Resource Summary Report

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NextGENe

RRID:SCR_011859
Type: Tool

Proper Citation

NextGENe (RRID:SCR_011859)

Resource Information

URL: https://www.softgenetics.com/NextGENe.php

Proper Citation: NextGENe (RRID:SCR_011859)

Description: Software tool for Next Generation sequence analysis. Analytical partner for analysis of desktop sequencing data produced by Illumina iSeq, Miniseq, MiSeq, NextSeq, HiSeq, and NovaSeq systems, Ion Torrent Ion GeneStudio S5, PGM, and Proton systems as well as other platforms. Software runs on Windows Operating System, which provides biologist friendly interface. It does not require scripting or other bioinformatics support.

Abbreviations: NextGENe

Synonyms: Next GENeration Sequence Analysis

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

Keywords: Next Generation Sequence Analysis, desktop sequencing data analysis, sequencing data

Availability: Commercial license

Resource Name: NextGENe

Resource ID: SCR_011859

Alternate IDs: OMICS_01131

Old URLs: http://softgenetics.com/NextGENe.html

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260731T042839+0000

Ratings and Alerts

No rating or validation information has been found for NextGENe.

No alerts have been found for NextGENe.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 368 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Guerra J, et al. (2025) The role of multi-organ cancer predisposition genes in the risk of inherited and histologically diverse gastric cancer. EBioMedicine, 116, 105759.

Ding Y, et al. (2025) Focusing on Rare Variants Related to Maturity-Onset Diabetes of the Young in Children. Pediatric diabetes, 2025, 8155443.

Kuehl J, et al. (2025) Genetic inactivation of FAAP100 causes Fanconi anemia due to disruption of the monoubiquitin ligase core complex. The Journal of clinical investigation, 135(11).

Özer L, et al. (2025) The retrospective data analysis of NLRP7 and KHDC3L mutations in Turkish patients with recurrent hydatidiform mole. Turkish journal of obstetrics and gynecology, 22(3), 230.

Dong L, et al. (2025) A Novel R140S ?c Variant Alters Cellular Distribution, Reduces Surface Expression, and Impairs Cytokine Signaling in Atypical X-SCID. Journal of clinical immunology, 45(1), 121.

Policarpio-Nicolas MLC, et al. (2025) Cytologic Findings and Ancillary Tests Results of Sclerosing Pneumocytoma: Our Institutional Experience. Diagnostic cytopathology, 53(1), 3.

Costa CIS, et al. (2025) Understanding rare variant contributions to autism: lessons from dystrophin-deficient model. NPJ genomic medicine, 10(1), 18.

Kwon YD, et al. (2025) Clinical usefulness of next-generation sequencing-based target gene sequencing in diagnosis of inherited bone marrow failure syndrome. Annals of hematology, 104(5), 2693.

Zheng Y, et al. (2025) Comparative sequencing study of mismatch repair and homology-directed repair genes in endometrial cancer and breast cancer patients from Kazakhstan. International journal of cancer, 156(4), 764.

Ouyang X, et al. (2025) Application of rapid clinical exome sequencing technology in the diagnosis of critically ill pediatric patients with suspected genetic diseases. Frontiers in genetics, 16, 1526077.

Kokemüller L, et al. (2025) Germline variants of homology-directed repair or mismatch repair genes in cervical cancer. International journal of cancer, 156(4), 700.

Yang G, et al. (2025) Novel POMT2 variants associated with limb-girdle muscular dystrophy R14: genetic, histological and functional studies. Orphanet journal of rare diseases, 20(1), 99.

Shi X, et al. (2025) Utility of whole exome sequencing in the evaluation of isolated fetal growth restriction in normal chromosomal microarray analysis. Annals of medicine, 57(1), 2476038.

Lee SY, et al. (2025) Comprehensive genetic profiling of sensorineural hearing loss using an integrative diagnostic approach. Cell reports. Medicine, 6(7), 102206.

Chen X, et al. (2025) dentification and characterization of novel PAX4 variants in patients with suspected MODY9. BMJ open diabetes research & care, 13(6).

Wang R, et al. (2025) Sperm DNA methylation profiling in patients with Kallmann syndrome. Endocrine connections, 14(10).

Özer L, et al. (2025) Reclassification of BRCA1 and BRCA2 Variants of Unknown Significance in a Turkish Cohort; A Single-Center, Retrospective Study. European journal of breast health, 21(4), 295.

Smith D, et al. (2025) Spatial and single cell mapping of castleman disease reveals key stromal cell types and cytokine pathways. Nature communications, 16(1), 6009.

Krizkova J, et al. (2025) Somatic mutations and outcomes in chronic myeloid leukemia adolescent and young adults compared to children, adults, and BCR::ABL1-positive acute lymphoblastic leukemia. Leukemia, 39(7), 1670.

Zhong L, et al. (2024) Clinical and genetic features of Fanconi anemia associated with a variant of FANCA gene: Case report and literature review. Medicine, 103(36), e39358.