

Resource Summary Report

Generated by [dkNET](#) 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 [dkNET](#) .

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.

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

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.

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.

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

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.

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.

Intorcia 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.