

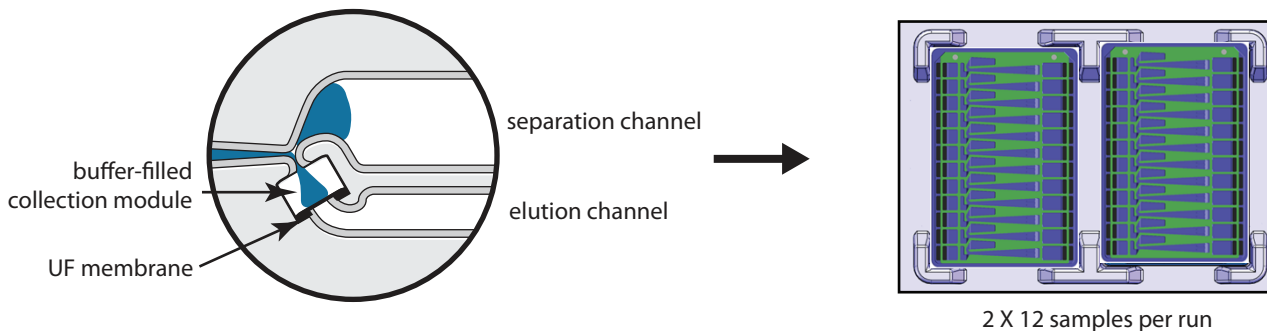
## Collect up to 24 Size-Selected DNA Fractions in 30 Minutes

### Benefits:

- Generates higher-quality libraries for improved sequence informatics
- Fragment sizes and ranges are reproducibly collected, providing consistent results, run-to-run
- Flexible programming allows collection of multiple size ranges, or up to 24 collections of the same fragment range



### Automated Preparative Electrophoresis



Sage Science's proprietary technology, featuring electro-elution from agarose, has been configured to run 12 samples on an SBS-footprint gel cassette— **for higher-throughput workflows and with a lower cost per sample.**

### Specifications:

Sample Capacity	Maximum Sample Load	Run Times	Target Range	Min. Size Distribution as Expressed by (CV)	Accuracy*	Reproducibility**
12 samples/cassette	1.5 µg	25-50 minutes	90 - 2000 bp	≤8%	≥ 90%	≥ 90%
2 cassettes (24 samples)/run		40 min for 500 bp				

\* 100% minus the deviation of actual target value (Agilent Bioanalyzer) from software input value divided by the actual value.

\*\* 100% minus 2X standard deviation of replicate samples.

# Take Good Care of Your Library.



## Automated size selection: An indispensable tool for NGS

### Selected References Citing Pippin DNA Size Selection

#### Paired-End Sequencing

Sheaffer, K.L. *et al.*, DNA methylation is required for the control of stem cell differentiation in the small intestine. *Genes Dev.* 28: 652-664 (2014)

#### Mate-Pair Sequencing

Srivastava, A. *et al.*, Discovery of transgene insertion sites by high throughput sequencing of mate pair libraries. *BMC Genomics.* 15:367 (2014)

#### Long-Read Sequencing

Benson, M.A. *et al.*, Evolution of hypervirulence by a MRSA clone through acquisition of a transposable element. *Molecular Microbiology* 93(4), 664-681 (2014)

#### miRNA Isolation

Singhal, R. *et al.* FOXO1 regulates expression of a microRNA cluster on X chromosome. *AGING*, 5:5. (2013)

#### ChIP-seq

Wharton, K., *et al.*, Methylation and Next-Generation Sequencing of free circulating DNA from human plasma. *BMC Genomics*, 15:476 (2014)

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