Source BioScience

Empower & Revolutionise Your Research with Next-Generation Sequencing

We are your Next-Generation Sequencing partner for life science research, molecular pathology and clinical diagnostics.

Applications

DNA Sequencing
de-novo sequencing
Targeted resequencing
Exome sequencing
Amplicon sequencing
Metagenomics

RNA Sequencing
de-novo sequencing
Targeted re-sequencing
Small RNA analysis

Epigenomics
ChIP sequencing
Bisulphite sequencing
MeDIP sequencing

Platforms

- **MiSeq**
- **NextSeq**
- **HiSeq**

Bioinformatic Analyses

- Genomics & targeted sequencing
- Transcriptomics - gene expression & regulation
- Differential gene expression
- Clinical informatics
- Epigenomics - gene regulation & epigenetic mechanisms
- DNA/RNA-protein interactions
- Metagenomics & metatranscriptomics

Why Source BioScience?

- Fast, effective & high-quality service
- GCP approved laboratories
- State of the art facilities in UK, Ireland, Germany & the USA
- Expert advice & support
- Dedicated project management
- Illumina CSPro certified provider
- Rapid turnaround times

All of our NGS projects are tailored to the individual customer requirements.

GCP

illumina CSPro CERTIFIED SERVICE PROVIDER

SERVICES

Bioinformatic Analyses for Next-Generation Sequencing

We offer a range of bioinformatics and computational analysis options to aid researchers in the interpretation of their data.

Genome *de-novo* Assembly of Read Data

- *de-novo* assembly of reads into sequence contigs
- Generation of contig sequences in FASTA format & a contig report
- Structural annotation

Metagenomics Analysis

- Blasting of reads against the GreenGenes database
- List of Taxonomic classification with percentage of each classification in the sample

ChIP Sequencing

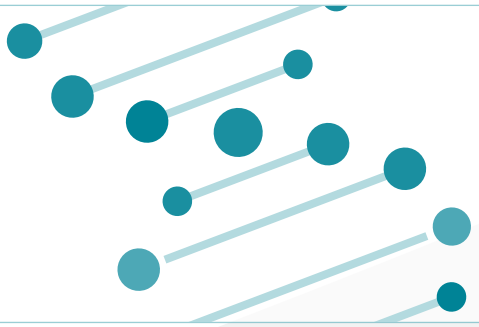
- Alignment of reads against a reference genome
- ChIP-seq analysis to determine peaks & their genomic regions
- Peak annotation (nearest gene information)

RNA Sequencing

- Alignment of reads against a reference genome
- Calculation of gene expression levels
- Calculation of differential gene expression levels between samples/groups
- Identification of exon splice crossing sequencing reads
- Pathway analysis & gene ontology

Transcriptome *de-novo* Assembly of Read Data

- *de-novo* assembly of reads into sequence contigs
- Generation of contig sequences in FASTA format & a contig report
- Functional annotation



Take the Hassle out of Nucleic Acid Extraction & Amplification with our DNA/RNA Preparation Services

- DNA Extraction
- RNA Extraction
- Whole Genome Amplification

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