







# **CORE FACILITY FOR BIOINFORMATICS** | SERVICES

# **DIRECT ACCESS SERVICE**

Categories	Client Type Rates (PHP)				
	UP Unit	Non-UP Government	Private		
DATA CRUNCHING					
Base Submission Fee (per day) <sup>1</sup>	100.00	120.00	140.00		
Usage-Hour Rate <sup>2,3</sup>	3.00	3.50	4.00		
DATA STORAGE					
Rate per Terabyte Chunk⁴ per day	30.00	36.00	50.00		

#### **NOTES**

- 1. Base Submission Fee is a fixed fee that will only take effect once within a calendar date, whenever a job has beem submitted through the queuing system. Logging in, data upload and download, as well as running simple UNI commands outside the queuing system will not activate this fee
- Failed runs will only be charged half the total cost of the run.
- Usage-hour is calculated from the number of reserved cores or memory/6, whichever is higher.
- A terabyte chunk refers to the range between two whole terabyte values (e.g., x < 1 TB, 1 TB < x < 2 TB, 2 TB < x < 3 TB, etc.)

# CUSTOM BIOINFORMATICS SERVICE

AVAILABLE WORKFLOWS				
1	Reads Quality Control	6	Molecular Phylogenetics	
2	Genome Assembly (De novo and/or Reference-based)	7	Simple Programming/ Parsing/ Scripting	
3	Variant Calling/ SNP Calling	8	Genome Annotation	
4	Transcriptome Assembly	9	Differential Gene Expression Analysis	
5	SSR/ Microsatellite Search and Primer Design	10	Metagenomics (Assembly, Diversity Analysis, Abundance Plotting, etc.)	

### **NOTES**

Costing for the above workflows will be given upon request. Kindly include the following information in your request for

- Availability and link to a reference if present (reference genome, similar workflow from a publication, etc.)
- Number of samples
- Sequencing coverage / throughput
- Sequencing platform used
- Desired output

## TRAINING AND WORKSHOPS

The facility offers training opportunities for various topics in bioinformatics and genomics. We also offer consultancy services for genomics-based projects. Please contact us for details and pricing.