



## Next Generation Sequencing Platform (NGS) Facility

BSBE Department, IIT Bombay

The **Next Generation Sequencing (NGS) Facility** is available for usage for **internal** and **external** users.

### Tapestation 4150 Requisition Form

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#### Basic Information

1. **Name of Student:**
  2. **Lab Name:**
  3. **Department:**
  4. **Contact Information** (Email and Phone):
  5. **Supervisor/PI Name:**
  6. **Procode:**
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#### Sample Information

7. **What type of sample will you analyze?**
  1. DNA
  2. RNA
  3. Other (Specify):
8. **Total number of samples:** (Specify if they will be analyzed at the same time or distributed over multiple runs)
9. **Sample Source** (e.g., tissue, blood, cell line, environmental sample):
10. **Sample Buffer Type:**
  1. TE
  2. Nuclease-free water
  3. Other (Specify):

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**Analysis Details****11. What type of assay do you require?**

- Genomic DNA ScreenTape
- D1000 ScreenTape
- D5000 ScreenTape
- RNA ScreenTape
- High Sensitivity Assay
- Other (Specify):

**12. What is the expected fragment size range?**

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**Facility and Instrument Usage Preferences****13. Do you intend to run the samples yourself in the facility?**

1. Yes
2. No

**14. If yes, do you require training on the TapeStation 4150 system?**

1. Yes
2. No

**15. If no, do you need facility staff assistance for sample processing?**

1. Yes
2. No

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**Any additional comments or requests:**



# **Next Generation Sequencing Platform (NGS) Facility**

## **BSBE Department, IIT Bombay**

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### **Sequencer Usage Charges:**

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#### **Basic Information**

1. **Name:**
  2. **Department:**
  3. **Institute / Company Name:**
  4. **Contact Information** (Email and Phone):
  5. **Supervisor/PI Name:**
  6. **Procode:**
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#### **Sequencing Requirements**

7. **Do you require paired-end or single-end sequencing?**
  1. Paired-end
  2. Single-end
8. **The sequencing platform available is Illumina NextSeq 550. Do you require any specific read length?**
  1. Yes (Specify):
9. **What is the expected genome/transcriptome size (if applicable)?**
10. **What is the desired depth of coverage?**
11. **What is the expected/required number of reads per sample?**
12. **Estimated data output size (e.g., GB per sample, total GB):**



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### NGS Requisition Form

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#### Basic Information

1. **Name of Student:**
  2. **Department:**
  3. **Contact Information** (Email and Phone):
  4. **Supervisor/PI Name:**
  5. **Procode:**
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#### Sample Information

6. **What type of sample will you handle? (Please tick appropriate)**
    - ☐ DNA (gDNA /cDNA/ Amplicons)
    - ☐ RNA
  7. **Organism** (e.g., human, mouse, plant, microbe):
  8. **Sample Source** (e.g., tissue, blood, cell line, environmental sample):
  9. **Total number of samples:**
    - ☐ Same Run
    - ☐ Distributed across multiple runs
  10. **DNA/RNA concentration range (ng/ $\mu$ L):**
  11. **Purity metrics** (e.g., A260/280, RIN for RNA):
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## **Project Details**

### **13. What type of sequencing is required?**

- Whole Genome Sequencing (WGS)
- Whole Exome Sequencing (WES)
- RNA Sequencing (RNA-Seq)
- Targeted Sequencing (Specify regions/genes):
- Other (Specify):

### **14. For RNA-Seq, specify the type of library preparation:**

- mRNA-Seq
- Total RNA-Seq (with/without rRNA depletion)
- Small RNA-Seq

**Any additional comments or requests:**