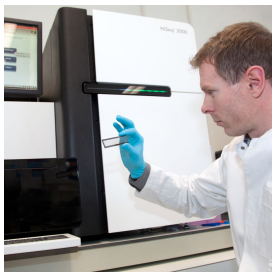
Illumina HiSeq2500

https://search.labfacilities.wur.nl/SearchDetail.aspx?deviceid=90a87259-cc74-4fad-8998-7c7740278ff8



Brand

Illumina

Type

Contact

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Organisation

Plant Sciences

Department

Bioscience

Description

The Illumina HiSeq2500 with v4 chemistry is based on the concept of ‘sequencing by synthesis’ to produce sequence reads up to 250 base pairs long derived from billions of surface-amplified DNA fragments simultaneously.
Depending on user specified settings, reads can be 125 or 250 base pairs long and derived from single read or paired end read chemistry, with a maximum throughput of 1 Tera bases per run.
Key advantages of the HiSeq2500 over other NGS platforms include:
• Highest throughput
• Lowest run cost/base
• Best-established technology
• Broadest range of biological applications

Technical Details

Mechanism

This sequencing starts with a mixture of single-stranded, adaptor ligated DNA fragments captured onto the surface of a glass flow cell containing up to eight separate channels. Isothermal polymerase clonally amplifies the DNA fragments in a discrete area or 'cluster' on the flow cell surfaces.
Two flow cells can be placed into the HiSeq2500 sequencer, where each cluster is supplied with polymerase and four differentially labelled fluorescent nucleotides with chemically inactivated 3'-OH to ensure a single base incorporated per cycle. Each base incorporation cycle is followed by an imaging step to identify the incorporated nucleotide at each cluster. Subsequently chemical cleavage of the fluorescent group and de-blocking the 3' end enables the next base incorporation cycle. At the end of the sequencing run, the sequence of each cluster is deduced by reading off the fluorescence at each successive nucleotide addition step resulting in billions of DNA sequence reads.

Publications

See how Illumina SBS (sequencing by synthesis) works, , ,
http://www.illumina.com/systems/hiseq_2500_1500/technology.html