Resource Summary Report

Generated by RRID on Aug 6, 2026

Prayoga: GenapSys Sequencer

RRID:SCR_017991
Type: Tool

Proper Citation

Prayoga: GenapSys Sequencer (RRID:SCR_017991)

Resource Information

URL: https://www.prayogalifesciences.com/genapsys_sequencer/

Proper Citation: Prayoga: GenapSys Sequencer (RRID:SCR_017991)

Description: Compact sequencer for DNA sequencing by GenapSys, Inc. Sequencing is carried out on microfluidic chips that have scalable number of detectors, allowing for applications ranging from targeted sequencing of specific amplicons to genome-scale data collection. System utilizes electrical sequencing chip., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: instrument resource

Defining Citation: DOI:10.1101/604553

Keywords: sequencing machine, hardware, high-throughput sequencing, instrument, equipment

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Prayoga: GenapSys Sequencer

Resource ID: SCR_017991

Alternate URLs: https://www.sopachem.com/lifesciences/wp-content/uploads/2020/04/GenapSys-Sequencer-Specification-Sheet.pdf

Old URLs: https://www.genapsys.com/products/

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260801T190609+0000

Ratings and Alerts

No rating or validation information has been found for Prayoga: GenapSys Sequencer.

No alerts have been found for Prayoga: GenapSys Sequencer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Lev A, et al. (2019) Reduced Function and Diversity of T Cell Repertoire and Distinct Clinical Course in Patients With IL7RA Mutation. Frontiers in immunology, 10, 1672.

Simon AJ, et al. (2016) Mutations in STN1 cause Coats plus syndrome and are associated with genomic and telomere defects. The Journal of experimental medicine, 213(8), 1429.

Lambert AJ, et al. (2015) Comparative sequence analyses of La Crosse virus strain isolated from patient with fatal encephalitis, Tennessee, USA. Emerging infectious diseases, 21(5), 833.

Evangelisti C, et al. (2015) A mutation screening of oncogenes, tumor suppressor gene TP53 and nuclear encoded mitochondrial complex I genes in oncocytic thyroid tumors. BMC cancer, 15, 157.

Zhang W, et al. (2014) Identification and characterization of a novel HIV-1 circulating recombinant form (CRF59_01B) identified among men-who-have-sex-with-men in China. PloS one, 9(6), e99693.

Oh BY, et al. (2011) Epidermal growth factor receptor mutations in colorectal cancer patients. Journal of the Korean Society of Coloproctology, 27(3), 127.

Nouws J, et al. (2010) Acyl-CoA dehydrogenase 9 is required for the biogenesis of oxidative phosphorylation complex I. Cell metabolism, 12(3), 283.

Munshi-South J, et al. (2008) Female-biased dispersal and gene flow in a behaviorally monogamous mammal, the large treeshrew (Tupaia tana). PloS one, 3(9), e3228.

Kim DW, et al. (2008) High tumour islet macrophage infiltration correlates with improved patient survival but not with EGFR mutations, gene copy number or protein expression in resected non-small cell lung cancer. British journal of cancer, 98(6), 1118.

Hemmerter S, et al. (2007) A curious coincidence: mosquito biodiversity and the limits of the Japanese encephalitis virus in Australasia. BMC evolutionary biology, 7, 100.

Yoshinari S, et al. (2006) Archaeal pre-mRNA splicing: a connection to hetero-oligomeric splicing endonuclease. Biochemical and biophysical research communications, 346(3),

1024.

Ren P, et al. (2005) Genomic organization and expression of 23 new genes from MATalpha locus of Cryptococcus neoformans var. gattii. Biochemical and biophysical research communications, 326(1), 233.

Yang JJ, et al. (2005) Hearing loss associated with enlarged vestibular aqueduct and Mondini dysplasia is caused by splice-site mutation in the PDS gene. Hearing research, 199(1-2), 22.

Lemos B, et al. (2004) Phylogenetic footprinting reveals extensive conservation of Sonic Hedgehog (SHH) regulatory elements. Genomics, 84(3), 511.