

Resource Summary Report

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GenBank

RRID:SCR_002760

Type: Tool

Proper Citation

GenBank (RRID:SCR_002760)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/Genbank/>

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Description: NIH genetic sequence database that provides annotated collection of all publicly available DNA sequences for almost 280 000 formally described species (Jan 2014) .These sequences are obtained primarily through submissions from individual laboratories and batch submissions from large-scale sequencing projects, including whole-genome shotgun (WGS) and environmental sampling projects. Most submissions are made using web-based BankIt or standalone Sequin programs, and GenBank staff assigns accession numbers upon data receipt. It is part of International Nucleotide Sequence Database Collaboration and daily data exchange with European Nucleotide Archive (ENA) and DNA Data Bank of Japan (DDBJ) ensures worldwide coverage. GenBank is accessible through NCBI Entrez retrieval system, which integrates data from major DNA and protein sequence databases along with taxonomy, genome, mapping, protein structure and domain information, and biomedical journal literature via PubMed. BLAST provides sequence similarity searches of GenBank and other sequence databases. Complete bimonthly releases and daily updates of GenBank database are available by FTP.

Abbreviations: GB

Synonyms: , Gen Bank, GenBank

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:24217914](#), [PMID:23193287](#), [PMID:21071399](#)

Keywords: genetic sequence, dna sequence, human genetics, human genome, nucleotide sequence, nucleotide, dna, dna data bank, gene mapping, genetics, gold standard

Funding: NLM

Availability: Free, Freely available

Resource Name: GenBank

Resource ID: SCR_002760

Alternate IDs: nif-0000-02873, r3d100010528, OMICS_01650

Alternate URLs: <https://doi.org/10.17616/R3D31X>

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260905T132453+0000

Ratings and Alerts

No rating or validation information has been found for GenBank.

No alerts have been found for GenBank.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 64417 mentions in open access literature.

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

Campbell AS, et al. (2026) Molecular insights into electroreceptor ribbon synapses from differential gene expression in sturgeon lateral line organs. *Journal of anatomy*, 248(5), 784.

Nail AN, et al. (2026) Deficient arsenic methylation and global proteomic reprogramming in human keratinocytes during arsenic-induced skin carcinogenesis. *Archives of toxicology*.

Dombaxe CP, et al. (2026) Proteomic Signatures of Regeneration: Uncovering Extracellular Matrix-Associated Cues in Goldfish Spinal Cord Repair. *The Journal of comparative neurology*, 534(5), e70170.

Sánchez-Mora P, et al. (2026) Detection and genetic characterization of Crimean-Congo hemorrhagic fever virus in ticks from western Spain (2017, 2020-2024). *Frontiers in veterinary science*, 13, 1789622.

Chen K, et al. (2026) Liquid?liquid phase separation of PHLDB2 promotes oral squamous cell carcinoma metastasis through regulating epithelial mesenchymal transition and PIK3CA expression. *Molecular medicine reports*, 33(1).

- Viruel J, et al. (2026) Phylogenomic Barcoding of Soil Seed Bank-Persistent and Wind-Dispersed Non-Native Plant Species in South Georgia. *Molecular ecology resources*, 26(1), e70068.
- Gwee CY, et al. (2026) Performance of Two Custom Probe Kits for In-Solution Enrichment of Ancient Avian DNA. *Molecular ecology resources*, 26(1), e70071.
- Mongkolphan C, et al. (2026) Molecular characterization of tick-borne piroplasms in captive megaherbivores in Thailand. *Parasitology research*, 125(1), 2.
- Klass LG, et al. (2026) Characterizing mixed strongyle infections in foals and broodmares using cytochrome c oxidase subunit I deep amplicon sequencing. *Parasites & vectors*, 19(1), 65.
- Shi X, et al. (2026) Nuclear factor IC promoting porcine reproductive and respiratory syndrome virus (PRRSV) replication and suppressing type I interferon transcription. *BMC veterinary research*, 22(1), 80.
- Li W, et al. (2026) Physiological and transcriptomic insights into the molecular mechanisms of salt stress adaptation in *Gardenia jasminoides*. *BMC plant biology*, 26(1), 203.
- Lee JK, et al. (2026) Distribution and characteristics of extended spectrum β -lactamase-producing *Escherichia coli* in stages of integrated broiler production in Korea. *Poultry science*, 105(3), 106340.
- Schnelle A, et al. (2026) Using Historic and Contemporary Genomes to Assess the Genetic Consequences of a Population Decline in an Endangered Tern Population. *Evolutionary applications*, 19(1), e70192.
- Sun Z, et al. (2026) Microsporidia keratoconjunctivitis identified as an emerging zoonotic threat from pet parrots: Clinical and metagenomic next-generation sequencing evidence. *Virulence*, 17(1), 2605385.
- Hu Q, et al. (2026) Rapid nucleic acid detection of *Mycoplasma synoviae* using dual-mode RAA-CRISPR/Cas12a system. *Poultry science*, 105(1), 106126.
- Barel M, et al. (2026) Colistin and Biofilm-Related Genes of Positive *Escherichia coli* O157:H7 in Cattle (*Bos taurus*) Carcasses Antibiotic Resistance Profiles, Biofilm and Molecular Characterisation of Isolates. *Veterinary medicine and science*, 12(1), e70730.
- Petersen NP, et al. (2026) ViMOP: a user-friendly and field-applicable pipeline for untargated viral genome nanopore sequencing. *Bioinformatics (Oxford, England)*, 42(1).
- Larsen BB, et al. (2026) Functional and antigenic constraints on the Nipah virus fusion protein. *bioRxiv : the preprint server for biology*.
- Gaorekwe RM, et al. (2026) Prevalence and Genetic Diversity of *Haemoproteus* and *Leucocytozoon* in Raptors and Other Captive Birds at the National Zoological Garden in South Africa. *Integrative zoology*, 21(1), 203.
- Li K, et al. (2026) Foot-and-mouth disease virus 3D polymerase antagonizes the interferon signaling pathway by blocking STAT2 nuclear translocation. *Virus research*, 363, 199671.