



Automated NGS Library Preparation Workstation. Simple and Fast



SynplStation 2400+

SynplStation 2400+ is a flexibleandefficient Automated Library Preparation Workstation. With its sophisticated design and built-in modules, it can complete all steps of

Next-Generation Sequencing (NGS) library preparation, free you from repetitive operations and significantly save your time.

APPLICATION

Comprehensive, Customized, Stable and Sophisticated Automated Library Preparation Workstation Ideal choice for NGS automation in infectious diseases, tumors, genetic diseases, etc.

FUNCTION

Fragmentation Washing Purification Purification End Repair A-tailing 04 02 06 08 01 03 05 07 09 Nucleic Acid Adaptor Amplification Hybridization Sequencing Extraction Ligation

SynplStation 2400+

PARAMETER

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Dimension (Length×Widt)	h×Height)	800mm×808mm×826mm
Throughput		1-24 Samples
Deck Capacity		16 Standard Position
PCR Module	Туре	Built-in
FCK Module	Temp. Accuracy	±0.2°C
	Temperature Control Module	2 (4-90°C)
Number of Modules	Shaker	1
Number of Modules	Magnetic Plate	1
	Auto Magnetic Plate	1
	Туре	Fixed 8 Channel
Pipette	Range	2-200µl
	CV	200µl CV<1%, 2µl CV<5%



FEATURE

Comprehensive

Built-in PCR module Capable of library preparation and target enrichment

Customized

1-24 samples per runUser-Friendly softwareCompatible with various librarypreparation reagentsSupport customized applications

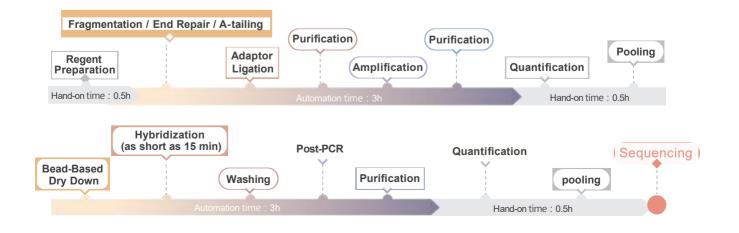
Stable

Good reproducibility High stability and success rate HEPA system and UV lamp

Sophisticated

Optimal deck layout design Efficient pipetting route planning Faster and more reliable

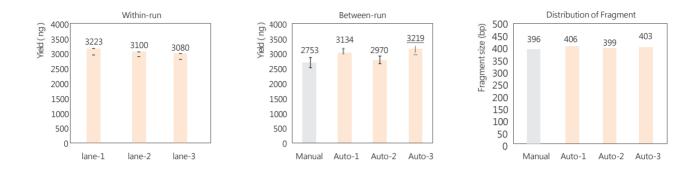
ACTUAL RUNTIME



I RESULTS

Library Preparation

50ng Human genomic DNA was used for library preparation through SynplStation 2400+ and manual operation. Library preparation kit: SynplSeq DNA library prep EF kit for Illumina.



Target Enrichment

After normalization, two human genomic DNA libraries were hybridized with a custom panel(610K) for 2 hours using Fast hybridization and wash kit.

Libraries sequenced on Novaseq, with sequencing data normalized to 150× raw data for analysis.

	Sample	Q30	Pct_Selected Bases	Fold_80_ Base_Penalty	Mean_Bait_ Coverage	Mean_Tamrget _Coverage	Pct_Target_ Bases_20X	Pct_Target_ Bases_30X	AT_ Dropout	GC_ Dropout
Manual	Lib1	0.922	0.78	1.49	83.16	55.22	0.959	0.883	0.234	7.744
Auto-1	Lib3	0.923	0.90	1.41	84.87	61.97	0.973	0.929	0.555	4.061
Auto-1	Lib4	0.918	0.88	1.44	83.51	60.38	0.969	0.920	0.538	4.068
Auto-2	Lib5	0.920	0.82	1.55	80.04	58.76	0.957	0.888	0.409	8.424
Auto-2	Lib6	0.918	0.84	1.54	81.09	60.10	0.964	0.898	0.475	8.218
	Lib7	0.923	0.87	1.39	80.35	54.24	0.972	0.915	0.875	1.949
Auto-3	Lib8	0.925	0.87	1.4	80.52	54.46	0.974	0.916	0.814	2.017

ORDER INFORMATION

Cat. No.	Product	Unit	
XS-S-001	SynplStation 2400	set	
XS-S-002	SynplStation 2400+	set	
	※ SynplStation 2400 can not complete h	ybridization and capture steps.	
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 $\,\,$ % If you have any needs, please consult local agent for details.