Tupper 5-D1, Pharmacology Dept.
Dalhousie University
5850 College St., Halifax NS B3H 4R2

Tel.: 902.494.2684
Email: imr@dal.ca
Web: imr.bio

IMR.bio
Integrated Microbiome Resource

IMR Sequencing Services – Pricing as of Nov.10, 2025

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 i100 (2x300 bp PE)

	Academic/Govt.	**Commercial**
	Per sample[1]	**Per sample[1]**
Library Preparation + Sequencing (max. 75k reads/sample[2])	$20	$30
or 2X depth (max. 150k reads/sample[2])	$30	$40
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 Vega (long reads)

	Academic/Govt.	**Commercial**
	Per sample[1]	**Per sample[1]**
Library Preparation + Sequencing (max. 35k HiFi reads/sample[2])	$30	$40
or 2X depth (max. 70k HiFi reads/sample[2])	$55	$65
DNA Extraction[3]	$35	$45
Standard Bioinformatics Analysis Pipeline[4]	$1000/project	$1500/project

Client-Prepared Pool of Amplicons (per whole run) – MiSeq i100 or Vega

	Academic/Govt.	**Commercial**
	Per run	**Per run**
MiSeq i100 5M 2x150 bp Run (~5 M PE reads & 1.5 Gb) - typically for ~75 samples	$1700	$2000
MiSeq i100 5M 2x300 bp Run (~5 M PE reads & 3 Gb) - typically for ~75 samples	$2300	$2500
MiSeq i100 25M 2x150 bp Run (~25 M PE reads & 7 Gb) - typically for ~380 samples	$2800	$3200
MiSeq i100 25M 2x300 bp Run (~25 M PE reads & 15 Gb) - typically for ~380 samples	$3300	$3600
Vega Whole Cell Run (~6 M HiFi reads, variable Gb) - typically for ~190 samples	$4000	$5000

Note: For clients wishing to use part of a 25M run with a prepared pool of amplicons, simply divide 380 by your sample # then multiply by the above 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) or Vega

	Academic/Govt.	Commercial
	Per run	**Per run**
NextSeq2000 P1 cell Run (~100 M PE reads = 200 M single reads & 30 Gb)	$4000	$5000
NextSeq2000 P2 cell Run (~400 M PE reads = 800 M single reads & 120 Gb)	$7500	$9000
NextSeq2000 P3 cell Run (~1.2 B PE reads = 2.4 B single reads & 360 Gb)	$11000	$12000
Vega Whole Cell Run (~6 M HiFi reads, variable Gb)	$4000	$5000

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

Viral/Phage Genomes (~1000X typical 150 kb gen.) – MiSeq i100 (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.)	$110	$165
DNA Extraction[3]	$35	$45
Custom Bioinformatics Analysis Pipeline	inquire	inquire

Prokaryote Genomes (~100X typical 5 Mb genome) – MiSeq i100 (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.)	$7200	$300	$9600	$400
DNA Extraction[3]	–	$35	–	$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Prokaryote Genomes (~100X typical 5 Mb genome) – PacBio Vega (long reads) – De novo Assembly

	Academic/Govt.		Commercial	
	Per run of 48	**Per genome**	**Per run of 48**	**Per genome**
Library Preparation + Sequencing (~500 Mb HiFi/genome)[5]	$9600	$200	$14400	$300
DNA Extraction[3]	–	$35	–	$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Fungal Genomes (~100X typical 30-40 Mb genome) – NextSeq2000 (2x150 bp PE) – Reseq. or Hybrid

	Academic/Govt.		Commercial	
	Per run of 96	**Per genome**	**Per run of 96**	**Per genome**
Library Preparation + Sequencing (~12 M PE reads = 24 M single reads & 3.6 Gb/genome)	$17280	$180	$26400	$275
DNA Extraction[3]	–	$35	–	$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Fungal Genomes (~100X typical 40 Mb genome) – PacBio Vega (long reads) – De novo *Assembly*

	Academic/Govt.		Commercial	
	Per run of 5	**Per genome**	**Per run of 5**	**Per genome**
Library Preparation + Sequencing (~4 Gb HiFi/genome)[5]	$6000	$1200	$8000	$1600
DNA Extraction[3]	–	$35	–	$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

(Micro)Eukaryote Genomes (20 Gb HiFi per cell)[5] – PacBio Vega (long reads) – De novo *Assembly*

	Academic/Govt.		Commercial	
	Per run of (X)	**Per genome**	**Per run of (X)**	**Per genome**
Library Preparation + Sequencing (~10 Gb HiFi)[5]	$6000 (2)	$3000	$8000 (2)	$4000
or whole cell (~20 Gb HiFi)[5]	$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)	$23040 (192)	$120	$34560 (192)	$180
or 2X depth (~12 M PE = 24 M single & 3.6 Gb/sample)	$17280 (96)	$180	$26400 (96)	$275
or 4X depth (~24 M PE = 48 M single & 7.2 Gb/sample)	$15600 (48)	$325	$24000 (48)	$500
or 6X depth (~36 M PE = 72 M single & 11 Gb/sample)	$14400 (32)	$450	$22400 (32)	$700
or 8X depth (~48 M PE = 96 M single & 14 Gb/sample)	$14400 (24)	$600	$21600 (24)	$900
or 12X depth (~72 M PE = 144 M single & 22 Gb/sam.)	$14000 (16)	$875	$21600 (16)	$1350
or 16X depth (~96 M PE = 192 M single & 29 Gb/sam.)	$13800 (12)	$1150	$21000 (12)	$1750
or 24X depth (~144 M PE = 288 M single & 43 Gb/sam.)	$13600 (8)	$1700	$20800 (8)	$2600
or 32X depth (~192 M PE = 384 M single & 58 Gb/sam.)	$13800 (6)	$2300	$21000 (6)	$3500
DNA Extraction[3]	–	$35	–	$45
Standard Bioinformatics Analysis Pipeline[4]	$1000/project		$1500/project	

Metagenomes – PacBio Vega (long reads) – Shallow Profiling

	Academic/Govt.		Commercial	
	Per run of 48	**Per sample**	**Per run of 48**	**Per sample**
Library Preparation + Sequencing (~500 Mb HiFi/sample)[5]	$9600	$200	$14400	$300
DNA Extraction[3]	–	$35	–	$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Metagenomes – PacBio Vega (long reads) – MAG Assembly

	Academic/Govt.		Commercial	
	Per run of (X)	**Per sample**	**Per run of (X)**	**Per sample**
Library Preparation + Sequencing (~10 Gb HiFi)[5]	$6000 (2)	$3000	$8000 (2)	$4000
or whole cell (~20 Gb HiFi)[5]	$5500 (1)	$5500	$6500 (1)	$6500
DNA Extraction[3]	–	$35	–	$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

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

	Academic/Govt.		Commercial	
	Per run of 48	**Per sample**	**Per run of 48**	**Per sample**
Library Preparation + Sequencing (~24 M PE reads = 48 M single reads & 7.2 Gb/sample)	$20400	$425	$31200	$650
RNA Extraction[3]	Not yet available		Not yet available	
Standard Bioinformatics Analysis Pipeline[4]	$1000/project		$1500/project	

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

	Academic/Govt.		Commercial	
	Per run of 8	**Per sample**	**Per run of 8**	**Per sample**
Library Preparation + Sequencing (~2.5 Gb HiFi and ~800k reads/sample)[5]	inquire	inquire	inquire	inquire
RNA Extraction[3]	Not yet available		Not yet available	
Standard PacBio Iso-Seq Pipeline	$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 Vega run (95 for a 2X run). Any batches >380/190 will need to be spread across multiple MiSeq/Vega runs.

2. These are generally maximum raw read outputs you will receive: there is inherent variability in runs and the performance of samples, depending on their quality, so expect a potential range of outputs as there is no way to guarantee the performance of complex DNA samples.

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

4. 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 are available on our IMR.bio Protocols page (http://imr.bio/protocols.html). Analyses will require a "mapping file" from the clients containing any relevant metadata for the study.

5. These Gb values are for the estimated HiFi (CCS) reads obtained and are dependent upon the final size of the library inserts, which can vary depending on the quality of the DNA and resulting library success.

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 Vega) 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 Vega.

Processing time: Time to completion may be variable depending upon the amount of other partial projects in the queue – amplicons are always full (so not a problem), but occurs more when submitting small numbers of samples for metagenomics runs (<<192 for NextSeq2000) or *de novo* genomes (<<48 for Vega).