INSTITUTE OF MENTAL HEALTH & NEUROSCIENCES (IMHANS)
An Autonomous Institution under the Government of Kerala
Government Medical College Campus, Kozhikode, Kerala, India, 673008
Telephone: +91-495-2359352 Email: office@imhans.ac.in Website: www.imhans.ac.in

No. A3/1331/2026/IMHANS 20-11-2026

NOTICE INVITING RATE CONTRACT PROPOSALS FOR THE YEAR 2026-2027

Proposals are invited for the Annual Rate Contract of Genomics Services for research activities for the year 2026 – 2027 at the Center for Interdisciplinary Brain Sciences (CIBS), Institute of Mental Health and Neurosciences (IMHANS), Kozhikode, Kerala

No.	Service Description
1	**Clinical exome sequencing (for germline genetic variants) > 100 X coverage with Analysis:** ○ **Source material:** Extracted genomic DNA samples and occasionally blood samples ○ **DNA Quality Check (QC):** [NanoDrop, fluorometric, electrophoresis system] ○ **Library preparation, QC & Exome Capture:** Standard clinical exome panel of genes with known disease associations (OMIM/HGMD/ClinVar). ○ **Sequencing:** Illumina Platform (NovaSeq X Plus or similar) with paired-end 2 x 150 bp read length and >100x coverage (4-5 GB data) per sample. ○ **Data QC criteria:** Coverage of ≥98% of targets at ≥20x, ≥99% of the clinical gene list at ≥20x, ≥99% of targets at ≥10x, On-target rate ≥70-75% and Fold-80 base penalty <1.6. ○ **Raw data delivery:** Demultiplexed paired-end FASTQ (R1/R2.fastq.gz) for each sample, with MD5 checksums. ○ **Bioinformatics analysis with standard deliverables:** Bioinformatics analysis (GRCh38 alignment, variant calling, annotation, and ACMG/AMP classification against the clinical gene panel), with standard deliverables: BAM with index, GVCF, VCF, variant annotation table, QC report, gene-level coverage report with gaps list, signed clinical report.
2a	**Whole exome sequencing (for germline genetic variants) 100 X coverage with Analysis:** ○ **Source material:** Extracted genomic DNA samples and occasionally blood samples. ○ **DNA Quality Check (QC):** [NanoDrop, fluorometric, electrophoresis system]. ○ **Library preparation and Quality Check (QC):** Twist Bio Comprehensive Exome panel & Exome Capture and QC as per manufacturer's specifications. ○ **Sequencing:** Illumina Platform (NovaSeq X Plus or similar) with paired-end 2 x 150 bp read length and 100x coverage (>7- 8 GB data) per sample. ○ **Data QC criteria:** Mean target coverage 100x; ≥97% of targets at ≥20x; ≥99% of targets at ≥10x; on-target rate ≥75%; Fold-80 base penalty <1.6. Variant calling performance should demonstrate sensitivity of >99% for SNVs, and >97% for small indels, validated against recognised reference standards such as Genome in a Bottle (GIAB) NA12878, with sensitivity, precision and false-positive rates reported wherever available. ○ **Raw data delivery:** Demultiplexed paired-end FASTQ (R1/R2.fastq.gz) for each sample, with MD5 checksums. ○ **Bioinformatics analysis:** Bioinformatics analysis (GRCh38 alignment, variant calling, annotation).Variant calling and filtering for SNVs and small indels with GATK. VQSR or hard filters, with minimum depth, genotype quality, and allele balance thresholds stated. Low-quality variants

Scanned with OKEN Scanner

	are flagged, not silently removed. Variant Annotation: gene, transcript (MANE Select where available), HGVS nomenclature, consequence, zygosity. read depth, gnomAD frequency (plus an Indian/South Asian dataset where available), ClinVar, and CADD, VEP, and REVEL annotations. Tools, reference genome, and database versions should be listed in the report. ○ **Standard deliverables per sample:** FASTQ files, aligned BAM with index, individual GVCF and VCF files, variant annotation table, QC report: DNA QC, library QC, sequencing metrics, and all data QC criteria above, with a pass/fail result. Batch summary: methods, tool and database versions, reference build, Twist panel version, and BED file.
2b	**Whole exome sequencing (for germline genetic variants) 100 X coverage with Trio Analysis:** ○ **Source material:** Extracted genomic DNA samples and occasionally blood samples. ○ **DNA Quality Check (QC):** [NanoDrop, fluorometric, electrophoresis system]. ○ **Library preparation and Quality Check (QC):** Twist Bio Comprehensive Exome panel & Exome Capture and QC as per manufacturer's specifications. ○ **Sequencing:** Illumina Platform (NovaSeq X Plus or similar) with paired-end 2 x 150 bp read length and 100x coverage (>7- 8 GB data) per sample. ○ **Data QC criteria:** Mean target coverage 100x; ≥97% of targets at ≥20x; ≥99% of targets at ≥10x; on-target rate ≥75%; Fold-80 base penalty <1.6. Variant calling performance should demonstrate sensitivity of >99% for SNVs and >97% for small indels, validated against recognised reference standards such as Genome in a Bottle (GIAB) NA12878, with sensitivity, precision and false-positive rates reported wherever available. ○ **Raw data delivery:** Demultiplexed paired-end FASTQ (R1/R2.fastq.gz) for each sample, with MD5 checksums. ○ **Bioinformatics analysis (GRCh38 alignment, variant calling, annotation):** Variant calling and filtering for SNVs and small indels with GATK. VQSR or hard filters, with minimum depth, genotype quality, and allele balance thresholds stated. Low-quality variants are flagged, not silently removed. Variant Annotation: gene, transcript (MANE Select where available), HGVS nomenclature, consequence, zygosity, read depth, gnomAD frequency (plus an Indian/South Asian dataset where available), ClinVar, and CADD, VEP, and REVEL annotations. Tools, reference genome, and database versions should be listed in the report. ○ **Trio-based analysis:** Joint variant calling and genotyping of all three individuals (proband and both biological parents), generating a multi-sample VCF and pedigree (PED) file. Trio-level QC, including sample identity, parentage/relatedness, sex concordance and Mendelian error assessment. Inheritance-based variant identification and separate reporting of: ○ De novo variants (SNVs and indels) present in the proband and absent in both parents. ○ Autosomal recessive homozygous variants. ○ X-linked variants, considering the sex of the proband. ○ Potentially relevant inherited autosomal dominant variants. For candidate de novo variants, parental read depth (minimum 20×), genotype quality, allele balance and reference/alternate read counts should be reported to assess confidence. ○ **Standard deliverables per sample:** FASTQ files, aligned BAM with index, individual GVCF and VCF files, variant annotation table, Joint multi-sample VCF and PED file, Separate candidate variant lists for each inheritance model, Trio QC and Mendelian consistency report. QC report: DNA QC, library QC, sequencing metrics, and all data QC criteria above, with a pass/fail result. Batch summary: methods, tool and database versions, reference build, Twist panel version, and BED file.

Scanned with OKEN Scanner

3	**Transcriptome sequencing** (Total RNA-seq): ○ Source Material: RNA or frozen cells ○ RNA extraction and Quality Check (QC) ○ Ribo-depletion using Ribo-Zero Kit & library preparation ○ Sequencing on Illumina Platform (NovaSeq X plus or similar) with 2 x 150bp read length with 60M reads/sample (9GB) data generation. ○ Raw data delivery: Demultiplexed paired-end FASTQ (R1/R2.fastq.gz) for each sample, with MD5 checksums. ○ Bioinformatics analysis: Alignment to an appropriate reference genome/transcriptome, Gene and transcript-level expression quantification, Differential gene expression analysis, where experimental groups and biological replicates are provided, Functional annotation and pathway enrichment analysis of differentially expressed genes, where applicable, Documentation of bioinformatics tools, reference genome and database versions, and analysis parameters ○ Standard deliverables: Raw FASTQ files, RNA extraction and RNA QC report, Library preparation and library QC report, Sequencing quality report, aligned BAM files with index, Gene/transcript expression quantification files, Differential expression results, where applicable, Functional annotation and pathway enrichment results, where applicable, Final bioinformatics analysis report documenting methodology, software versions, reference genome and databases used.
4	**Transcriptome sequencing** (polyA RNA-seq) ○ Source Material: RNA or frozen cells ○ RNA extraction and Quality Check (QC) ○ Polyadenylation using Poly-A tail Kit & library preparation. ○ Sequencing on Illumina Platform (NovaSeq X plus or similar) with 2 x 150bp read length with 30M reads/sample (4.5GB) data generation. ○ Raw data delivery: Demultiplexed paired-end FASTQ (R1/R2.fastq.gz) for each sample, with MD5 checksums. ○ Bioinformatics analysis: Alignment to an appropriate reference genome/transcriptome, Gene and transcript-level expression quantification, Differential gene expression analysis, where experimental groups and biological replicates are provided, Functional annotation and pathway enrichment analysis of differentially expressed genes, where applicable, Documentation of bioinformatics tools, reference genome and database versions, and analysis parameters ○ Standard deliverables: Raw FASTQ files, RNA extraction and RNA QC report, Library preparation and library QC report, Sequencing quality report, aligned BAM files with index, Gene/transcript expression quantification files, Differential expression results, where applicable, Functional annotation and pathway enrichment results, where applicable, Final bioinformatics analysis report documenting methodology, software versions, reference genome and databases used.

Scanned with OKEN Scanner

General Terms and Conditions

1. The service provider should have published evidence (peer-reviewed research papers) for providing the genomics services requested, specifically in human samples for large-scale studies during the last three years. The details should be enclosed with the application.
2. The service provider should perform all the genomics services requested within their facility in India & NOT be outsourced to other companies in India or abroad.
3. The clinical exome sequencing services should be accredited by the College of American Pathologists (CAP)
4. Samples will be submitted as blood samples or nucleic acids (DNA/RNA). The company representative should collect the samples for sequencing in appropriate temperature packaging on a pre-decided day, every time, from the indenter at no extra charge.
5. The cost should be inclusive of sample collection, DNA/RNA isolation, purification, library construction, data curation, quality control, and appropriate bioinformatic analysis, depending on the service.
6. The quantity and quality of the sequencing data should match the indenter's needs as mentioned in the order.
7. The raw data of sequencing reads, results, and data analysis should be handed over to the indenter on an external hard disk or via online data-sharing portals.
8. The turnaround time for results from the submission of samples should be 4-6 weeks
9. The price quoted must be valid for the entire one-year rate contract period.
10. The rate contract is valid for one year from the date of execution of the rate contract. Hence, quote the validity of the rate contract period as one year from the date of execution of the rate contract order, instead of the specified period, such as the financial year or the Calendar Year
11. The price quoted for each service should be submitted along with the application in the form of a Hard/Soft copy
12. Dealers should submit the authorisation letter from the firm concerned.
13. The tax rate applicable to the educational/research institution may be mentioned in the proposal for the rate contract.
14. All other terms and conditions per the store purchase rules of the Government of Kerala also apply to this rate contract.
15. The application containing other terms and conditions that are not acceptable will be rejected.
16. Other details can be obtained from IMHANS Website (www.imhans.ac.in) or the undersigned during office hours (Phone: +91495-2359352; +91-9400061163; email: office@imhans.ac.in).

Scanned with OKEN Scanner

ior providing
es during the

Tender Details

1	Tender No. & date		A3/1331/2026/IMHANS dated 20/11/2026
2	Last date and time for receipt of Tender		04.12.2026, 12 noon
4	Date and time for opening of tender		04.12.2026, 2 PM
5	Price of tender form		Rs.1000 /- + GST 18%
7	E.M.D		Rs. 5000 /-

Director

Dr. Shibukumar T. M.
MBBS, MD (Psychiatry)
Reg No.28628
Director, IMHANS
Kozhikode

To: Notice board/Website

Scanned with OKEN Scanner