

Bioinformatics and Expression Analysis core facility



DECEMBER NEWSLETTER

BEA located in the Neo building at 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.

The **NextSeq 2000** Sequencing system is the most recent instrument addition and is now up and running at BEA. The NextSeq 2000 uses patterned flow cells and a novel resolution optics system that yields highly accurate imaging data higher sensitivity than previous systems. Different output reagents sizes are available from 50-300 cycles generating >1000 Mreads/run. Please inquire for details about different library protocols, sequencing workflows and prices.

iLabs

From 2021 all projects at BEA will be handled with the new cloud based core facility management system iLab. The iLabs system will be supplied by Agilent. The core facilities at KI are currently using different processes for bookings of instruments, request for services and invoicing. By using iLab, a common way of working will be achieved for all core facilities. For more information see homepage: www.bea.ki.se or talk to a BEA employee.

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 on January 7. We strongly recommend visitors to contact the core facility before visiting.

*We wish you a Merry Christmas
and a Happy New Year!*



BEA contact information

Fredrik Fagerström-Billai Group Leader fredrik.fagerstrom-billai@ki.se
08-524 835 43

Visiting Address

Department of Biosciences and Nutrition at Neo,
Blickagången 16
Karolinska Institutet,
SE-141 57 Huddinge, SWEDEN
Homepage: www.bea.ki.se