

Resource Summary Report

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RefSeq non-redundant proteins

RRID:SCR_022748

Type: Tool

Proper Citation

RefSeq non-redundant proteins (RRID:SCR_022748)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/refseq/about/nonredundantproteins/>

Proper Citation: RefSeq non-redundant proteins (RRID:SCR_022748)

Description: Non-redundant RefSeq protein records are currently provided for archaeal and bacterial RefSeq genomes, with exception of selected reference genomes, by NCBI prokaryotic genome annotation pipeline. This scope definition may change in the future to include additional RefSeq sub-kingdoms or other organism groups and some GenBank conceptual translation protein records may provide cross-links to RefSeq non-redundant proteins.

Resource Type: data or information resource

Keywords: NIH, NLM, Non-redundant RefSeq protein records, RefSeq protein records, NCBI prokaryotic genome annotation, protein records

Availability: Free, Freely available

Resource Name: RefSeq non-redundant proteins

Resource ID: SCR_022748

Record Creation Time: 20220916T050153+0000

Record Last Update: 20260801T190801+0000

Ratings and Alerts

No rating or validation information has been found for RefSeq non-redundant proteins.

No alerts have been found for RefSeq non-redundant proteins.

Data and Source Information

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Yi L, et al. (2025) Chromosome-level genome assemblies of sunflower oilseed and confectionery cultivars. *Scientific data*, 12(1), 24.

Yao H, et al. (2025) Unveiling the developmental dynamics and functional role of Odorant Receptor Co-receptor (Orco) in *Aedes albopictus*: A novel mechanism for regulating odorant receptor expression. *PLoS neglected tropical diseases*, 19(11), e0013753.

Mehabooba B, et al. (2025) De novo transcriptome analysis of *Perna perna* L. (Bivalve) with functional and metabolic pathway analysis. *Scientific data*, 12(1), 1742.

Gu T, et al. (2025) *Faucicola mancuniensis* isolated from human respiratory tract and its genomic characteristics. *BMC microbiology*, 25(1), 587.

Safarchi A, et al. (2025) Understanding dysbiosis and resilience in the human gut microbiome: biomarkers, interventions, and challenges. *Frontiers in microbiology*, 16, 1559521.

Mousa AA, et al. (2025) Metagenomic analysis reveals rumen microbiome enrichment and functional genes adjustment in carbohydrate metabolism induced by different sorting behavior in mid-lactation dairy cows. *Animal microbiome*, 7(1), 82.

Lu L, et al. (2025) Two novel phages infecting *Erythrobacter* isolated from the epipelagic ocean. *Frontiers in microbiology*, 16, 1592355.

Chen XX, et al. (2025) Microbial dysbiosis with tryptophan metabolites alteration in lower respiratory tract is associated with clinical responses to anti-PD-1 immunotherapy in advanced non-small cell lung cancer. *Cancer immunology, immunotherapy* : CII, 74(4), 140.

Yu Z, et al. (2025) Analysis of post-transcriptional regulatory signatures and immune cell subsets in premature ovarian insufficiency based on full-length transcriptome. *Scientific reports*, 15(1), 5533.

Zang T, et al. (2025) Structural and functional changes in the oral microbiome of patients with craniofacial microsomia. *Scientific reports*, 15(1), 5400.

Yuan J, et al. (2025) Whole genome sequencing analysis of a novel exopolysaccharide-producing *Bacillus velezensis* and its impact on the quality of soy sauce. *Food chemistry*: X, 28, 102585.

Feng B, et al. (2025) Short-Term Fertilization with the Nitrogen-Fixing Bacterium (*NFB*) *Kosakonia radicincitans* GXGL-4A Agent Can Modify the Transcriptome Expression Profiling of Cucumber (*Cucumis sativus* L.) Root. *Microorganisms*, 13(3).

Wang T, et al. (2025) Integrated metabolite profiling and transcriptome analysis identify candidate genes involved in diterpenoid alkaloid biosynthesis in *Aconitum pendulum*. *Frontiers in plant science*, 16, 1547584.

Borelli TC, et al. (2025) DeepSEA: an alignment-free explainable approach to annotate antimicrobial resistance proteins. *BMC bioinformatics*, 26(1), 224.

Fox BW, et al. (2024) Evolutionarily related host and microbial pathways regulate fat desaturation in *C. elegans*. *Nature communications*, 15(1), 1520.

Xu R, et al. (2024) Pectin supplementation accelerates post-antibiotic gut microbiome reconstitution orchestrated with reduced gut redox potential. *The ISME journal*, 18(1).

Zhang X, et al. (2024) Temporal genomics in Hawaiian crickets reveals compensatory intragenomic coadaptation during adaptive evolution. *Nature communications*, 15(1), 5001.

Song Y, et al. (2024) Chromosome level genome assembly of endangered medicinal plant *Anisodus tanguticus*. *Scientific data*, 11(1), 161.

Guo G, et al. (2024) Genome-wide identification of GA2ox genes family and analysis of PbrGA2ox1-mediated enhanced chlorophyll accumulation by promoting chloroplast development in pear. *BMC plant biology*, 24(1), 166.

Wang J, et al. (2024) Identification of molecular markers and candidate regions associated with grain number per spike in Pubing3228 using SLAF-BSA. *Frontiers in plant science*, 15, 1361621.