Department of Zoology

University of Calcutta

35,BC Road , Kol-700019

Notice

No-WBDBT/1st/SEQ-1/2020 **Date-24/8/2020**

The quotation in sealed envelope is being invited from the listed companies of this university within 10 days, from the publication of notice. Companies are requested to submit their quotations to **Dr. Madhusudan Das**

Quotation requirement for whole exome sequencing for 11 samples

Technical requirements

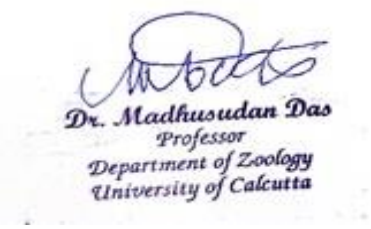
1. Sample run on Illumina hiseq X10 sequencer to generate 2X150bp

2. QC, exome capture, sequencing-ready library preparation using **Sure Select XT Human All Exon V5+UTR**., cluster generation.

3.Average Sequencing depth/sample should be 100x

4. 8-10 gb data yeild.
5. Complete Bioinformatics Analysis required.
6. phred score Q30≥ i.e minimum of 75% of the sequenced bases will be of Q30 value

Project investigator



Department of Zoology

University of Calcutta

35,BC Road , Kol-700019

Notice

No-WBDBT/1st/SEQ-2/2020 **Date-24/8/2020**

The quotation in sealed envelope is being invited from the listed companies of this university within 10 days, from the publication of notice. Companies are requested to submit their quotations to **Dr. Madhusudan Das**

Quotation Requirement for Epigenome-Wide Profiling of CpGs methylation status sequencing for 13 samples

Technical requirements

1. Illumina's 850K Infinium Methylation EPIC BeadChip.

2. Illumina iScan system.

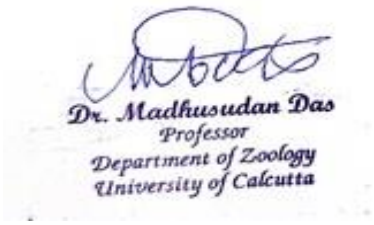
3.gDNA QC, Bisulfite conversion, whole genome amplification

4. Relative methylation levels between two samples or sample groups.

5. Methylation array data processing and analysis

6. Corrected resulting p- should be provided .

Project investigator



Department of Zoology

University of Calcutta

35,BC Road , Kol-700019

Notice

No-WBDBT/1st/SEQ-3/2020 **Date-24/8/2020**

The quotation in sealed envelope is being invited from the listed companies of this university within 10 days, from the publication of notice. Companies are requested to submit their quotations to **Dr. Madhusudan Das**

Quotation Requirement for Methylation Study Using Illumina Hiseq X Ten for 14 Samples.

Technical requirements

1. Illumina X10 platform.

2 Minimum of 10 x of effective genome coverage for each sample.

3. Read length- 2x150bp

4. Data yield- 30 Gb/Sample

5. Data processing and analysis

The Standard Deliverables:

1. The Raw fastq files and QC report containing the read information, data size, average base quality, GC percentage, Base quality distribution.
2. Alignment files (sorted bam files) and alignment statistics, chromosome wise read alignment distribution, Distribution of the methylated sites in the genic/intergenic regions.
3. Statistics on the raw methylation calls and their distance from Transcription Start sites.

Differentially methylated regions in the test and control samples (if any) along with Gen ontology annotations.

Project investigator