Resource Summary Report

Generated by dkNET on Apr 30, 2025

GensearchNGS

RRID:SCR_010802
Type: Tool

Proper Citation

GensearchNGS (RRID:SCR_010802)

Resource Information

URL: http://www.phenosystems.com/www/index.php/products/gensearchngs

Proper Citation: GensearchNGS (RRID:SCR_010802)

Description: An integrated software solution for the analysis of DNA-Seq data from commonly used NGS equipments such as Roche/454, Illumina and Ion Torrent.

Abbreviations: GensearchNGS

Resource Type: software resource

Keywords: bio.tools

Funding:

Availability: Commercial license

Resource Name: GensearchNGS

Resource ID: SCR_010802

Alternate IDs: OMICS_00287, biotools:gensearchngs

Alternate URLs: https://bio.tools/gensearchngs

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014510+0000

Ratings and Alerts

No rating or validation information has been found for GensearchNGS.

No alerts have been found for GensearchNGS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Koparir A, et al. (2024) Zebrafish as a model to investigate a biallelic gain-of-function variant in MSGN1, associated with a novel skeletal dysplasia syndrome. Human genomics, 18(1), 23.

Bürtin F, et al. (2024) ctDNA responds to neoadjuvant treatment in locally advanced rectal cancer. Journal of cancer research and clinical oncology, 150(9), 428.

Pluta N, et al. (2023) Whole-Genome Sequencing Identified New Structural Variations in the DMD Gene That Cause Duchenne Muscular Dystrophy in Two Girls. International journal of molecular sciences, 24(17).

Lippert J, et al. (2022) Prognostic Role of Targeted Methylation Analysis in Paraffin-embedded Samples of Adrenocortical Carcinoma. The Journal of clinical endocrinology and metabolism, 107(10), 2892.

Bahena P, et al. (2022) Unraveling the genetic complexities of combined retinal dystrophy and hearing impairment. Human genetics, 141(3-4), 785.

Scheiper-Welling S, et al. (2022) Variant interpretation in molecular autopsy: a useful dilemma. International journal of legal medicine, 136(2), 475.

Shemer Y, et al. (2021) Investigating LMNA-Related Dilated Cardiomyopathy Using Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes. International journal of molecular sciences, 22(15).

Köffer J, et al. (2021) Post-mortem genetic investigation of cardiac disease-associated genes in sudden infant death syndrome (SIDS) cases. International journal of legal medicine, 135(1), 207.

Jouinot A, et al. (2020) Intratumor heterogeneity of prognostic DNA-based molecular markers in adrenocortical carcinoma. Endocrine connections, 9(7), 705.

Doll J, et al. (2020) Novel Loss-of-Function Variants in CDC14A are Associated with

Recessive Sensorineural Hearing Loss in Iranian and Pakistani Patients. International journal of molecular sciences, 21(1).

Kolokotronis K, et al. (2020) New Insights on Genetic Diagnostics in Cardiomyopathy and Arrhythmia Patients Gained by Stepwise Exome Data Analysis. Journal of clinical medicine, 9(7).

Lekszas C, et al. (2020) Biallelic TANGO1 mutations cause a novel syndromal disease due to hampered cellular collagen secretion. eLife, 9.

Doll J, et al. (2020) A novel missense variant in MYO3A is associated with autosomal dominant high-frequency hearing loss in a German family. Molecular genetics & genomic medicine, 8(8), e1343.

Scheiper-Welling S, et al. (2020) Characterization of an N-terminal Nav1.5 channel variant - a potential risk factor for arrhythmias and sudden death? BMC medical genetics, 21(1), 227.

Doll J, et al. (2020) Genetic Spectrum of Syndromic and Non-Syndromic Hearing Loss in Pakistani Families. Genes, 11(11).

Kariminejad A, et al. (2019) Homozygous Null TBX4 Mutations Lead to Posterior Amelia with Pelvic and Pulmonary Hypoplasia. American journal of human genetics, 105(6), 1294.

Böck J, et al. (2018) Single CpG hypermethylation, allele methylation errors, and decreased expression of multiple tumor suppressor genes in normal body cells of mutation-negative early-onset and high-risk breast cancer patients. International journal of cancer, 143(6), 1416.

Hofrichter MAH, et al. (2018) The conserved p.Arg108 residue in S1PR2 (DFNB68) is fundamental for proper hearing: evidence from a consanguineous Iranian family. BMC medical genetics, 19(1), 81.

Wolf B, et al. (2015) DNAseq Workflow in a Diagnostic Context and an Example of a User Friendly Implementation. BioMed research international, 2015, 403497.