

Q: What types of sequencing studies are you performing on the system?

RM: We like the flexibility of the NextSeq 500 system. We're performing RNA-Seq — both reference-based and *de novo* — as well as whole-genome sequencing at the moment. Where it really has the edge over other systems is its ability to generate 2 × 150 paired-end reads. That's what we're running most. Because of the speed, we're also using it for small RNA sequencing and ChIP-Seq®. We have also run whole exomes.

Q: Do you use BaseSpace® genomics computing in performing data analysis?

RM: All the NextSeq 500 data can be uploaded automatically to the BaseSpace cloud. However, most of our analysis happens at our servers.

Q: Has the NextSeq 500 system impacted the number of customer studies you can perform?

RM: The faster sequencing speed of the NextSeq 500 system is enabling us to handle a higher workload. It's reducing our project turnaround time by 2-3 weeks.

Q: If somebody had told you in the early 2000s that you'd be able to sequence a whole genome in a little over a day what would you have thought?

RM: In 2000, it was a dream that we'd sequence a whole genome in a day. Now it's a reality with the NextSeq 500 system.

References

1. www.genotypic.co.in/
2. www.linkedin.com/company/236387

AAAGAATGATAACAGTAAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCA
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