Resource Summary Report

Generated by RRID on Aug 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: database, data or information resource

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: 20260805T044141+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 230 mentions in open access literature.

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

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.

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

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.

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.

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.

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.

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

Kline I, et al. (2025) Human cytomegalovirus promotes de novo PC synthesis during early virus replication. Journal of virology, 99(9), e0057925.

Shang X, et al. (2025) Benchmarking large language models for genomic knowledge with GeneTuring. Briefings in bioinformatics, 26(5).

Levy M, et al. (2025) Exome sequencing in every pregnancy? Results of trio exome sequencing in structurally normal fetuses. Prenatal diagnosis, 45(3), 276.

Bayrak H, et al. (2024) RMND1 Mutation Case Report and Literature Review. Molecular syndromology, 15(6), 487.

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

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.

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

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.

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.

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