

# 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:** 20260815T182723+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 55 mentions in open access literature.

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

Hazinia S, et al. (2026) Integrated Metabolomics, Transcriptomics, and Ultrastructural Assessment of the Myco-Heterotrophic Plant, *Monotropa uniflora*. *Plant direct*, 10(4), e70165.

Tigabu A, et al. (2026) Broad-spectrum antibiotic treatment reshapes the gut microbiome, resistome, and colonization potential of opportunistic pathogens: a metagenomics study. *Gut pathogens*, 18(1).

Perrone GCM, et al. (2026) Structural basis of ligand selectivity in FAD/NAD(P)H-dependent dehydrogenases: insights from trypanothione reductase and type II NADH dehydrogenase. *Protein science : a publication of the Protein Society*, 35(7), e70664.

Jiang HS, et al. (2026) A novel single-cell NAD-ME C4 subtype integrated with CAM and bicarbonate use in an aquatic plant. *The New phytologist*, 249(5), 2386.

Cheng Z, et al. (2026) A chromosome-level reference genome of an endangered plant *Craigia yunnanensis*. *Scientific data*, 13(1).

Zhang H, et al. (2026) Allelic variation at a single locus distinguishes spring and winter faba beans. *Nature genetics*, 58(3), 655.

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.

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.

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.

Wang M, et al. (2025) Biocontrol Potential, Plant Growth-Promotion, and Genomic Insights of *Pseudomonas koreensis* CHHM-1 Against Bacterial Canker in *Actinidia arguta*. *Microorganisms*, 13(10).

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.

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

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.

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

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

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.

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.