Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 17, 2025

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: database, data or information resource

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

Funding:

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

Alternate URLs: ftp://ftp.ncbi.nlm.nih.gov/refseq, https://bio.tools/refseq

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250412T054839+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 16092 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lhamo D, et al. (2025) Genome-wide association studies on resistance to powdery mildew in cultivated emmer wheat. The plant genome, 18(1), e20493.

Peters Haugrud AR, et al. (2025) Identification of robust yield quantitative trait loci derived from cultivated emmer for durum wheat improvement. The plant genome, 18(1), e20398.

Symonds ALJ, et al. (2025) Memory Phenotype Tfh Cells Develop Without Overt Infection and Support Germinal Center Formation and B Cell Responses to Viral Infection. European journal of immunology, 55(1), e202451291.

Zin OA, et al. (2025) Genotype-Phenotype Correlations of Nance-Horan Syndrome in Male and Female Carriers of a Novel Variant. Genes, 16(1).

Almirón C, et al. (2025) Functional and genomic analyses of plant growth promoting traits in Priestia aryabhattai and Paenibacillus sp. isolates from tomato rhizosphere. Scientific reports, 15(1), 3498.

Zhao K, et al. (2025) IS15DIV-flanked composite transposon harboring bla NDM-5 in multidrug-resistant Salmonella Typhimurium. iScience, 28(2), 111720.

Graça AP, et al. (2025) MftG is crucial for ethanol metabolism of mycobacteria by linking mycofactocin oxidation to respiration. eLife, 13.

Wang W, et al. (2025) Non-additive dosage-dependent effects of TaGS3 gene editing on grain size and weight in wheat. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(2), 38.

Tang G, et al. (2025) Metagenomic estimation of absolute bacterial biomass in the mammalian gut through host-derived read normalization. bioRxiv : the preprint server for biology.

Qin L, et al. (2025) Utilizing Targeted Next-Generation Sequencing for Rapid, Accurate, and Cost-Effective Pathogen Detection in Lower Respiratory Tract Infections. Infection and drug resistance, 18, 329.

Mughal F, et al. (2025) Evolution of intrinsic disorder in the structural domains of viral and cellular proteomes. Scientific reports, 15(1), 2878.

Liu G, et al. (2025) oriTDB: a database of the origin-of-transfer regions of bacterial mobile genetic elements. Nucleic acids research, 53(D1), D163.

Wang X, et al. (2025) Spatial and Single-Cell Analyses Reveal Heterogeneity of DNAM-1 Receptor-Ligand Interactions That Instructs Intratumoral ??T-cell Activity. Cancer research, 85(2), 277.

Yang Y, et al. (2025) Systematic identification of secondary bile acid production genes in global microbiome. mSystems, 10(1), e0081724.

Raynaud M, et al. (2025) PRDM9 drives the location and rapid evolution of recombination hotspots in salmonid fish. PLoS biology, 23(1), e3002950.

Ferreira C, et al. (2025) Comparative genomics analyses of Actinobacteriota identify Golgi phosphoprotein 3 (GPP34) as a widespread ancient protein family associated with sponge symbiosis. Microbiome, 13(1), 4.

Guccione C, et al. (2025) Incomplete human reference genomes can drive false sex biases and expose patient-identifying information in metagenomic data. Nature communications, 16(1), 825.

Bernal Astrain G, et al. (2025) The small GTPase MRAS is a broken switch. Nature communications, 16(1), 647.

Kentistou KA, et al. (2025) Rare variant associations with birth weight identify genes involved in adipose tissue regulation, placental function and insulin-like growth factor signalling. Nature communications, 16(1), 648.

Megrian D, et al. (2025) Evolutionary plasticity and functional repurposing of the essential metabolic enzyme MoeA. Communications biology, 8(1), 49.