Rapid EZ DNA-Seq.

PRODUCT SHEET

Simple and robust PCR-free solution for DNA-Seq libraries

The Rapid EZ DNA-Seq library preparation kit is an end-to-end solution for generating PCR-free NGS libraries in 2.5 hours. This kit with optimization-free, robust enzymatic fragmentation and DimerFree® library construction is suitable for a wide range of sequencing applications, and is particularly useful for applications sensitive to PCR bias or PCR artifacts, such as microbiome and prokaryotic samples, or sequencing of GC- or AT-rich regions of the human genome.

Why use Rapid EZ DNA-Seq library preparation kit?

1. Single kit provides all the reagents necessary for PCR-free NGS library preparation, including pre-plated adaptors
2. Short, 'add and incubate' workflow can be completed in 2.5 hours
3. Flexible and robust enzymatic fragmentation to generate insert sizes from 200-500 bp, without optimization
4. Up to 96 Unique Dual Index (UDI) adaptors for flexible multiplexing
5. Eliminate adaptor dimers without adaptor titration – regardless of sample input – using DimerFree technology
6. PCR-free workflow enables high quality data for any sample type, including microbial genomes with a broad range of GC content

Applications

- Whole genome sequencing with varied GC content
- Whole genome metagenomics
- Amplicon sequencing
- PCR-free libraries

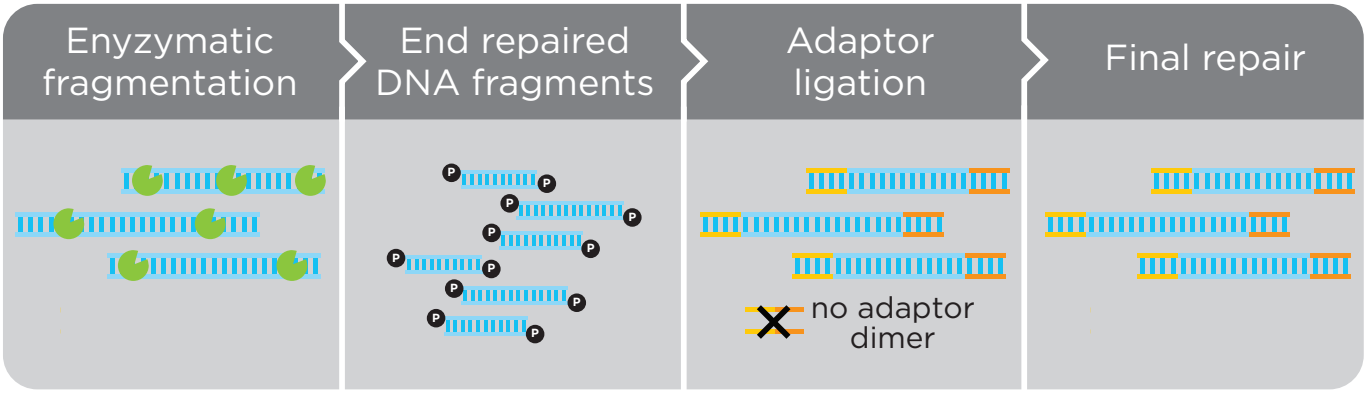


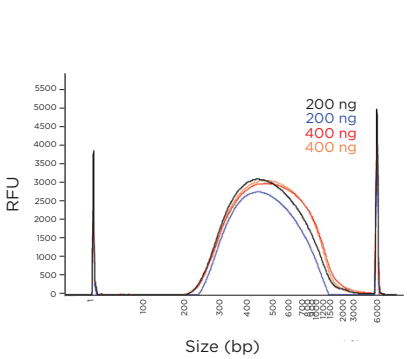
Figure 1: Rapid EZ DNA-Seq library preparation kit integrates robust enzymatic fragmentation for a simple PCR-free workflow.

Tecan's enzymatic fragmentation:

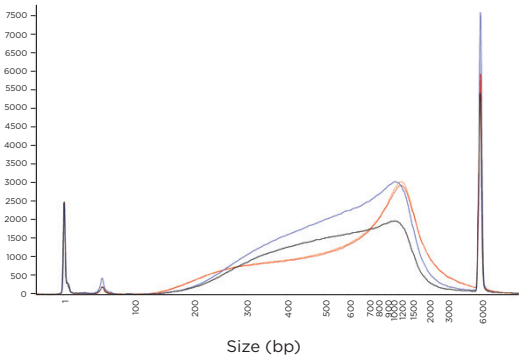
Our enzymatic fragmentation technology is a simple, robust and consistent method for fragmentation of genomic DNA into homologous sized fragments, suitable for a broad range of sequencing applications.

This technology provides greatly improved fragmentation without optimization, outperforming competitor kits for a broad range of sample types and concentrations to provide the best possible starting material for your sequencing protocol.

2A: Tecan's enzymatic fragmentation, 20 mins



2B: QiaSeq FX enzymatic fragmentation, 8-10 mins



2C: Kapa HP enzymatic fragementation, 17mins

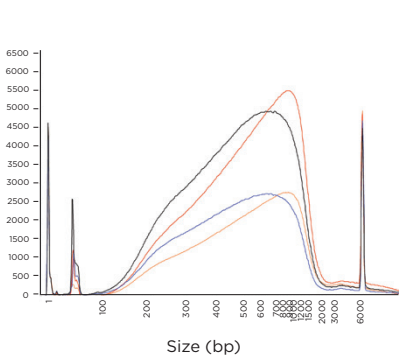


Figure 2: Comparison of the final library traces generated with kits from various vendors at different input ranges, demonstrating the consistency and robustness of Tecan's enzymatic fragmentation technology. Competitors' libraries show under fragmentation and inconsistent fragmentation across replicates after optimization. Primer dimer peaks were also observed with QiaSeq FX and Kapa HP workflows (Figures 2B and 2C) which would require an additional bead clean-up step. Tecan's enzymatic fragmentation (Figure 2A) yields consistent fragment sizes without the need for optimization, regardless of input. (Human NA12878 samples 200 and 400 ng input in replicates, fragmented to 300 bp insert size).

	Sample input	Total reads	*S. aureus* fraction of total aligned	*S. aureus* uniformity	*E. coli* fraction of total aligned	*E. coli* uniformity	*R. sphaeroides* fraction of total aligned	*R. sphaeroides* uniformity	Avg insert size
Sample 1a	200 ng	2124866	35.22%	1	31.27%	0.996	33.51%	0.9998	267
Sample 1b	200 ng	2116963	35.09%	1	31.30%	0.996	33.60%	0.9999	269
Sample 2a	400 ng	1939499	35.19%	1	31.41%	0.996	33.40%	0.9998	266
Sample 2b	400 ng	1983577	34.94%	1	31.33%	0.996	33.74%	0.9998	266
Sample 3a	500 ng	2307945	34.63%	1	31.47%	0.996	33.89%	0.9998	267
Sample 3b	500 ng	2753734	34.99%	1	31.43%	0.996	33.59%	0.9998	275

Table 1: DNA-Seq libraries from equimolar mixture of 3 bacterial blend samples with varying GC content (*S. aureus* - 33% GC, *E. coli* – 50% GC, *R. sphaeroides* – 69% GC) at different inputs (200 ng – 500 ng) were prepared using Rapid EZ kit. The sequencing data of Rapid EZ libraries demonstrate that the bacterial strains are equally well represented across replicates and different inputs in the samples with nearly perfect uniformity of coverage for each strain in a mixed bacterial sample.

Technical details

- Input: 200 to 500 ng intact DNA
- Up to 96 Unique Dual Index adaptors available
- Automation-friendly workflow
- Compatible with Illumina sequencing platforms

Ordering information

Product Name	Part no.	No. of reactions	Barcodes
Rapid EZ DNA-Seq	0567-24	24	1-24
Rapid EZ DNA-Seq	0567-A01	96	1-96

www.tecan.com

For Research Use Only. Not for use in diagnostic procedures.

Australia +61 3 9647 4100 **Austria** +43 62 46 89 330 **Belgium** +32 15 42 13 19 **China** +86 21 220 63 206 **France** +33 4 72 76 04 80 **Germany** +49 79 51 94 170 **Italy** +39 02 92 44 790 **Japan** +81 44 556 73 11 **Netherlands** +31 18 34 48 17 4 **Nordic** +46 8 750 39 40 **Singapore** +65 644 41 886 **Spain** +34 93 595 25 31 **Switzerland** +41 44 922 89 22 **UK** +44 118 9300 300 **USA** +1 919 361 5200 **Other countries** +41 44 922 81 11

401546 V 1.0, 2020-05