

# Bioinformatics and Expression Analysis core facility



## • Order Form Updated May 2021

BEA Project Number:	<input type="text"/>	iLabs:	<input type="text"/>	Starting Date:	<input type="text"/>
<b>Contact Information</b>					
Name			Department/Section		
Phone			e-mail		
<b>Invoice Address (KI customers only)</b> Karolinska Institutet Fakturor Box 23 109, SE-104 35 Stockholm			<b>Invoice Address (Non-KI customers)</b>		
Reference code: <u>ZZ</u>					
<b>KI Account</b> Projectnumber: .....			<b>Cost Center:</b>		

### Important information regarding iLabs Project Submission

#### Electronic submission using the iLabs system.

- From 2021 all projects at BEA are demanded to be handled with the new cloud based core facility management system iLab.
- All BEA users need to be registered and approved by PIs in iLabs to initiate a project request at BEA. <https://karolinska.corefacilities.org/account/login>
- After registration in iLabs BEA staff will create a project for the customer to approve. You can use this BEA order form to specify the desired service for your project.
- The integration between iLab and UBW (ERP system) will make it possible to generate invoices in iLab and send them for automatic handling in UBW.
- If you are a PI (Principal Investigator), you will manage your research group within iLab and give your team members access to the projects/funds you are managing.
- Further information about iLabs and project submission can be found at the KI CFM Web page: <https://staff.ki.se/the-cfm-project-and-ilab>
- Information about BEA services and prices can be found at the BEA Web page: <http://www.bea.ki.se/>

## Core facility platforms and applications.

### Indicate desired type of service.

<b>Platform:</b> <input type="checkbox"/> Affymetrix microarray <input type="checkbox"/> Illumina Microarray <input type="checkbox"/> Illumina Miseq <input type="checkbox"/> Illumina Nextseq 550 <input type="checkbox"/> Illumina Nextseq 2000 <input type="checkbox"/> Illumina Novaseq NGI	<b>Application:</b> <input type="checkbox"/> Gene/Exon Expression <input type="checkbox"/> miRNA Expression <input type="checkbox"/> Genotyping / CNV <input type="checkbox"/> ChIP seq <input type="checkbox"/> RNA seq <input type="checkbox"/> Methylation <input type="checkbox"/> User provided library	<b>Additional services:</b> <input type="checkbox"/> RNA isol. and purif. <input type="checkbox"/> ABI TLDA <input type="checkbox"/> Agilent Bioanalyzer QC <input type="checkbox"/> Agilent TapeStation QC <input type="checkbox"/> Small sample (Pico) <input type="checkbox"/> Other	<b>Additional Info:</b> <input type="checkbox"/> Sequencing only <input type="checkbox"/> Bioinformatic services <b>Indicate type/species:</b> <input type="text"/>
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## Core facility Sequencing sample information

### Indicate sequencing specifications and library type.

<b>Sequencing run/flowcell:</b>  <b>Sequencing Type:</b> <input type="checkbox"/> SR <input type="checkbox"/> PE <b>Single or Dual index:</b> <input type="checkbox"/> Single <input type="checkbox"/> Dual  <b>Sequencing cycle numbers:</b> <input type="checkbox"/> Read 1 _____ <input type="checkbox"/> Read 2 _____ <input type="checkbox"/> Index 1 _____ <input type="checkbox"/> Index 2 _____	<b>Indicate library type:</b>  <b>Library information:</b> Library has been pooled Yes <input type="checkbox"/> No <input type="checkbox"/> Library has been QC Yes <input type="checkbox"/> No <input type="checkbox"/> <b>Indicate:</b> <b>Library size (bp):</b> <input type="text"/> <b>Conc. qubit (ng/ul):</b> <input type="text"/> <b>Molar conc. (nM):</b> <input type="text"/> <b>Library loading (pM):</b> <input type="text"/>	<b>Sample sheet submitted:</b> Yes <input type="checkbox"/> No <input type="checkbox"/> <b>Data delivery:</b> <input type="checkbox"/> Fastq only <input type="checkbox"/> RAW data <input type="checkbox"/> MFT data delivery <input type="checkbox"/> Hard drive delivery <b>Bioinformatic services</b> <input type="checkbox"/> Multi QC <input type="checkbox"/> Sequence mapping <b>Indicate type/species:</b> <input type="text"/>
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### Order information and Invoicing:

	No	Cost/Sample	Total Cost
Platform/Type/Array/Assay:			
Labeling/Library/Assay/Protocol:			
Additional Lab Services:			
Service fees charged by BEA :			<input type="text"/>

### Additional Information:

## Confirmation

I fully agree with the conditions for using the core facility and the different platforms/assays terms and conditions for academic press. The core facility cannot take any responsibilities for damaged or lost samples or data. **It is the responsibility of the customer to secure and pick up remaining samples and data which will otherwise be disposed after 12 months.** Although raw data will be stored, the BEA core facility holds no responsibility to store pre-processed data or further analyzed data. It is important that the customer has reflected and responded to all the questions found in this order form. **I fully understand all the conditions and routines applied to the specific project and confirm my agreement by signing below.**

Date	Signature	Signature in block letters
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**Sample and Project Information**

**Sample preparation and sample submission checklist**

RNA/DNA purification method used:

Column cleanup performed:  Yes  No      DNase treatment:  Yes  No

Concentration measured:  Yes  No      Electronic submission of sample information:  Yes  No

Store remaining RNA/DNA:  Yes  No

**Labeling and Description (indicated by the customer)**

#	Label	Description	Additional sample information
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**Storage (indicated by the core facility)**

## Bioinformatics

### Basic bioinformatics

Basic bioinformatics of microarray data at BEA includes QC of data, normalisations, annotations, experimental group comparisons with fold change and p-value calculations. For sequencing projects we offer bcl conversion and demultiplexing of pooled sequencing reads to fastq files. In the basic service we also include sequencing alignment to sam/bam format if desired.

For annotation and alignment please indicate species and genomic build:

### Extended bioinformatics

Depending on the design of the project, bioinformaticians at BEA can assist in further analyses tailored for the specific project. See BEA's homepage (<http://apt.bea.ki.se/>) for examples and requirements for further applied bioinformatics help.

Indicate type of desired analysis:

## Data delivery

**BEA will always provide the customer with all raw data as well as pre-processed data with annotations for each assay, including Quality Control plots.** The processed data is normalized using the appropriate methods and operating software (depending on assays). This procedure will generate signal values for each measurable point and the document will also include biological annotations for respective platform and assay. If the customer agreed on bioinformatical help from BEA in forms of Comparative analysis, statistical and bioinformatical lists are generated for the customer to filter biologically interesting data from. This analysis will also be accompanied by an Analysis report for the specific project.

**The customer will receive a link by e-mail where the all data and results can be downloaded from the KI Own Cloud or the BEA server.**

**Please use the field below for special requests regarding data delivery, including additional persons to be contacted, only raw data delivery etc.**

### Delivery notes

## Acknowledgement

**Important:**

**In case of publications, please cite:**

*"We also would like to thank the core facility at NEO, BEA, Bioinformatics and Expression Analysis, which is supported by the board of research at the Karolinska Institute and the research committee at the Karolinska hospital".*