Bioinformatics and Expression Analysis core facility











Contact Information











NEWSLETTER JUNE -19

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 the Karolinska Institute 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.

10X Genomics Single Cell sequencing

BEA will provide single cell gene expression analysis with the 10X genomics platform which provides solutions for cell characterization and gene expression of thousands of cells simultaneously. BEA will initially offer 10X single cell RNA-Seq gene expression and single cell ATAC-Seq as a BEA staff assisted service. BEA will help users to design experiments, provide reagents and service starting from the initial cell separation step. The 10x chromium controller device, which is used for separating cells and reagent oligos, has been jointly bought by several departments and groups at KI south campus and is placed at ANA Futura. After library preparation and sequencing data can be analyzed with the free Cell Ranger and Loupe cell browser software which will be installed at BEA

Increased prices from 1st July

BEA prices for many sequencing services will be raised from 1st Jul 2019. The increase is due to vendor price increases and currency adjustments. BEA will be adjusting service prices mainly for library preparations and many of the sequencing solutions with Nextseq and Miseq. Prices will be presented in the new online pricelist and valid for projects delivered after the 1st July 2019.

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 <u>reference list</u> 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.

Summer vacation

BEA will be partly open during the whole summer but the staff will be reduced and the service will be limited. We strongly recommend visitors to contact the core facility before visiting and to make sure that we are present before visiting or delivering samples.

BEA will have limited opening hours between the 8th of July and the 5th of August. Please contact before visiting!



We wish you all a nice summer!

Bioinformatics and Expression Analysis core facility (BEA)

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