pathogenicity. Twin research and human genetics : the official journal of the International Society for Twin Studies, 1.

Wickland DP, et al. (2026) Identification of tumor-associated antigens with multi-cancer therapeutic potential. Frontiers in immunology, 17, 1839980.

Ostroverkhova D, et al. (2026) Integrating evidence from protein domains to identify cancer driver mutations. Protein science : a publication of the Protein Society, 35(2), e70422.

Lee H, et al. (2026) Multimodal antigenic escape to GPRC5D-targeted T cell engagers in multiple myeloma. Nature medicine, 32(3), 964.

Brock DC, et al. (2026) Rare heterozygous missense variants in VSX2 are associated with retinal detachment. PLoS genetics, 22(2), e1012027.

Mao B, et al. (2026) Mutation in MSH5 Causes Primary Ovarian Insufficiency and Successful Therapeutic Intervention by In Vitro Fertilisation. Journal of cellular and molecular medicine, 30(9), e70745.

Li L, et al. (2026) Identification and functional characterization of a novel CRYBB1 deletion mutation causing autosomal dominant congenital cataract in a Chinese family. BMC ophthalmology, 26(1), 85.

Lee DB, et al. (2026) Disease- and gene-specific deep learning for pathogenicity prediction of rare missense variants in cancer predisposition genes. BioData mining,

19(1).

Chen P, et al. (2025) Comparative Cochlear Transcriptomics in Echolocating Bats and Mouse Reveals Hras as Protector Against Noise-Induced Hearing Loss. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(44), e08466.

Schlesinger D, et al. (2025) A large-scale sORF screen identifies putative microproteins involved in cancer cell fitness. iScience, 28(3), 111884.

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.

Pittman SK, et al. (2025) Witnessing community violence and its consequences: Changes across middle school. Journal of research on adolescence : the official journal of the Society for Research on Adolescence, 35(2), e70031.

Kline I, et al. (2025) Human cytomegalovirus promotes de novo PC synthesis during early virus replication. bioRxiv : the preprint server for biology.

Emmanuel N, et al. (2025) Hydrophobicity causes anomalous migration of cystine/glutamate antiporter SLC7A11 in SDS-PAGE with low acrylamide concentration. FEBS open bio, 15(6), 994.

Fu M, et al. (2025) Genotype-phenotype correlations and functional characterization of novel PAX2 variants in a 10-patient pediatric cohort. Renal failure, 47(1), 2552911.

Cao K, et al. (2025) Case Report: Identification and functional characterization of a novel heterozygous splice-donor (c.647+1G>A) site mutation in the SPTB gene that causes hereditary spherocytosis with hemolytic anemia. Frontiers in genetics, 16, 1626155.

Mahajan M, et al. (2025) Detecting known neoepitopes, gene fusions, transposable elements, and circular RNAs in cell-free RNA. Bioinformatics (Oxford, England), 41(5).

Spargo TP, et al. (2025) Haploinsufficiency of ITSN1 is associated with a substantial increased risk of Parkinson's disease. Cell reports, 44(3), 115355.

Ergin V, et al. (2025) Exploring Shootin1's oncogenic role within FGFR2 gene fusions. Turkish journal of biology = Turk biyoloji dergisi, 49(7), 811.