

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

RefSeq

RRID:SCR_003496

Type: Tool

Proper Citation

RefSeq (RRID:SCR_003496)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/RefSeq/>

Proper Citation: RefSeq (RRID:SCR_003496)

Description: Collection of curated, non-redundant genomic DNA, transcript RNA, and protein sequences produced by NCBI. Provides a reference for genome annotation, gene identification and characterization, mutation and polymorphism analysis, expression studies, and comparative analyses. Accessed through the Nucleotide and Protein databases.

Synonyms: RefSeq, , Reference Sequence Database, Reference Sequence, Reference Sequences, NCBI

Resource Type: data or information resource, database

Defining Citation: [PMID:24316578](#), [PMID:24259432](#), [PMID:22121212](#), [PMID:18927115](#), [PMID:17130148](#), [PMID:15608248](#)

Keywords: reference sequence, transcript, protein, dna, rna, plasmid, organelle, virus, genome, nucleic acid, ortholog, paralog, haplotype, nucleotide sequence, gene expression, blast, gold standard, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: RefSeq

Resource ID: SCR_003496

Alternate IDs: SCR_016579, nif-0000-03397, OMICS_01659, biotools:refseq, r3d100011306

Alternate URLs: <ftp://ftp.ncbi.nlm.nih.gov/refseq>, <https://bio.tools/refseq>, <https://doi.org/10.17616/R3HP70>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260729T044043+0000

Ratings and Alerts

No rating or validation information has been found for RefSeq.

No alerts have been found for RefSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18049 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Dalley R, et al. (2026) Human Neocortical Glutamatergic Neurons Revealed Through Multimodal Profiling. *bioRxiv : the preprint server for biology*.

Chang LJ, et al. (2026) Assessment of Circulating Tumor DNA for Early Detection of Hepatocellular Carcinoma in Alpha-Fetoprotein-Negative Patients With Cirrhotic Nodules. *JGH open : an open access journal of gastroenterology and hepatology*, 10(1), e70331.

Zamparo S, et al. (2026) Metabarcoding Reveals a Potentially Undescribed Columnaris-Causing Bacterium in Peracute Skin Disease of Rainbow Trout (*Oncorhynchus mykiss*, Walbaum). *Journal of fish diseases*, 49(1), e70004.

Richmond JQ, et al. (2026) A chromosome-level reference genome assembly for Gilbert's skink *Plestiodon gilberti*. *The Journal of heredity*, 117(1), 115.

Santos M, et al. (2026) Comprehensive Mapping of Functional Enhancers in Chinese Hamster Ovary Cells. *Biotechnology and bioengineering*, 123(1), 196.

Mantzana-Oikonomaki V, et al. (2026) Pigments, Chromatophore Structure, and Gene Expression Underlying Colour Polytypy of a Panamanian Poison Frog. *Molecular ecology*, 35(1), e70214.

Bag A, et al. (2026) Genetic mapping and candidate gene identification for key physiological traits associated with heat tolerance in wheat (*Triticum aestivum* L.) using a MAGIC population. *PLoS one*, 21(1), e0339966.

Liu Y, et al. (2026) A Novel MPT-Driven Necrosis-Related lncRNA Signature for Prognostic Prediction in Hepatocellular Carcinoma: Validation Using Organoids. *Cancer medicine*, 15(1), e71445.

Luo Z, et al. (2026) Host adaptation and genome evolution of the broad host range fungal rust pathogen, *Austropuccinia psidii*. *G3* (Bethesda, Md.), 16(1).

Dockman RL, et al. (2026) Improved chromosome-level genome assembly of the American cockroach, *Periplaneta americana*. *G3* (Bethesda, Md.), 16(1).

Cusick KN, et al. (2026) Proteomic Characterization of Bottlenose Dolphin (*Tursiops truncatus*) Urine. *Journal of proteome research*, 25(1), 290.

Niazian M, et al. (2026) CRISPR-induced knockouts reveal a dual role for the soybean *NFR5* gene in symbiotic nitrogen fixation and root hair development. *The plant genome*, 19(1), e70143.

Silva-Llanes I, et al. (2026) GASDERMIN D-mediated pyroptosis as a therapeutic target in TAU-dependent frontotemporal dementia mouse model. *Journal of biomedical science*, 33(1), 6.

Huttunen M, et al. (2026) Canine parvovirus infection affects host cell nucleolar organization and ribosome biogenesis. *Communications biology*, 9(1), 10.

Lemaire ON, et al. (2026) Carbon-monoxide-driven bioethanol production operates through a tungsten-dependent catalyst. *Nature chemical biology*, 22(1), 28.

Zhang L, et al. (2026) Gut microbiome-mediated transformation of dietary phytonutrients is associated with health outcomes. *Nature microbiology*, 11(1), 94.

Ruiz E, et al. (2026) Benchmarking the Taxonomic Resolution of Fish eDNA Metabarcodes Against COI Barcodes. *Molecular ecology resources*, 26(1), e70069.

Lim KHJ, et al. (2026) Cross-presentation of dead cell-associated antigens shapes the neoantigenic landscape of tumor immunity. *Nature immunology*, 27(1), 72.

Hershberger CE, et al. (2026) The alternative splicing landscape of hepatocellular carcinoma and its potential for HCC detection. *Hepatology communications*, 10(1).

Kunzelman GW, et al. (2026) Chromatin Profiling Reveals Distinct Male and Female Trajectories for Developmental Learning Potential. *Developmental neurobiology*, 86(1), e23017.