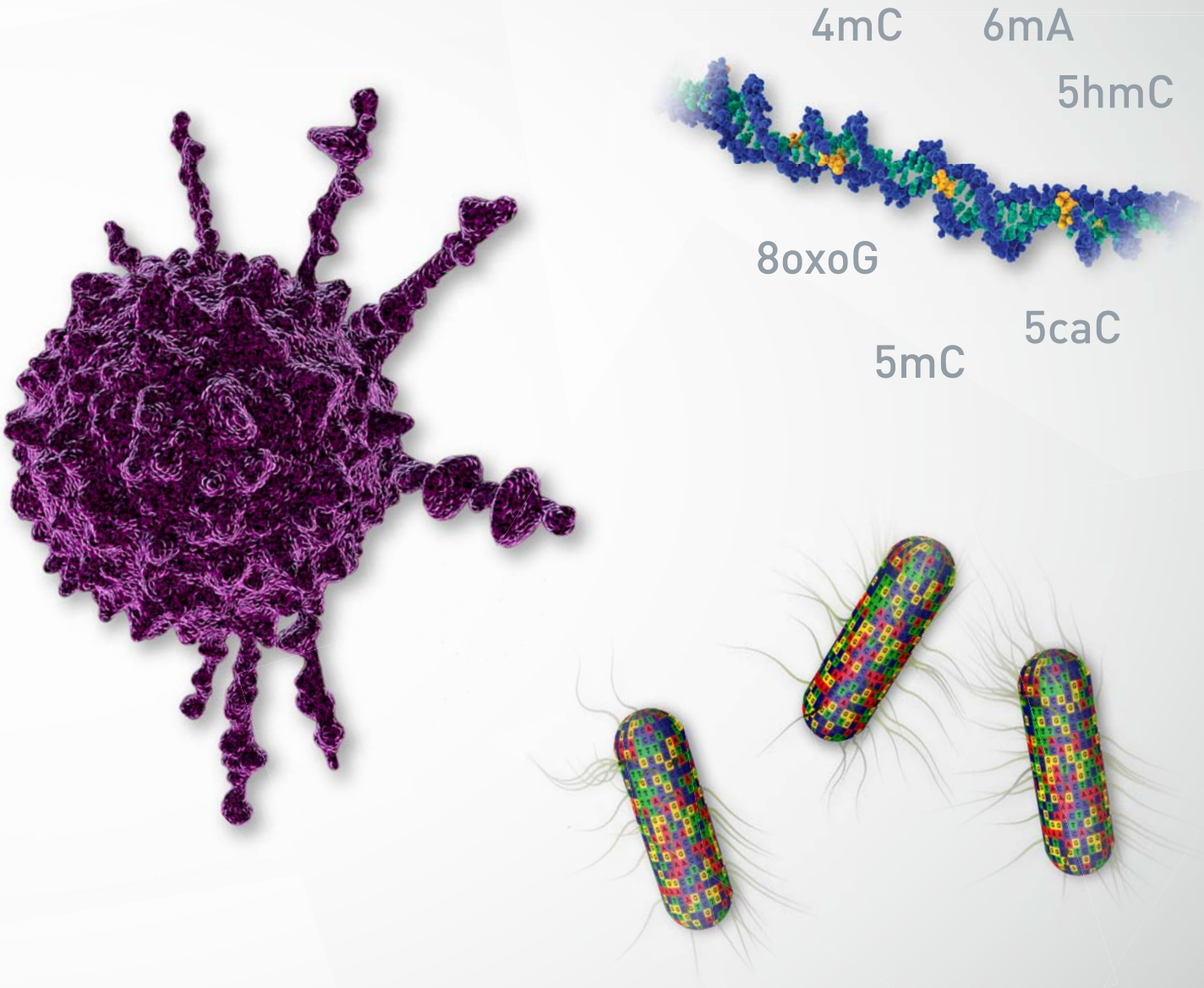
PACIFIC BIOSCIENCES®

PacBio RS II Sequencing System



FIND MEANING IN COMPLEXITY

Genome finishing • Epigenetics • Haplotype phasing

Repeat expansions • Full-length transcripts • Minor variants

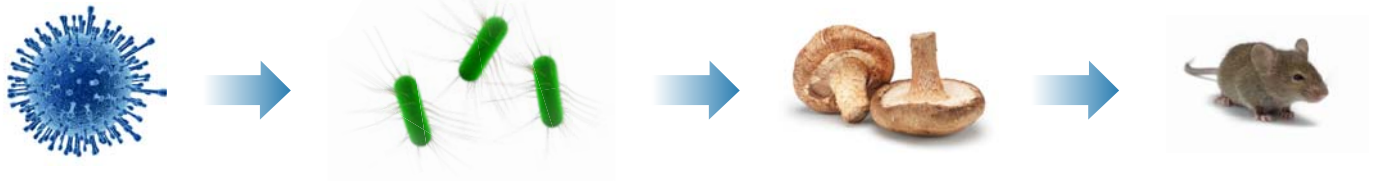
Extraordinary Read Lengths with the PacBio RS II

The PacBio® RS II sequencing system allows scientists to rapidly and cost effectively generate finished genome assemblies, reveal and understand epigenomes, and characterize genomic variation. It achieves the industry's longest read lengths and highest consensus accuracy.

Generate Finished Genomes

The PacBio RS II finishes microbial genomes and improves assembly of larger organisms with multi-kilobase reads and unbiased coverage regardless of GC content. No amplification is required.

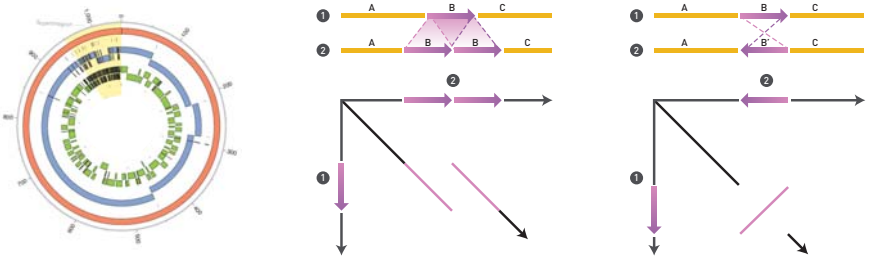
Range of Genome Sizes



Viruses / BACs | Bacteria | Lower Eukaryotes | Higher Eukaryotes

Benefits

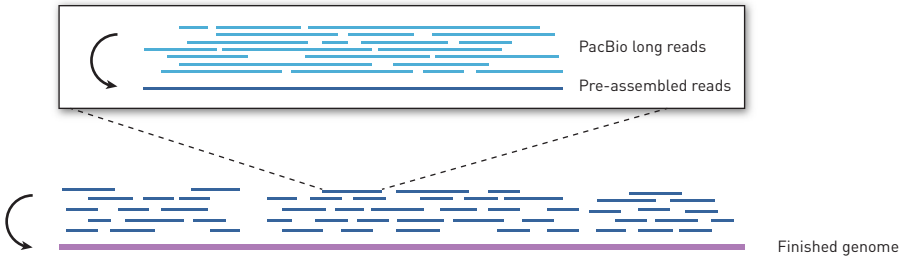
- Highest N50
- Fewest contigs
- Detect structural variation
- 99.999% accuracy
- Genome finishing at 1/10th the cost



Finished bacterial genome | Tandem duplication | Inversion

De Novo Assembly Methods

- Hierarchical Assembly
- Hybrid Assembly
- Scaffolding
- Gap Filling



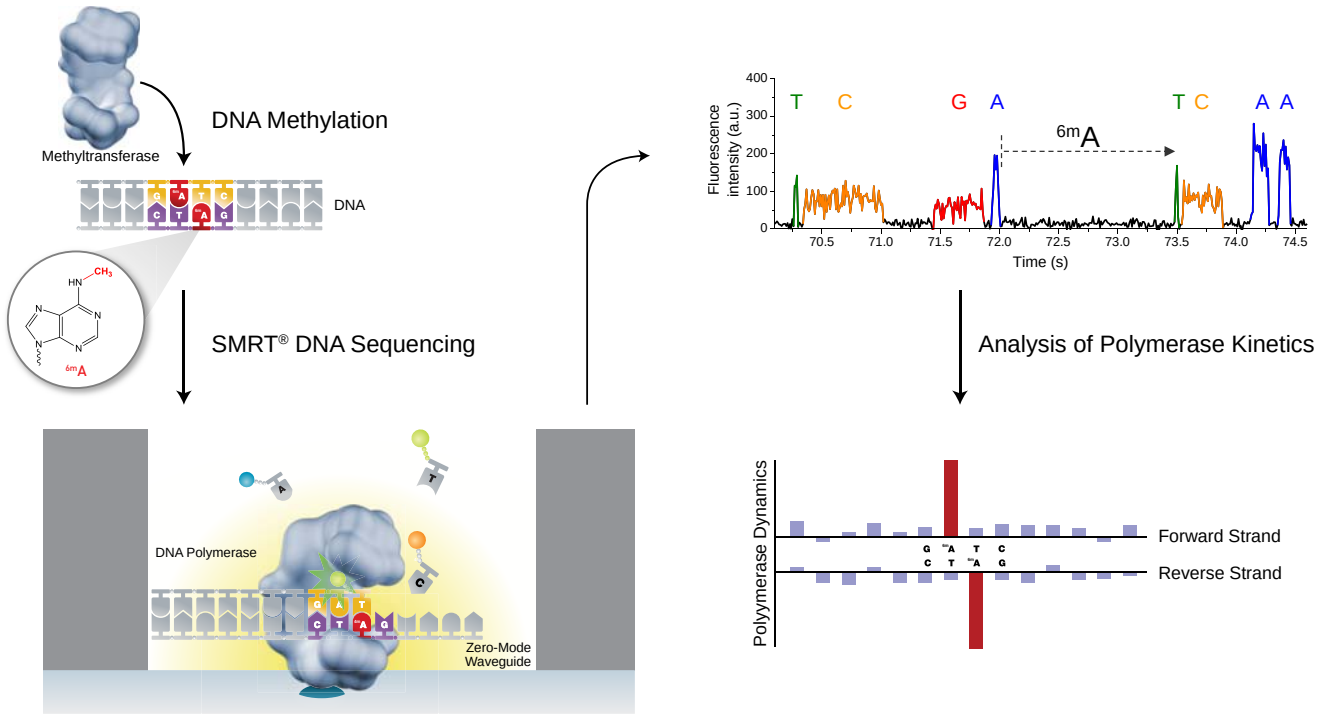
Hierarchical Genome Assembly Process (HGAP)

Paper: PloS One: Mind the gap: Upgrading genomes with Pacific Biosciences *RS* long-read sequencing technology
Paper: Nature Biotechnology: Hybrid error correction and *de novo* assembly of single-molecule sequencing reads
Paper: Nature Biotechnology: A hybrid approach for the automated finishing of bacterial genomes

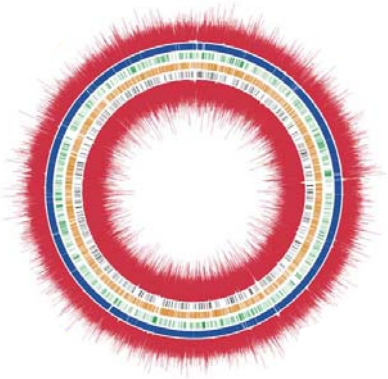
www.pacb.com/denovo

Discover the Epigenome

The PacBio® RS II detects DNA base modifications using the kinetics of the polymerization reaction during sequencing.



Methyltransferases bind specifically to DNA motifs in a genome and methylate bases. PacBio software locates modified sites and motifs.



Methylome of the German *E. coli* outbreak strain. The inner and outer red circles show the kinetic signals. The colored internal tracks show the different methylation motif distributions.

Motif	Occurrence in Genome	Modified in Genome	% Modified
5'-G**A**TC-3' 3'-CT**A**G-5'	42,992	41,969	97.6%
5'-ACC**A**CC-3' 3'-TGGTGG-5'	4,569	4,492	98.3%
5'-CTGC**A**G-3' 3'-G**A**CGTC-5'	2,746	2,678	97.5%
5'-CC**A**CN$_6$TGAY-3' 3'-GGTGN$_6$**A**CTR-5'	492 492	478 484	97.2% 98.4%

Genome-wide detection of methylation for the German *E. coli* outbreak strain.

Paper: Current Opinions in Microbiology: Entering the era of bacterial epigenomics with SMRT DNA sequencing
Paper: Nature Biotechnology: Genome-wide mapping of methylated adenine residues in pathogenic *Escherichia coli*
Paper: Nucleic Acids Research: The methylomes of six bacteria

www.pacb.com/basemod

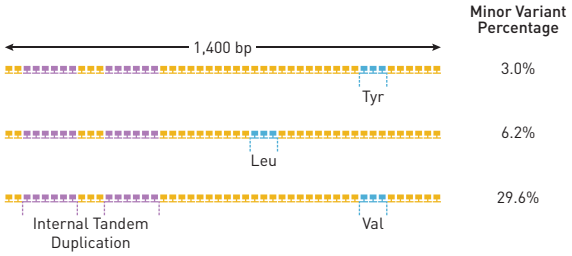
Characterize Genomic Variation

The PacBio® RS II provides exquisite sensitivity and specificity with extraordinarily long reads to fully characterize genetic complexity.

Compound Mutations and Haplotype Phasing

Multi-kilobase reads facilitate the study of linked mutations hundreds, even thousands, of bases apart.

Paper: Nature: Validation of FLT3-ITD as a therapeutic target in human acute myeloid leukemia

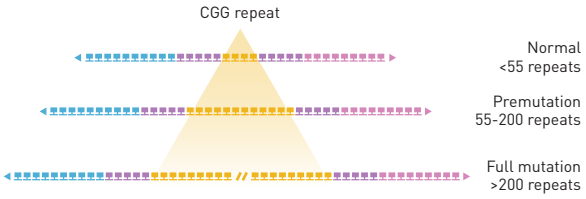


FLT3 gene model in acute myeloid leukemia

Repeat Expansions

Long reads and low bias allow accurate sequencing across repeat expansions, even in low complexity regions.

Paper: Genome Research: Sequencing the unsequenceable: Expanded CGG-repeat alleles of the fragile X gene

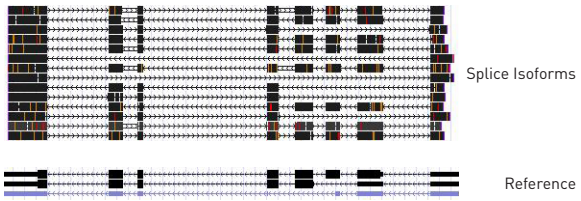


FMR1 gene

Full-Length Transcripts and Splice Variants

Single-molecule resolution and long reads span entire cDNAs, allowing full characterization of splicing in the transcriptome.

Poster: AGBT 2012: Full length cDNA sequencing on the PacBio® *RS*

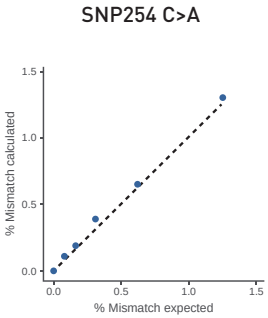


Minor Variants and Quasispecies

Single molecule sequencing simplifies the analysis of mixed populations of sequences. Exquisitely sensitive and specific.

Linear variant detection to < 0.1% frequency

Poster: CROI 2013: Sensitive detection of minor variants and viral haplotypes using SMRT® sequencing

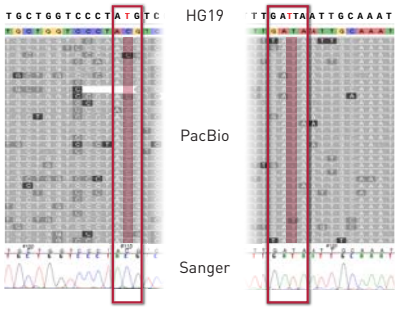


SNP Detection and Validation

Single molecule sequencing detects and validates SNPs with high accuracy by avoiding mapping errors and systematic error.

99.999% consensus accuracy

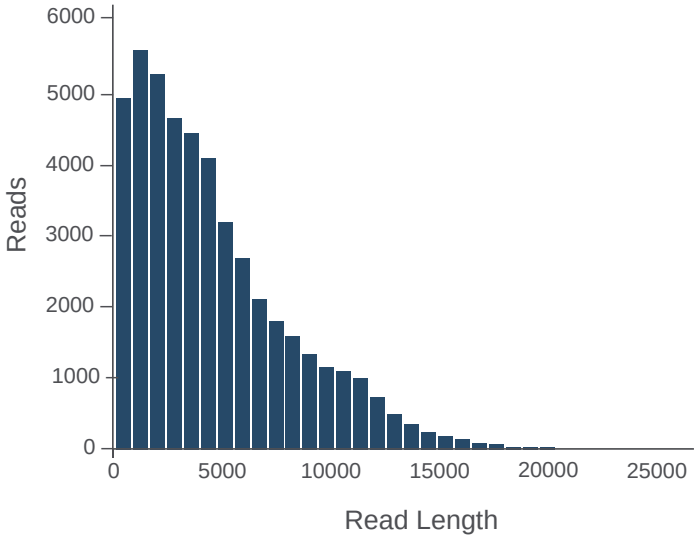
Paper: BMC Genomics: Pacific Biosciences sequencing technology for genotyping and variation discovery in human data



www.pacb.com/target

PacBio RS II Typical Results

Read Length Distribution



Typical Results

Read Length:

Average:	4,606 bp
95th Percentile:	11,792 bp
Maximum:	23,297 bp

Throughput per SMRT® Cell: 216 Mb

47,197 reads

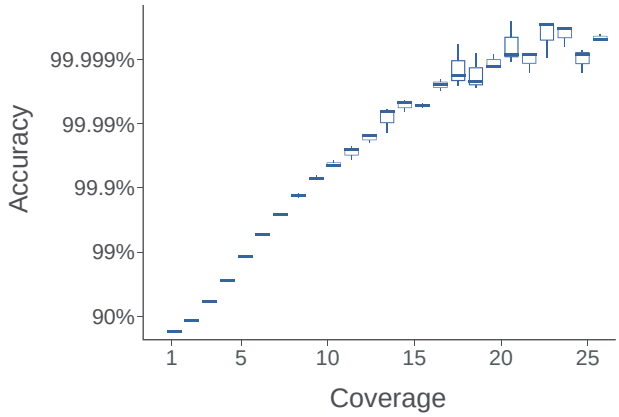
Based on data from 11 kb plasmid library using a 120 minute movie

Template Preparation

Insert Size (bp)	Input DNA per prep (ng)
250 – 500	250
1,000 – 2,000	500
5,000 – 10,000	1,000

Each library prep typically supports >35 SMRT Cells.

Accuracy



Based on data from *E. coli* with 10 kb libraries using a 90 minute movie

Products and Workflow

The PacBio® RS II system, consumables and software provide a simple, fast, end-to-end workflow.

Library Preparation

DNA Template Prep Kit
DNA Polymerase Binding Kit
MagBead Kit

No amplification required

Instrument Run

PacBio RS II with touch screen
RS Remote for run design
SMRT Cells
DNA Sequencing Kit

Sequencing time 30 to 120 min per SMRT Cell

Data Analysis

SMRT Analysis
SMRT Portal
SMRT View

Open source, open standards

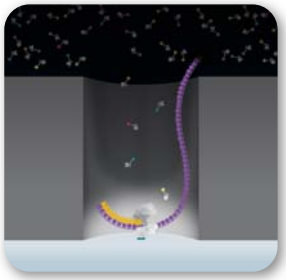
Results in as few as 10 hours

SMRT® Technology

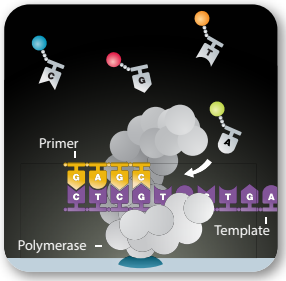
The PacBio RS II is based on novel Single-Molecule, Real-Time (SMRT) technology which enables the observation of natural DNA synthesis by a DNA polymerase in real time. Sequencing occurs on SMRT Cells, each containing thousands of Zero-Mode Waveguides (ZMWs) in which polymerases are immobilized. The ZMWs provide a window for watching the DNA polymerase as it performs sequencing by synthesis.

SMRT® Cells

Zero-Mode Waveguides

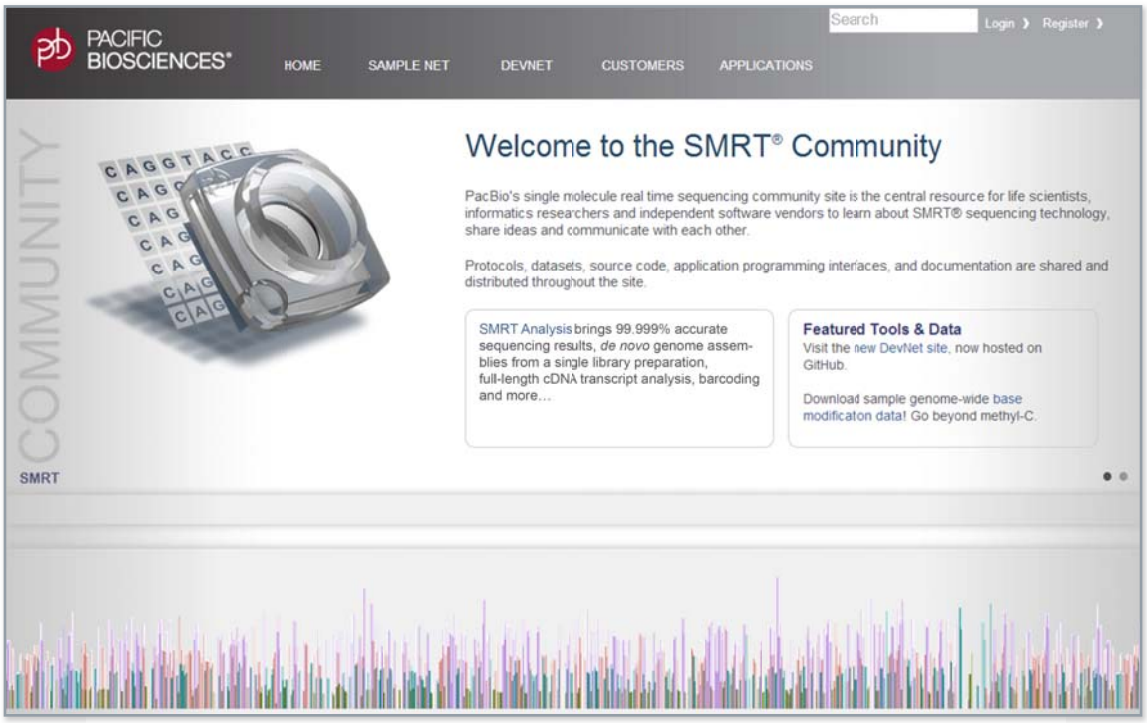


Phospholinked Nucleotides



Join the SMRT® Community

Our SMRT Sequencing community site is the central resource for life scientists, informatics researchers and independent software vendors to learn about our technology, share ideas and communicate with each other.



www.smrtcommunity.com

Operating Environment

Instrument and environmental cabinet

Power requirements:	208 – 240 VAC. UPS recommended
Operating temperature:	15 °C – 25 °C (59 °F – 77 °F) ± 2 °C per hour
Humidity:	20% – 80%, noncondensing
Ventilation:	HVAC capacity of up to 22,720 BTU (6654 Watts)
Nitrogen:	90 – 125 PSI (4,654 – 6,464 torr)
WxDxH:	78.9 in x 30.3 in x 62.2 in (200.4 cm x 77.0 cm x 158.0 cm)
Weight:	2,405 lb (1,091 kg)

Blade Center

Includes integrated computation and storage for performing single molecule, real-time sequencing, kinetic data generation, basecalling and quality assessment.

WxDxH:	27.5 in x 27 in x 39.2 in (69.9 cm x 68.6 cm x 99.6 cm)
Weight:	250 lb (113 kg)

PACIFIC
BIOSCIENCES®

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