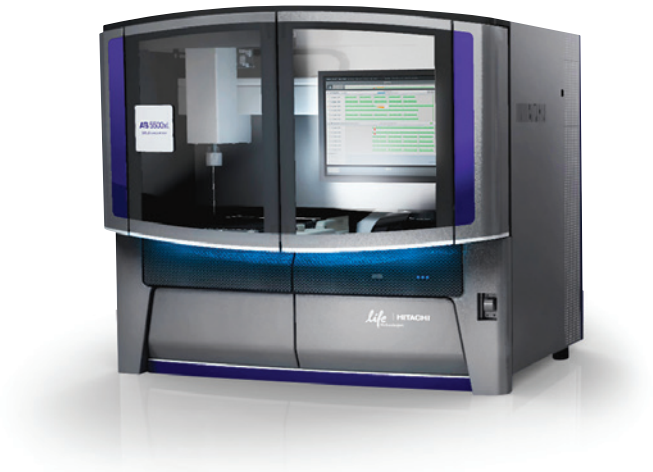
5500 W SERIES GENETIC ANALYZERS

Wildfire technology provides radical improvements in cost, simplicity and throughput



Key advancements

Lower cost
Up to 50% savings in running cost with direct library amplification

Simplified workflow
Template preparation reduced to 1/4 the time by replacing beads with direct amplification on FlowChip

Increased throughput
Faster time to result from high density sequencing colonies that provide 2–4X higher throughput

Wildfire technology radically simplifies template preparation, reducing the time required from approximately 8 hours to 2 hours, typically with less than 30 minutes of hands-on time. The template preparation is powered by direct library amplification on the FlowChip with an isothermal step (Figure 1). This results in reduction of up to 50% in template preparation cost. Wildfire sequencing colonies also enable higher densities and more efficient sequencing chemistry, facilitating increased throughput on 5500 W Series Genetic Analyzers.

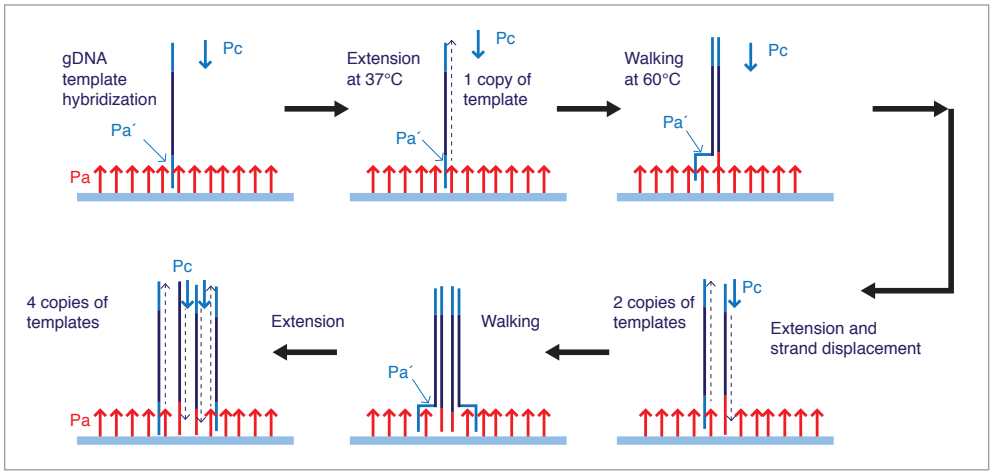


Figure 1. Overview of the Wildfire template walking process.

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5500 W Series Genetic Analyzer V2.0 specifications*

System and features	5500 W System (1 FlowChip)	5500xl W System* (2 FlowChips)
Pay-per-lane sequencing	Reagent consumption engineered independently for each lane; users pay only for the consumables in the active lanes when performing a partial run.	
Application-per-lane sequencing	Independent FlowChip lanes allow users to configure read length of chemistry for each lane, enabling multiple applications in a single run.	
Multiplexing	96 barcodes for both RNA and DNA applications	
Instrument throughput[1] 1 x 50 1 x 75 2 x 50 MP 50 x 50 Paired-End	 ~ 80 Gb ~ 120Gb ~ 160 Gb ~160 Gb	 ~ 160 Gb ~ 240 Gb ~ 320 Gb ~ 320 Gb
Exomes/run[2]	Up to 18	Up to 36
Transcriptomes/run[3]	Up to 12	Up to 24
Small RNA/run[4]	Up to 144	Up to 288
Maximum read lengths[5]	1 x 75 Frag, 2 x 50 MP, 50 x 50 Paired-End	

1. Instrument throughput is estimated using typical runs at a density of 700,000/panel, 65%–70% passing filter. Actual throughput will depend on the samples being run. Throughput uses the quality reads from the instrument that pass the primary analysis filter.
2. ~50 Mb exome, >100x average coverage using fragment chemistry, 1 x 75 bp run.
3. Transcriptome assumes > 100 million reads/sample using fragment chemistry, 1x 50 bp run.
4. ~8 million reads/sample for each small-RNA sample and utilizing barcodes (48).
5. Paired-End mapping percentage is ~45%.

Ordering information

Product	Cat. No.
5500xl W Instrument	4473730
5500 to 5500 W Upgrade	4473719
5500xl to 5500xl W Upgrade	4473720
5500 to 5500 W with PC Upgrade	4476693
5500xl to 5500xl W with PC Upgrade	4476634
5500 W Computer Upgrade Kit	4476413
5500 to 5500 W with PC and PE Upgrade	4481471
5500xl to 5500xl W with PC and PE Upgrade	4481479

Visit **lifetechnologies.com/5500w** to learn more about the 5500 W Series Genetic Analyzers and related products

*The content provided herein may relate to products that have not been officially released and is subject to change without notice.

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