



अखिल भारतीय आयुर्विज्ञान संस्थान, भोपाल
ALL INDIA INSTITUTE OF MEDICAL SCIENCES (AIIMS) BHOPAL

Saket Nagar, Bhopal-462020 (India)
Website : www.aiimsbhopal.edu.in

Pre- Bid Clarifications

E-Tender No. 056 AIIMS/BPL/STORES/CIF/NGS/2019-20 Dated: 10.12.2019
(Next Generation Sequencer to the Central Instrumentation Facility)

1. M/s Imperial Life Sciences (P) Limited.

Refer- ence	Tender Specifications	Request for Amendment	AIIMS Bhopal Response
1	2	3	4
Point - 1	The System should be a simple bench top instrument to support various applications like: metagenomics, Targeted amplicon sequencing, Targeted Expression profiling, Gene expression profiling, Genomic sequencing (de novo/ resequencing) for bacteria, viruses and other small pathogens, Targeted Sequencing (Variant validation) and more advance applications like CHiP seq, mi RNA, Transcriptome sequencing, whole exome sequencing and small RNA profiling and sequencing.	Please add Whole Genome Sequencing in existing list of applications.	Suggested amendment accepted
Point- 4	System should be capable of generating up to 100M reads per run.	System should be capable of generating 300M - 500M reads per run	Specification amended as system should be capable of generating up to 400M reads per run or more.
Point- 6	Throughput: up to 22- 25 GB per run	Throughput: Up to 150GB per run	Specification amended as Throughput: up to 25 GB or more per run
Point- 9	The system should offer a range of fast and simple library solutions and kits with low sample input requirements for a range of research applications such as whole genome sequencing, targeted gene panels, CHIP-seq, exome, miRNA discovery & quantification and RNA sequencing	Please replace "whole genome sequencing" to "whole human genome sequencing" in existing specification.	Suggested amendment Not accepted
Point- 11	The instrument should have a complete end-to-end on board solution with necessary software's & server (internal or external) of > 200 GB RAM & internal usable Storage of > 20 TB for processing signals, calling bases, variants and alignment of sequences	The instrument should have a complete end-to-end on board solution with necessary software's & server (internal or external) of > 256 GB RAM & internal usable Storage of 30 TB for processing signals, calling bases, variants and alignment of sequences for automated clinical friendly reporting on VCF files for exomes, NIPT, Metagenomics etc.	Specification amended as The instrument should have a complete end-to-end on board solution with necessary software's & server (internal or external) of > 200 GB RAM & internal usable Storage of 20 TB or more for processing signals, calling bases, variants and alignment of sequences for automated clinical friendly reporting on VCF file formats.

31/12/19

Shashank
30/12/19

Atoria
30.12.19.

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2. M/s Premas Life Sciences Pvt Ltd.

Reference	Tender Specifications	Request for Amendment	AIIMS Bhopal Response
Point-4	System should be capable of generating up to 100M reads per run.	System should be capable of generating 25M or more reads per run. Explanation:- MiSeq system can produce 25M reads (max 50M paired end). Majority of the applications are covered using 50M paired en reads. Nextseq can generate 400M reads (no other instrument can match this point)	Specification amended as system should be capable of generating up to 400M reads per run or more.
Point-6	Throughput: up to 22- 25 GB per run	Throughput: Should be 15 GB or more per run Explanation:- Miseq offers max 15gb data output. Nextseq offers 120Gb (no other instrument can match this point)	Specification amended as Throughput: up to 25 GB or more per run

S. Kashyap
30/12/19

Akroia
30.12.19.

TSU
30/12/19

S. Singh
30/12/2019

K. K.
31/12/19

R. K.
30-12-19