



IMR Sequencing Services – Pricing as of April 16th, 2024

All prices listed are in Canadian Dollars (CAD). GST/HST will be added to all Canadian orders. A fee of \$25/shipment to cover Customs costs will be added to all international orders.

16S/18S/ITS Short Amplicons (per sample, per amplicon) - MiSeq (2x300 bp PE)

	Academic/Govt. Per sample ¹	Commercial Per sample ¹
Library Preparation + Sequencing (max. 50k reads/sample ²)	\$30	\$40
or 2X depth (max. 100k reads/sample ²)	\$45	\$55
DNA Extraction ³	\$35	\$45
Standard Bioinformatics Analysis Pipeline ⁴	\$1000/project	\$1500/project

16S/18S/ITS Full-Length Amplicons (per sample, per amplicon) - PacBio Sequel2 (long reads)

	Academic/Govt. Per sample ¹	Commercial Per sample ¹
Library Preparation + Sequencing (max. 10k CCS reads/sample ²)	\$35	\$45
or 2X depth (max. 20k CCS reads/sample ²)	\$65	\$75
DNA Extraction ³	\$35	\$45
Standard Bioinformatics Analysis Pipeline ⁴	\$1000/project	\$1500/project

Client-Prepared Pool of Amplicons (per whole run) – MiSeq (150/250/300 PE)

	Academic/Govt. Per run	Commercial Per run
MiSeq Nano 2x250 bp Run (~1 M PE reads & 0.5 Gb)	\$2400	\$3000
MiSeq Micro 2x150 bp Run (~4 M PE reads & 1.2 Gb)	\$2600	\$3200
MiSeq Standard 2x300 bp Run (~20-25 M PE reads & 12-15 Gb)	\$6000	\$7000

Note: For clients wishing to use part of a run with a prepared pool of amplicons, simply divide 380 by your sample # then multiply by the above standard run price to determine your pool cost (this is for a 1X depth, simply double the amount for 2X).

Client-Prepared Pool of Metagenomes (per whole run) – NextSeq2000 (2x150 bp PE)

	Academic/Govt. Per run	Commercial Per run
NextSeq2000 P1 cell Run (~100 M PE reads)	\$4700	\$5700
NextSeq2000 P2 cell Run (~400 M PE reads)	\$11000	\$12000
NextSeq2000 P3 cell Run (~1.2 B PE reads)	\$18000	\$19000

Note: For clients wishing to use part of a run with a prepared pool of metagenomes, simply divide 192 by your sample # then multiply by the above P3 cell price to determine your pool cost (this is for a 1X depth).

Viral/Phage Genomes (1000X typical 150 kb genome) – MiSeq (2x300 bp PE) – De novo Assembly

	Academic/Govt.		Commercial	
	Per genome		Per genome	
Library Preparation + Sequencing (~0.25 M PE reads = 0.5 M single reads & 150 Mb/gen.)	\$200		\$300	
DNA Extraction ³	\$35		\$45	
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Small Genomes (>100X typical 5 Mb genome) – MiSeq (2x300 bp PE) – Resequencing

	Academic/Govt.		Commercial	
	Per run of 24	Per genome	Per run of 24	Per genome
Library Preparation + Sequencing (~0.9 M PE reads = 1.8 M single reads & 540 Mb/gen.)	\$12000	\$500	\$14400	\$600
DNA Extraction ³	–	\$35	–	\$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Small Genomes (>400X typical 5 Mb genome) – PacBio Sequel2 (long reads) – De novo Assembly

	Academic/Govt.		Commercial	
	Per run of 48	Per genome	Per run of 48	Per genome
Library Preparation + Sequencing (~2 Gb/genome)	\$14400	\$300	\$19200	\$400
DNA Extraction ³	–	\$35	–	\$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

(Micro)Eukaryote Genomes (100 Gb per cell) – PacBio Sequel2 (long reads) – De novo Assembly

	Academic/Govt.		Commercial	
	Per run of (X)	Per genome	Per run of (X)	Per genome
Library Preparation + Sequencing (~50 Gb/genome)	\$6000 (2)	\$3000	\$8000 (2)	\$4000
or whole cell (~100 Gb/genome)	\$5500 (1)	\$5500	\$6500 (1)	\$6500
DNA Extraction ³	–	\$35	–	\$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Metagenomes – NextSeq2000 (2x150 bp PE P3 cell) – Profiling and Contig Assembly

	Academic/Govt.		Commercial	
	Per run of (X)	Per sample	Per run of (X)	Per sample
Library Preparation + Sequencing (~6 M PE reads = 12 M single reads & 1.8 Gb/sample)	\$42240 (192)	\$220	\$57600 (192)	\$300
or 2X depth (~12 M PE = 24 M single & 3.6 Gb/sample)	\$31200 (96)	\$325	\$38400 (96)	\$400
or 4X depth (~24 M PE = 48 M single & 7.2 Gb/sample)	\$25200 (48)	\$525	\$33600 (48)	\$700
or 6X depth (~36 M PE = 72 M single & 11 Gb/sample)	\$24000 (32)	\$750	\$32000 (32)	\$1000
or 8X depth (~48 M PE = 96 M single & 14 Gb/sample)	\$22800 (24)	\$950	\$28800 (24)	\$1200
or 12X depth (~72 M PE = 144 M single & 22 Gb/sam.)	\$22400 (16)	\$1400	\$28800 (16)	\$1800
or 16X depth (~96 M PE = 192 M single & 29 Gb/sam.)	\$22200 (12)	\$1850	\$28800 (12)	\$2400
or 24X depth (~144 M PE = 288 M single & 43 Gb/sam.)	\$21600 (8)	\$2700	\$28000 (8)	\$3500

or 32X depth (~192 M PE = 384 M single & 58 Gb/sam.)
 DNA Extraction³
 Standard Bioinformatics Analysis Pipeline⁵

Academic/Govt.		Commercial	
Per run of 48	Per sample	Per run of 48	Per sample
\$21600 (6)	\$3600	\$27600 (6)	\$4600
–	\$35	–	\$45
\$1000/project		\$1500/project	

Metagenomes – PacBio Sequel2 (long reads) – Shallow Profiling

Library Preparation + Sequencing (~2 Gb/sample)
 DNA Extraction³
 Custom Bioinformatics Analysis Pipeline

Academic/Govt.		Commercial	
Per run of 48	Per sample	Per run of 48	Per sample
\$14400	\$300	\$19200	\$400
–	\$35	–	\$45
inquire		inquire	

Metagenomes – PacBio Sequel2 (long reads) – MAG Assembly

Library Preparation + Sequencing (~50 Gb/sample)
 or whole cell (~100 Gb/sample)
 DNA Extraction³
 Custom Bioinformatics Analysis Pipeline

Academic/Govt.		Commercial	
Per run of (X)	Per sample	Per run of (X)	Per sample
\$6000 (2)	\$3000	\$8000 (2)	\$4000
\$5500 (1)	\$5500	\$6500 (1)	\$6500
–	\$35	–	\$45
inquire		inquire	

(Meta)transcriptomes – NextSeq2000 (2x150 bp PE P3 cell) – Total Stranded w/rRNA Depletion

Library Preparation + Sequencing (~24 M PE reads = 48 M single reads & 7.2 Gb/sample)
 RNA Extraction³
 Standard Bioinformatics Analysis Pipeline⁵

Academic/Govt.		Commercial	
Per run of 48	Per sample	Per run of 48	Per sample
\$31200	\$650	\$38400	\$800
Not yet available		Not yet available	
\$1000/project		\$1500/project	

Iso-Seq – PacBio Sequel2 (long reads) – Full-Length Isoform Transcripts

Library Preparation + Sequencing (~12 Gb and ~500k reads/sample)
 RNA Extraction³
 Standard PacBio Iso-Seq Pipeline

Academic/Govt.		Commercial	
Per run of 8	Per sample	Per run of 8	Per sample
inquire	inquire	inquire	inquire
Not yet available		Not yet available	
\$1000/project		\$1500/project	

Notes/Details:

1. One control well is required per 96-well PCR library plate, hence a maximum of 4x95=380 samples can be done together on one MiSeq run (190 for a 2X run) or 2x95=190 samples on a Sequel2 run (95 for a 2X run). Any batches >380/190 will need to be spread across multiple MiSeq/Sequel2 runs.

2. These are generally maximum raw read outputs you will receive, but there is inherent variability in runs, meaning averages can be closer to 30k/60k (MiSeq 1X/2X) or 12k/24k (Sequel2 1X/2X).

3. Extra costs may be incurred if samples, due to their nature, require more specialized (length, cost, etc.) extraction procedures.

4 & 5. Details of our amplicon and metagenomics pipelines are available at https://github.com/LangilleLab/microbiome_helper/wiki, but a summary of the major deliverables clients will receive (analyses will require a "mapping file" from the clients containing any relevant metadata for the study) are available on our IMR.bio Protocols page (<http://imr.bio/protocols.html>).

Custom Bioinformatics: Additional bioinformatic analyses can be requested at a project-based rate or through research collaboration. Please contact us for more details.

Customs primers/amplicons: Beyond the 16S/18S/ITS amplicons offered "in-stock", essentially any PCR amplicon (max. size ~550 bp, best ~450-500 bp for MiSeq; no size limit for Sequel2) can be adapted to our systems. Please consults us for primer design/protocol details. Pricing is as follows (one-time extra oligo ordering charge): \$1050/1400/2100 for oligos for 1-95/96-190/191-380 samples for MiSeq; \$350/700 for oligos for 1-95/96-190 samples for Sequel2.

Processing time: Time to completion may be variable depending upon the amount of other partial projects in the queue – this generally no longer applies to amplicons as we are at capacity, but occurs more when submitting small numbers of samples for metagenomics runs (<<192 for NextSeq2000) or *de novo* genomes (<<48 for Sequel2).