

Resource Summary Report

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Geospiza

RRID:SCR_003264

Type: Tool

Proper Citation

Geospiza (RRID:SCR_003264)

Resource Information

URL: <http://www.geospiza.com/>

Proper Citation: Geospiza (RRID:SCR_003264)

Description: Developer of enterprise-class software systems for workflow management of genetic analysis. Geospiza has established itself as the life science industry's top software developer for meeting the combined laboratory, data management and analytical needs of biotechnology and pharmaceutical companies, universities, researchers, contract core and diagnostic laboratories involved in genetic testing and manufacturing bio-therapeutics. Geospiza's products are designed and built by biologists, enabling researchers to focus on the science, not the software. *GeneSifter Analysis Edition: Access easy-to-use statistical, visualization and annotation tools for Microarray and Next Generation Sequencing data. *GeneSifter Lab Edition: Manage cross-platform core lab operations from a single interface out-of-the-box.

Abbreviations: Geospiza

Synonyms: Geospiza Inc.

Resource Type: material service resource, software resource, production service resource, commercial organization, service resource

Keywords: genetic analysis, microarray, next generation sequencing, data management

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Geospiza

Resource ID: SCR_003264

Alternate IDs: OMICS_01127, nif-0000-31431

Old URLs: <http://www.geospiza.com/finchtv.html>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260819T044102+0000

Ratings and Alerts

No rating or validation information has been found for Geospiza.

No alerts have been found for Geospiza.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 130 mentions in open access literature.

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

Ramadan SI, et al. (2026) Associations of genetic polymorphisms with boldness, stress response, and route efficiency in homing pigeons (*Columba livia*). *Physiology & behavior*, 305, 115211.

Badry A, et al. (2026) DNA Barcoding and Phylogenetic Relationship of *Parabuthus liosoma* (Ehrenberg, 1828) (Scorpiones: Buthidae) in Saudi Arabia. *Biology*, 15(4).

Selcuk MA, et al. (2026) Molecular epidemiology and population genetic diversity of caprine hemoplasmas in Southeastern Türkiye: First detection of *Candidatus Mycoplasma haemovis*. *BMC veterinary research*, 22(1).

Dercksen M, et al. (2025) Diagnosis of Primary Trimethylaminuria in an Affected Patient With a Rare Genotype in Sub-Saharan Africa. *JIMD reports*, 66(2), e70005.

Franzo G, et al. (2025) Porcine reproductive and respiratory syndrome virus 2 in Europe: neither wild nor tamed. *Porcine health management*, 11(1), 62.

Alhnaity HM, et al. (2025) Genetic variants in QRICH2 gene among Jordanians with sperm motility disorders. *The Libyan journal of medicine*, 20(1), 2481741.

Rollins RE, et al. (2025) Analysis of ticks (Acari: Ixodida) and associated microorganisms collected on the North Sea Island of Heligoland. *Parasitology research*, 124(3), 34.

Gunyakti Kilinc S, et al. (2025) Comparative Analysis of Nuclear (Ef1?) and Mitochondrial (mt-CO1 and mt-Nad5) Markers for Molecular Characterization of Sheep Isolates of *Echinococcus granulosus sensu lato*. *Veterinary medicine and science*, 11(2), e70313.

Darlan DM, et al. (2025) Molecular and serological detection of *Leptospira interrogans* among wild rats in flood-prone residential areas of Indonesia. *Open veterinary journal*, 15(1), 437.

Kumar N, et al. (2025) Impact of altitudinal variations on plant growth dynamics, nutritional composition, and free living rhizospheric N₂ fixing bacterial community of *Eruca sativa*. *Scientific reports*, 15(1), 13839.

Sonowal H, et al. (2025) Preclinical Development of Tuspetinib for the Treatment of Acute Myeloid Leukemia. *Cancer research communications*, 5(1), 74.

Dinh QM, et al. (2025) Genetic Relationship and Diversity of *Ellochelon vaigiensis* in the Vietnamese Mekong Delta Using Cytochrome b Gene Sequences. *Ecology and evolution*, 15(6), e71639.

Ceylan O, et al. (2025) Sequence-based analysis of *Theileria annulata* reveals high Tams1 gene diversity and conservation of 18 S rRNA in Türkiye. *BMC veterinary research*, 21(1), 578.

Korsak D, et al. (2025) Characterization of *Cronobacter* spp. isolated from food products in Poland and comparative genomic analysis of *Cronobacter sakazakii* isolate MK_10 and a clinical strain associated with a fatal neonatal infection. *Frontiers in microbiology*, 16, 1713963.

Che Alias MA, et al. (2024) Morphological and genetic identification of *Halophila* species and a new distribution record of *Halophila nipponica* at the Tanjung Adang Laut shoal, Johor, Malaysia. *PloS one*, 19(10), e0309143.

Lea V, et al. (2024) Toward the Development of the Trojan Female Technique in Pest Insects: Male-Specific Influence of Mitochondrial Haplotype on Reproductive Output in the Seed Beetle *Acanthoscelides obtectus*. *Evolutionary applications*, 17(12), e70065.

Kisielinski K, et al. (2024) The bacterial burden of worn face masks-observational research and literature review. *Frontiers in public health*, 12, 1460981.

Suhendro I, et al. (2024) Association of heat-shock protein 70.1 gene with physiological and physical performance of Bali cattle. *Veterinary world*, 17(1), 17.

Jaiswal P, et al. (2024) Morphological and Molecular Characterization of *Trichoderma* Isolates from Vegetable Crop Rhizospheres in Nepal. *F1000Research*, 13, 1088.

Karakoc S, et al. (2024) Genetic diversity and haplotypes of *Cysticercus tenuicollis* isolates from slaughtered sheep and goats in Elazig and Bingol provinces of Turkey. *Veterinary medicine and science*, 10(4), e1411.