INDIAN BIOLOGICAL SCIENCES AND RESEARCH INSTITUTE
भारतीय जैविक विज्ञान एवं अनुसंधान संस्थान
An ISO 9001:2015 Certified Institute
Knowledge Leads Innovation

Every genome has a story. We help you read it.

A student-friendly guide to Next-Generation Sequencing at IBRI Noida — what it is, how our facility performs it, and where the sequence data actually comes from.

WHAT IS NGS?

Next-Generation Sequencing (NGS) is a high-throughput technology that reads millions of short DNA or RNA fragments **at the same time**, instead of one fragment at a time like older Sanger sequencing. The fragments are reassembled by computer to reveal a genome, a transcriptome, or the microbes in a sample — turning biological material into readable, searchable data.

Millions

of DNA fragments read in parallel, in a single run

Hours

not weeks — from sample to raw sequence data

1 sample

can answer genomic, transcriptomic & microbial questions

What we sequence

Whole Genome Sequencing

Reads a sample's entire DNA — every gene and the regions between them.

Whole Exome Sequencing

Focuses on the protein-coding regions where most disease-linked variants sit.

RNA Sequencing

Captures which genes are active, and how strongly, in a cell or tissue.

Targeted Gene Panels

Deep, focused sequencing of a chosen set of genes of interest.

16S / Metagenomics

Identifies and profiles microbial communities in a sample.

Amplicon Sequencing

Sequences a specific PCR-amplified region across many samples at once.

THE WORKFLOW

How we perform NGS

From a biological sample to an interpreted report, every run at IBRI Noida follows the same rigorous, six-stage pipeline.

01 Sample collection & quality check

DNA or RNA is extracted from the submitted sample and checked for purity, concentration and integrity (e.g. via Qubit / TapeStation / Bioanalyzer) before it moves forward.

02 Library preparation

The DNA/RNA is fragmented, and short adapter sequences are attached to each fragment so the sequencer can recognise, amplify and read it.

03 Cluster generation & sequencing

Fragments are amplified into clusters on a flow cell and sequenced base-by-base on our NGS platform, generating millions of short "reads".

04 Base calling & demultiplexing

Raw signals are converted into A/T/G/C base calls with quality scores, and reads are sorted back to their original sample.

05 Bioinformatics analysis

Reads are quality-trimmed, aligned to a reference genome (or assembled from scratch), and variants, expression levels or taxa are called computationally.

06 Interpretation & report

Findings are annotated against biological databases and delivered as a clear report, alongside the raw and processed data files.

Where the dataset comes from

GENERATED IN-HOUSE

Your own sequencing run

- Raw reads produced on our NGS platform from the sample you submit
- Delivered as FASTQ files (raw reads) and BAM/VCF files (aligned & variant-called data)
- You own this data — it is specific to your sample, not shared or reused

PUBLIC REFERENCE DATA

Used for alignment & comparison

- NCBI SRA & GEO — archives of published raw sequencing data
- Ensembl / UCSC Genome Browser — reference genomes & annotations
- 1000 Genomes Project & gnomAD — population variant frequencies
- TCGA — cancer genomics data for comparative studies

For students & early researchers

Get hands-on with real sequencing data — from wet-lab library prep to running your first alignment and variant call.

Hands-on workshops · Internships · Project collaborations · Guest lectures

ADMISSIONS OPEN

Join our next NGS batch

Register for hands-on NGS project training / dissertation at IBRI Noida.

Register online:

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