# Resource Summary Report

Generated by dkNET on Apr 29, 2025

## 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 processing software, sequence analysis software, data analysis software, software resource, software application

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

**Funding:**

**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:** 20250429T054651+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 dkNET.


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.

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).

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.

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

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

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

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).

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).

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.

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.

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.

Kumar AKH, et al. (2024) Effect of Metformin on Plasma Exposure of Rifampicin, Isoniazid, and Pyrazinamide in Patients on Treatment for Pulmonary Tuberculosis. Therapeutic drug monitoring, 46(3), 370.

Neto A, et al. (2024) Thermostability study of virulent Newcastle disease viruses isolated in Southern Angola. The Onderstepoort journal of veterinary research, 91(1), e1.

Zhang H, et al. (2024) Scaled and Efficient Derivation of Loss of Function Alleles in Risk Genes for Neurodevelopmental and Psychiatric Disorders in Human iPSC. bioRxiv : the preprint server for biology.

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).