

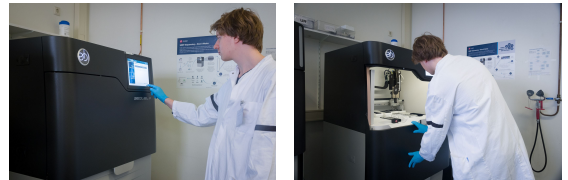
## Pacbio Sequel Ii System

<https://search.researchequipment.wur.nl/SearchDetail.aspx?deviceid=8774d1eb-031d-4f2a-a1aa-0a1aab98af45>

### Brand

Pacific Biosciences

### Type



### Contact

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### Organisation

Plant Sciences Group

### Department

Bioscience

### Description

Pacbio Sequel Ii offers single molecule real-time (SMRT), long-read, DNA sequencing technology on at large though flexible scale. You may find Sequel Ii suitable for large scale projects such as de-novo sequencing of large and complex (plant) genomes, full length transcriptome analysis (Isoseq) large amplicon sequencing, Structural Variation detection and haplotype phasing.

The Sequel Ii system offers the ability to run multiple chips (SMRT cells) allowing flexible on-demand sequencing, using variable sequencing run time per SMRT cell analysis. Users deploy multiple flow cells as well as variable run times (up to 30 Hours) onto single experiments for greater speed or throughput resulting in high quality long read sequences (HiFi reads).

The performance of SMRT sequencing - whether that is data yields, accuracy or ease of use - has improved tremendously in recent years. Each Sequel II SMRT cell now allows up to 8 Million ZMW wells to be loaded for sequencing simultaneous.

### Technical Details

- Variable, up to 30 hour run time per SMRT cell
- Each Sequel Ii SMRT cell has approximately eight times the sequencing capacity of a Sequel SMRT cell
- 8M wells per SMRT cell resulting typically in >5M reads
- As much as 150 Gb per flow cell
- Read lengths are determined by your sample and experimental needs
- High Quality per base (<1% error rate) in HiFi reads, therefore making assembly, structural variation detection and phasing much more reliable, easier and faster
- Sequel Ii sequences (native) DNA — meaning no amplification bias and retained modification information

### Applications

- De-novo sequencing of large genomes
- Structural Variation analysis
- Haplotype phasing
- Full length transcriptome sequencing (isoSeq)
- DNA modifications
- High throughput high fidelity Long amplicon sequencing
- Multiplexing bacterial genome sequencing
- Target enrichment Long read sequencing