Bioinformatics and Expression Analysis core facility





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NEWSLETTER JUNE -18

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-forservice" 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.

Targeted Resequencing

Targeted resequencing, allows a subset of genes or regions to be separated and sequenced with NGS techniques which allow researchers to focus on specific areas of interest. The approach reduces turnaround time compared to broader approaches and enables deep sequencing at high coverage levels for rare variants. Price example for preparing and running a custom NGS panel with 48 target genes in 48 samples: 40 000 SEK, including OH and all handling costs. Please inquire for details and other formats.

Illumina DNA methylation analysis at BEA

BEA continues to offer service for DNA methylation analysis with the new Illumina Infinium methylation EPIC 850K bead array which is the successor of the popular 450K array. It covers >90% of CpGs from the 450K plus some 350K CpGs in enhancer regions which have been shown to be critical sites for differential methylation. Illumina's 450K arrays are no longer available for order from Illumina but we still have a supply of arrays which are available for a lower price per sample.

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 <u>contact</u> 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 9th of July and the 6th of August. Please contact before visiting!



We wish you all good luck in the championship and a nice summer!

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