

Resource Summary Report

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NGSEP

RRID:SCR_012827

Type: Tool

Proper Citation

NGSEP (RRID:SCR_012827)

Resource Information

URL: <http://sourceforge.net/projects/ngsep/>

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Description: Software whose main functionality is the variants detector, which allows to make simultaneous discovery of SNVs, small indels, and CNVs. Accurate variant calling across species and sequencing protocols. Used for analysis of DNA high throughput sequencing data.

Abbreviations: NGSEP

Synonyms: NGSEP3, Next Generation Sequencing Eclipse Plugin, Next Generation Sequencing Experience Platform

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

Defining Citation: [PMID:31099384](#)

Keywords: matlab, variants detector, SNVs discovery, CNVs discovery, variant calling, species, sequencing protocols, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: NGSEP

Resource ID: SCR_012827

Alternate IDs: OMICS_00067, biotools:NGSEP

Alternate URLs: <https://bio.tools/NGSEP>

License: GNU General Public License version 3.0

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260731T042851+0000

Ratings and Alerts

No rating or validation information has been found for NGSEP.

No alerts have been found for NGSEP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 69 mentions in open access literature.

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

Gonzalez-Garcia LN, et al. (2025) Genetic diversity and comparative genomics across Leishmania (Viannia) species. Communications biology, 8(1), 925.

Gonzalez-Garcia LN, et al. (2025) Genomic characterization of Leishmania (V.) braziliensis associated with antimony therapeutic failure and variable in vitro tolerance to amphotericin B. Scientific reports, 15(1), 12973.

Cruz-Saavedra L, et al. (2025) Variation in surface protein expression leads to heterogeneous Trypanosoma cruzi populations during host cell infection. Nature communications, 16(1), 9949.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three Ormosia species: repetitive sequences distribution and structural rearrangement. GigaScience, 14.

Mendoza-Bustamante MÁ, et al. (2025) Exploring the genetic factors of nitrogen use efficiency in potato. PloS one, 20(11), e0325578.

Lee YB, et al. (2025) Genetic diversity and population structure analysis of Forsythia ovata, a Korean endemic, based on genotyping-by-sequencing. PloS one, 20(2), e0317278.

Soler-Garzón A, et al. (2025) Mapping resistance to Sclerotinia white mold in two pinto bean recombinant inbred line populations. The plant genome, 18(1), e20538.

Medina CA, et al. (2025) Genome-Wide Association and Genomic Prediction of Alfalfa (Medicago sativa L.) Biomass Yield Under Drought Stress. International journal of molecular sciences, 26(2).

Fuentes L, et al. (2024) Genetic diversity of Anadara tuberculosa in two localities of the Colombian Pacific Coast. Scientific reports, 14(1), 28467.

Ospina JA, et al. (2024) Genome-wide association study of cassava brown streak disease resistance in cassava germplasm conserved in South America. *Scientific reports*, 14(1), 23141.

Hoyos Sanchez MC, et al. (2024) A phased genome assembly of a Colombian *Trypanosoma cruzi* TcI strain and the evolution of gene families. *Scientific reports*, 14(1), 2054.

Izquierdo P, et al. (2024) Genome-wide association and genomic prediction for iron and zinc concentration and iron bioavailability in a collection of yellow dry beans. *Frontiers in genetics*, 15, 1330361.

Garcia-Abadillo J, et al. (2024) Sparse testing designs for optimizing predictive ability in sugarcane populations. *Frontiers in plant science*, 15, 1400000.

Saavedra-Díaz C, et al. (2024) Genetic association analysis in sugarcane (*Saccharum* spp.) for sucrose accumulation in humid environments in Colombia. *BMC plant biology*, 24(1), 570.

Soler-Garzón A, et al. (2024) GWAS of resistance to three bacterial diseases in the Andean common bean diversity panel. *Frontiers in plant science*, 15, 1469381.

Ghidoli M, et al. (2024) Genetic study of *Camelina sativa* oilseed crop and selection of a new variety by the bulk method. *Frontiers in plant science*, 15, 1385332.

Gaitán N, et al. (2024) A graph clustering algorithm for detection and genotyping of structural variants from long reads. *GigaScience*, 13.

Bezandry R, et al. (2024) The evolutionary history of three *Baracoffea* species from western Madagascar revealed by chloroplast and nuclear genomes. *PloS one*, 19(1), e0296362.

Logachev A, et al. (2024) Pangenomics of flax fungal parasite *Fusarium oxysporum* f. sp. lini. *Frontiers in plant science*, 15, 1383914.

Arias CL, et al. (2023) Metabolic and transcriptomic study of pennycress natural variation identifies targets for oil improvement. *Plant biotechnology journal*, 21(9), 1887.