



Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu
School of Biotechnology, FoA, Chatha -180009

NIT No:AUJ/SBT/20-21/F-3/1141

Dated:21-10-2020

Due on: 13-11-2020

Notice Inviting Tender

On behalf of the Vice-Chancellor, SKUAST-Jammu, Coordinator, School of Biotechnology invites tenders from the principal manufacturers or authorized firms/ dealers dealing with sequencing services for the following works with detailed specification given as Annexure-I

S. No.	Name of the work	Qty.	Earnest Money Deposit (in Rs.)	Cost of Tender Document (in Rs.)
1.	Metagenome Sequencing of Basmati rhizosphere samples	06	3800.00	1000/-
2	Genotyping by sequencing of Brassica samples	40	4000.00	1000/-

Terms and Conditions

1. The Bidding documents/NIT can be downloaded from the website www.skuast.org w.e.f 22-10-2020 from 9:30 A.M onwards.
2. The tender can be submitted from 22-10-2020 (9:30 AM) to 13-11-2020 upto 2:00 P.M.
3. Tender documents for two works shall be submitted separately
4. List of tender documents (**as pre-qualification bid**) to be submitted:-
 - i. EMD in the form of CDR/FDR pledged to Comptroller, SKUAST-J, Main Campus, Chatha, Jammu.
 - ii. PAN/TIN number.
 - iii. Demand draft towards tender processing charges, drawn in favour of Comptroller, SKUAST-J, Main Campus, Chatha, Jammu.
 - iv. CDR/FDR amount as specified against each work pledged in favour of "Comptroller, SKUAST-Jammu" towards Earnest Money Deposit.
 - v. Copies of Registration Certificate of GST
 - vi. Authorization certificate from principal manufacturer.
 - vii. The copy of the relevant Quality certificates (ISO).
 - viii. List of sequencing services being provided
 - ix. Undertaking of not being blacklisted by any Govt. Agency/ department.
 - x. List of clients being served (Agricultural Universities/ Educational Institutes/National Institutes/others separately in the last three years) with Contact name & address with mobile no.
 - xi. Bank Details on letter head along with cancelled cheque.
5. Services Related Terms and Conditions:
 - I. Sample should be collected from the University/Institute.
 - II. Raw data and bioinformatics analysis in standard file formats
 - III. Analysis report containing complete methodology from Sample QC to data analysis with all the tables, figures & results.
 - IV. Data storage and delivery through external hard drive.
 - V. Turnaround time should be ≤ 40 working days from sample QC acceptance to filtered raw data availability.

6. Each tender shall be submitted in two separate sealed envelopes subscribed as, “Technical Bid” and “Financial Bid” and thereafter, sealed in envelopes duly subscribed as “Tender for Metagenome sequencing or GBS”.
7. The tender must be delivered in the office of the **Coordinator, School of Biotechnology, SKUAST-J, Main Campus, Chatha, Jammu-180009 (J&K)** on or before due date by speed post/registered post. If the office happens to be closed on the last date of receipt as specified, the same will be received on the next working day at the same time and venue.
8. Offers without processing tender Fee and EMD shall summarily be rejected.
9. The rates quoted shall remain valid atleast for 180 days.
10. Incomplete or tenders received after the due date shall not be entertained.
11. The distributors/ dealers/supplier should have experience in this field and satisfactorily completed the similar nature of works.
12. In case of any controversy between the Supplier and the University, the decision of the Vice Chancellor of SKUAST-Jammu shall be final and binding on the tenderer.
13. Bids will be opened in the presence of the members of the Divisional Purchase Committee.
14. Financial bids of only those bidders will be opened; who will qualify the technical bid.

**Coordinator
School of Biotechnology**

No: AUJ/SBT/2020-21/F- 3/1142-44

Date: 21-10-2020

Copy to:

- Dean, FoA, Chatha, for kind information
- Incharge Data Centre for uploading on University Website
- SVC for timely Publishing of NIT in two local daily for wide publicity

Annexure-I

S. No.	Name of the service to be provided	Qty.	Detailed specifications
1.	Metagenome Sequencing of Basmati rhizosphere samples	06	<ul style="list-style-type: none"> ○ Raw reads of ~6 GB per sample with an average read length of 2×150bp PE ○ Preparation of paired-end library for the metagenomic DNA File ○ Enrichment of library ○ Sequencing and bioinformatics ○ Format : fastq
2	GBS/ddRAD-sequencing of plant samples	40	<p>Data deliverables:</p> <ul style="list-style-type: none"> ○ 250-300 MB data for each sample with a base call accuracy of 99 percent ○ Paired-end reads in 2 x 100 bases format ○ Aligned and filtered files in BAM and SAM filter format ○ SNP files after alignment of all samples ○ Variant comparison from all samples ○ Samples specific SNPs ○ SNPs in hmp format ○ Library preparation, sequencing and bioinformatics