

**GENOMICS
FRAGMENT ANALYSIS
External**



Date	_____	Contact Name	_____
Company	_____	Contact Phone	_____
Customer #	_____	PI Name	_____
PO #	_____	Contact Location	_____
Authorized Signature	_____	FRED Account	_____

Data Export Information

Data can be exported over the Shared Resources Network (fred) for retrieval onto Mac or PC computers. Log on to the server "fred". In your "home" directory there will be a folder called "geneticanalysis" which will contain your data.

GeneScan and GeneMapper programs are available from the biocomputing center as shared software. For computer programs and locations, see the Genomics website at: www.fhcr.org/science/shared_resources/genomics/

Charges for FRAGMENT ANALYSIS:	Quantity	Charge Code
Number of samples (if 87 or less)	_____	GRE__0111
Number of samples (if 88 or more)	_____	GRE__0112

Charges for SNPlex:

Number of samples	_____	GRE__0113
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For Resource Use Only			
Circle One:	Consortium (2)	External (4)	SCCA (5)

Please remember to complete sample information on reverse side.

Leave this invoice in the inbox when you turn your samples in (DE-302). Only 1-2ul of sample is required. Fragment Analysis is available to run Monday through Friday during regular business hours on the ABI Prism 3100 and 3730xl DNA Analyzers. Please contact Elizabeth Jensen (x4470) if you have any questions. Turn around time is typically 1-2 business days, but may be longer due to high volume in Fragment Analysis requests.

Thank you.

SAMPLE SHEET INFORMATION

Select the appropriate dye set:

- Filter Set D (6-FAM, HEX, NED, ROX)
- Filter Set G5 (6-FAM, VIC, NED, PET, LIZ)
- Filter Set F (6-FAM, JOE, NED, ROX)

SAMPLE NAME	SAMPLE NAME
1	25
2	26
3	27
4	28
5	29
6	30
7	31
8	32
9	33
10	34
11	35
12	36
13	37
14	38
15	39
16	40
17	41
18	42
19	43
20	44
21	45
22	46
23	47
24	48

Sample names can only have letters, numbers, and the following characters: -_(){}#+

Only 1-2ul of sample is required. Please place the samples in a clearly marked 96-well plate or set of strip tubes. Place samples in the freezer in the box labeled “Genotyping Samples.”

96-well plates MUST be loaded vertically from A to H with no spaces.
(E.g.: A1=1, B1=2...H1=8, A2=9, B2=10...H2=16, etc.)