

[Infrastructure name]: NextGen Sequencing (NGS)

[Name of infrastructure manager/contact person]: Johan Jakobsson

1. Short description of the infrastructure.

The MultiPark next generation sequencing (NGS) facility is located at the BMC in Lund. The core offers state-of-the art next generation sequencing technology for experimental and preclinical studies with particular expertise in transcriptome analysis. It is a core facility providing you with a full service – from RNA isolation to initial bioinformatics analysis.

The facility is open to all MultiPark researchers, Lund University affiliates and external users. The services provided include:

- RNA isolation
- Initial QC of RNA/DNA (BioAnalyzer +Qubit)
- Library preparation
- QC of sequencing libraries (BioAnalyzer +Qubit)
- Next generation sequencing (the core has a Illumina NextSeq500 instrument)
- Data storage
- Initial bioinformatics analysis

In addition to RNA-seq, other NGS-based techniques such as various forms of DNA-analysis and ChIP-seq are available upon request.

The core has expertise in handling many different types of tissues and cells, including the analysis of samples with very small amount of RNA.

2. Is this infrastructure receiving support also from other Strategic Research Areas (SRAs) or organizations at Lund University (e.g. Medical faculty, LBIC). If yes, please specify the type of support and its amount.

Salary research engineer (ca 50%) financed by StemTherapy

3. Number and names of MultiPark senior researchers using the infrastructure in the period 2018-2020¹. - 8

Daniella Ottosson
Gesine Paul-Visse
Maria Swanberg
Niklas Marklund
Tomas Deierborg
Johan Jakobsson
Malin Parmar
Cecilia Lundberg

4. Number and names of senior researchers outside of Multipark and/or non-academic partners using the infrastructure 2018-2020. - 8

Anders Enjin
David Ley 314372
Isabella Artner
Karolinska Institutet (seq 13)
Marco Ledri
Mattias Belting
Nils Wierup 314093
Per Ekström

5. Does the infrastructure have a steering document accessible to the users? If yes, when was it last updated?²

¹ If the infrastructure was first established in 2020, please include this information.

² Note that the Multipark leadership may ask to see this document with a very short notice.

See website: <https://www.multipark.lu.se/technical-platforms/next-generation-sequencing-ngs>

Is the infrastructure charging user fees? If yes, state the amount and what is covered by the user fees.

Use of the core facility is free of charge and users only pay for reagents. Approximate costs for one single RNA-seq sample typically range from 1000 SEK – 3000 SEK per sample but are dependent on the design of the project.

6. List publications generated with the help of this infrastructure during the past 3 years (2018-2020). Do not include manuscripts in preparation and please give the full reference (i.e., complete author list, complete title, journal name with year, volume, pages)³.

Fredrik Nilsson, Petter Storm, Edoardo Sozzi, David Hidalgo Gil, Marcella Birtele, Yogita Sharma, Malin Parmar, Alessandro Fiorenzano. Single-Cell Profiling of Coding and Noncoding Genes in Human Dopamine Neuron Differentiation, *Cells*, 2021. 10(1).

Di Maria V, Moindrot M, Ryde M, Bono A, Quintino L, Ledri M. Development and Validation of CRISPR Activator Systems for Overexpression of CB1 Receptors in Neurons. *Front Mol Neurosci*. 2020 Sep 8;13:168.

Brattås PL, Hersbach BA, Madsen S, Petri R, Jakobsson J, Pircs K
[Impact of differential and time-dependent autophagy activation on therapeutic efficacy in a model of Huntington disease.](#)
Autophagy. 2020 May 6:1-14

Katarína Tiklová, Sara Nolbrant, Alessandro Fiorenzano, Åsa K. Björklund, Yogita Sharma, Andreas Heuer, Linda Gillberg, Deirdre B. Hoban, Tiago Cardoso, Andrew F. Adler, Marcella Birtele, Hilda Lundén-Miguel, Nikolaos Volakakis, Agnete Kirkeby, Thomas Perlmann & Malin Parmar, Single cell transcriptomics identifies stem cell-derived graft composition in a model of Parkinson's disease, *Nat Commun*, 2020. 11(1): p. 2434.

Grassi DA, Brattås PL, Jönsson ME, Atacho D, Karlsson O, Nolbrant S, Parmar M, Jakobsson J.
[Profiling of lincRNAs in human pluripotent stem cell derived forebrain neural progenitor cells.](#)
Heliyon. 2019 Dec 31

Jönsson ME, Ludvik Brattås P, Gustafsson C, Petri R, Yudovich D, Pircs K, Verschuere S, Madsen S, Hansson J, Larsson J, Månsson R, Meissner A, Jakobsson J.
[Activation of neuronal genes via LINE-1 elements upon global DNA demethylation in human neural progenitors.](#)
Nat Commun. 2019 Jul 18

Petri R, Brattås PL, Sharma Y, Jönsson ME, Pircs K, Bengzon J, Jakobsson J.
[LINE-2 transposable elements are a source of functional human microRNAs and target sites.](#)
PLoS Genet. 2019 Mar 13

Kutsche LK, Gysi DM, Fallmann J, Lenk K, Petri R, Swiersy A, Klapper SD, Pircs K, Khattak S, Stadler PF, Jakobsson J, Nowick K, Busskamp V.
[Combined Experimental and System-Level Analyses Reveal the Complex Regulatory Network of miR-124 during Human Neurogenesis.](#)
Cell Syst. 2018 Sep 28

Pircs K, Petri R, Madsen S, Brattås PL, Vuono R, Ottosson DR, St-Amour I, Hersbach BA, Matusiak-Brückner M, Hult Lundh S, Petersén Å, Déglon N, Hébert SS, Parmar M, Barker RA,

³ If the infrastructure was first established in 2020, please include this information here too.

Multipark infrastructure report form 2021

Jakobsson J.

[Huntingtin Aggregation Impairs Autophagy, Leading to Argonaute-2 Accumulation and Global MicroRNA Dysregulation](#)

Cell Reports 24, 1397–1406, August 7, 2018