Resource Summary Report

Generated by NIF on Apr 27, 2025

RefSeqGene

RRID:SCR_013787
Type: Tool

Proper Citation

RefSeqGene (RRID:SCR_013787)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/refseq/rsg/

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Description: A data set of defined genomic sequences used as reference standards for well-characterized genes. These standard nucleotide sequences serve as foundations for locating mutations, establishing conventions for numbering exons and introns, and defining the coordinates of other variations. Sequences are aligned to reference chromosomes. RefSeqGene is a subset of NCBI RefSeq.

Synonyms: NCBI RefSeqGene, RefSeqGene Project

Resource Type: information resource

Defining Citation: PMID:18927115

Keywords: data set, genomic sequences, reference standard

Funding:

Availability: Free, Public

Resource Name: RefSeqGene

Resource ID: SCR_013787

License URLs: http://www.nlm.nih.gov/privacy.html

Record Creation Time: 20220129T080318+0000

Record Last Update: 20250420T014703+0000

Ratings and Alerts

No rating or validation information has been found for RefSeqGene.

No alerts have been found for RefSeqGene.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

Huang X, et al. (2025) Mutation spectra and genotype?phenotype analysis of congenital hypothyroidism in a neonatal population. Biomedical reports, 22(2), 30.

Lv W, et al. (2024) Extrachromosomal circular DNA orchestrates genome heterogeneity in urothelial bladder carcinoma. Theranostics, 14(13), 5102.

Pugacheva EM, et al. (2024) BORIS/CTCFL epigenetically reprograms clustered CTCF binding sites into alternative transcriptional start sites. Genome biology, 25(1), 40.

Pranck?nien? L, et al. (2023) Microevolutionary processes analysis in the Lithuanian genome. Scientific reports, 13(1), 11941.

Chou KJ, et al. (2022) A new missense mutation of calcium sensing receptor with isoleucine replaced by serine at codon 857 leading to type V Bartter syndrome. Experimental cell research, 414(1), 113080.

Markova TV, et al. (2022) Clinical and genetic characterization of three Russian patients with pycnodysostosis due to pathogenic variants in the CTSK gene. Molecular genetics & genomic medicine, 10(5), e1904.

Ikeda S, et al. (2022) Disruption of piRNA machinery by deletion of ASZ1/GASZ results in the expression of aberrant chimeric transcripts in gonocytes. The Journal of reproduction and development, 68(2), 125.

Erdo?an M, et al. (2021) The Genetic Analysis of Cystic Fibrosis Patients With Seven Novel Mutations in the CFTR Gene in the Central Anatolian Region of Turkey. Balkan medical journal, 38(6), 357.

Markova T, et al. (2021) Clinical and genetic characterization of autosomal recessive stickler syndrome caused by novel compound heterozygous mutations in the COL9A3 gene. Molecular genetics & genomic medicine, 9(3), e1620.

Penitenti F, et al. (2021) Clinical presentation, genotype-phenotype correlations, and outcome of pancreatic neuroendocrine tumors in Von Hippel-Lindau syndrome. Endocrine, 74(1), 180.

Urnikyte A, et al. (2021) Genome-Wide Landscape of North-Eastern European Populations: A View from Lithuania. Genes, 12(11).

Ziadi W, et al. (2021) STAT3 polymorphisms in North Africa and its implication in breast cancer. Molecular genetics & genomic medicine, 9(8), e1744.

Liu W, et al. (2021) Analysis of STAG3 variants in Chinese non-obstructive azoospermia patients with germ cell maturation arrest. Scientific reports, 11(1), 10077.

Hirsch D, et al. (2021) Molecular characterization of ulcerative colitis-associated colorectal carcinomas. Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc, 34(6), 1153.

Wu CY, et al. (2021) Lipopolysaccharide stimulation test on cultured PBMCs assists the discrimination of cryopyrin-associated periodic syndrome from systemic juvenile idiopathic arthritis. Scientific reports, 11(1), 11903.

Hirsch D, et al. (2020) Newly established gastrointestinal cancer cell lines retain the genomic and immunophenotypic landscape of their parental cancers. Scientific reports, 10(1), 17895.

Keppens C, et al. (2020) Variation in nomenclature of somatic variants for selection of oncological therapies: Can we reach a consensus soon? Human mutation, 41(1), 7.

Yamaguchi T, et al. (2020) Pathological processes in aqueous humor due to iris atrophy predispose to early corneal graft failure in humans and mice. Science advances, 6(20), eaaz5195.

Dobon B, et al. (2020) The shaping of immunological responses through natural selection after the Roma Diaspora. Scientific reports, 10(1), 16134.

Ahn YH, et al. (2020) Targeted Exome Sequencing Provided Comprehensive Genetic Diagnosis of Congenital Anomalies of the Kidney and Urinary Tract. Journal of clinical medicine, 9(3).