

Bioinformatics and Expression Analysis core facility



Karolinska
Institutet

Christmas Holidays

Dear colleagues and friends,

As the holiday season approaches, the BEA team would like to take this opportunity to wish you and your loved ones a very happy and healthy Christmas. We are grateful for your continued support and collaboration in our pursuit of scientific discovery. Our team is dedicated to providing cutting edge genomics technology and expertise, and we are committed to advancing the field of biomedical research.

We hope that this holiday season brings you 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 6th 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 9th 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 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. 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 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 Agilent platforms and offers a wide range of options. RNA sequencing is a highly sensitive and accurate tool for measuring gene expression across the transcriptome, which allows detection of both known and novel features without prior knowledge. BEA offers many different protocols targeting different parts of the transcriptome from a wide variety of sources. 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.

10X Genomics Single Cell sequencing

10X single cell sequencing is a cutting-edge technique that allows scientists and researchers to study the genetic makeup of individual cells. 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. BEA will help users to design experiments, provide reagents and service starting from the initial cell separation step.

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. Contact us today to learn more about how we can support your research.

Bioinformatics and Expression Analysis core facility (BEA)

Fredrik Fagerström-Billai	Group Leader	fredrik.fagerstrom-billai@ki.se
Tassos Damdimopoulos	Bioinformatician	tassos.damdimopoulos@ki.se
Ashwini Gajulapuri	Research Engineer	Ashwini.gajulapuri@ki.se
Carolina Bonilla Karlsson	Research Engineer	carolina.bonilla.karlsson@ki.se
Susann Fält	Research Engineer	susann.falt@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