

ABI 3730 PRISM® DNA Analyzers for:

- **Sanger DNA sequence analysis**
- **fragment analysis**

The ABI 3730 PRISM® DNA Analyzer enables high quality sequencing up to 900 bases and high resolution (1 bp) fragment analysis. The ABI 3730 instruments is in the 96 or 384 well format using a 48 x 36cm capillary array.

For DNA sequencing we have the appropriate matrices set up on the instruments for BigDye™ terminators v.3.1 and 1.1 (Applied Biosystems).

For fragment analysis the DNA can be labelled with up to four different fluorescent dyes. The fourth or fifth color, depending on the Dye Set used, is reserved for the internal lane size standard. We are using DS-33 (6-FAM; blue; VIC; green; NED; yellow; PET; red; LIZ, orange size standard).and DS-30 (6-FAM; blue; HEX; green; NED; yellow; ROX, red, size standard). We recommend the use of DS-33.

The core facility will provide start up theoretical and technical assistance for “hands-on” users. Each user reserves a date and time for occupying the instrument by a booking system.

Information regarding our “hands-off” and “full-service” options:

- **How we want your pre-made fragment analysis samples**

Fragment analysis samples that will be analysed on the ABI3730 instrument, should be supplied to us as fluorescently labeled, pooled PCR products in 96-wells plates. The concentration of products needs to be optimized by the user.

An internal size standard, that allows precise size calling by providing a means to normalize mobility during the run, is added to each well. The users can bring their own internal standards or KIGene will supply the appropriate internal size standard. Each user must book an entire run (a minimum of 48 samples).

- **How we want your pre-made Sanger sequence samples**

After completion of the sequence reaction, each sequence sample is precipitated and dried before delivery to us.

Only mark the side of the tubes with sample numbers and your initials. It is sufficient to write the complete sample names in the order form.

- **How we want your full-service Sanger sequence samples**

In order to optimize the sequencing reaction we need information about template and primer concentrations, size of the template DNA and annealing temperature of the primer. Our requirements for template and primer concentrations can be found at <http://www.cmm.ki.se/wp-content/uploads/2014/11/Requirements-for-full-service-DNA-sequence-samples-and-primer-list.pdf>

- **Our universal sequence primers**

We stock the most common universal primers. Please note that the oligo sequences might differ between universal primers from different companies despite the same

name. Remember to check that our universal primer can anneal to the target DNA. Our universal primers and their sequences are listed at <http://www.cmm.ki.se/wp-content/uploads/2014/11/Requirements-for-full-service-DNA-sequence-samples-and-primer-list.pdf>

- **Sample delivery.**

Put your samples in an envelope together with the appropriate order form. Preferably use padded envelope and parafilm over the tube lids if you are sending them by post.

Internal Users: Send samples by internal mail or place samples in any of our three drop boxes at Solna Campus area:

CMM

Pick-up time:

- 10:00 and 13:00 each business day

Drop box location:

- outside the Neurogenetics Unit, L8:00 (CMM entrance floor)

BioClinicum

Pick-up time:

- 10:00 each business day
- After 10:00, note that your samples might be processed faster if you place them in our CMM drop box

Drop box location:

- Plan 5, close to the Skyway entrance

BioMedicum

Pick-up time:

- 10:00 each business day
- After 10:00, note that your samples might be processed faster if you place them in our CMM drop box

Drop box location

- Plan 4, outside the lunch room located close to the Skyway entrance

External Users: KIGene, MMK, Neurogenetics unit CMM L8:00, Karolinska University Hospital at Solna, 171 76 Stockholm.

- **Turn-around time**

- 10:00 AM: sample-to-result within the same day
- 13:00 PM: pre-made sample-to-result within the same day

Note: In rare cases delays may occur if we experience unusually heavy loads or equipment failure.

Note: We always reload failed sequence reactions **without charge** in case we assess that they might improve in a second analysis.

- **Data storage.**
We store all data from pre-made and full-service sequence samples for three years. Therefore, if you lose raw data files we can retrieve these for you if you give us the relevant information (date and sample names).
- **Sample storage.**
We save primers and templates for full-service sequence samples a month in our freezers.
- **For order forms and more information regarding DNA sequencing, go to <http://www.cmm.ki.se/team/kigene-genetic-analysis-at-cmm/>.**

Price list

ABI 3730: Sanger DNA sequencing and fragment analysis		
<i>“Hands on” service</i>		
DNA sequence or fragment analysis	600 SEK/96-well plate ^{1,2}	2 400 SEK/384-well plate ^{1,2}
<i>“Hands off” service</i>		
Fragment analysis, 1-48 samples/run	750 SEK/run (excl. size std) ^{1,2}	1 000 SEK/run (incl. size std) ^{1,2}
DNA sequence reaction: “full service”	100 SEK/sample ^{1,2}	70 SEK/sample (≥48 samples) ^{a,1,2}
DNA sequence reaction: “pre-made”	40 SEK/sample ^{1,2}	25 SEK/sample (≥96 samples) ^{b,1,2}
PCR product purification	20 SEK/sample ^{1,2}	10 SEK/sample (≥48 samples) ^{b,1,2}
Plasmid DNA extraction from bacteria	40 SEK/sample (1-10) ^{1,2}	25 SEK/sample (>12 samples) ^{1,2}

^a Provided that the template DNAs have the same concentrations and are placed in 96-well plates. No more than eight sequence primers per plate. The same annealing temperature will be used for all primers.

^b Provided that the samples are placed in 96-well plates and can be treated in the same way

¹ The KI INDI fee will be added to the price for users within KI.

² An administrative fee of 30 % will be added for users outside KI.

The indicated prices are exclusive of value-added tax.

Please note: Bookings regarding “hands-on” service that are missed and that are not cancelled at least 24hrs in advance will be charged by 50% of the running cost.