

BHABHA ATOMIC RESEARCH CENTRE
NUCLEAR AGRICULTURE AND BIOTECHNOLGY DIVISION
MUMBAI 400 085

Reference No: NABTD/2022/I/12505

25th January, 2022

Sub: Whole genome transcriptome analysis of *B. juncea*

1. Quotations are invited for Whole genome transcriptome analysis of *B. juncea* (samples: 12).

Service description:

2. Taxes and excise duties shall be quoted separately. Form AF shall be provided wherever necessary.
3. The quotations are to be strictly in printed letter head and the quotation format should consist of sales tax registration number registered with local ST authority/CST authority, PAN number of the firm, service tax registration number etc.
4. The quotation must reach the undersigned by **February 20, 2022** and must be sent in a sealed envelope superscribed **with the above reference number and due date** given above, **by registered/speed post only**.
5. The address on the envelope should read
Dr. Archana N. Rai
Nuclear Agriculture And Biotechnology Division
Bhabha Atomic Research Centre, Mumbai 400 085.
6. There is no need of inspection.
7. Payment will be made against delivery.
8. The bidder shall deliver the finished components within six weeks from the date of firm purchase order issued to the bidder.
9. Director, BioScience Group, BARC reserves the right to accept/reject any or all quotations without any reason.

Dr. Archana N. Rai
SO/F, MBSII, NABTD

Forwarded through

Dr. T. R. Ganpathi
Head, N.A.B.T.D.

To,
Web display and Notice Boards.....

Annexure 1

- RNA extraction, QC and reporting.
- Library preparation, library validation and quantitation .
- Sequencing using Illumina Hiseq 100X2 PE chemistry, ~40 million reads per sample and FASTQ conversion.
- Raw data quality check, Data cleaning, Read alignment, alignment quality check and marking/removal of PCR duplicates, Transcripts assembly and assembly statistics.
- Identification of known, conserved and putative genes, Differential gene expression profiling including expression pattern analysis, comparative transcriptomic study across the samples and reporting.
- Identification of SSR, Transposable element and Novel transcripts