



**JAWAHARLAL INSTITUTE OF POSTGRADUATE MEDICAL EDUCATION &
RESEARCH (JIPMER)**

(An institution of National Importance under the Ministry of Health & Family Welfare, Govt. of India)
Dhanvantari Nagar, Puducherry-605006.

Dated: 08 January 2025

Enq.No. JIP/ SSTD/Limited tender/Extramural/SR/IADVL/1/2025-26

LIMITED TENDER

Project title: Transcriptome analysis of Stevens Johnson syndrome and Toxic epidermal necrolysis with focus on cell death pathways in disease mechanisms.

Dear Sir/Madam,

Sub: Limited tender invited by Department of Skin & STD for extramural project for RNA sequencing. –
Reg.,

Please quote your lowest rate for RNA sequencing service as per the list given overleaf/attached, subject to the following terms and conditions.

- 1 Rates should be quoted only for the items which are available in stock and can be supplied immediately on receipt of order.
- 2 GST as applicable.
- 3 No insurance charges are payable as per the rules in the Government. As such, the firms before quoting should take into consideration all the risks in the transit and then furnish limited tender which should cover insurance charges also. If any point is raised as regards insurance charges after orders are issued, the same will not be entertained and the firms thereafter should affect the supply at their own cost.
- 4 Rates should be quoted F.O.R Department of Skin & STD office, JIPMER, Puducherry door delivery. Extra packing, forwarding charges etc. should not be quoted.
- 5 Delivery is required urgently. Tenders should please state the guarantee delivery period they can offer. As delivery date is essence of the contract, this should be strictly adhered to by the successful tenders. Items to be supplied within 30 days of receipt of supply order.
- 6 No supply, which is not according to the specifications and not meeting our requirement, will be accepted.
- 7 The Director/ Principal investigator shall have the right of rejecting the limited tender in whole or part without assigning any reason therefore.
- 8 In case of high precision instruments, the firms should give a guarantee certificate for their satisfactory performance.
- 9 HSN code should be included of each item and GST should be given as per govt rules.
- 10 All products should be mentioned as per specification in the tender document mentioned.
- 11 Limited tender quotations should be sent only by Certificate of Posting/ Registered Post/ Speed Post. Hand quotations & Emails are not accepted.



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- 12 Brand name, Model as applicable is to be mentioned for every item quoted.
- 13 The firms participating in the limited quotation must have registered with the Purchase section of JIPMER before last day to submission. If not, the firms may be registered before quoting their rates. Quotations from unregistered firms will not be accepted. For more details in this regard please see "Tender section of JIPMER website <https://www.ipmer.cdu.in/tender>.
- 14 Rate quoted has to be valid up to 3 years from the purchase order and the vendor has to ensure that they will supply for three years.
- 15 Some of the items may require staggered supply. Vendor should comply to this request.
- 16 The manufacturer and the items have to be approved by standard regulatory bodies.
- 17 The firm should ensure that they are supplying at least all the components of particular one item.
- 18 Tender should contain technical as well as price bid.
- 19 Please furnish your limited tender in a sealed cover superscribing as: **Limited tender for RNA sequencing service.** Limited tender quotation should be in the name of "The Director, JIPMER" and sent to the **postal address: Dr. Sivaranjini R, Additional Professor, Department of Skin & STD, JIPMER, Dhanvantari Nagar, Puducherry-605006, India.**

Enq.No. JIP/ SSTD/Limited tender/Extramural/SR/IADVL/1/2025-26, Dated :08.01.2025


Limited tender quotations should reach this office on or **before 23-01-2025 by 4.30 P.M.**

Limited Tender received after the due date will be summarily rejected.

Attach the below listed annexures in addition to compliance certificate with the specifications (both general and technical)

1. Proof of the equipment in name of the company/ Authorization access to Respective Sequencing platforms.
2. List of publications done with above services.
3. Atleast 3 reference from previous clients.
4. Filled and signed Evaluation table as in the document
5. JIPMER vendor registration certificate.
6. Pamphlet of service information with the quotation

Yours faithfully


Sivaranjini R
अपर आचार्य / ADDITIONAL PROFESSOR
त्वचा व रक्तरोम विज्ञान विभाग
Department of Dermatology & STD
जिपमेर, पुदुच्चेरी / JIPMER, Puducherry -6.



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General specifications for RNA Sequencing services

Sample details: The work concerns transcriptome analysis from **skin biopsy specimens** of those with drug reactions like Stevens Johnson syndrome/Toxic epidermal necrolysis/erythema multiforme. A total of **40 samples** (20 samples from lesional skin and 20 uninvolved skin samples from the same subjects) will need to be sequenced in this project to identify the differentially expressed genes.

- The complete scope of work should be done by the vendor within India. Samples should not be sent out of India
- The vendor should provide a facility certificate to testify the possession of an in-house Illumina HiSeq 2500/HiSeq 4000/latest model Illumina NovaSeq 6000 installed, and NGS facility explicitly in the name of the company (it should not be in lease agreement or tie-up/collaborative mode).
- Biopsy tissue will be provided by the client. It will be the responsibility of the service provider to collect the samples from the lab and transport to the sequencing center under proper conditions. The client will not be responsible for any payment for the transportation of the samples.
- The PI/representative should be allowed to visit and train in both wet lab and bioinformatics process. If not specified clearly in your tender document, the tender will stand to be rejected.
- For the tissue samples provided by the PI, RNA extraction should be done using a standard kit and confirmed with spectrophotometer and Qubit test prior to further processing.
- The vendor should provide confirmed order copies from government institutions for working on whole exome sequencing projects where at least 1400 samples (cumulative) have been processed.
- Proof of Bioinformatics facility: Declaration for in-house bioinformatics/dry lab facility in India should be provided. Partner/collaborator company installation certificate located abroad will not be considered.
- The vendor should have demonstrated scientific capability for the successful completion of undertaking genomics, as documented by the vendor having research publica-



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tions in peer-reviewed journals for at least 3 sequencing projects using NGS platform. The vendor should have done at least one such project in an INI/ Government Institute. Appropriate documents to support this claim should accompany the proposal.

- Establishment of firm: The firm should have a minimum of 4 years of experience in handling NGS projects, and testimonials for the successful completion should be provided.
- Either one order of 60-70 lacs or 2 orders of 40 lacs in the last 2 years should be furnished, or proof should be provided.
- The vendor should specify the government service tax in the financial bid.
- Acknowledged recognition for the vendor's repute as demonstrated by its participation in any multi-nation and multi-ethnic genomics study project(s) would be preferred.
- The firm should not be blacklisted/debarred/banned by any government department/public sector undertaking.
- If required, the vendor will be called for a technical presentation to showcase their expertise.
- Necessary training and bioinformatics support would be provided by the vendor.
- NCBI data submission along with publication support to be provided.
- Project timeline: 90 days from the receipt of samples.
- Raw data and analysis results to be maintained by the firm on their servers for more than 120 days.
- Sample RNA QC analysis should be done at no extra cost, and the report should be submitted within 5 days after receiving the samples. Raw FastQ file, Clean FastQ file, and sequencing details should reach the client within 85 days after sample QC is completed.
- Price for each service must be quoted separately. The rate for sequencing with and without bioinformatics analysis and data size has to be mentioned separately.
- The bidder should provide 3 customer feedbacks mainly highlighting data analysis support for NGS projects provided by the company.
- The bidder should provide evidence of atleast 3 publications, in Pubmed indexed journals from the NGS work carried out by them.



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- Reagents/consumables used in the library preparation and subsequent process must be of standard quality. They should be used as per the tender document. DNA insert size report using a bioanalyzer of the final RNA library must be provided along with the Q30 report of every sequencing run. Any deviation during the process will result in termination of the contract.
- Capability to deliver high-quality raw sequencing data and bioinformatics analysis output in a timely and efficient manner (90-95% of total data have Phred-score >Q30). Summary of complete sequencing runs, raw FastQ file, and Clean FastQ file should be provided. QC reports should be provided (with data size, adapters, read length and depth, Phred quality score, GC content, base quality distributions). Details of the bioinformatics tools should be mentioned clearly in the tender document.

Technical specification for RNA Sequencing

1. Library Preparation

Library construction should be carried out using an Illumina-specific library preparation kit. Library prep is designed to be compatible with all Illumina sequencing systems and is extensively validated on the NextSeq 500/550 and NovaSeq 6000 Systems to generate 30 M, 2 * 150 bp reads/sample. Up to 95% of the sequenced bases should be of Q30 value. Sequenced data should be processed to generate FASTQ files and uploaded on the FTP server for download.

2. Sequencing and Data Quality

- RNA sequencing should be performed using the Illumina HiSeq or NovaSeq 6000 platforms.
- Each sample should be sequenced at the mean coverage of 150-fold (150X) with 101/150-bp paired-end sequencing method.
- Minimum 12-13 GB clean data per sample (after removal of adapters and low-quality sequence/reads).
- Capability to deliver high-quality raw sequencing data and bioinformatics analysis output in a timely and efficient manner (90-95% of total data have Phred-score >Q30). Summary of complete sequencing runs, raw FastQ file, and Clean FastQ file should be provided. QC reports should be provided (with data size, adapters, read length and depth, Phred quality



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score, GC content, base quality distributions). Details of the bioinformatics tools should be mentioned clearly in the tender document.

3. Standard and Advanced Analysis

- Standard Analysis: Pre-processing of reads including Quality Filtering, trimming low-quality reads, Replication removal, Sequence reconstruction and grouping, Gene prediction, Functional Annotation.

-Advanced Bioinformatics Analysis: Standard Analysis Deliverables, Differential gene expression analysis, Statistical analysis, Differential abundance analysis, COG, KEGG Analysis, Gene Ontology and Pathway analysis (Functional Analysis), Integration with clinical data, Data to NCBI SRA, Support in providing write-up on methods for manuscript purpose.

4. Additional Requirements

-Price for each service must be quoted separately. Rate for sequencing with and without bioinformatics analysis and data size has to be mentioned separately.

-The vendor should have demonstrated scientific capability for the successful completion of undertaking genomics, as documented by the vendor having research publications in peer-reviewed journals for 3 sequencing projects using NGS platform. Appropriate documents to support this claim should accompany the proposal.

-The PI/representative should be allowed to visit and train both the wet lab and bioinformatics process free of cost. If not specified clearly in your tender document, the tender will stand to be rejected.

-Reagents/consumables used in the library preparation and subsequent process must be of standard quality. They should be used as per the tender document. DNA insert size report using a bioanalyzer of the final RNA library must be provided along with the Q30 report of every sequencing run. Any deviation during the process will result in termination of the contract.

-Capability to deliver high-quality raw sequencing data and bioinformatics analysis output in a timely and efficient manner (90-95% of total data have Phred-score >Q30). Summary of complete sequencing runs, raw FastQ file, and Clean FastQ file should be provided. QC



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reports should be provided (with data size, adapters, read length and depth, Phred quality score, GC content, base quality distributions). Details of the bioinformatics tools should be mentioned clearly in the tender document.

- Vendor should provide access to an online platform for real-time tracking of samples and accessing reports. Pamphlet of service information should be attached along with the quotation.

-Turnaround time: Reports should be provided within a maximum of 90 working days. (Any delay beyond 90 days will attract a penalty of 10% of the tender value).



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Evaluation table

No.	Specification for 40 samples	Unit price (per sample)	Total price for 40 samples	GST	Total with GST
1.	RNA Extraction: Including purification and quantification.				
2.	Sequencing: RNA sequencing should be performed using the Illumina HiSeq or NovaSeq 6000 platforms. Each sample should be sequenced at the mean coverage of 150-fold (150X) with 150-bp paired-end sequencing method. Minimum 12-13 GB clean data per sample (after removal of adapters and low-quality sequence/reads). Capability to deliver high-quality raw sequencing data and bioinformatics analysis output in a timely and efficient manner (90-95% of total data have Phred-score >Q30). Summary of complete sequencing runs, raw FastQ file, and Clean FastQ file should be provided. QC reports should be provided (with data size, adapters, read length and depth, Phred quality score, GC content, base				



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	<p>quality distributions). Details of the bioinformatics tools should be mentioned clearly in the tender document.</p> <p>Standard Analysis: Pre-processing of reads including Quality Filtering, trimming low-quality reads, Replication removal, Sequence reconstruction and grouping, Gene prediction, Functional Annotation.</p>				
3.	<p>Advanced Bioinformatics Analysis: Standard Analysis Deliverables, Differential gene expression analysis, Statistical analysis, Differential abundance analysis, COG, KEGG Analysis, Gene Ontology and Pathway analysis (Functional Analysis), Integration with clinical data, Data to NCBI SRA, Support in providing write-up on methods for manuscript purpose.</p>				