



Next Generation Sequencing Platform Price List



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Tariff 1 is for University of Bern and Inselspital internal accounts

Tariff 2 is for all external accounts*

* The University of Bern will apply a 20% overhead charge + VAT to the final invoice of commercial customers.

-Library Preparation Services

Sequencing libraries compatible with illumina platforms

-DNA Sequencing Libraries	Min. Input	Cat. No.	Tariff 1	Tariff 2
~Mechanical DNA Fragmentation				
DNA PCR-free library - Standard & no PCR	1 µg gDNA	LIBD01	225	266
DNA PCR-free library - Low Input & no PCR	250 ng gDNA	LIBD02	210	248
DNA library - Standard & with PCR	100 ng gDNA	LIBD03	225	266
DNA library - Low Input, with PCR & UMIs	500 pg gDNA	LIBD04	220	260
DNA library for FFPE & cfDNA - Low Input, with PCR & UMIs	10 ng DNA	LIBD05	240	284
ssDNA library - precious, damaged, degraded ds & ssDNA	10 pg DNA	LIBD06	230	272
~Enzymatic DNA Fragmentation				
DNA PCR-free library - no PCR	50 ng gDNA	LIBD07	165	195
DNA library - Standard & PCR	1 ng small genome or 100 ng large genome	LIBD08	150	177
DNA library - Low Input, with PCR & UMIs	100 pg DNA	LIBD09	175	207
DNA library for FFPE - Low Input, with PCR & UMIs	10 ng FFPE DNA	LIBD10	220	260
PlexWell service HTP DNA-Seq 96 samples Examples for use: Microbial WGS, low depth WGS, metagenomics	3-30ng DNA	LIBD011	2'500	2'954
Hi-C library for genome scaffolding - human	enquire	LIBD012a	1'300 Sample 2 = 1'000 CHF	1'536
Hi-C library for genome scaffolding - animal/plant/microbial/fungal	enquire	LIBD012b	1'500 Sample 2 = 1'000 CHF	1'772

UMI = Unique Molecular Identifier

-Amplicon libraries	Input	Cat. No.	Tariff 1	Tariff 2
Amplicon PCR indexing service/12 samples Incl. PCR amplicon clean-up, unique dual indexing step, 2 nd PCR step clean-up and QC PCR products with illumina compatible overhangs only	10 µL of 1 st step PCR	LIBA01a	185	219
Amplicon PCR service/12 samples Bring your own primers, incl., clean-up and quantification	DNA; protocol specific	LIBA01b	110	135
Large amplicons Illumina compatible overhangs are not necessary.	1 ng (≥300 bp)	LIBA02	140	165

-Epigenomics	Input	Cat. No.	Tariff 1	Tariff 2
Chromatin Immunoprecipitation sequencing library (ChIP-Seq)	10 pg ChIP'ed DNA	LIBE01	220	260
CUT & RUN library	10 pg DNA fragments	LIBE02	230	272
Assay for Transposase-Accessible Chromatin sequencing library (ATAC-Seq)	nuclei prep. from 50'000 cells	LIBE03	290	343
Whole Genome bisulfite sequencing library (WGBS)	100 pg-50 ng gDNA ≥5 ng FFPE or cfDNA	LIBE04	330	390
Enzymatic Methyl-Seq (EM-Seq)	10 -200 ng gDNA	LIBE05	320	378
Reduced Representation Bisulfite Sequencing library (RRBS)	10-500 ng gDNA	LIBE06	260	307

-Microbiomics	Input	Cat. No.	Tariff 1	Tariff 2
Amplicon libraries for 16S (V3-V4) or ITS Including community standards & NTC	Microbial DNA: 10 ng/ µL	LIBM01a 16S LIBM01b ITS	25	30
Amplicon library for full-length 16S (V1-9)- ITS Including community standards & NTC	1 ng/ µL	LIBM02	40	47
Shotgun metagenomic sequencing library - Standard & PCR	1 ng DNA	LIBM03	150	177
Shotgun metagenomic sequencing library - Low Input, with PCR & UMIs	100 pg DNA	LIBM04	175	207

-RNA libraries	Min. Input	Cat. No.	Tariff 1	Tariff 2
Small RNA Size selected libraries according to project	100 ng total RNA 50 pg enriched small RNA	LIBR01	390	461
miRNA-Seq Price includes miRNA spike-in at point of extraction	100 ng total RNA 5uL of RNA from 200 uL serum/plasma	LIBR02	370	437
Quant-Seq 3'mRNA-Seq	100 ng total RNA (RNA with polyA mRNA)	LIBR03	160	189
Stranded mRNA -standard	200 ng	LIBR04	255	301
Stranded mRNA – no fragmentation, low input & with UMIs	1 ng total RNA	LIBR05	225	266
Stranded mRNA - Ultra-low input	1-1'000 cells 10 pg of total RNA	LIBR06	340	402
Stranded Total RNA – standard - human, blood, rat, mouse & Plant	100 ng	LIBR07	350	414
Stranded Total RNA – no fragmentation, low input & with UMIs Compatible with diverse species for tailored rRNA depletion incl. bacteria	1 ng	LIBR08	325	384
Stranded Total RNA – Ultra Low input -mammalian RNA	10 ng total RNA	LIBR09	350	414
FFPE RNA	10 ng FFPE RNA	LIBR10	340	402
Spike-In RNA Control		LIBR11	12	14
BRB-Seq 48 samples, NextSeq 1000 sequencing, 90-100bp reads, 8M/sample	50 ng total RNA (RNA with polyA mRNA)	LIBR12	3'400	3'899
BRB-Seq 96 samples- NovaSeq 6000 sequencing, 90-100 bp reads, 8M/sample		LIBR13	5'900	6'734
Stranded mRNA library package deal/8 samples	50 ng total RNA (RNA with polyA mRNA)	LIBR14	800	945
24 x stranded mRNA-Seq libraries, 25 M reads, at 2 x 50bp or 1 x 100bp		LIBR15	4'900	5'789

Volume discounts on illumina sequencing libraries:

≥ 12 identical libraries	-10%
≥ 24 identical libraries	-20%

-10 x Genomics - Chromium single cell/nuclei services	Target recovery	Cat. No.	Tariff 1	Tariff 2
Chromium Single Cell Gene Expression (3') v3.1 Cells to 3' gene expression library + Feature barcode library for cell surface protein	500-10'000 cells	LIBSC01a LIBSC01b	2'400 160	2'836 189
Chromium Single Cell ATAC v2 Nuclei to ATAC library	500-10'000 nuclei	LIBSC02	2'300	2'717
Chromium Single Cell Multiome ATAC + Gene Expression (3') Nuclei to ATAC library and gene expression library	500-10'000 nuclei	LIBSC03	4'000	4'726
Chromium Single Cell Immune Profiling -cells to ds cDNA v2 + 5' gene expression library + VDJ enrichment library + Feature barcode library for cell surface protein	500-10'000 cells	LIBSC04a LIBSC04b LIBSC04c LIBSC04d	2'300 320 450 160	2'717 378 532 189
LIBSC01-04: 16% reduction in price for sample 2, up to sample 8, from the same GEM generation batch				

Chromium Single Cell Gene Expression (3') v3.1 bundle* 8 x Cells to 3' gene expression library (one submission of 8 samples)	500-10'000 cells	LIBSC05	16'000	18'904
Chromium Single Cell Immune Profiling -cells to ds cDNA v2 bundle* 8 x 5' gene expression library (one submission of 8 samples) 8 x VDJ enrichment library 8 x Cell surface protein library	500-10'000 cells	LIBSC06a LIBSC06b LIBSC06c	16'000 1'600 1'280	18'904 1'890 1'512
Chromium Single Cell Gene Expression (3') v3.1 HT Cells to 3' gene expression library + Feature barcode library for cell surface protein + Cell multiplexing library (3'Cell Plex)	2'000-20'000 cells	LIBSC07 LIBSC01b LIBSC07b	2'100 160 160	2'481 189 189
Chromium Single Cell Immune Profiling -cells to ds cDNA v2 HT** + 5' gene expression library + VDJ enrichment library + Feature barcode library for cell surface protein + 5' BEAM library	2'000-20'000 cells	LIBSC08a LIBSC04b LIBSC04c LIBSC04d LIBSC08b	2'000 320 450 160 160	2'363 387 532 189 189
Single Cell Gene Expression Flex Chromium Fixed RNA Kit, Human/Mouse Transcriptome Chromium Fixed RNA Kit, Human/Mouse Transcriptome	4 barcodes 16 barcodes	LIBSC09 LIBSC10	4'200 9'400	6'616 10'870

* Bundle offers can be adapted to batch sizes of 6 or 7 samples/submission.

** Less than 8 samples/GEM generation batch requires a 1'700 CHF chip payment.

-10 x Genomics - Visium Spatial Transcriptomics Services	Capture Area	Cat. No.	Tariff 1	Tariff 2
Visium Spatial Gene Expression - 4 samples	Capture area in %	LIBSC11a	7'200	8'507
Fresh Frozen - 16 samples	4'992 spots	LIBSC11b	25'600	30'246
Visium Spatial Gene Expression FFPE CytAssist human/mouse 6.5 mm²	Capture area in %			
-4 samples	4'992 spots	LIBSC12a	7'560	8'932
-16 samples		LIBSC06b	26'400	31'191
Visium Spatial Gene Expression FFPE CytAssist human/mouse 11 mm²	Capture area in %			
-2 samples	14'336 spots	LIBSC13a	7'700	9'097
-8 samples		LIBSC13b	27'200	32'136
~Other single cell RNA-Seq workflows	Target recovery	Cat. No.	Tariff 1	Tariff 2
SMART-Seq/96 samples	1 -1,000 cells 2 pg- 10 ng RNA	LIBSC14	4'200	4'962

Sequencing libraries compatible with the Pacific Bioscience Sequel Platform

~PacBio DNA Sequencing Libraries*	Min. Input	Cat. No.	Tariff 1	Tariff 2
HiFi SMRTbell Library -standard & metagenome	300ng-10 µg – project dependent	LIBP01	400	473
HiFi SMRTbell Library - Low input	300 ng	LIBP02	420	496
HiFi SMRTbell Library – Ultra Low input Size selections are not included in the price	5 ng	LIBP03	550	662
HiFi Microbial multiplexed library (total 200-300 Mb/SMRTcell)	300ng-2 µg/microbe	LIBP04a LIBP04b	140	165
≤ 48			130	154
≥ 48				
~PacBio Amplicon Sequencing				
PCR BARCODED SAMPLES 1 pool of PCR barcoded amplicons or barcoded cDNA/(barcoded) SMRTbell library	Total input DNA per SMRT Cell: 300 ng for <3 kb 500 ng for 3 - 10 kb ≥1000 ng for ≥10 kb	LIBP05	300	354
ADAPTER BARCODED SAMPLES 1 amplicon/barcoded SMRTbell library		LIBP06	330	390
~PacBio RNA Sequencing Libraries		Cat. No.	Tariff 1	Tariff 2
Iso-Seq Library (full-length (FL) transcripts)	300 ng total RNA, High quality	LIBP07	400	473
Barcoded FL cDNA 1 st sample	300 ng total RNA, High quality	LIBP08a	400	473
Samples 2-12, same batch		LIBP08b	200	237
Kinnex PCR & Array formation FL RNA-Seq 1 st sample	Requires 55 ng cDNA (LIBP08)	LIBP09a	800	944
Samples 2-4, same batch		LIBP09b	600	708
~PacBio single cell RNA Sequencing Libraries		Cat. No.	Tariff 1	Tariff 2
MAS-Seq for 10 x Genomics Single Cell 3'kit 1 st sample	Requires 15-75 ng 10 x Genomics 3' cDNA	LIBP10a	950	1121
Samples 2-4, same batch		LIBP10b	600	708
Kinnex single cell RNA-Seq 1 st sample	Requires 15-75 ng 10 x Genomics 3' or 5' cDNA	LIBP11a	950	1121
Samples 2-4, same batch		LIBP11b	600	708

* Subsequent identical libraries (samples 2- 12) in any single submission for LIBP01-LIBP07 are charged at **35% off** the stated price.

~PacBio special services		Cat. No.	Tariff 1	Tariff 2
HMW DNA extraction/sample 1-4 samples- cells or blood samples		LIBPS01	400	472
HMW DNA extraction/sample 1-4 samples - plant, tissue, insect samples etc.		LIBPS02	650	767
HMW DNA extraction manual/16 samples – microbial		LIBPS03a	430	507
HMW DNA extraction on robot/48 samples – microbial		LIBPS03b	840	991
HMW DNA extraction on robot/96 samples – microbial		LIBPS03c	1'500	1'770
RNA extraction/sample - cells or blood samples		LIBPS04	30	35
RNA extraction/sample - bacteria, plant, tissue samples		LIBPS05	52	61
PacBio short read eliminator service/sample		LIBPS06	46	54
~PacBio Metabarcoding				
16S rRNA V1-V9 (bacterial) or ITS1-2 (fungal) 1-2 ng input DNA, 192 barcodes One step PCR & including community standards & NTCs ≤ 96 ≥ 96		LIBPS07a LIBPS07b	20 10	24 12
Kinnex 16S rRNA V1-V9 (batches of ≥ 96, max 384 barcodes) 1-2 ng input DNA One step PCR & including community standards & NTCs <i>Followed by Kinnex PCR & Array formation (LIBP08)</i>		LIBPS08	15	18

NOTE: Other library preparations are possible upon request for illumina (WES, myBAITs), 10x Genomics and PacBio.

-Accessory DNA/RNA Services

-DNA Fragmentation services	Cat. No.	Tariff 1	Tariff 2
Covaris E220evolution Focused Ultrasonicator Shearing gDNA (50-130 µL) in the 100-1'000 bp range; microTUBE & service incl. QC/8 Rxn	AD01	150	177
Covaris g-TUBE DNA shearing Shearing of gDNA in the 6-20 kb range using centrifugal force; g-TUBE service incl. QC /sample	AD02	74	87
Diagenode Megaruptor 2 DNA fragmentation in the 3-75 kb range; Hydropore devices & service, incl. QC /sample	AD03	47	56
-DNA Size Selection			
Sage Science Blue Pippin 3% agarose for size selections in the range of 100-250 bp/5 samples 2% agarose for size selections in the range of 100-600 bp/5 samples 0.75% agarose for size selections in the range of 1-40 kb/4 samples All size selection services are inclusive of QC	AD04a AD04b AD04c	218 218 254	258 258 300
-Purify and concentrating services			
DNA concentrating service - speed vac	AD05	3	4
Clean, concentrate & DNase I treatment for RNA samples – column based ≤ 24 ≥ 24	AD06a AD06b	20 10	24 12
Clean, concentrate treatment for DNA samples – column based ≤ 24 ≥ 24	AD07a AD07b	18 8	21 9
Clean, concentrate treatment for genomic DNA samples – column based ≤ 24 ≥ 24	AD08a AD08b	21 9	25 11
bead-based DNA clean-up service with quantification /12 samples	AD09	75	89
-DNA & RNA QC services			
Spectrophotometric analysis	AD010	1	1
Advanced Analytics Fragment Analyzer CE12 - capillary gel electrophoresis QC for libraries, RNA & DNA; reagents & service/1 lane (11 samples & ladder)	AD011	80	95
Advanced Analytics FEMTO Pulse CE - pulsed field capillary gel electrophoresis QC for libraries, RNA & HMW DNA; reagents & use/1 lane (11 samples & ladder)	AD012	123	145
LifeTechnologies Qubit Fluorimetry - Accurate quantitation for RNA or DNA; reagents/sample	AD013	3	3
qPCR based illumina NGS Library Quantification/8 samples	AD014	123	145
Sample equimolar pooling service/24 samples	AD015	80	94

-Ready-to-Load Library Services

- Ready-to-Load Library (RTL) services	Cat. No.	Tariff 1	Tariff 2
Custom-made library extra light service RTL projects handling only	LIBRTL01	53	63
Custom-made library light service RTL quantitation (concentration) & pooling service/8 samples	LIBRTL02	80	94
Custom-made library standard service RTL quantitation (size and concentration) & pooling service/11 samples	LIBRTL03	140	165
Custom-made standard service for low concentrated libraries RTL quantitation (size and concentration) & pooling service/11 samples	LIBRTL04	180	213
Custom-made library full service RTL quantitation (size and concentration), purification & pooling service/11 samples	LIBRTL05	215	254

-Sequencing Services

illumina sequencing service

illumina iSeq 100	Cycles	No. reads	Output	Cat. No.	Tariff 1	Tariff 2
i1 Reagent v2	300	4 M	1.2 Gb	SEQi01	700	827
i1 Reagent v2 QC run	300	4 M	1.2 Gb	SEQi02	680	803
Custom sequencing i				SEQi03	enquire	enquire

illumina MiSeq	Cycles	No. reads	Output	Cat. No.	Tariff 1	Tariff 2
v2 nano flow cell	300	1 M	300 Mb	SEQM01	550	650
v2 nano flow cell	500	1 M	500 Mb	SEQM02	640	756
v2micro flow cell	300	4 M	1.2 Gb	SEQM03	760	898
v2 standard flow cell	50	12 M	750 Mb	SEQM04	1'300	1'536
v2 standard flow cell	300	12 M	4.5 Gb	SEQM05	1'600	1'890
v2 standard flow cell	500	12 M	7.5 Gb	SEQM06	1'800	2'127
v3 flow cell	150	22 M	3.3 Gb	SEQM07	1'400	1'654
v3 flow cell	600	22 M	13.2 Gb	SEQM08	2'300	2'717
Custom sequencing M				SEQM09	60	71

illumina NextSeq 1000	Cycles	No. reads	Output	Cat. No.	Tariff 1	Tariff 2
P1 100 cycles	100	100 M	10 Gb	SEQNX01	1'150	1'359
P1 300 cycles	300	100 M	30 Gb	SEQNX02	1'560	1'843
P1 600 cycles	600	100 M	60 Gb	SEQNX03	2'320	2'741
P2 100 cycles	100	400 M	40 Gb	SEQNX04	1'800	2'127
P2 200 cycles	200	400 M	80 Gb	SEQNX05	3'280	3'875
P2 300 cycles	300	400 M	120 Gb	SEQNX06	4'320	5'104
P2 600 cycles	600	300 M	180 Gb	SEQNX07	4'720	5'577
Custom sequencing NX				SEQNX08	enquire	enquire

illumina NovaSeq 6000³	Cycles	No. reads	Output	Cat. No.	Tariff 1	Tariff 2
SP flow cell	100	650 M	65 Gb	SEQN01	2'900	3'426
SP flow cell	200	650 M	134 Gb	SEQN02	3'800	4'490
SP flow cell	300	650 M	200 Gb	SEQN03	4'100	4'844
SP flow cell	500	650 M	325 Gb	SEQN04	5'700	6'734
S1 flow cell	100	1.3 B	134 Gb	SEQN05	5'100	6'026
S1 flow cell	200	1.3 B	266 Gb	SEQN06	6'500	7'680
S1 flow cell	300	1.3 B	400 Gb	SEQN07	7'100	8'388
S2 flow cell	100	3.3 B	333 Gb	SEQN08	9'500	11'224
S2 flow cell	200	3.3 B	667 Gb	SEQN09	11'900	14'060
S2 flow cell	300	3.3 B	1'000 Gb	SEQN10	12'800	15'123
SP, S1, S2 flow cell XP workflow				SEQN11	550	650
S4 flow cell	200	8.0 B	1'600 Gb	SEQN12	16'500	19'494
S4 flow cell	300	8.0 B	2'400 Gb	SEQN13	18'400	21'739
S4 flow cell XP workflow				SEQN14	910	1'075
Custom sequencing N				SEQN15	120	145

NOTE: M = million, B = billion, Mb = Mega base pairs, Gb= Giga base pairs; please note that the stated number (No.) of reads and data output figures are stated at the lower end of what illumina guarantees and will vary according to sample type, quality and clusters passing filter.

Pacific Biosciences sequencing service

<u>PacBio Sequel IIe system</u>	Cat. No.	Tariff 1	Tariff 2
1 SMRT cell 8M	SEQP01	2'100	2'481
<u>PacBio Revio System</u>			
1 SMRT cell 25M	SEQP02	1'440	1'700

Service Considerations

Costs: The NGSP is a non-profit core facility serving three faculties of the University of Bern, Inselspital, and the many external academic and commercial researchers. Tariff 1 costs cover all consumables, lab technician hands-on working time, all quality control steps and the direct informatics time required from sample delivery to data release via our LIMS. Tariff 2 prices are the full costs of the service which include the direct costs attributed to tariff 1 prices, other direct costs (personnel time dedicated to projects that is not hands-on lab-based working time, instrument maintenance, instrument depreciation, infrastructure) and indirect costs (administrative costs). Tariff 2 is charged to all external researchers/customers. Furthermore, Value Added Tax (7.7%) will be added to the final invoice, as well as an overhead charge from the University of Bern (20%).

Consultation/quote requests: Please tell us what your deadlines are and give us as much information as you can about your needs. The lab manager will contact you as soon as possible to discuss your project in more depth followed by providing a start-to-finish quotation for your project. Please allow up to a week for this process. In your initial contact email to pamela.nicholson@unibe.ch, please include: your full name, organisation, PI, project description, desired sequencing platform, species, genome size, number of samples and whether you would like bioinformatics support beyond the generation of data.

Storage Rules:

Samples – 3 months

cDNA & Libraries – 24 months

Data Storage – 6 months

Turn-around times: Unless communicated otherwise and as a general guide: *Standard RNA or DNA-Seq is 1.5-3 weeks. Any other service is up to 6 weeks.*

Contact details: NGS Platform - University of Bern

E-mail: ngs.lab@vetsuisse.unibe.ch

Tel: 031 684 22 85

-Miscellaneous Services

<u>Miscellaneous</u>	Cat. No.	Tariff 1	Tariff 2
Additional Data Handling or consumable use in NGSP lab	MISC01	50	59
Urgent Project Service Priority samples QC & library prep.	MISC02	10%	15%

Prices and conditions are subject to change without notice.