**System for Next-Generation Sequencing**

**Equipment:** IonTorrent PGM™ System for Next-Generation Sequencing

**No. of Equipment: TUL7**

**Responsible coordinator:** Mgr. Jana Steinová

**Name of Institution:** Technical University of Liberec

**Address of Institution:** Bendlova 1407/7, 46117 Liberec

**E-mail:** jana.steinova@tul.cz

**Telephone:** 734 396 937

**Homepage:** cxi.tul.cz

**Contact person:** Jana Steinová

**E-mail:** jana.steinova@tul.cz

**Telephone:** 734 396 937

**Equipment Description**

**Description of equipment:**

IonTorrent PGM™ System for Next-Generation Sequencing consists of:

1. Ion OneTouch™ 2 Instrument for the emulsion PCR
2. Ion OneTouch™ ES (enrichment system)
3. Ion Personal Genome Machine® (PGM™) System (for sequencing)

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

**WP9**

**Detailed description of expertise**

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

IonTorrent PGM™ System for Next-Generation Sequencing utilizes massively parallel sequencing to generate thousands of megabases of sequence information per day. The key IonTorrents’ applications are: targeted sequencing, transcriptome sequencing, exome sequencing, genotyping sequencing, or microbial sequencing. The last mentioned is used routinely at TUL.

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

* Small RNA and miRNA Sequencing
* Aneuploidy and CNV Analysis
* Viral Typing
* Bacterial Typing
* De Novo Sequencing

**Keywords describing research area:**

**Sequencing, amplicon, gene expression, DNA, RNA, genome, bacteria**

**Competence**

**Relevance for applied and industrial research:**

Ion Torrent PGM™ System for Next-Generation Sequencing represents a very powerful tool for monitoring the bacterial diversity changes in different matrices, and therefore it is used for studying the environmental impact of different treatments.

**Relevance for fundamental studies:**

Diversity studies (targeting different groups of organisms), genome sequencing, transcriptome sequencing and many others.