

Resource Summary Report

Generated by [NIF](#) on Aug 26, 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: 20260821T193711+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 19506 mentions in open access literature.

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

Andersen L, et al. (2026) Cell-Free DNA-Derived Immune Cell Ratios Uncover Cancer-Associated Systemic Changes. Cancer research communications, 6(4), 811.

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.

Weissman S, et al. (2026) Clonal dynamics of HIV-infected and uninfected T cells. EBioMedicine, 126, 106163.

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

Bruckner I, et al. (2026) Extrachromosomal microDNA Signature as a Candidate Biomarker in Pediatric Acute Lymphoblastic Leukemia. Cancer research communications, 6(1), 143.

Lee JB, et al. (2026) Lazertinib with stereotactic body radiotherapy in oligometastatic EGFR-mutant non-small-cell lung cancer. ESMO open, 11(2), 106057.

Yu L, et al. (2026) Systematic characterization of PBP2 as the primary siderophore recognizer in Actinomycetes and other Gram-positive bacteria. Microbial genomics, 12(4).

Arimura T, et al. (2026) Arboreal Squirrels Have a Segregated Vomeronasal System With a Regressed Type 2 Receptor (V2R)-Domain. The Journal of comparative neurology, 534(5), e70171.

Lassila M, et al. (2026) Progressive intestinal tumor cell plasticity, Myc activation, and loss of Lgr5+ tumor stem cell lineage commitment upon Wnt depletion. Science advances, 12(28), eaeb8564.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Phanaphitakkul S, et al. (2026) Comparative Genomics of High-Yielding *Komagataeibacter diospyri* Mutants Induced by Ultraviolet Light. *Molecular biotechnology*, 68(6), 2704.

VanBuren R, et al. (2026) Variability in drought gene expression datasets highlights the need for paired physiology and community standardization. *Plant physiology*, 200(1).

Wakatake T, et al. (2026) Transcriptomic prey-capture responses in convergently evolved carnivorous pitcher plants. *The New phytologist*, 249(5), 2559.

Intorcchia V, et al. (2026) Hfq orchestrates a robust RNA-RNA interaction network in *Acinetobacter baumannii*. *mBio*, 17(1), e0323125.

Akotenou G, et al. (2026) MegaPlantTF: a machine learning framework for comprehensive identification and classification of plant transcription factors. *Bioinformatics (Oxford, England)*, 42(1).

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.

Sánchez-Casiano NE, et al. (2026) Molecular epidemiology and population structure of *Providencia stuartii* obtained from humans and other sources. *Microbiology spectrum*, 14(2), e0203225.

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.

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.