

Resource Summary Report

Generated by T1D on Aug 1, 2026

Wafergen: Apollo 324 NGS Library Prep

RRID:SCR_018027

Type: Tool

Proper Citation

Wafergen: Apollo 324 NGS Library Prep (RRID:SCR_018027)

Resource Information

URL: http://www.thunderbiosci.co.kr/wp-content/uploads/2017/07/Apollo-324_brochure.pdf

Proper Citation: Wafergen: Apollo 324 NGS Library Prep (RRID:SCR_018027)

Description: Compact benchtop platform that enables rapid and full walk-away automation of next generation sequencing applications. Paired with PrepX reagents, Apollo 324 line offers complete sample-to-answer solution for NGS library prep. Apollo 324 automated protocols and PrepX reagent kits combine liquid handling and proven chemistries to produce high quality libraries for all major NGS platforms. System provides complete, walkaway solution using validated protocols and chemistries that produce consistent libraries for DNA-seq, RNA-seq, and ChIP-seq applications.

Synonyms: Apollo 324 NGS Library Prep System, Apollo 324 NGS Library Prep Robot

Resource Type: instrument resource

Keywords: ABRF, Library Preparation System, Wafergen Biosystems, next generation sequencing, DNA-seq, RNA-seq, CHIP-seq, instrument, equipment

Specification URL: https://raw.githubusercontent.com/SciCrunch/RRID-Instruments/main/PDF/SCR_018027.pdf

Resource Name: Wafergen: Apollo 324 NGS Library Prep

Resource ID: SCR_018027

Alternate IDs: Model_Number_324

Alternate URLs: http://www.thunderbiosci.co.kr/wp-content/uploads/2017/07/Apollo-324_brochure.pdf

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260725T190843+0000

Ratings and Alerts

No rating or validation information has been found for Wafergen: Apollo 324 NGS Library Prep.

No alerts have been found for Wafergen: Apollo 324 NGS Library Prep.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Li Y, et al. (2024) Detection of Hybrid Fusion Transcripts, Aberrant Transcript Expression, and Specific Single Nucleotide Variants in Acute Leukemia and Myeloid Disorders with Recurrent Gene Rearrangements. Pathobiology : journal of immunopathology, molecular and cellular biology, 91(1), 76.