

Bidhan Chandra Krishi Viswavidyalaya

CROP RESEARCH UNIT

RESEARCH DIRECTORATE

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e-Tender Notification

Ref: CRU/2223/ Ten 7

Date...17.11.22.

Officer in Charge, Crop Research Unit, and PI, IAEA/ICAR-funded project is inviting price-quotation from the competent and *bonafide* vendors/ dealers having registration of GST for the supply of the following to the University within **fifteen days** from the date of publication of this notice as per specifications appended below (Table 1). **Vendors are requested to quote for the cost of a single sample, and the quoted price must be included GST and be valid for 31st March 2023.** They are also requested to upload the technical specification and other requirements, as appended in Table 1, in a separate file for Technical comparison. A demand draft of Rs 2000.00 (Two thousand only) in favour of Comptroller, BCKV, must have to be produced as the EMD charges. The quoted price will not be considered for comparison until the servicing laboratory is CAP/NABL/DSR certified and comply the technical specification as appended in table 1. Vendors must have to produce experience certificate/credintials in transcriptome sequencing in the form of at least five independent orders in last one year. The payment will be processed only after completing the service desired in the issued order.

Table -1: Tender specification of CRU/2223/ Ten 7 of 17.11.22

S.No	Name of the Item	No of Samples required.	Desired Specification	Quote Price (Rs.) with GST for a single sample
1	NGS based Transcriptome sequencing of plant samples (De Novo, Lentil),	25	Transcript Sequencing & Analysis of plant samples involving the cost of total RNA libraries (coding and non-coding) preparation and sequencing at least 30GB data in Illumina Novaseq6000; 100-150bp paired end reads per sample and at least 80% of the sequenced bases should be of Q30 value. Sequenced data with FASTQ files should be uploaded on the FTP server for download and review; other file formats required are: SOFT formatted family files, MINiML formatted family files and Series Matrix Files. Comprehensive bioinformatics analysis of sequenced data should include: a. The Raw fastq files and QC report containing the read information, data size, average base quality, GC percentage, Base quality distribution. b. 5' and 3' read bias should be measured. c. Aligned reads distribution and splice	

			<p>junction information d. Genes and isoforms expression values e. List of genes differentially expressed globally. f. GO annotation for differentially expressed genes such as biological process, molecular function and cellular component, pathway information (KEGG & Reactome). g. Gene Set Enrichment Analysis. h. Cluster analysis and heat maps. i. Publication and training support. j) Additional Analysis as per instruction for the next six months after completion of the project. The servicing laboratory must be CAP/NABL/DSR. Free pick up of sample in dry ice from BCKV must be assured in the quotation.</p>	
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17/11/22
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