Resource Summary Report

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Genome Reference Consortium

RRID:SCR_006553
Type: Tool

Proper Citation

Genome Reference Consortium (RRID:SCR_006553)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/projects/genome/assembly/grc/

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Description: Consortium that puts sequences into a chromosome context and provides the best possible reference assembly for human, mouse, and zebrafish via FTP. Tools to facilitate the curation of genome assemblies based on the sequence overlaps of long, high quality sequences.

Abbreviations: GRC

Synonyms: Genome Reference Consortium

Resource Type: consortium, data or information resource, database, organization portal, portal

Keywords: sequnence, chromosome, reference, assembly, human, mouse, zebrafish, genome, sequence, overlap

Funding: NIH

Resource Name: Genome Reference Consortium

Resource ID: SCR_006553

Alternate IDs: nif-0000-20983

Alternate URLs: http://genomereference.org

Old URLs: http://www.ncbi.nlm.nih.gov/genome/assembly/grc/index.shtml

Record Creation Time: 20220129T080236+0000

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Ratings and Alerts

No rating or validation information has been found for Genome Reference Consortium.

No alerts have been found for Genome Reference Consortium.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. Cancer research, 86(5), 1300.

Pekkoc-Uyanik KC, et al. (2025) Next-generation sequencing of CCR5, CXCR4, and IFNAR1 variants in relation to HIV-1 disease progression and ART response. Scientific reports, 15(1), 26511.

Ruggiero R, et al. (2025) Genetic variants linked to type 2 diabetes in CDKN1B and TCF7L2 influence survival outcomes in metastatic colorectal cancer. International journal of cancer, 157(9), 1853.

Ennis CS, et al. (2025) Plasma exosomes from individuals with type 2 diabetes drive breast cancer aggression in patient-derived organoids. Communications biology, 8(1), 1276.

Fléchon A, et al. (2024) Association of Tumor Mutational Burden and PD-L1 with the Efficacy of Pembrolizumab with or without Chemotherapy versus Chemotherapy in Advanced Urothelial Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(23), 5353.

Chia R, et al. (2024) Genome sequence analyses identify novel risk loci for multiple system atrophy. Neuron, 112(13), 2142.

Marrero RJ, et al. (2023) SAMHD1 single nucleotide polymorphisms impact outcome in children with newly diagnosed acute myeloid leukemia. Blood advances, 7(11), 2538.

Faria JAD, et al. (2023) Cytogenomic Investigation of Syndromic Brazilian Patients with Differences of Sexual Development. Diagnostics (Basel, Switzerland), 13(13).

Khandelwal A, et al. (2023) Mbnl2 loss alters novel context processing and impairs object recognition memory. iScience, 26(5), 106732.

Masuelli S, et al. (2022) When left does not seem right: epigenetic and bioelectric differences between left- and right-sided breast cancer. Molecular medicine (Cambridge,

Mass.), 28(1), 15.

Qu LH, et al. (2021) Targeted next-generation sequencing identifies ABCA4 mutations in Chinese families with childhood-onset and adult-onset Stargardt disease. Bioscience reports, 41(6).

Yu L, et al. (2020) Identification of SPRR3 as a novel diagnostic/prognostic biomarker for oral squamous cell carcinoma via RNA sequencing and bioinformatic analyses. PeerJ, 8, e9393.

Qu LH, et al. (2020) Identification of 13 novel USH2A mutations in Chinese retinitis pigmentosa and Usher syndrome patients by targeted next-generation sequencing. Bioscience reports, 40(1).

Meira JGC, et al. (2018) Diagnosis of Atelosteogenesis Type I suggested by Fetal Ultrasonography and Atypical Paternal Phenotype with Mosaicism. Revista brasileira de ginecologia e obstetricia : revista da Federacao Brasileira das Sociedades de Ginecologia e Obstetricia, 40(9), 570.

Bauer E, et al. (2018) From metagenomic data to personalized in silico microbiotas: predicting dietary supplements for Crohn's disease. NPJ systems biology and applications, 4, 27.

Cooper A, et al. (2017) APOL1 renal risk variants have contrasting resistance and susceptibility associations with African trypanosomiasis. eLife, 6.

Matyas JJ, et al. (2017) Truncated TrkB.T1-Mediated Astrocyte Dysfunction Contributes to Impaired Motor Function and Neuropathic Pain after Spinal Cord Injury. The Journal of neuroscience : the official journal of the Society for Neuroscience, 37(14), 3956.

Chu A, et al. (2016) Large-scale profiling of microRNAs for The Cancer Genome Atlas. Nucleic acids research, 44(1), e3.

Narayanasamy S, et al. (2016) IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. Genome biology, 17(1), 260.

Zhang X, et al. (2016) Single-cell analyses of transcriptional heterogeneity in squamous cell carcinoma of urinary bladder. Oncotarget, 7(40), 66069.