

**University of Michigan DNA Sequencing Core
Services, Pricing and Information for UMich internal Clients**

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The University of Michigan DNA Sequencing Core (“UMDSC”) provides analytical services to UMich-affiliated researchers (“internal clients”) and non-UMich-affiliated researchers (“external clients”) . This document lists the services provided to internal clients of the UMDSC, including the prices of those services as of the above revision date. Revisions to this document will be made periodically with approval of the UM Office of Financial Analysis (OFA), and may include changes in prices or services. Revisions become effective upon the date of OFA approval, and at that time supersede all previous price lists. *Actual prices charged will be those approved by the OFA. In event of errors in this document, the OFA approved prices supersede those stated here.*

The UMDSC offers nucleic acid analysis services as listed in the following table. For definitions or for detailed information on the services, please consult the Core’s web site (<http://seqcore.brcf.med.umich.edu>) or with Core staff members. The actual prices that a client will pay generally requires a complicated mixture of the below charges. All prospective clients should contact the Sequencing Core (seqcore@umich.edu) for discussion and clarification of costs for *their* project.

Discounts are available for members of certain Centers. In most cases, these are provided by the Center administration in the form of rebates, after the service is rendered by the Core and after payment has been made by the Investigator. Please contact your Center administrators to discuss potential discount opportunities.

Sanger Sequencing:

Sanger DNA Sequencing, regular service:	\$3.00/lane
Sanger DNA sequencing, “Rush” (“Next Day”) service:	\$4.50/lane
Sanger DNA sequencing, “Ultra-Rush” (“Same Day”) service: (<i>Ultra-Rush is available only if enabled on the Sample Submission form.</i>)	\$5.70/lane
Sanger DNA sequencing, full 96-well plates:	\$2.40/lane
Sanger DNA sequencing, “Reduced Service”, full 96-well plates: (<i>Please consult Core staff before attempting to use this service.</i>)	\$2.25/lane
Sanger DNA sequencing, “siRNA Construct”:	\$6.00/lane
Sanger DNA Sequencing, “Large DNA”:	\$6.00/lane
Sanger DNA sequencing, bulk submissions, very large projects:	contact us.

Fragment Analysis:

Fragment Analysis, purchase one “CE Loading Plate”:	\$26.00/plate
Fragment Analysis, Capillary electrophoresis on one 96-well plate:	\$54.00/plate
Fragment Analysis, “Identifiler Plus” service:	\$32.00/sample

Taqman analysis:

Taqman, run one ready-to-load 96-well plate in real time:	\$18.00/plate
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Sequenom services:

Sequenom MassARRAY, one “Pinset” of reactions (24), materials only:	\$190.00/pinset
Sequenom MassARRAY, one “Quadrant” of reactions (96), materials only:	\$460.00/quadrant
Sequenom MassARRAY, one “Half Chip” of reactions (192), materials only:	\$750.00/half chip
Sequenom MassARRAY, one “Full Chip” of reactions (384), materials only:	\$1340.00/full chip
Extra materials, EpiTyper analysis, priced as fraction of a chip:	\$630.00/full chip
Sequenom technician time (assay design, data analysis):	\$76.00/hour

PyroMark pyrosequencing services:

One full plate, materials and standard labor time:	\$320.00/plate
Partial plate – 24 wells, materials and standard labor time:	\$220.00/plate
Extra effort, hourly technician time beyond standard labor:	\$58.00/hr

Illumina Microarray services:

Illumina Microarray services: Microarray expendables at market price.	
Illumina Microarray technician time:	\$47.00/hour
Reagent costs, per 96-well plate:	\$230.00/plate
Scanning cost, instrument use per hour:	\$9.40/hour

Illumina Sequencing services, Library generation:

Standard Genomic libraries:	\$68.00/library
Ultra-low input genomic libraries:	\$106.00/library
Non-stranded mRNA-seq (i.e. standard mRNA-seq libraries):	\$116.00/library
Stranded mRNA-seq, polyA-selected:	\$136.00/library
Stranded mRNA-seq, Ribo-Zero rRNA depletion:	\$194.00/library
NEB Ultra non-stranded mRNA-seq (ribo-depletion reagents purchased separately):	\$124.00/library
NEB Ultra stranded mRNA-seq (ribo-depletion reagents purchased separately):	\$124.00/library
SMARTer stranded mRNA-seq (ribo-depletion reagents purchased separately):	\$195.00/library
smRNA-seq libraries:	\$140.00/library
PCR-free genomic libraries:	\$74.00/library
Exome captures, pools	\$520.00/pool
Multiplexing costs	\$18.00/sample
Size selections (fragment size-specific isolation):	\$18.00/hour
Illumina Library Technician time, special services:	\$74.00/hour

Illumina Sequencing Services, Sequencing lanes:

V4 Single-end sequencing, 50 nt read length:	\$880.00/lane
V4 Single-end sequencing, 125 nt read length:	\$1160.00/lane
V4 Single-end sequencing, 150 nt read length:	\$1430.00/lane
V2 Single-end sequencing, 50 nt read length, RAPID:	\$930.00/lane
V2 Single-end sequencing, 100 nt read length, RAPID:	\$1170.00/lane
V2 Single-end sequencing, 200 nt read length, RAPID:	\$1570.00/lane
V4 Paired-end sequencing, 50 nt read length:	\$1390.00/lane
V4 Paired-end sequencing, 125 nt read length:	\$2020.00/lane
V4 Paired-end sequencing, 150 nt read length:	\$2290.00/lane
V2 Paired-end sequencing, 50 nt read length, RAPID:	\$1400.00/lane
V2 Paired-end sequencing, 100 nt read length, RAPID:	\$1790.00/lane
V2vPaired-end sequencing, 150 nt read length RAPID:	\$2300.00/lane
H4K Single-end sequencing, 50 nt read length:	\$840.00/lane
H4K Paired-end sequencing, 50 nt read length, RAPID:	\$1400.00/lane
H4K Paired-end sequencing, 75 nt read length, RAPID:	\$1490.00/lane
H4K Paired-end sequencing, 150 nt read length RAPID:	\$2020.00/lane
MiSeq 50 cycle sequencing:	\$1180.00/run
MiSeq 150 cycle sequencing:	\$1260.00/run
MiSeq 300 cycle sequencing:	\$1390.00/run
MiSeq 500 cycle sequencing:	\$1500.00/run
MiSeq 600 cycle sequencing:	\$1860.00/run
Duo cBot RAPID kit:	\$194.00/ea
Drive, 1T:	\$72.00/ea
Technician time, extra effort:	\$140.00/hr

Pacific Biosciences Sequencing services:

PacBio shearing/QC:	\$89.00/sample
DNA library preparation:	\$468.00/sample
<i>Additional reagents may be required, in certain cases. Discuss with Core staff.</i>	
BluePippin Isolation:	\$111.00/sample
Special technician hours:	\$75.00/hour
PacBio SMRT Cell sequencing:	\$425.00/SMRT cell

Ion Torrent/Ion Proton Sequencing services:

Ion sample shearing/QC:	\$56.00/sample
Ion Library, Genomic:	\$400.00/sample
Ion Library Exome selection:	\$960.00/sample
Ion Library Custom Capture:	\$600.00/sample
<i>Additional reagents may be required, in certain cases. Discuss with Core staff.</i>	
Ion Library special services, additional technician time:	\$78.00/hour
Ion Torrent sequencing, 100 nt reads:	\$630.00/run
Ion Torrent sequencing, 200 nt reads:	\$680.00/run
Ion Proton sequencing, P1 cell:	\$1740.00/run
Ion Proton P1 Run Only (user-supplied chip/kit)	\$1,161.00/run

Affymetrix Services:

(Note: Except as noted below, all Affymetrix microarrays provided by customer; prices are for processing costs ONLY)

Standard GeneChip expression profiling, whole-transcriptome:	\$257.00/sample
Standard GeneAtlas expression profiling, whole-transcriptome:	\$230.00/sample
Standard GeneTitan expression profiling, whole-transcriptome:	\$156.00/sample
Standard GeneChip expression profiling, 3':	\$257.00/sample
Standard GeneAtlas expression profiling, 3':	\$230.00/sample
Standard GeneTitan expression profiling, 3':	\$156.00/sample
Standard GeneChip expression profiling, NuGen whole-transcriptome:	\$222.00/sample
Standard GeneAtlas expression profiling, NuGen whole-transcriptome:	\$206.00/sample
Standard GeneTitan expression profiling, NuGen whole-transcriptome:	\$155.00/sample
Partial service, GeneChip expression profiling:	\$81.00/sample
Partial service, GeneAtlas expression profiling:	\$30.41/sample
Partial service, GeneTitan expression profiling:	\$41.73/sample
GeneChip SNP typing:	\$290.00/sample
GeneChip SNP typing, hybridization only:	\$43.00/sample
Axiom (GeneTitan/GeneAtlas) SNP typing:	\$27.00/sample
OncoScan SNP typing: <i>includes chips</i>	\$765.00/sample

qPCR Arrays:

Qiagen Superarray sample processing (labor only), 96- or 384-well plates:	\$244.00/plate
<i>Materials are charged at market prices.</i>	
Life Technologies OpenArray sample processing (labor only):	\$128.00/run
<i>Materials are charged at market prices.</i>	
Life Technologies OpenArray microRNA sample processing (labor only):	\$150.00/run
<i>Materials are charged at market prices.</i>	

DNA Purification Services:

Whole blood DNA isolation:	\$40.50/sample
Whole blood-finish only:	\$28.50/sample
Compromised blood DNA isolation:	\$49.00/sample
Compromised blood-finish only:	\$33.00/sample
Saliva DNA isolation:	\$19.50/sample
Subaliquotting, transfer or dilution of one sample (DNA, RNA):	\$1.70/sample
Nanodrop or Qubit measurement on one sample:	\$1.70/sample

Sample Quality Control/manipulation:

Agilent Bioanalyzer DNA 1000, full LabChip:	\$70.00/chip
Agilent Bioanalyzer, DNA High Sensitivity, full chip:	\$92.00/chip
Agilent Bioanalyzer RNA 6000 Nano, full chip:	\$68.00/chip
Agilent Bioanalyzer, RNA 6000 Pico, full chip:	\$72.00/chip
Agilent Tape Station DNA 1K analysis:	\$18.50/sample
Agilent Tape Station High-sensitivity DNA 1K analysis:	\$20.40/sample
Agilent Tape Station Genomic DNA:	\$20.40/sample
Agilent Tape Station RNA 6K analysis:	\$18.60/sample
Agilent Tape Station High sensitivity RNA 6K analysis:	\$19.00/sample

Please note the following:

The UM DNA Sequencing Core will process samples on a first-come, first-served basis. Samples from external clients will be processed at lower priority than internal clients. For the Pacific Biosciences sequencer, HHMI Investigators have priority above that of UM researchers, up to certain limits. Clients must be registered with the UM DNA Sequencing Core via our computer system (see the "PI Administration" section of Core's web site). All samples must be entered into our computer system, and must be properly labeled with our tracking number(s) *before* they are delivered to this Core. We reserve the right to discard any samples that are not properly labeled. The Core does not return unused samples or portions of samples after completion of work; they are discarded.

Prices listed in this document are those charged to internal (University of Michigan) clients, as determined by the method of billing employed by the University of Michigan Financial Operations. If a client pays using funds from a “shortcode” within the UM Financial Operations, that client will be charged the rate for internal clients, and the prices listed in this document are applicable. If a client pays by *any* other method, then the prices listed in this document are not applicable. No exception to this policy will be made for any actual or perceived affiliation the client may have with the University of Michigan, nor for any collaborative agreement the client may have with a University of Michigan employee, faculty, student, officer or agent.

An analysis performed by the UMDSC can fail for many reasons, including failures on the Core’s part (e.g. instrument malfunction, Core technician error) and failures on the Customer's part (e.g. misquantitated sample, misdesigned experiment, impure sample). We will, to the best of our ability, assess whether a failed analysis is due to a failure on the part of the Core, and we may in such cases repeat an analysis at our cost. When, in our sole judgment, a failure is not due to error on the part of the Core, we reserve the right to refuse repeating the analysis. We will not be held liable for analytical failures arising due to errors or problems in the Client’s laboratory. We will not bear the cost of repeat runs unless we explicitly state that we are doing so of our own accord. If, on completion of any repeat, the results prove that the Core was at fault in the original failure, we may at that time choose to absorb the cost of the repeat analysis. Determination of the cause of failure is based solely on the judgment of the Core staff members, and ultimate decision making in such cases resides with the Director of the UM DNA Sequencing Core.