Resource Summary Report

Generated by T1D on Aug 4, 2026

LifeScope

RRID:SCR_013234
Type: Tool

Proper Citation

LifeScope (RRID:SCR_013234)

Resource Information

URL: http://www.lifetechnologies.com/fr/fr/home/technical-resources/software-downloads/lifescope-genomic-analysis-software.html

Proper Citation: LifeScope (RRID:SCR_013234)

Description: Genomic Analysis Software designed to match the accuracy of the next generation 5500 Genetic Analyzers with Exact Call Chemistry (ECC).

Abbreviations: LifeScope

Synonyms: LifeScope Genomic Analysis Software

Resource Type: software resource

Keywords: unix/linux, life technologies, linux, next-generation sequencing

Availability: Acknowledgement requested

Resource Name: LifeScope

Resource ID: SCR_013234

Alternate IDs: OMICS_00667

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260801T190457+0000

Ratings and Alerts

No rating or validation information has been found for LifeScope.

No alerts have been found for LifeScope.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 199 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Li C, et al. (2025) Ferrostatin-1 inhibits tracheal basal cell ferroptosis to facilitate the rapid epithelization of 3D-printed tissue-engineered tracheas. Stem cell research & therapy, 16(1), 147.

Preda MB, et al. (2025) miR-210 locus deletion disrupts cellular homeostasis: an integrated genetic study. Scientific reports, 15(1), 22659.

Zhou H, et al. (2024) Light regulates nuclear detainment of intron-retained transcripts through COP1-spliceosome to modulate photomorphogenesis. Nature communications, 15(1), 5130.

Schmitz AS, et al. (2024) Novel variants in CSF1R associated with adult-onset leukoencephalopathy with axonal spheroids and pigmented glia (ALSP). Journal of neurology, 271(9), 6025.

Wang J, et al. (2024) Deficiency of autism susceptibility gene Trio in cerebellar Purkinje cells leads to delayed motor impairments. Frontiers in psychiatry, 15, 1396716.

Wirkus JM, et al. (2024) Changes of pulse wave transit time after haemodynamic manoeuvres in healthy adults: a prospective randomised observational trial (PWTT volunteer study). BJA open, 11, 100291.

Buck TM, et al. (2023) CRB1 is required for recycling by RAB11A+ vesicles in human retinal organoids. Stem cell reports, 18(9), 1793.

Kinmonth-Schultz H, et al. (2023) Oligosaccharide production and signaling correlate with delayed flowering in an Arabidopsis genotype grown and selected in high [CO2]. PloS one, 18(12), e0287943.

Martin Cerezo ML, et al. (2023) Population structure and hybridisation in a population of Hawaiian feral chickens. Heredity, 130(3), 154.

Tropitzsch A, et al. (2022) Diagnostic Yield of Targeted Hearing Loss Gene Panel Sequencing in a Large German Cohort With a Balanced Age Distribution from a Single Diagnostic Center: An Eight-year Study. Ear and hearing, 43(3), 1049.

Kulkarni P, et al. (2022) Mast Cells Differentiated in Synovial Fluid and Resident in Osteophytes Exalt the Inflammatory Pathology of Osteoarthritis. International journal of molecular sciences, 23(1).

Carrell AA, et al. (2022) Novel metabolic interactions and environmental conditions mediate the boreal peatmoss-cyanobacteria mutualism. The ISME journal, 16(4), 1074.

Kim EJ, et al. (2022) ZEB1-regulated lnc-Nr2f1 promotes the migration and invasion of lung adenocarcinoma cells. Cancer letters, 533, 215601.

Fot EV, et al. (2022) Invasive and Non-invasive Dynamic Parameters to Predict Fluid Responsiveness After Off-pump Coronary Surgery. Turkish journal of anaesthesiology and reanimation, 50(1), 59.

Sharma KL, et al. (2021) Mitogen-induced transcriptional programming in human fibroblasts. Gene, 800, 145842.

Blythe MJ, et al. (2021) LINE-1 transcription in round spermatids is associated with accretion of 5-carboxylcytosine in their open reading frames. Communications biology, 4(1), 691.

Fern??ndez-Rozadilla C, et al. (2021) Exome sequencing of early-onset patients supports genetic heterogeneity in colorectal cancer. Scientific reports, 11(1), 11135.

Linders PTA, et al. (2021) Congenital disorder of glycosylation caused by starting site-specific variant in syntaxin-5. Nature communications, 12(1), 6227.

Fritz D, et al. (2021) Whole genome sequencing identifies variants associated with sarcoidosis in a family with a high prevalence of sarcoidosis. Clinical rheumatology, 40(9), 3735.

Lo Iacono L, et al. (2021) Early life adversity affecting the attachment bond alters ventral tegmental area transcriptomic patterning and behavior almost exclusively in female mice. Neurobiology of stress, 15, 100406.