

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

Whole Genome Shotgun (WGS) Project

RRID:SCR_016637

Type: Tool

Proper Citation

Whole Genome Shotgun (WGS) Project (RRID:SCR_016637)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/genbank/wgs/>

Proper Citation: Whole Genome Shotgun (WGS) Project (RRID:SCR_016637)

Description: Project for assemblies of incomplete genomes or incomplete chromosomes of prokaryotes or eukaryotes that are being sequenced by a whole genome shotgun strategy. WGS projects may be annotated, but annotation is not required. The nucleotide and protein data from all WGS projects go into the BLAST database.

Abbreviations: WGS

Synonyms: Whole Genome Shotgun WGS Project, Whole Genome Shotgun WGS, WGS Projects, Whole Genome Shotgun

Resource Type: data processing software, software application, software resource

Keywords: assembly, incomplete, chromosome, prokaryote, eukaryote, sequenced, whole, genome, shot, gun, strategy, data

Funding: National Library of Medicine

Resource Name: Whole Genome Shotgun (WGS) Project

Resource ID: SCR_016637

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260821T194108+0000

Ratings and Alerts

No rating or validation information has been found for Whole Genome Shotgun (WGS) Project.

No alerts have been found for Whole Genome Shotgun (WGS) Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Robinson E, et al. (2026) STK11 mutations and deletions define a distinct subtype of cervical adenocarcinoma. medRxiv : the preprint server for health sciences.

Zhang X, et al. (2025) MTA-Cooperative PRMT5 Inhibitors Are Efficacious in MTAP-Deleted Malignant Peripheral Nerve Sheath Tumor Models. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(22), 4779.

Vasquez I, et al. (2023) Comparative Genomics of a Polyvalent Escherichia-Salmonella Phage fp01 and In Silico Analysis of Its Receptor Binding Protein and Conserved Enterobacteriaceae Phage Receptor. Viruses, 15(2).

Adriaenssens EM, et al. (2023) Guidelines for public database submission of uncultivated virus genome sequences for taxonomic classification. Nature biotechnology, 41(7), 898.

DeSantis TZ, et al. (2023) StrainSelect: A novel microbiome reference database that disambiguates all bacterial strains, genome assemblies and extant cultures worldwide. Heliyon, 9(2), e13314.

Thomès L, et al. (2021) Mosaic Evolution of the Phosphopantothenate Biosynthesis Pathway in Bacteria and Archaea. Genome biology and evolution, 13(2).

Wang H, et al. (2021) Synonymous mutations and the molecular evolution of SARS-CoV-2 origins. Virus evolution, 7(1), veaa098.

Vannier T, et al. (2020) Diversity and evolution of bacterial bioluminescence genes in the global ocean. NAR genomics and bioinformatics, 2(2), lqaa018.

Cao R, et al. (2019) Identification and Functional Characterization of Squamosa Promoter Binding Protein-Like Gene TaSPL16 in Wheat (Triticum aestivum L.). Frontiers in plant science, 10, 212.