

# Illumina Next Generation Sequencing Service

## SERVICE REQUEST FORM

### Instructions

Fill out both 'Page 1' and 'Page 2' of the Service Request Form. Enter sample details using either the *Sample Submission Sheet* or *Library Submission Sheet* [available on ATGC (SMF)'s website]. Please submit one service request form per application.

Please email all submission forms to : [NGSSubmissions@mdanderson.org](mailto:NGSSubmissions@mdanderson.org).

All samples should be accompanied by a printed and signed version of the completed Service Request Form. The ATGC is located in BSRB Room S15.8425. We accept samples M-F, 9am - 5pm.

### For SMF Lab Only

Project ID: \_\_\_\_\_ Date: \_\_\_\_\_

### Contact Information

Principal Investigator: \_\_\_\_\_ Department: \_\_\_\_\_

User Name: \_\_\_\_\_ User Email: \_\_\_\_\_

### Project Information

Project Title: \_\_\_\_\_ Are these Xenograft \_\_\_\_\_

Sample Source: \_\_\_\_\_ Reference Genome: \_\_\_\_\_

Is this continuation of a previous project?      Yes      No      Previous SMF Project ID: \_\_\_\_\_

Sample Type:	ChIP DNA	Circulating DNA	Circulating RNA	Total RNA
	FFPE DNA	FFPE RNA	Genomic DNA	Plasmid DNA
	PCR Product	Premade Libraries	RIP RNA	

Sequencing Application:	<u>DNA Seq Application</u>	<u>RNA Seq Application</u>	<u>Single Cell</u>
	Amplicon-seq	microRNA-Seq	10x Genomics
	ChIP-seq	Ultra Low Input mRNA-seq	Tapestri Single Cell
	Whole Genome	TCR a/b Profiling	
	<u>Capture Seq</u>		
	Clinical Exome-seq (Agilent)	<u>Strand Specific</u>	<u>Other</u>
	Exome-seq (Agilent)	Stranded mRNA-seq	Stranded      Must specify application
	Exome-seq (NimbleGen)	Total RNA-seq	RNA Access
	Exome-seq (Twist)	(Human only) Ultra Low Input	
	T200.1 Panel	Total RNA seq	
	Targeted-seq (User supplied probes)		

**ChIP-Seq Only:** May we shear your samples to an appropriate size range?      Yes      No  
 We add ERCC spike in control mix1 as default for stranded mRNA-seq.

<b>No. of Samples(library pools):</b>	<b>No. of Lane or Run</b>									
Sequencing Instrument:	HiSeq4000	NovaSeq6000	MiSeq	V2	V3	Nano	iSeq	NextSeq500	MID	High
Sequencing Format:	50nt SR	76nt SR	100nt SR	150nt SR						
	76nt PE	100nt PE	150nt PE	250nt PE						
NovaSeq Only. flow cell type:	SP	S1		S2		S4				
	SP-Xp	S1-Xp		S2-Xp		S4-Xp				

Sequencing Format:      Read 1      Read2      Index1      Index2  
 (Required only for premade libraries)      Note1. the Xp workflow divides the flow cell into 2 (SP, S1, S2) or 4 (S4) lanes. If selecting Xp, please indicate the number of lanes requested.  
 Note2. Please submit full flow cell libraries for HiSeq4000, except sequencing format 76nt PE.

Custom Primer Use:      Are you using a custom primer for sequencing?      Yes      No  
 If yes was selected, please continue to answer next two questions. 1. Do you want us to spike in PhIX and mix the custom primer with Illumina primers?      Yes      No      2. The custom primer Conc

## Data Analysis

Bioinformatician  
Name:

Bioinformatician Email:

SMF will provide sequencing data in "fastq files" format. Alignment data is available upon request only but will add additional processing time.

## Billing Information

Billing Contact Name:

Billing Contact Email:

**Note:**  
To split service charges between two accounts, please provide 'Account 2' information. If service charges are to be split between 3 or more accounts, please provide additional account information in the 'Additional Account Information' section below.

Account 1:

Account 2:

Dept ID (6 digits):

Dept ID (6 digits):

Fund Group (2 digits):

Fund Group (2 digits):

Fund (6 digit)

Fund (6 digit)

Fund Type (2 digits)

Fund Type (2 digits)

PCBU (5 letters)

PCBU (5 letters)

Project (6 digits)

Project (6 digits)

Activity (4 digits)

Activity (4 digits)

Expiration Date:

Expiration Date:

Amount/Percentage to

Amount/Percentage

be Billed:

to be Billed:

Additional Account

Information:

Dept Administrator or  
Authorized Financial  
Designee (Signature here):

Please Print Name and  
Title(Person of Signature):

## Project Description/Custom Requests

**Notes:** 1. Samples should be submitted in 1.5ml eppendorf tubes. 2. If you use your own label, please place the label on the 1.5ml tube vertically or horizontally around on the bottom 2/3 of the tube. Please Keep the top 1/3 of the tube free for core lab use.

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