NOTICE INVITING TENDER

Whole Exome Sequencing Study for 21 Patients, BARC Hospital

Sealed Quotation is invited by Head, Medical Division, BARC Hospital, Anushaktinagar, Mumbai – 400 094 for “Whole Exome Sequencing Study for 21 Patients, BARC Hospital.

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<tr>
<td>1. Name of Item</td>
<td>Whole Exome Sequencing Study</td>
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<td>2. Scope of work</td>
<td>As Per Annexure</td>
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<td>3. Quantity</td>
<td>21 Patients</td>
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<td>4. Location of work</td>
<td>Pathology Unit, BARC Hospital</td>
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<td>5. Estimated cost of work</td>
<td>₹ 651,000/- (Inclusive of Taxes)</td>
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<td>6. Last date of receipt of Sealed Quotations</td>
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<td>7. Date of Opening</td>
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The Quotation must be placed in a sealed cover with the name of work and quotation number clearly written on the envelope addressed to “Administrative Officer – III, BARC Hospital, Anushakti Nagar, Mumbai – 400 094”. It should reach to Assistant Personnel Officer, Hospital Administration, F-541, 4th Floor, Annex Building, BARC Hospital, Anushaktinagar, Mumbai – 400 094 by Post only on or before 11.2019 at 13.00 hrs. and it will be opened at 15.00 hours on the same day. The Quotations should have the seal of the Company, Signature of the Proprietor of the firm, PAN and GSTN registration Number, failing which your quotation is liable to be rejected.
**General Terms and Condition**

1. The work should be completed within **90 days** from the receipt of Work order.

2. The firm should give rates, showing taxes, if any, and levies, packing forwarding and insurance charges separately giving full breakup details.

3. The offers should be legibly hand written or type written giving full address of the firm. The tenders should quote in figures as well as in words the rates amount tendered by him. Any discrepancy between the figures and words, the amount written in words will prevail. Alterations/overwriting, unless legibly attested by the tenderer, shall disqualify the tenders.

4. The tender rates should be kept open / valid for a period of six month from the date the tenders are opened.

5. In case of non-supply of materials/items, non-completion of work, within the due date/within the date of delivery, the Head, Medical Division will have the right to impose penalty, as deemed fit, to resort to risk purchase in full or part thereof at his/her discretion, his/her decision shall be final and binding.

6. Any other statutory levy imposed by the Govt. of India from time to time will be paid extra on demand with adequate proof thereof.

7. The Head, Medical Division shall be the final authority to reject full or any part of the supply/service which is not confirming to the specification/s and other terms and conditions.

8. Payment shall be made through Electronic Clearing System only after satisfactory completion of work.

Yours faithfully,

(Smt. Meerakshi S.)

Administrative Officer III

For and on behalf of President of India

1. AAO (Works), BARC
Quotations are invited by firms having excellent and demonstrable experience in providing clinical next generation sequencing services should be NABL/CAP accredited. Firms with Indian population variation database will be preferred.

1. The samples should be processed in India and samples should not be send out of India under any conditions.
2. The firm should provide CLINICAL REPORT of whole exome sequencing (WES) of patient DNA, by target capture methods to enrich the sequences for uniform coverage across all the genomic exons. Exonic regions of genes from fragmented total gDNA, followed by massively parallel, next generation sequencing of the captured fragments.
3. Firm should provide DNA QC analysis of the samples.
4. DNA library preparation, enrichment capture of exonic region by an exome capture kit and enrichment kit, cluster amplification, paired end run to obtain 2x150bp reads with at least 100X mean depth coverage.
5. The library preparation should ensure that all the genes are represented and there are no gaps in the genes.
6. Approximately 7GB cleaned data/samples (adapter and low quality sequences/reads removed) should be delivered. Proportion of clean data and raw data should be 90% and above.
7. >80-85% of total data should have >Q30 Phred score.
8. Detailed quality report before and after trimming should be provided. It should include base quality and sequence quality score, distribution details, average base content and GC distribution in the reads, PCR amplification details, check for over-represented sequences, adaptor trimming details, read length details (percentage of read length distribution), parameters used for trimming and details of software used for trimming/removal of low quality sequences/reads etc.
9. Alignment and recalibration, variant calling using appropriate software. Details of read alignment statistics and quality metrics obtained for each sample, and list of software's and parameters should be provided.
10. Depth of coverage details, percentage and details of target regions captured and regions missed should be provided for each sample.
11. Alignment of sequence data to human reference GRCh37/hg19 or the latest build on demand.
12. Variant calling (SNP and INDELS) should be performed using standard procedures of GATK or Samtools. Summary report of variants called from each sample to be provided. Variant calling should be done individually and together (all samples together to produce single VCF file for all samples). Variant filtration should be done using standard procedures and parameters used for filtering. List of software's and parameters used for annotation should be provided.
13. Delivery Time: Sample DNA QC report should be submitted within 10 days after receiving the samples. Raw FastQ file, clean FastQ file and other quality and parameter files mentioned should be delivered within 40 days after initial QC report. BAM file, Filtered and unfiltered VCF files (VCF of individual samples and all samples together) and other parameters and quality files mentioned above should be delivered within 50 days after initial sample QC report. FASTQ files should be provided on demand.
14. A final clinical report should be provided along with trio/quad analysis of patients. Novel variants should be compared with the existing Indian population database in addition to existing global database.