

Directors

Jens HJERLING-LEFFLER, PhD | Karolinska Institutet, Sweden



Dr. Jens Hjerling-Leffler Ph.D. is a group leader at Karolinska Institutet, Stockholm, Sweden. He obtained his PhD from Karolinska Institutet in 2006. He then performed postdoctoral work in developmental neuroscience at University College London, UK and New York University School of Medicine, NY, USA before returning to Sweden to start his independent group in 2011. The work in Dr. Hjerling-Leffler's laboratory is based on the conviction that by bringing analyses to the level of definite types of cells in vivo we can drastically increase our understanding of the nervous system. He thus focuses on understanding the neuronal diversity of the brain, and how this knowledge can be applied to understand complex disorders by bridging neuroscience with genetics. He is a member of the Young academy of Sweden and the scientific director for the Karolinska Institutet Virus Tech core facility which he established in 2016. In 2018, Dr. Hjerling-Leffler was awarded an ERC consolidator grant for work on Schizophrenia.

Selected publications:

- Xiaoyan Qian, Kenneth D. Harris, Thomas Hauling, Dimitris Nicoloutsopoulos, Ana B. Muñoz-Manchado, Nathan Skene, Jens Hjerling-Leffler & Mats Nilsson. *Probabilistic cell typing enables fine mapping of closely related cell types in situ.* *Nat Methods.* 2019
- Muñoz-Manchado AB, Bengtsson Gonzales C, Zeisel A, Munguba H, Bekkouche B, Skene NG, Lönnerberg P, Ryge J, Harris KD, Linnarsson S, Hjerling-Leffler J. *Diversity of Interneurons in the Dorsal Striatum Revealed by Single-Cell RNA Sequencing and PatchSeq.* *Cell Rep.* 2018 Aug 21;24(8):2179-2190.e7. doi: 10.1016/j.celrep.2018.07.053. PMID: 30134177
- Harris KD, Hochgerner H, Skene NG, Magno L, Katona L, Bengtsson Gonzales C, Somogyi P, Kessaris N, Linnarsson S, Hjerling-Leffler J. *Classes and continua of hippocampal CA1 inhibitory neurons revealed by single-cell transcriptomics.* *PLoS Biol.* 2018 Jun 18;16(6):e2006387. doi: 10.1371/journal.pbio.2006387. eCollection 2018 Jun. PMID: 29912866
- Skene NG, Bryois J, Bakken TE, Breen G, Crowley JJ, Gaspar HA, Giusti-Rodriguez P, Hodge RD, Miller JA, Muñoz-Manchado AB, O'Donovan MC, Owen MJ, Pardiñas AF, Ryge J, Walters JTR, Linnarsson S, Lein ES; Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium, Sullivan PF*, Hjerling-Leffler J.* *Genetic identification of brain cell types underlying schizophrenia.* *Nat Genet.* 2018 Jun;50(6):825-833. doi: 10.1038/s41588-018-0129-5. Epub 2018 May 21 PMID: 29785013 * Shared corresponding authors
- Zeisel A, Muñoz-Manchado AB, Codeluppi S, Lönnerberg P, La Manno G, Juréus A, Marques S, Munguba H, He L, Betsholtz C, Rolny C, Castelo-Branco G, Hjerling-Leffler J*, Linnarsson S*. *Brain structure. Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq.* *Science.* 2015 Mar 6;347(6226):1138-42. doi: 10.1126/science.aaa1934. Epub 2015 Feb 19. PMID: 25700174 *Shared corresponding author

Peter KHARCHENKO, PhD | Harvard Medical School, USA

Peter Kharchenko, Ph.D, is the Gilbert S. Omenn Associate Professor of Biomedical Informatics the Harvard Medical School. His lab specializes in developing statistical and computational methods for analysis of high-throughput assays, in particular analysis of single-cell datasets. Dr. Kharchenko has received his Ph.D from the Biophysics program at Harvard University, studying transcriptional regulation of metabolism under the mentorship of George Church. He then conducted his postdoctoral training with Peter Park at the Harvard Medical School, focusing on analysis

of epigenetic regulation in model organisms and mammalian tissues. These efforts, part of the ENCODE consortium, provided first detailed maps of genome-wide chromatin states, their association with transcriptional and regulatory factors. Dr. Karchenko's own group has developed some of the initial statistical models for single-cell RNA-seq measurements, initially designed to determine the distinguishing characteristics of cells comprising hematopoietic stem cell niche. Further studies of hematopoiesis, hematological malignancies, as well as solid tumors have provided the basis for development of more complex computational methods for analysis of single-cell data. Dr. Kharchenko's group has also been applying these techniques to study transcriptional and epigenetic states in neural tissues, including both sensory and central nervous system. As part of the NIH BRAIN initiative, the group is studying the organization of the human and mouse brains using a combination of single-cell techniques, including spatially-resolved transcriptomics.

Selected publication:

- Kharchenko et al. "Bayesian approach to single-cell differential expression analysis." *Nat. Methods* 2014
- Lake et al. "Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain." *Nat. Biotech* 2018
- La Manno et al. "RNA velocity of single cells." *Nature* 2019
- Soldatov et al. "Spatiotemporal structure of cell fate decisions in murine neural crest." *Science* 2019
- Barkas et al. "Joint analysis of heterogeneous single-cell RNA-seq dataset collections." *Nat. Methods* 2019