



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

NIT No. AUJ/SBT/18-19/4196

Date: 08-03-2019

Due on: 22-03-2019

TENDER NOTICE

For and behalf of the Vice Chancellor, SKUAST-Jammu, sealed tenders are invited from the authorized distributors/dealers/suppliers for supply of Next Generation Sequencing services. The detailed specifications, terms, conditions and tender document can be downloaded from University website www.skuast.org

(Dr. Mehak Gupta)

Principal Investigator, N-PDF, SERB Project

No. AUJ/SBT/18-19/4212-4215

Date: 08-03-2019

Copy to:

1. Director Research, SKUAST-J, Chatha, for kind information
2. Coordinator, SBT, SKUAST-J, Chatha, for kind information
3. Incharge Data Centre, SKUAST-J for uploading on University Website
4. SVC for timely Publishing of NIT in two local dailies (one each in Hindi and English)



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For and behalf of the Vice Chancellor, SKUAST-Jammu, sealed tenders are invited from the authorized distributors/dealers/suppliers for supply of Next Generation Sequencing services as per the specifications (Annexure-I); terms & conditions given hereunder.

S. No.	Description	Samples
1.	High quality Transcriptome sequencing using NGS	06

Terms and conditions

1. Date of Publishing from 11-03-2019
2. NIT can be downloaded from the website www.skuast.org w.e.f 11-03-2019 from 2:00 PM onwards.
3. The bids shall be deposited from 11-03-2019 (2:00 PM) to 22-03-2019 Upto 2:00 P.M. The bids received will be opened at 3:30 P.M on 22-03-2019.
4. List of tender documents (as technical bid) to be submitted are PAN/TIN/GST number and authorization certificate from principal supplier, if any.
5. The tender shall be submitted in two separate sealed envelopes i.e. Technical Bid and Financial Bid duly subscribed on two envelopes, "Technical Bid" and "Financial Bid" and thereafter, sealed in one envelop duly subscribed as "UPS".
6. Prices quoted must be FOR, SKUAST-J, Chatha and inclusive of transit insurance. Discount, if any, should be shown separately. Additional charges on account of Excise Duty, GST, Entry Tax or any other charge / levy must be specifically quoted.
7. The offer should be valid for a period of 180 days.
8. The specifications of the NGS services should conform to the highest standards.
9. Late, delayed and incomplete tenders and amendments and additions to the tender after opening of the same will not be accepted.
10. The successful tenderer shall be responsible for providing the facility at the University with following points:
 - a) Sample should be collected from the University/Institute.
 - b) Sequence report containing complete methodology from Sample QC to sequence data generated with all the tables, figures & results.
 - c) Data storage and delivery through external hard drive.
 - d) Turnaround time should be ≤ 40 working days from sample QC acceptance to filtered raw data availability.
 - e) Support for the raw data submission to public repository.
11. 100% payment shall be made on completion of assigned job.
12. The tender must be delivered in the office of Dr. Mehak Gupta, Principal Investigator, N-PDF, SERB project, School of Biotechnology, SKUAST-J, Main Campus, Chatha, Jammu-180009 (J&K) on or before 22-03-2019 upto 2:00 PM by speed post/registered post/by hand. 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.

Sd/
Principal Investigator
N-PDF, SERB

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Detailed Technical Specifications:

Name of the Item	No. of samples	Specification
High quality Transcriptome sequencing using NGS	06	<ol style="list-style-type: none"> 1. QC report of RNA samples using Suitable Bioanalyzer with RIN value of > 8 to be taken to perform the experiment. 2. Each library to be prepared using Illumina adapters. 3. All the libraries to be validated using suitable Bioanalyzer and libraries passing in-house QC standards to be taken further for sequencing using Illumina Hi-Seq with : <ul style="list-style-type: none"> • mRNA enrichment and rRNA removal • Regular and strand-specific transcriptome library • 2x150 bp paired end sequencing • ≥ 25 Million reads per sample recommended • Q-30 for more than 80% data

Principal Investigator, N-PDF, SERB Project