

Bioinformatics and Expression Analysis core facility



Home About BEA Contact Information Where to find us



Karolinska
Institutet

NEWSLETTER DEC

BEA located in the NEO building in Huddinge

BEA –the core facility for Bioinformatics and Expression Analysis is a core facility providing access to a broad repertoire of genomic technologies located in the NEO building under the authority of the department of Biosciences and Nutrition at Karolinska Institutet in Huddinge.

BEA has extensive experience of implementing and maintaining microarray and sequencing technologies as core facility services which are highly requested by researchers at KI and researchers from other Swedish universities.

BEA operates as a core facility offering services with a strict "fee-for-service" principle. The overall principle is that customer fees cover costs for reagents, operating investments and service agreements.

Sequencing at BEA

BEA is offering services for different sequencing applications on the Illumina platforms in Huddinge. The service can be adapted for your needs and we provide different library construction and sequencing methods together with complete bioinformatics service for your research project. Please inquire for details about different library protocols, sequencing workflows and prices.

New personnel at BEA

BEA research engineer Ashwini Gajulapuri will be on maternal leave from January 2020. At the same time Carolina Bonilla, who previously has been working at Bionut, Scilife and Astra, will start at BEA. We wish both Ashwini and Carolina good luck with the New Year.

10X Chromium single cell service at BEA

The 10 X Genomics Chromium single cell system enables the analysis of large cell numbers at the highest capture efficiency. The technology allows for high-throughput single cell transcriptomics of many different cell types. The workflow allows separation and encapsulation of hundreds to thousands of cells per library together with reagent beads into nano-droplet that can now be prepared and sequenced at BEA. We offer a full data analysis pipeline with Cell Ranger and Loupe cell browser software.

Sequence analysis support

The core facility aims to improve NGS analysis services in terms of customer options for mapping methods, reference genomes and downstream analysis, together with more extensive quality control summaries. A recently acquired server dedicated to NGS analysis will increase analysis speed and storage capacity

Request to our customers

We would like to request our customers to inform BEA about publications that have resulted from projects at the core facility. BEA provides a [reference list](#) on our webpage which continuously needs to be updated.

We would also like to urge our customers to collect their samples after completed analysis since we have limited space in our freezers.

Christmas and New Year vacation

The core facility will be closed or partially closed during the holidays, and will reopen at January 7. We strongly recommend visitors to contact the core facility before visiting.

Contact information can be found at our [contact page](#).

The core facility wishes all a

Merry Christmas and a Happy new Year!



Bioinformatics and Expression Analysis core facility (BEA)

Fredrik Fagerström-Billai	Group Leader	fredrik.fagerstrom-billai@ki.se
Marika Rönholm	Research Engineer	marika.ronholm@ki.se
Tassos Damdimopoulos	Bioinformatician	tassos.damdimopoulos@ki.se
Susann Fält	Research Engineer	susann.falt@ki.se
Ashwini Gajulapuri	Research Engineer	ashwini.gajulapuri@ki.se
Patrick Müller	Research Engineer	patrick.muller@ki.se
David Brodin	Bioinformatician	david.brodin@ki.se

Visiting Address

Department of Biosciences and Nutrition at NEO
Karolinska Institutet,
SE-141 57 Huddinge, SWEDEN
Homepage: www.bea.ki.se