

Cellomics Platform

High content screening (HCS) / Analysis (HCA)

Anna Hammarberg

1. Short description of the infrastructure.

The Cellomics ArrayScan VTI HCS Reader is available for everyone to use. Cellomics, or HCS / HCA, enables automated acquisition, visualization and quantification of a large number of images:

- Automated fluorescence and brightfield microscopy
- Extraction of quantitative data from intensity and area measurements
- High through-put format

Examples of dynamic processes that may be measured are:

- Migration
- Changes in morphology, expression pattern and intensity.

Acquisition and analysis of images of:

- Live and fixed cells
- Subcellular targets
- Small organisms

The high throughput format enables a time-saving, unbiased acquisition and analysis of cells in a multiwell format, or on slides. We have the competence and available time to help you get more data out of your images.

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.

NO

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

Daniella Ottosson
Johan Jakobsson
Malin Parmar
Oxana Klementieva
Håkan Toresson

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

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

Gustav Smith
Kristian Pietras
Henric Ahlenius
Tania Ramos Moreno

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

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

MultiPark user fee:

180 SEK/hour scan time

180 SEK/hour Introduction and protocol setup

External user fee:

240 SEK/hour scan time

240 SEK/hour Introduction and protocol setup

Introduction to Cellomics ArrayScanVTI HCS reader instrument, Scan software and View software takes 3-4 hours.

7. 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.

1. Pircs K, Petri R, Madsen S, Brattås PL, Vuono R, Ottosson DR, St-Amour I, Hersbach BA, Matusiak-Brückner M, Lundh SH, Petersén Å, Déglon N, Hébert SS, Parmar M, Barker RA, Jakobsson J. Huntingtin Aggregation Impairs Autophagy, Leading to Argonaute-2 Accumulation and Global MicroRNA Dysregulation. *Cell Rep.* 2018 Aug 7;24(6):1397-1406. doi: 10.1016/j.celrep.2018.07.017. PMID: 30089251
2. Davidsson M, et al., *RNA.* 2018 May;24(5):673-687
3. Davidsson M, et al., bioRxiv 335372; doi: <https://doi.org/10.1101/335372>
4. Activation of neuronal genes via LINE-1 elements upon global DNA demethylation in human neural progenitors. Marie E Jönsson et al, *Nature Communications* volume 10, Article number: 3182 (2019).
NATURE COMMUNICATIONS | (2019)10:3182
5. Davidsson M, Wang G, Aldrin-Kirk P, Cardoso T, Nolbrant S, Hartnor M, Mudannayake J, Parmar M, Björklund T.
6. A systematic capsid evolution approach performed in vivo for the design of AAV vectors with tailored properties and tropism

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

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

7. Proc Natl Acad Sci U S A. 2019 Dec 9. pii: 201910061. doi: 10.1073/pnas.1910061116. PMID: 31818949
8. A Phenotypic Screening Assay Identifies Modulators of Diamond Blackfan Anemia
9. Kavitha Siva, Fredrik Ek, Jun Chen, Abdul Ghani Alattar, Kristmundur Sigmundsson, Roger Olsson, Marcin Wlodarski, Thomas Lundbäck, Johan Flygare
SLAS Discov. 2019 Mar;24(3):304-313
10. Bruzelius A, Hidalgo I, Boza-Serrano A, Hjelmér AG, Tison A, Deierborg T, Bengzon J, Ramos-Moreno T. **The human bone marrow harbors a CD45- CD11B+ cell progenitor permitting rapid microglia-like cell derivative approaches.** Stem Cells Transl Med. 2020 Dec 9. doi: 10.1002/sctm.20-0127. Epub ahead of print. PMID: 33295698.
11. Jessica Giacomoni, Andreas Bruzelius, Christina-Anastasia Stamouli, Daniella Rylander Ottosson. **Direct Conversion of Human Stem Cell-Derived Glial Progenitor Cells into GABAergic Interneurons.** Cells 2020, 9(11), 2451; <https://doi.org/10.3390/cells9112451>
12. [Single cell transcriptomics identifies stem cell-derived graft composition in a model of Parkinson's disease.](#)
Tiklová K, Nolbrant S, Fiorenzano A, Björklund ÅK, Sharma Y, Heuer A, Gillberg L, Hoban DB, Cardoso T, Adler AF, Birtele M, Lundén-Miguel H, Volakakis N, Kirkeby A, Perlmann T, Parmar M. *Nat Commun.* 2020 May 15;11(1):2434. doi: 10.1038/s41467-020-16225-5. PMID: 32415072
13. Direct Reprogramming of Human Fetal- and Stem Cell-Derived Glial Progenitor Cells into Midbrain Dopaminergic Neurons
Sara Nolbrant¹, Jessica Giacomoni¹, Deirdre B Hoban¹, Andreas Bruzelius², Marcella Birtele¹, Devin Chandler-Militello³, Maria Pereira¹, Daniella Rylander Ottosson², Steven A Goldman⁴, Malin Parmar⁵
Stem Cell Reports. 2020 Oct 13;15(4):869-882. Epub 2020 Sep 24
PMID: 32976765 PMCID: [PMC7562948](https://pubmed.ncbi.nlm.nih.gov/33426328/) DOI: [10.1016/j.stemcr.2020.08.013](https://doi.org/10.1016/j.stemcr.2020.08.013)
14. Pimpalwar N, Czuba T, Landenhed Smith M, Nilsson J, Gidlöf O, Smith JG. **Methods for isolation and transcriptional profiling of individual cells from the human heart.** Heliyon 2020;6:e05810. <https://pubmed.ncbi.nlm.nih.gov/33426328/>