**MiSeq System**

**Equipment:** MiSeq System Illumina

**No. of Equipment: IEM6**

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**Equipment Description**

The Illumina MiSeq is a desktop sequencer with integrated computer which enables a broad range of applications, from targeted gene sequencing to metagenomics, small genome sequencing, targeted gene expression analysis, [amplicon sequencing](http://www.illumina.com/content/illumina-marketing/amr/en_US/techniques/sequencing/dna-sequencing/targeted-resequencing/amplicon-sequencing.html) starting at 10 ng DNA, and HLA typing. [New MiSeq reagents](http://www.illumina.com/content/illumina-marketing/amr/en_US/products/miseq-reagent-kit-v3.html) enable up to 15 Gb of output with 25 M sequencing reads and 2x300 bp read lengths. The MiSeq integrates cluster generation, sequencing and data analysis on a single instrument.

**Components:** flow cell compartment

enclosed optics module

status bar

touch screen monitor

external USB ports

reagent compartment

**Instrument configuration:**

RFID tracking for consumables

MiSeq control software

MiSeq reporter software

**Instrument control computer (internal):**

Base Unit: Intel Core i7-2710QE 2.10 GHz CPU

Memory: 16 GB RAM

Hard drive: 750 GB

Operating system: Windows 7

**Light Emitting Diode:** 500 nm, 660 nm

**Radio Frequency identifier:**

Frequency: 13,56 MHz

Power: 100 mW

**Miseq Performance Parameters:**

|  |  |  |
| --- | --- | --- |
| **MiSeq reagent kit v3** | | |
|  |  |  |
| **Read lenght** | **Total time** | **Output** |
| 2 x 75 bp | 21 hours | 3.3-3.8 GB |
| 2 x 300 bp | 56 hours | 13.2-15 GB |
|  |  |  |
| **Reads Passing Filter** | | |
| Single Reads | 20-25 M | |
| Paired-End Reads | 44-50 M | |
|  |  |  |
| **Quality Scores** | | |
| > 85% bases higher than Q30 at 2 x 75 bp | | |
| > 70% bases higher than Q30 a 2 x 300 bp | | |

|  |  |  |
| --- | --- | --- |
| **MiSeq reagent kit v2** | | |
|  |  |  |
| **Read lenght** | **Total time** | **Output** |
| 1 x 36 bp | 4 hours | 540-610 Mb |
| 2 x 25 bp | 5.5 hours | 750-850 Mb |
| 2 x150 bp | 24 hours | 4.5-5.1 Gb |
| 2 x 250 bp | 39 hours | 7.5-8.5 Gb |
|  |  |  |
| **Reads Passing Filter** | | |
| Single Reads | 12-15 M | |
| Paired-End Reads | 24-30 M | |
|  |  |  |
| **Quality Scores** | | |
| > 90% bases higher than Q30 at 1 x 36 bp | | |
| > 90% bases higher than Q30 at 2 x 25 bp | | |
| > 80% bases higher than Q30 at 2 x 150 bp | | |
| > 75% bases higher than Q30 at 2 x 250 bp | | |

**Specification of expertise relevant to NanoEnviCz workpackages:**

**WP3**a,d,f,g,h, **WP4**a,b, **WP6**a,d, **WP7**a,c,e,h,i, **WP9**a,b,c,d

**Detailed description of expertise**

**Please, specify the main research topics connected with equipment**:

The MySeq System is an instrument primarily used in nanotoxicology. It may be applied for the analysis of genotoxicity of nanomaterials by measuring various changes on the level of DNA or RNA, including detection of mutations and changes in gene expression levels.

**Please, specify the secondary research topics connected with equipment**:

The system may be used in toxicology in general to monitor toxic effects of compounds or materials of interest on the level of DNA or RNA. It is suitable for both *in vitro* studies on cell lines, and *in vivo* applications in laboratory animals.

**Keywords describing research area:**

genomics, sequencing, mutations, gene expression

**Competence**

**Relevance for applied and industrial research:**

A system that can be used for detection of biologigacal toxic effects of new materials *in vitro* and *in vivo.*

**Relevance for fundamental studies:**

A system suitable to study mechanisms of effects of new compounds and materials, including nanomaterials, on molecular level with the aim to identify possible toxicity resulting in both gene expression changes and induction of mutations.