

Bioinformatics and Expression Analysis core facility



Karolinska
Institutet

Christmas Holidays

Dear colleagues and friends,

The BEA team would like to wish all of our friends, colleagues and customers a Merry Christmas and a Happy New Year. We are grateful for your continued support and collaboration in our pursuit of scientific discovery. We hope the holidays will bring joy, peace, and happiness. We look forward to working with you in the new year.

Merry Christmas and a Happy New Year

*Best wishes, The BEA
team*



Request to our customers

During the holidays BEA will have limited opening hours. Please contact us before visiting! From the 22nd of December to the 4th of January BEA will only be partly open.

The staff will be reduced and the service will be limited and we strongly recommend visitors to contact the core facility before visiting and to make sure that we are present before visiting or delivering samples. We will resume normal business hours on the 8th of January.

BEA located in the NEO building in Huddinge

BEA—the core facility for Bioinformatics and Expression Analysis provides access to a broad repertoire of genomic technologies. We are located in the NEO building under the authority of the department of Biosciences and Nutrition at the Karolinska Institute in Huddinge.

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. All projects and invoicing are handled with the KI iLabs system.

Sequencing at BEA

BEA is offering services for different sequencing applications on the Illumina Nextseq and Miseq 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. We have an established collaboration with NGI for larger sequencing projects on the Illumina Novaseq Plus platform. Please inquire for details about different library protocols, sequencing workflows and prices.

Expression analysis

The core facility provides expression analysis services for the Illumina, Affymetrix and 10X Genomics platforms and offers a wide range of options. BEA offers many different protocols targeting different parts of the transcriptome from a wide variety of sources. With 10X single cell sequencing, researchers can study the expression of genes in different cell types, identify rare cell populations, and uncover new biological pathways and processes. Our services are extensive and ranges from experimental planning to bioinformatic support. We are also offering services for RNA and DNA purification, nucleic acid quality control and different qPCR based assays.

Oxford Nanopore Technologies

BEA is introducing service for Oxford Nanopore Technologies (ONT) for rapid, long-read, real-time sequencing of DNA or RNA.

Nanopore sequencing technology uses flow cells containing nanopores which can detect unique electrical currents when DNA and RNA are passed through the pores enabling accurate base calling. In addition, epigenetic marks such as 5mC and 5hmC can also be detected within the same sequencing run.

Initially BEA will provide service for amplicon sequencing in different formats with Minion and Flongle flowcells but we are willing to discuss any other type of project.

Standard Amplicon sequencing requires a ~150 fmol pure PCR amplified DNA as input with the ONT v14 Ligation sequencing protocol. Please contact us for more information.

RRBS

BEA provides service for Reduced representation bisulfite sequencing (RRBS). This technique combines a methylation independent restriction enzyme digest and bisulfite sequencing in order to enrich for the areas of the genome that have a high CpG content. The fragments that comprise the reduced genome include the majority of promoters, as well as regions such as repeat sequences that are difficult to profile using conventional bisulfite sequencing approaches.

Bioinformatic support

Are you in need of expert Bioinformatic support for your research or analysis? Look no further! Our team of highly trained Bioinformaticians can provide you with the guidance and support you need to successfully analyze and interpret your data. We offer help with both basic analysis and long term support. Contact us today to learn more about how we can support your research.

BEA Web

The BEA web pages has recently been updated with new information about our applications instrumentation.

ki.se/en/research/bioinformatics-and-expression-analysis-core-facility-bea

<http://www.bea.ki.se/>

Bioinformatics and Expression Analysis core facility (BEA)

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