Resource Summary Report

Generated by kravitz2 on Sep 18, 2026

SeqScape Software

RRID:SCR_001604
Type: Tool

Proper Citation

SeqScape Software (RRID:SCR_001604)

Resource Information

URL: http://www.lifetechnologies.com/order/catalog/product/4327091

Proper Citation: SeqScape Software (RRID:SCR_001604)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on March 28, 2017. A resequencing package designed for mutation detection and analysis, SNP discovery and validation, pathogen sub-typing, allele identification and sequence confirmation.

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

Keywords: mutation, sequencing, thermofisher scientific, snp, pathogen sub-typing

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SeqScape Software

Resource ID: SCR_001604

Alternate IDs: OMICS_01819

Alternate URLs: http://www.thermofisher.com/order/catalog/product/4327091

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260912T195528+0000

Ratings and Alerts

No rating or validation information has been found for SeqScape Software.

No alerts have been found for SeqScape Software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 543 mentions in open access literature.

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

Emeru BA, et al. (2025) Newcastle disease virus genotype VII.1.1 identified from backyard chickens with low antibody titer: Jimma Zone, Southwest Ethiopia. BMC veterinary research, 21(1), 23.

Rubino E, et al. (2025) Exome sequencing reveals a rare damaging variant in GRIN2C in familial late-onset Alzheimer's disease. Alzheimer's research & therapy, 17(1), 21.

Nka AD, et al. (2025) Tenofovir and Doravirine Are Potential Reverse-Transcriptase Analogs in Combination with the New Reverse-Transcriptase Translocation Inhibitor (Islatravir) Among Treatment-Experienced Patients in Cameroon: Designing Future Treatment Strategies for Low- and Middle-Income Countries. Viruses, 17(1).

Binder C, et al. (2024) His108Arg Transthyretin Amyloidosis-Shedding Light on a Distinctively Malignant Variant. Journal of clinical medicine, 13(24).

Juul-Madsen K, et al. (2024) Amyloid-? aggregates activate peripheral monocytes in mild cognitive impairment. Nature communications, 15(1), 1224.

Knoll A, et al. (2024) Haplotype Diversity in mtDNA of Honeybee in the Czech Republic Confirms Complete Replacement of Autochthonous Population with the C Lineage. Insects, 15(7).

Silverj A, et al. (2024) Origin and evolution of West Nile virus lineage 1 in Italy. Epidemiology and infection, 152, e150.

Buchholtz NVEJ, et al. (2024) Development of a highly sensitive and specific intact proviral DNA assay for HIV-1 subtype B and C. Virology journal, 21(1), 36.

Gautheron J, et al. (2024) ADH1B, the adipocyte-enriched alcohol dehydrogenase, plays an essential, cell-autonomous role in human adipogenesis. Proceedings of the National Academy of Sciences of the United States of America, 121(24), e2319301121.

Molitor A, et al. (2024) A pleiotropic recurrent dominant ITPR3 variant causes a complex multisystemic disease. Science advances, 10(37), eado5545.

Selvatici R, et al. (2024) Relevance of Next-Generation Sequencing in the Diagnosis of Thalassemia and Hemoglobinopathies: The Experience of Four Italian Diagnostic Hubs. Genes, 16(1).

Cho E, et al. (2024) Frequency of Fabry disease in chronic kidney disease patients including patients on renal replacement therapy in Korea. Kidney research and clinical

practice, 43(1), 71.

Votsi C, et al. (2024) RFC1 Repeat Distribution in the Cypriot Population: Study of a Large Cohort of Patients With Undiagnosed Ataxia and Non-Disease Controls. Neurology. Genetics, 10(3), e200149.

Nguidi M, et al. (2024) Impact of patrilocality on contrasting patterns of paternal and maternal heritage in Central-West Africa. Scientific reports, 14(1), 15653.

Kamali K, et al. (2024) Integrating phylogenetic, phylogeographic, and morphometric analyses to reveal cryptic lineages within the genus Asaccus (Reptilia: Squamata: Phyllodactylidae) in Iran. BMC zoology, 9(1), 12.

Hany U, et al. (2024) Heterozygous COL17A1 variants are a frequent cause of amelogenesis imperfecta. Journal of medical genetics, 61(4), 347.

Pérez-Serra A, et al. (2024) Implementing a New Algorithm for Reinterpretation of Ambiguous Variants in Genetic Dilated Cardiomyopathy. International journal of molecular sciences, 25(7).

Pacot L, et al. (2024) Prenatal diagnosis for neurofibromatosis type 1 and the pitfalls of germline mosaics. NPJ genomic medicine, 9(1), 41.

Zhang J, et al. (2024) Simultaneous high throughput genotyping of 36 blood group systems using NGS based on probe capture technology. Heliyon, 10(13), e33608.

Ek T, et al. (2024) Long-Lasting Response to Lorlatinib in Patients with ALK-Driven Relapsed or Refractory Neuroblastoma Monitored with Circulating Tumor DNA Analysis. Cancer research communications, 4(9), 2553.