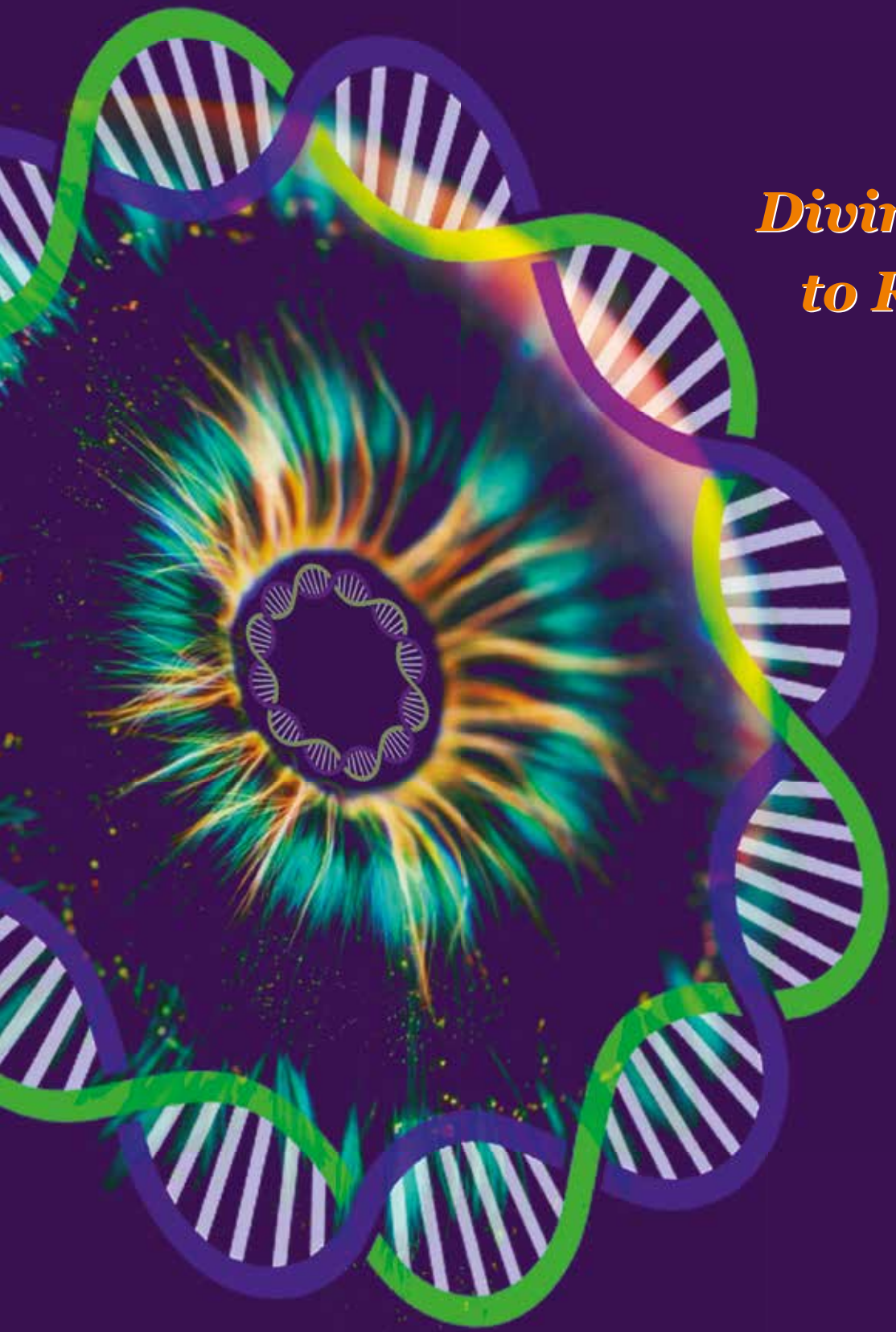
HiGenoMB® HIMEDIA
Unzipping Genes

Hi-G® 360

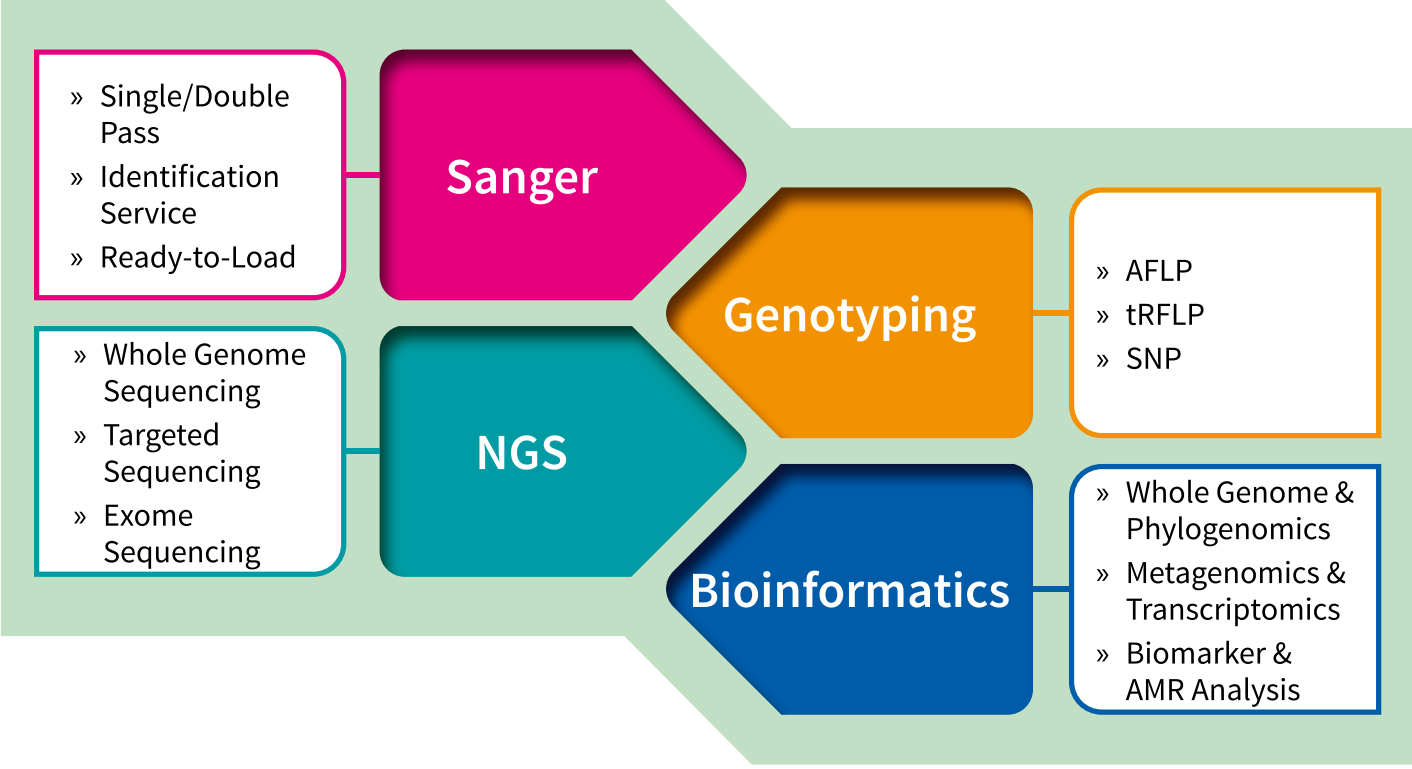
Sequencing and Bioinformatics Services



Diving Deeper to Rise Higher

HIMEDIA®
For Life is Precious

Hi-Gx360® Sequencing and Bioinformatics Services

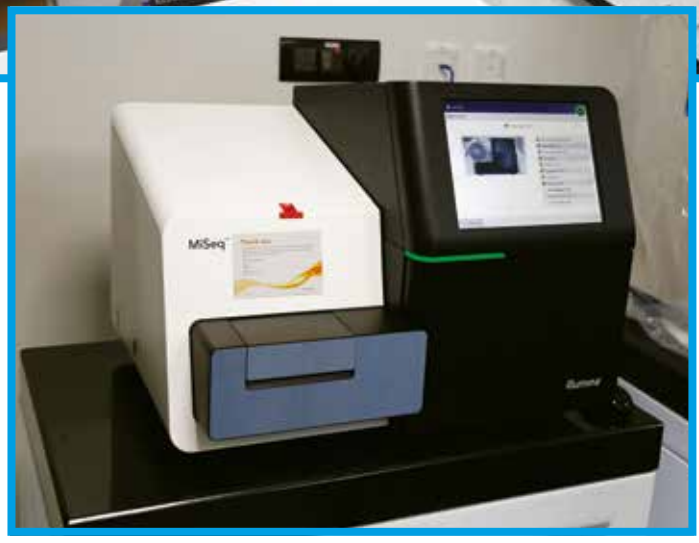


We stand for :-

- High quality data output for a broad range of sequencing applications
- No hidden fees
  - Standard vector primers or universal gene primers added at no-extra cost
  - No extra charge for difficult-to-sequence templates
  - Help troubleshoot sequencing projects at no extra charge
- Fully customized solutions that fit your project objectives
- Functionally tested, optimized, and validated analyses pipelines built using opensource tools
- Direct Support by Sequencing and Bioinformatics experts
- Shared knowledge base and resources to empower you

State-of-Art Hi-Gx360® Lab

Sanger Sequencer :
3500XL Genetic Analyzer



Next generation Sequencer (NGS) : MiSeq™

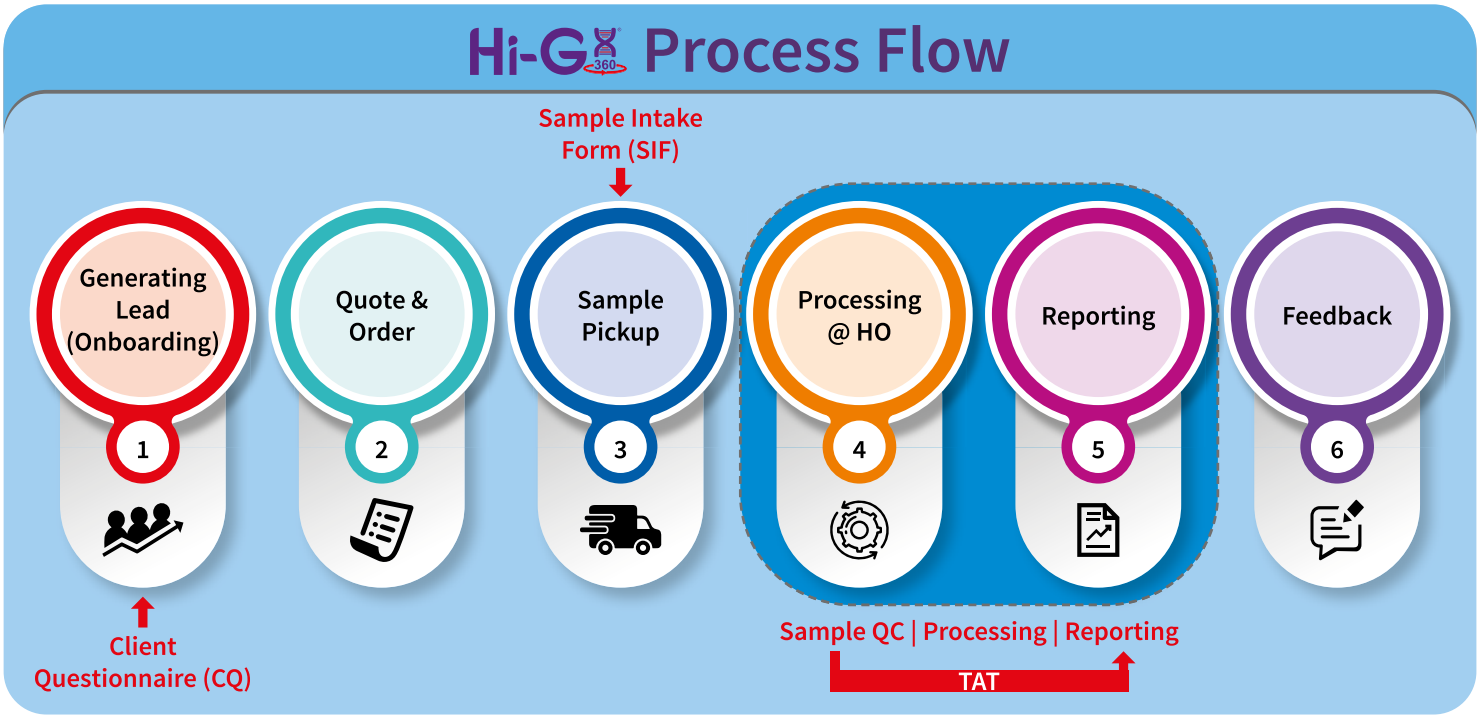
Bioinformatics Cluster

Next generation Sequencer (NGS) :
NextSeq™ 550

Sanger Sequencing Applications

- **Highly accurate** 'chain termination based' 'first generation' DNA sequencing method
- **Gold standard** for benchmarking all other **sequencing** technologies, including NGS
- **Confirm sequence variants** or fill 'gaps' of genomic regions determined by NGS
- **Predesigned identification service** under **Isolate-to-Identity** covering all organisms
- **Detailed reports** always include .ab1 files and other useful information
- **Standard** vector **primers** and universal gene markers added free-of-cost
- AFLP, tRFLP and SNP **genotyping services**
- Gene sequence based **phylogenetic analysis** service
- Stuck with **NCBI** GenBank **submissions**, connect with us!

Note: Bioinformatics services provided for above mentioned codes are included on page no.16 onwards.



Sanger Sequencing Services

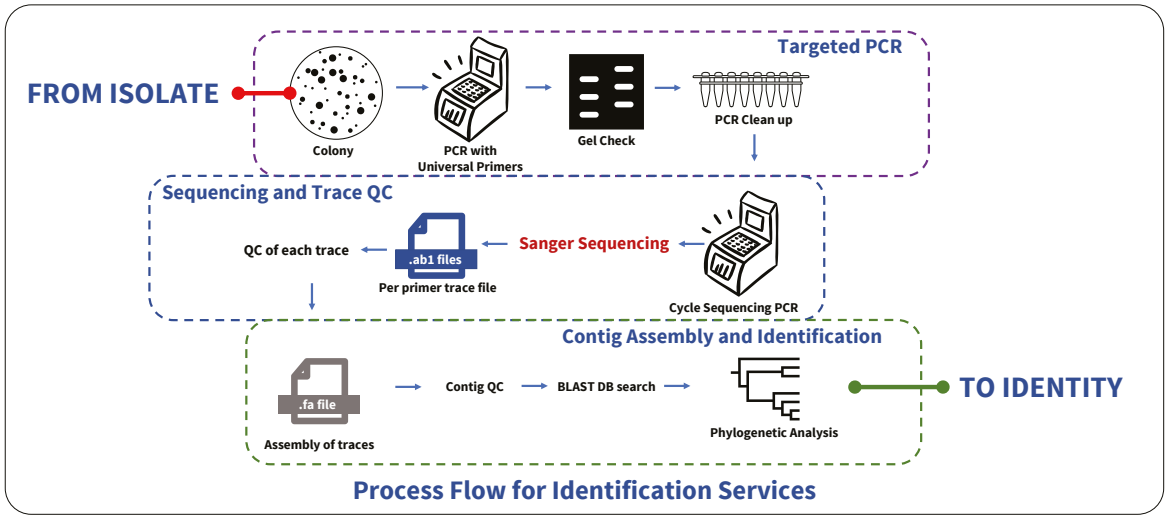
Description		Service Codes
Single pass sequencing ~700 bp	purified PCR/Plasmid	MBS101
	unpurified PCR/Plasmid	MBS102
Single strand F & R primer sequencing ~1200 bp	purified PCR/Plasmid	MBS103
	unpurified PCR/Plasmid	MBS104
Single strand F&R primer sequencing & BLAST analysis ~1200 bp	unpurified PCR/Plasmid	MBS104A
Double pass both strands 1.5-2 kb	purified PCR/Plasmid	MBS105
	unpurified PCR/Plasmid	MBS106
96-well plate single pass sequencing ~700 bp	purified PCR/Plasmid	MBS107
	unpurified PCR/Plasmid	MBS108
Primer walking (upto 2 kb)		MBS121
Primer walking (upto 5 kb) with DNA extraction		MBS121A
Ready-to-Run 96-well plate single pass sequencing (~700 bp)		MBS122
gDNA-to-Sequence 96-well plate single pass sequencing (~700 bp)		MBS123
gDNA-to-Sequence 96-well plate F & R primer sequencing (~1200 bp)		MBS124

Supplemental Services

Only offered in combination with other service codes, NOT separately

Description	Service Codes
Agarose Gel Extraction	MBS301
Plasmid DNA Isolation	MBS302
Purification of PCR Products	MBS303
Agarose Gel-based QC	MBS305

Identification of Organisms (Isolate-to-Identity)



Identification Services

Description		Service Codes
Bacterial/Archaeal 16S rRNA-based Identification	from genomic DNA to identity	MBS109
	from Pure Isolate to Identity	MBS110
rRNA-based partial Identification (gDNA to BLAST, ~700 bp single pass)	Does not include phylogenetic analysis (MBS020).	MBS109A
rRNA-based partial Identification (gDNA to BLAST, ~1200 bp single pass)	Does not include phylogenetic analysis (MBS020).	MBS109B
Fungal ITS-based Identification	Genomic DNA	MBS111
	Pure Isolates	MBS112
Fungal 18S rRNA-based Identification	from genomic DNA	MBS113
	from Pure Isolates	MBS114
Algal 18S rRNA-based Identification	from genomic DNA	MBS115
	from Pure Isolates	MBS116
Algal 23S rRNA-based Identification	from genomic DNA	MBS117
	from Pure Isolates	MBS118
Identification of other Eukaryotes	from genomic DNA	MBS119
	from Biological Sample	MBS120

Genotyping Services

Description	Service Codes
AFLP-based DNA Fingerprinting	MBS151
tRFLP-based DNA Fingerprinting	MBS152
SNP Genotyping	MBS153

Regulatory/NABL Compliant Services

Description	Service Codes
Hi-Gx360® Single pass sequencing (~700 bp, purified PCR/Plasmid)	MBS401
Hi-Gx360® Single pass sequencing (~700 bp, unpurified PCR/Plasmid)	MBS402
Hi-Gx360® Single pass F&R primer sequencing (~1200 bp, purified PCR/Plasmid)	MBS403
Hi-Gx360® Single pass F&R primer sequencing (~1200 bp, unpurified PCR/Plasmid)	MBS404
Hi-Gx360® Double pass (for 1.5-2 kb, purified PCR/Plasmid)	MBS405
Hi-Gx360® Double pass (for 1.5-2 kb, unpurified PCR/Plasmid)	MBS406
Hi-Gx360® Microbial Identification by 16S rRNA gene sequencing from genomic DNA	MBS409
Hi-Gx360® Microbial Identification by 16S rRNA gene sequencing from pure isolate	MBS410
Hi-Gx360® Fungal Identification by ITS sequencing from genomic DNA	MBS411
Hi-Gx360® Fungal Identification by ITS sequencing from Pure Isolates	MBS412
Hi-Gx360® Fungal Identification by 18S rRNA gene sequencing from genomic DNA	MBS413
Hi-Gx360® Fungal Identification by 18S rRNA gene sequencing from Pure Isolates	MBS414
Hi-Gx360® Algal Identification by 18S rRNA gene sequencing from genomic DNA	MBS415
Hi-Gx360® Algal Identification by 18S rRNA gene sequencing from Pure Isolates	MBS416
Hi-Gx360® Algal Identification by 23S rRNA gene sequencing from genomic DNA	MBS417
Hi-Gx360® Algal Identification by 23S rRNA gene sequencing from Pure Isolates	MBS418

Next Generation Sequencing

Whole Genome Sequencing Applications

Whole Genome Sequencing (WGS) has enabled comprehensive decoding of the sequence of entire genomes of organisms. Such information is crucial for understanding functional and evolutionary history of organisms,as well as to identify mutations and genetic variations that are responsible for causing genetic disorders,development of cancer, disease outbreaks, evolution of strains with novel pathogenic traits, etc. At Hi-Gx360 ®, we use a read-to-annotation approach to generate in detail all the information needed to understand functions of all predicted genes present in the organism. Assembled genomes may not be 100% complete, hence, further gap-filling can be achieved using one of many long read sequencing technologies.

- ☐ Sequence close relatives of reference-organisms or entirely novel organisms (de-novo)
- ☐ Obtain high-resolution and accurate genomic characterization using 2 x 150 or 2 x 300 bp reads
- ☐ Data supplied with interactive QC report.
- ☐ Receive raw sequence reads, assembled contigs & scaffolds Along with bioinformatics analysis customised to fit your needs
- ☐ Choose from basic or advanced bioinformatics.*

*** Note: Bioinformatics services provided for above mentioned codes are included on page no.16 onwards.**

Recommendations

	Resequencing	De-novo Sequencing
Depth/Coverage	50X - 100X	>100X
Read length chemistry	2x75 to 2x300	
Sample Requirements	Minimum quantity 0.5 µg, Minimum concentration = 20 ng/µl, A260/280 = 1.8 - 2.0	

Deliverables

- ☐ Run information, Statistics of raw data & FASTQ files
- ☐ Reference Genome Mapping files/ De-novo Genome Mapping files, Functional Annotations, Gene predictions, Gene annotations, Pangenome analysis
- ☐ Advanced analysis customized to your project needs

WGS Services

Description	Service Codes
Whole Genome Sequencing (0.5 Gb Data) eg., Mycoplasma/Gram -ve Bacteria/Archaea	MBS201
Whole Genome Sequencing (1 Gb Data) eg., Gram +ve Bacteria/Archaea	MBS201-1G
Whole Genome Sequencing (2 Gb Data) eg., Yeast	MBS201-2G
Whole Genome Sequencing (4 Gb Data)	MBS201-4G
Whole Genome Sequencing (6 Gb Data) eg., Fungi/Algae	MBS201-6G
Whole Genome Sequencing (8 Gb Data)	MBS201-8G
Whole Genome Sequencing (10 Gb Data)	MBS201-10G
Whole Genome Sequencing (12 Gb Data) eg., Worms	MBS201-12G
Whole Genome Sequencing (16 Gb Data)	MBS201-16G
Whole Genome Sequencing (20 Gb Data)	MBS201-20G
Whole Genome Sequencing (25 Gb data)	MBS201-25G
Whole Genome Sequencing (30 Gb data)	MBS201-30G
Whole Genome Sequencing (50 Gb data)	MBS201-50G
Whole Genome Sequencing (60 Gb data)	MBS201-60G
Whole Genome Sequencing (100 Gb data)	MBS201-100G
Whole Genome Sequencing (30 Mb data, eg., Mycoplasma @50X)	MBS201-30M
Whole Genome Sequencing (250 Mb data, eg., Bacteria @50X)	MBS201-250M
Whole Genome Sequencing (Virus)	MBS202
Whole Genome Sequencing (Virus, 10Kb @ 100X)	MBS202-1K
Whole Genome Sequencing (Virus, 20Kb @ 100X)	MBS202-2K
Whole Genome Sequencing (Virus, 50Kb @ 100X)	MBS202-5K
COVIDSeq on MiSeq (per sample for 95 samples)	MBS222

*** Gb - Gigabases, Mb-Millionbases, KB - Kilobases**

Note: Bioinformatics services provided for above mentioned codes are included on page no.16 onwards.

Whole Exome Sequencing Applications

The human genome has 180,000 coding regions which account for 1.7% of the genome. An estimated 85% of human diseases with genetic basis occur due to aberrations in these coding regions. Targeted sequencing of this region of the genome is termed as whole exome sequencing (WES). Exome sequencing is a more cost-effective option than sequencing the whole human genome. This sequencing method uses a targeted capture approach where biotinylated probes are deployed against the coding regions of the fragmented human genome to capture and pull down these parts with streptavidin coated beads. The fragments thus obtained are sequenced on the NextSeq™ 550 platform. This strategy results in a 100-fold increase in coverage of the relevant sections of the genome.

- ☐ Lower cost and wide availability
- ☐ Sequencing coverage on target upto 30X
- ☐ Detection of coding single-nucleotide polymorphism (SNP) variants as sensitive as whole genome sequencing
- ☐ A smaller data set for faster and easier analysis compared to whole genome sequencing
- ☐ Standard sequencing coverage ≥ 50X; cancer sample ≥ 100X. More SNPs can be gained by increasing the coverage.
- ☐ Cost-effective library preparation and exome enrichment solutions

Exome Sequencing Recommendations

	Whole Exome Sequencing	Cancer Specific and/or Rare Variant Detection
Depth/Coverage	100-300X	500–1000X
Read length chemistry	2x75 to 2x150	
Capture Region	Agilent SureSelect Human All Exon V8, Design size 41.6 Mb, Target region 35.1 Mb	
Sample Requirements	Required quantity 1.0 – 0.2 µg, Minimum concentration = 20 ng/µl, $A_{260/280}$ = 1.8 - 2.0	

Deliverables

- ☐ Run information, Statistics of raw data & FASTQ/VCF files
- ☐ Mapping statistics, Statistics of sequencing reads
- ☐ SNPs and InDels calling, Variant annotation, SNVs concordance, Tumor-Normal paired analysis

WES Services

Description	Service Codes
Whole Exome Sequencing (45 Mb Capture)	MBS212-45M
Whole Exome Sequencing (64 Mb Capture)	MBS212-64M

*** Gb - Gigabases, Mb-Millionbases, KB - Kilobases**

Note: Bioinformatics services provided for above mentioned codes are included on page no.16 onwards.

Metagenomics and Microbiome Applications

Microorganisms are crucial for the survival of life on our planet. Descriptive metrics, such as the assemblage of microorganisms present in a defined environment, i.e., the microbiota, and the collection of genes & genomes of this microbiota, i.e., the metagenome, yield information for the functional potential of microbial communities. Microbiome interactions, which refers to the entire habitat, including the microorganisms, their genomes, and the surrounding environmental conditions allows a more robust understanding for hypothesis testing. With Hi-Gx360® NGS service, you can now:

- ☐ Sequence a collection of genes or genomes of the microbiota in any sample
- ☐ Sequence 16S rRNA genes,18S rRNA genes or other marker genes & genomic regions.
- ☐ Obtain comprehensive insight into microbial diversity and its functional role.
- ☐ Detect low-abundance microbial species by performing in-depth sequencing.

Metagenome sequencing

Shotgun metagenomics is a proven tool to study environmental, agricultural & human microbiomes, pathogen identification & surveillance as well as monitoring of anti-microbial resistance genes in the environment. Some of the most common applications include:

- ☐ Identification and classification of microbial communities
- ☐ Novel biomarker discoveries
- ☐ De-novo assembly & characterizations of novel genomes
- ☐ Discovery of novel enzymes and metabolic pathways
- ☐ Relative abundance analysis of microbial communities

Amplicon-based microbiome sequencing

- ☐ A potential tool for high-throughput phylogenetic analysis of microbial communities.
- ☐ Based on phylogenetic marker genes; 16S, 18S rRNA genes & ITS region
- ☐ Allows species identification and taxonomic diversity characterization
- ☐ Provides detail insight of genus and species

Note: Bioinformatics services provided for above mentioned codes are included on page no.16 onwards.

Advantages of amplicon-based phylogenetic gene marker sequencing

- ☐ Marker genes are omnipresent
- ☐ Marker genes are highly abundant to those of other genes
- ☐ Measures phylogenetic relationships across different taxa
- ☐ Easily estimate relative abundance of microbial communities
- ☐ Highly cost-effective

Recommendations

	Shotgun Metagenome	Amplicon-based MiCrobiome
Objective	• Discovery metagenomics • Relative abundance of microbial communities • Metagenome assembled genome sequencing	Taxonomic profiling
Reads per sample	25-500 Million paired end reads*	Over 1 Lakh paired end reads*
Read length chemistry	1x150 to 2x300	
Sample Requirements	Minimum Quantity 1 µg, Minimum Concentration = 50 ng/µl, OD 260/280=1.8~2.0	

* Note: **Number of reads may be decided by client and may vary depending on the diversity in the sample**

Deliverables

- ☐ Run information, Statistics of raw data & FASTQ files
- ☐ Taxonomic profiles, Functional Annotations, Metagenome assembled genomes (MAGs)
- ☐ Advanced analysis customized to your project needs

Shotgun-Metagenome Based Services

Description		Service Codes
Metagenome sequencing (soil/ sediment/water)	(5 Gb Data)	MBS213-5G
	(10 Gb Data)	MBS213-10G
	(15 Gb Data)	MBS213-15G
	(20 Gb Data)	MBS213-20G
Metagenome sequencing (Clinical)	(1 Gb Data)	MBS214-1G
	(5 Gb Data)	MBS214-5G
	(10 Gb Data)	MBS214-10G
	(15 Gb Data)	MBS214-15G
	(20 Gb Data)	MBS214-20G
Metagenome sequencing Environmental DNA (eDNA)	(5 Gb Data)	MBS215-5G
	(10 Gb Data)	MBS215-10G
	(15 Gb Data)	MBS215-15G
	(20 Gb Data)	MBS215-20G

*** Gb - Gigabases, Mb-Millionbases, KB - Kilobases**

Note: Bioinformatics services provided for above mentioned codes are included on page no.16 onwards.

Amplicon-based Microbiome Services

Description		Service Codes
Microbiome sequencing from Community DNA (16S)	(1 lakh PE reads)	MBS203
	(2.5 lakh PE reads)	MBS203-2L
	(5 lakh PE reads)	MBS203-5L
	(10 lakh PE reads)	MBS203-10L
Microbiome sequencing from Insect/Food sample (16S)	(1 lakh PE reads)	MBS204
	(2.5 lakh PE reads)	MBS204-2L
	(5 lakh PE reads)	MBS204-5L
Microbiome sequencing from Swabs/body fluids (16S)	(1 lakh PE reads)	MBS205
	(2.5 lakh PE reads)	MBS205-2L
	(5 lakh PE reads)	MBS205-5L
Microbiome sequencing from Soil/Sediment/ Water/Fecal (16S)	(1 lakh PE reads)	MBS206
	(2.5 lakh PE reads)	MBS206-2L
	(5 lakh PE reads)	MBS206-5L
Microbiome sequencing from Community DNA (ITS)	(1 lakh PE reads)	MBS207
	(2.5 lakh PE reads)	MBS207-2L
	(5 lakh PE reads)	MBS207-5L
Microbiome sequencing from Insect/Food sample (ITS)	(1 lakh PE reads)	MBS208
	(2.5 lakh PE reads)	MBS208-2L
	(5 lakh PE reads)	MBS208-5L
Microbiome sequencing from Swabs/body fluids (ITS)	(1 lakh PE reads)	MBS209
	(2.5 lakh PE reads)	MBS209-2L
	(5 lakh PE reads)	MBS209-5L
Microbiome sequencing from Soil/Sediment/ Water/Fecal (ITS)	(1 lakh PE reads)	MBS210
	(2.5 lakh PE reads)	MBS210-2L
	(5 lakh PE reads)	MBS210-5L
Microbiome sequencing (protein coding genes)	(1 lakh PE reads)	MBS211
	(2.5 lakh PE reads)	MBS211-2L
	(5 lakh PE reads)	MBS211-5L
16S Microbiome ready-to-load	(50,000 PE reads)	MBS216
	(1 lakh PE reads)	MBS216-1L
	(2.5 lakh PE reads)	MBS216-2L
	(5 lakh PE reads)	MBS216-5L

Supplemental Services

Only offered in combination with other service codes, NOT separately

Description	Service Codes
DNA Fragment QC	MBS304
RNA QC with RIN value	MBS306

Note: Bioinformatics services provided for above mentioned codes are included on page no.16 onwards.

Transcriptomics

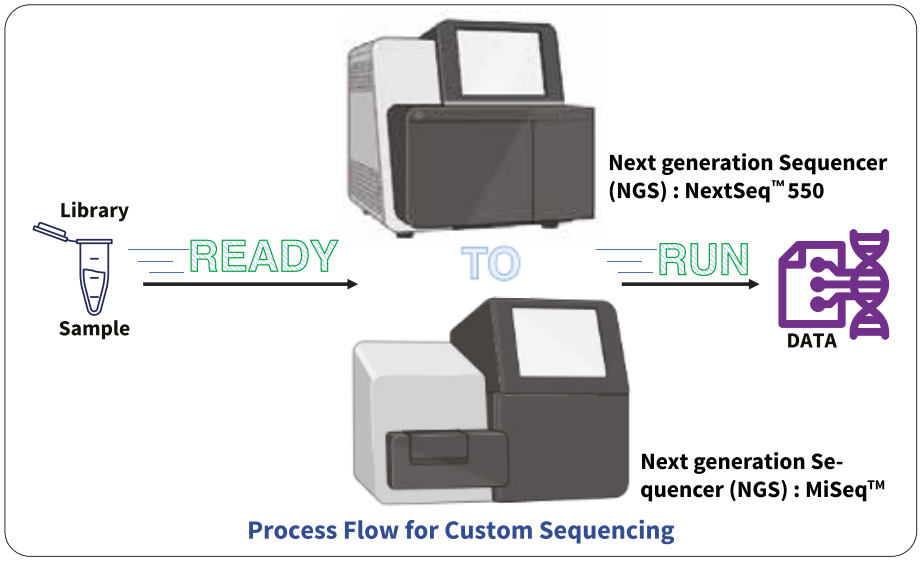
RNA sequencing (RNA-seq) is a powerful and widely used technique for transcriptome analysis that has revolutionized the field of molecular biology. It allows researchers to study gene expression at an unprecedented level of detail, providing valuable insights into the mechanisms of cellular processes and disease pathogenesis. RNA-seq works by converting RNA molecules into a library of cDNA fragments that are then sequenced using high-throughput sequencing technologies.

- ☐ Identify and quantify gene expression levels, detect novel transcripts & investigate alternative splicing patterns
- ☐ Detect post-transcriptional modifications such as RNA editing
- ☐ Wide dynamic range and low input requirements
- ☐ Work with a variety of sample types, from single cells to complex tissues.
- ☐ Integrate with other types of omics data to obtain a more comprehensive view of biological systems.

RNA Sequencing Services

Description	Service Codes
de novo RNA Sequencing/Transcriptome Sequencing (10M PE reads, 2x150)	MBS230-10M
de novo RNA Sequencing/Transcriptome Sequencing (20M PE reads, 2x150)	MBS230-20M
de novo RNA Sequencing/Transcriptome Sequencing (30M PE reads, 2x150)	MBS230-30M
Top Up Sequencing (10M PE reads, 2x150)	MBS230-10MTUP
RNA Sequencing/Transcriptome Sequencing, 10Gb data(W~67M PE reads, 2x150)	MBS230-10G
mRNA Sequencing/RNA Sequencing/Whole Transcriptome Sequencing (10M PE reads, 2x75)	MBS231-10M
mRNA Sequencing/RNA Sequencing/Whole Transcriptome Sequencing (20M PE reads, 2x75)	MBS231-20M
mRNA Sequencing/RNA Sequencing/Whole Transcriptome Sequencing (30M PE reads, 2x75)	MBS231-30M
Top Up Sequencing (10M PE reads, 2x75)	MBS231-10MTUP
Small RNA/miRNA Sequencing/Gene expression Profiling (10M reads, 75bp)	MBS232-10M
Small RNA/miRNA Sequencing/Gene expression Profiling (20M reads, 75bp)	MBS232-20M
Small RNA/miRNA Sequencing/Gene expression Profiling (30M reads, 75bp)	MBS232-30M
Top Up Sequencing (10M PE reads, 75bp)	MBS232-10MTUP

Custom Sequencing

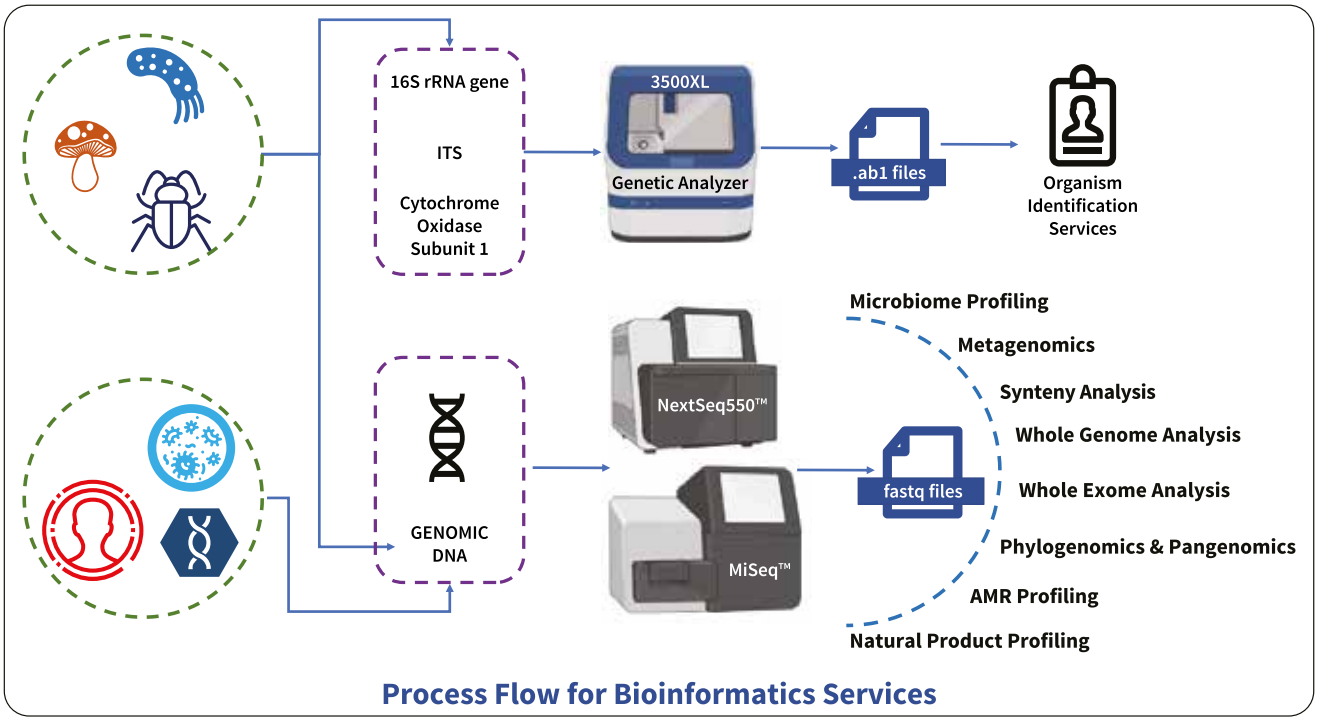


Process Flow for Custom Sequencing

Sequencing Services

Category	Description		Service Codes
NGS	16S Microbiome ready-to-load	(50,000 PE reads)	MBS216
NGS		(1 lakh PE reads)	MBS216-1L
NGS		(2.5 lakh PE reads)	MBS216-2L
NGS		(5 lakh PE reads)	MBS216-5L
NGS	MiSeq ready-to-load	(1 Gb data)	MBS217
NGS		(2 Gb data)	MBS217-2G
NGS		(4 Gb data)	MBS217-4G
NGS		(16 Gb data)	MBS217-16G
NGS	NextSeq ready-to-load	(upto 5 Gb)	MBS218-5G
NGS		(upto 30 Gb)	MBS218-30G
NGS		(upto 60 Gb)	MBS218-60G
NGS		(upto 100 Gb)	MBS218-100G
NGS		(upto 120 Gb)	MBS218-120G
NGS	NextSeq 550 Rental (no consumables) for ready-to-run	(upto 20-40 Gb)	MBS219-20G
NGS		(upto 40-80 Gb)	MBS219-40G
NGS		(upto 80+ Gb)	MBS219-80G
NGS	Custom Sequencing on MiSeq	(DNA to sequence, 2x300)	MBS220-10L
NGS		(DNA to sequence, 2x150)	MBS220-25K
NGS	NextSeq 550 Rental (no consumables) for microarray scanning		MBS221

Bioinformatics Services



Process Flow for Bioinformatics Services

Whether you have smaller sequence datasets or large datasets from NGS, one of the biggest challenges especially in massively parallel sequencing is their analysis. Problems arise mainly due to lack of scalable computational power and lack of knowledge regarding how different bioinformatic (BioIT) tools work under the hood. Data privacy too remains a daunting challenge for researchers who are working with patient data. At Hi-Gx360® we have systematically addressed each of these concerns in our state-of-the-art bioinformatics data center. This includes :

- ☐ **Secure Datasets** that are never shared over the open internet
- ☐ **Transparent and Open information** sharing about analysis workflow.
- ☐ Highly **Scalable and validated open-source packages** used for analysis.
- ☐ **Secure Interactive reports** that are comprehensive and information rich.
- ☐ **Publication** grade **data** visualizations
- ☐ Direct **Consultations with** our highly **qualified scientists** on project design

With our bioinformatics services, you can accurately achieve the following

- ☐ Identify organisms with confidence
- ☐ Assemble, annotate and analyze whole genomes
- ☐ Locate low frequency mutations & identify InDels
- ☐ Uncover genetic traits, such as antibiotic resistance markers, etc.
- ☐ Combine with short and long reads libraries to obtain complete genome sequence
- ☐ Identify repetitive regions, structural variants and complex rearrangements for de-novo assemblies

Bioinformatics Services

BioIT Services for Sanger Data

Description	Service Codes
Phylogenetic Analysis (16S/18S/ITS/any other gene based)	MBS020
NCBI submissions	MBS021
Primer Designing	MBS024
Custom Analysis for Sanger Data	MBS029

BioIT Services for NGS Data

Description	Service Codes
Whole Genome analysis for Bacteria/ Archaea (Basic)	MBS001
Whole Genome analysis for Bacteria/ Archaea (Advanced)	MBS002
Whole Genome analysis for Fungi (Basic)	MBS003
Whole Genome analysis for Fungi (Advanced)	MBS004
Whole Genome analysis for Virus	MBS005
Whole Genome analysis using Short & Long Reads for Bacteria/Archaea (Basic)	MBS006
Whole Genome analysis using Short & Long Reads for Bacteria/Archaea (Advanced)	MBS007
Whole Genome analysis using Short & Long Reads for Fungi (Basic)	MBS008
Whole Genome analysis using Short & Long Reads for Fungi (Advanced)	MBS009
Genome Mining for Natural Products from Bacteria/Archaea (Requires MBS001)	MBS010
Genome Mining for AMR and other features from Bacteria/Archae (Requires MBS001)	MBS011
Genome Based Microbial identification (Requires MBS001)	MBS012
Microbiome profiling (Basic Analysis 16S/18S/ITS/any other gene based)	MBS013
Microbiome profiling (Advanced Analysis 16S/18S/ITS/any other gene based)	MBS014
Shotgun Metagenomics (Bacterial/ Archaeal/Viral communities)	MBS015
Genome resolved Metagenomics (Bacterial/Archaeal/Viral communities)	MBS016
Transcriptome analysis (Kallisto/Salmon or prokaryote)	MBS017
Transcriptome analysis (HiSat/Star or eukaryote)	MBS018
In-silico genome isolation for mixed cultures	MBS019
Whole Genome analysis for Yeast (Basic)	MBS022
Whole Genome analysis for Yeast (Advanced)	MBS023
SRA Submission of NGS Dataset	MBS025
Whole Exome Analysis (Human)	MBS027
Mitochondrial Whole Genome Analysis	MBS028
Small RNA/miRNA Data Analysis	MBS030
Custom Analysis for NGS Data	MBS026

Specialized *in-silico* genome mining services

Natural Product Discovery

Microorganisms are some of the greatest chemists known to man and produce several bioactive chemicals. Genome mining can allow us to **predict** the **biosynthetic potential** of the organism even before attempting a costly process of chemical characterization. Such mining of genomes can also inform the chemical synthesis process thus making the process from **discovery to production** shorter.

MBS010 Genome Mining for Natural Products from Bacteria Archaea (requires MBS001)

Antimicrobial Resistance Profile

Antimicrobial resistance (AMR) is a global threat to human health and development. In fact, AMR is one of the top 10 global public health threats facing humanity as declared by WHO. Hence, it is integral to identify control and prevention strategies to combat the increasing threat of AMR. Among the many options, genome mining allows for an **accurate prediction of AMR** for bacteria. At Hi-Gx360®, our team will help you **identify the AMR markers** from the genomic sequence of your organism.

MBS011 Genome Mining for AMR and other features from Bacteria/Archaea (Requires MBS001)

In-silico Isolation for Mixed Cultures

Sometimes mixed microbial colonies are inadvertently sequenced together. In such cases all is not lost, it is possible to **separate** these **genomes bioinformatically**. Often this approach offers critical insights into the two organisms allowing for **devising strategies to isolate them** and further analyze them. Genome segregation can also offer clues into why these organisms grow together thus **revealing mechanisms of cross-feeding** based associations.

MBS019 In-silico genome isolation for mixed cultures

HiGenoMB Unzipping Genes

Consumables for Sequencing

Extraction Kit

Product Name	Product Code
HiPurA® Blood Genomic DNA Miniprep Purification Kit	MB504
HiPurA® Bacterial Genomic DNA Purification Kit	MB505
HiPurA® Mammalian Genomic DNA Purification Kit	MB506
HiPurA® Insect DNA Purification Kit	MB529
HiPurA® Paraffin-Embedded Tissue DNA Purification Kit	MB530

Product Name	Product Code
HiPurA® Soil DNA Purification Kit	MB542
HiPurA® Fungal DNA Purification Kit	MB543
HiPurA® PCR Product and Gel Purification Combo Kit	MB563
HiPurA® SuperPlant DNA Purification Kit (For Purification of DNA from plants rich in polyphenols)	MB571
HiPurA® HP Fungal DNA Purification Kit (following bead beating method)	MB576

Reagents

Product Name	Product Code
1kb DNA Ladder	MBT051
50bp DNA Ladder	MBT084
100bp DNA Ladder	MBT049
6X Gel Loading Buffer	ML015
2X PCR TaqMixture	MBT061
2-Propanol	MB063
Poly(ethylene glycol) MW 8000	MB150
1N Sodium hydroxide	ML195
5M Sodium chloride	ML008
1M Tris-Cl, pH 8.5	ML152
1M Tris-Cl, pH 7.0	ML090

Product Name	Product Code
3M Sodium acetate, pH 5.2-5.4	ML009
0.5M EDTA, pH 8.0	ML014
Molecular Biology Grade Water for PCR	ML065
RNA Liv™	ML161
RNase Kil™	ML162
1X PBS Solution	ML116
Diluent for DNA Extraction	MB228
Agarose, Ultrapure, Low EEO	MB229
Hi-SYBr Safe Gel Stain (10,000X in DMSO)	ML053
HiPurA® Mag Beads for Cleanup	ML239
DNA Kil™	ML221

Consumables

Product Name	Product Code
PCR Blocks	PR2
PCR Blocks	PR3
PCR Blocks	PR19
Aluminium Sealing Film	PR20
Optical Sealing Film 96 well PCR plate	PR18
96 Well Plate for Sequencing /PCR	PR26
Hi-PCR® Applicator for Sealing Film	PR28
Silicone Mat for 96- well plates (PCR)	PR27
8-Strip tubes with optically clear flat caps for Real-time PCR	PR17
PCR Tubes, Flat lid Autoclavable, Conical Bottom, with Graduation	CG281

Product Name	Product Code
PCR Tubes, Thin walled DNase/RNase free, Autoclavable, Conical Bottom, without Graduation, Flat lid	PW1255
Micro Centrifuge Tube - B	PW146
HiPer® Lock MicroCentrifuge Tube, 2.0ml	MBLA017
Barrier Tips, 10µl	LA749A
Barrier Tips XL, Max. capacity 10µl	LA749XL
Barrier Tips, 20µl	LA750A
Barrier Tips XL, Max Capacity 20µl	LA750XL
Barrier Tips, 100µl	LA1104A
Barrier Tips, 200µl	LA751A
Barrier Tips, 1000µl	LA859A
Polypropylene Cryogenic Storage Box	PW1215

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