



Internal Price List for UniBe, UniFr & Inselspital

All prices in CHF

-Library Preparation Services

Sequencing libraries compatible with illumina platforms

<i>-DNA Sequencing Libraries</i>	Input	Price	Cat. No.
DNA PCR-free library	1 µg gDNA	215	LIBD01 ¹
DNA PCR-free library - Low input	100 ng gDNA 10 ng cfDNA	240	LIBD02
DNA library - Mechanical fragmentation and PCR	100 ng gDNA	215	LIBD03 ¹
DNA library - enzymatic fragmentation and PCR	1 ng small genome or 100 ng large genome	150	LIBD04 ¹
ssDNA library - precious, damaged, degraded ds & ssDNA	10 pg DNA	200	LIBD05
Formalin Fixed Paraffin Embedded (FFPE) DNA library	10 pg FFPE DNA	200	LIBD06

<i>-Amplicon libraries</i>	Input	Price	Cat. No.
Amplicon indexing service/12 samples (unique dual indexing step and QC) Clean PCR products with illumina compatible overhangs	10 µL of 1 st step PCR	140	LIBA01
Large amplicons Illumina compatible overhangs are not necessary	1 ng (≥300 bp)	130	LIBA02

<i>-Epigenomics</i>	Input	Price	Cat. No.
Chromatin Immunoprecipitation sequencing library (ChIP-Seq)	10 pg ChIP'ed DNA	220	LIBE01
CUT & RUN library	10 pg DNA fragments	220	LIBE02
Assay for Transposase-Accessible Chromatin sequencing library (ATAC-Seq)	nuclei prep. from 50'000 cells	290	LIBE03
Whole Genome bisulfite sequencing library (WGBS)	100 pg-50 ng gDNA ≥5 ng cfDNA	310	LIBE04
Reduced Representation Bisulfite Sequencing library (RRBS)	10-500 ng gDNA	220	LIBE05

<i>-Metagenomics</i>	Input	Price	Cat. No.
Amplicon libraries for 16S V1-V2 or V3-V4 Including community standard Recommended for > 48 samples 10% off MiSeq v3 600 cycles sequencing	Microbial DNA: 10 ng/ µL	23	LIBM01a V1-2 LIBM01b V3-4
Amplicon library for full-length 16S (V1-9) or ITS Including community standard Recommended for > 48 samples 10% off MiSeq v3 600 cycles sequencing	10 pg for microbial isolates; 1-50 ng for metagenomic samples	53	LIBM02a 16S LIBM02b ITS
Shotgun metagenomic sequencing library	1-500 ng DNA	150	LIBM03 ¹

-RNA libraries	Input	Price	Cat. No.
Small RNA Size selected libraries according to project	≥ 100 ng total RNA ≥ 50 pg enriched small RNA	390	LIBR01
Quant-Seq 3'mRNA-Seq - with unique molecular identifiers	≥ 100 ng total RNA	170	LIBR02
Stranded mRNA	≥ 200 ng	250	LIBR03 ¹
Stranded mRNA - Low input	10 ng total RNA	250	LIBR04
Stranded mRNA - Ultra-low input	1-1'000 cells 10 pg of total RNA	380	LIBR05
Stranded Total RNA - RNA from human, blood, rat, mouse, bacteria	≥ 100 ng	340	LIBR06 ¹
Stranded Total RNA Plant - RNA from plant tissue	≥ 100 ng	340	LIBR07 ¹
Stranded Total RNA-Seq universal - RNA from any species	≥ 100 ng	310	LIBR08
Stranded Total RNA - Low input RNA from human, rat, mouse, blood RNA from bacterial samples	10 ng total RNA	320 300	LIBR09a LIBR09b
FFPE RNA	10 ng FFPE RNA	340	LIBR10
Spike-In RNA Control		12	LIBR11
-Immune Profiling			
Human BCR IgG IgM H/K/L Profiling library/12 samples	≥ 1 ng total RNA	3'000	LIBR12
Human TCR a/b Profiling library/12samples	≥ 1 ng total RNA 1'000-10'000 purified T cells	4'000	LIBR13
Mouse BCR IgG H/K/L Profiling library /12 samples	≥ 10 ng total RNA	2'500	LIBR14
Mouse TCR a/b Profiling library/12 samples	≥ 10 ng total RNA 1'000-10'000 purified T cells	2'600	LIBR15

¹Volume discounts on standard illumina sequencing libraries:

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

-10 x Genomics	Target recovery	Price	Cat. No.
Chromium Single Cell Gene Expression (3') Cells to 3' gene expression library + Cell surface protein library	500-10'000 cells	2'000 140	LIBSC01a LIBSC01b
Chromium Single Cell ATAC Nuclei to ATAC library	500-10'000 nuclei	1'900	LIBSC02
Chromium Single Cell Multiome ATAC + Gene Expression (3') Nuclei to ATAC library and gene expression library	500-10'000 nuclei	3'100	LIBSC03
Chromium Single Cell Immune Profiling -cells to ds cDNA + 5' gene expression library + VDJ enrichment library + Cell surface protein library	500-10'000 cells	1'600 360 400 140	LIBSC04a LIBSC04b LIBSC04c
Visium Spatial Gene Expression	Capture area in %	2'000	LIBSC05

Sequencing libraries compatible with the Pacific Bioscience Sequel Platform

-PacBio DNA Sequencing Libraries	Input	Price	Cat. No.
HiFi SMRTbell Library	15 µg	700	LIBP01
HiFi SMRTbell Library - Low input	150 ng/300 Mb genome	720	LIBP02
Genomic DNA library (> 15 kb)	1-5 µg	750	LIBP03
Microbial multiplexed library (total 30-40 Mb) up to 8 barcodes up to 16 barcodes	1 µg/microbe	1'050 1'600	LIBP04a LIBP04b
-PacBio Amplicon Sequencing			
SMRTbell Libraries using Barcoded Universal Primers (BUP) 24 amplicons 48 amplicons 96 amplicons	250-500 ng for 250-1000 bp 500-1000 ng for 1-3 kb 1000-2000 ng for 3-10 kb	820 1'440 2'500	LIBP05a LIBP05b LIBP05c

SMRTbell Libraries using Barcoded Overhang Adapters (BOA) 8 amplicons 16 amplicons	1500-3000 ng for 15 kb	735 1'100	LIBP06a LIBP06b
-PacBio RNA Sequencing Libraries		Price	Cat. No.
Iso-Seq Library (full-length transcripts) Standard library targeting ~2 kb transcripts Two libraries; standard targeting 2 kb transcripts + a special library targeting >3 kb transcripts or < 2 kb transcripts	300 ng total RNA	650 1'100	LIBP7a LIBP7b

-PacBio special services		Price	Cat. No.
HMW DNA extraction/sample (≥ 50 kb), 1-4 samples; including QC		650	LIBPS01
Microbial WGS from DNA extraction to assembly (8 samples) package (up to total 30 Mb)		1'580	LIBPS02
Microbial WGS from DNA extraction to assembly (16 samples) package (up to total 30 Mb)		2'400	LIBPS03
Full-length 16S gene with barcoded primers for multiplexed SMRTbell library DNA to demultiplexed reads Including community standard Recommended for > 20 samples 10% off 1 SMRT cell 1M v3 sequencing		38	LIBPS04

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

-Accessory DNA/RNA Services

-DNA Fragmentation services		Price	Cat. No.
Covaris E220evolution Focused Ultrasonicator Shearing of gDNA (50-130 µL) in the 100-1'000 bp range; microTUBE & service incl. QC/sample		60	AD01
Covaris g-TUBE DNA shearing Shearing of gDNA in the 6-20 kb range using centrifugal force; g-TUBE service incl. QC /sample		40	AD02
Diagenode Megaruptor 2 DNA fragmentation in the 3-75 kb range; Hydropore devices & service, incl. QC /sample		50	AD03
-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		160 160 170	AD04a AD04b AD04c
-Clean and concentrator services			
DNA/RNA concentrating service speed vac		5	AD05
RNase treatment for DNA samples		15	AD06
DNase treatment for RNA samples		15	AD07
Column based DNA/RNA purification		10	AD08
ChIP sample clean-up		10	AD09
Bead-based DNA/RNA clean-up		12	AD10
PCR amplicon bead-based clean-up service /12 samples		90	AD11
-DNA & RNA QC services			
Spectrophotometric analysis		1	AD012
Advanced Analytics Fragment Analyzer CE12 - capillary gel electrophoresis QC for libraries, RNA & DNA; reagents & service/1 lane (11 samples & ladder)		80	AD013
Advanced Analytics FEMTO Pulse CE - pulsed field capillary gel electrophoresis QC for libraries, RNA & HMW DNA; reagents & use/1 lane (11 samples & ladder)		110	AD014
LifeTechnologies Qubit Fluorimetry Accurate quantitation for RNA or DNA; reagents/sample Lightening RNA quality assessment/samples (10 min)		3.5 5.5	AD015a AD015b
qPCR based illumina NGS Library Quantification/8 samples		110	AD016

<i>-Ready-to-Load Library (RTL) services</i>	Price	Cat. No.
Custom-made library extra light service RTL projects handling only	50	LIBRTL01
Custom-made library light service RTL quantitation (concentration) & pooling service/8 samples	66	LIBRTL02
Custom-made library standard service RTL quantitation (size and concentration) & pooling service/11 samples	140	LIBRTL03
Custom-made library standard service for low concentrated samples RTL quantitation (size and concentration) & pooling service/11 samples	170	LIBRTL04
Custom-made library full service RTL quantitation (size and concentration), purification & pooling service/11 samples	150	LIBRTL05
Custom-made PacBio SMRTbell enzyme clean-up service To enrich for intact circular SMRTbell templates prior to PacBio sequencing	60	LIBRTL06

-Sequencing Services

illumina sequencing service

illumina iSeq 100	Cycles	No. reads	Output	Price	Cat No.
i1 Reagent v2	300	4 M	1.2 Gb	660	SEQi01
i1 Reagent v2 QC run ²	500	1 M	500 Mb	600	SEQi02

illumina MiSeq	Cycles	No. reads	Output	Price	Cat No.
v2 nano flow cell	300	1 M	300 Mb	530	SEQM01
v2 nano flow cell	500	1 M	500 Mb	600	SEQM02
v2micro flow cell	300	4 M	1.2 Gb	700	SEQM03
v2 standard flow cell	50	≥ 12 M	≥ 750 Mb	1'070	SEQM04
v2 standard flow cell	300	≥ 12 M	≥ 4.5 Gb	1'300	SEQM05
v2 standard flow cell	500	≥ 12 M	≥ 7.5 Gb	1'480	SEQM06
v3 flow cell	150	≥ 22 M	≥ 3.3 Gb	1'200	SEQM07
v3 flow cell	600	≥ 22 M	≥ 13.2 Gb	1'890	SEQM08
Custom sequencing				60	SEQM09

illumina NovaSeq 6000³	Cycles	No. reads	Output	Price	Cat No.
SP flow cell	100	≥ 650 M	≥ 65 Gb	2'800	SEQN01
SP flow cell	200	≥ 650 M	≥ 134 Gb	3'800	SEQN02
SP flow cell	300	≥ 650 M	≥ 200 Gb	4'200	SEQN03
SP flow cell	500	≥ 650 M	≥ 325 Gb	5'700	SEQN04
S1 flow cell	100	≥ 1.3 B	≥ 134 Gb	5'000	SEQN05
S1 flow cell	200	≥ 1.3 B	≥ 266 Gb	6'300	SEQN06
S1 flow cell	300	≥ 1.3 B	≥ 400 Gb	7'200	SEQN07
S2 flow cell	100	≥ 3.3 B	≥ 333 Gb	9'500	SEQN08
S2 flow cell	200	≥ 3.3 B	≥ 667 Gb	11'200	SEQN09
S2 flow cell	300	≥ 3.3 B	≥ 1'000 Gb	12'600	SEQN10
SP, S1, S2 flow cell XP workflow				800	SEQN11
S4 flow cell	200	≥ 8.0 B	≥ 1'600 Gb	16'000	SEQN12
S4 flow cell	300	≥ 8.0 B	≥ 2'400 Gb	17'500	SEQN13
S4 flow cell XP workflow				1'200	SEQN14

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 estimates and will vary according to sample type, quality and clusters passing filter.

²precedes a NovaSeq 6000 run for the same NGS library set at the NGSP

³Version 1.5 NovaSeq 6000 sequencing chemistry

Pacific Biosciences Sequel sequencing service

PacBio Sequel⁴	Price	Cat No.
1 SMRT cell 1M v3	1'520	SEQP01
1 SMRT cell 1M v3 LR	1'600	SEQP02

⁴Sequel II sequencing service is also available, please enquire.

-Miscellaneous Services

Miscellaneous	Price	Cat No.
Additional Data Handling for unexpected additional data handling tasks	50	MISCO1

Service Considerations

Costs: The NGSP is a non-profit core facility serving three faculties of the University of Bern, Inselspital, and the University of Fribourg. The costs stated above include all consumables, lab technician hands-on working time, quality control steps and the informatics required from sample delivery to data release via our LIMS. Our prices do not include bioinformatics. If you need bioinformatics support, please contact: info@bioinformatics.unibe.ch

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@vetsuisse.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.

Sample requirements: Your sample is the foundation of your sequencing project. Therefore, please consult our sample requirements information section on our website: www.ngs.unibe.ch.

As of December 2020, the website will have all information concerning our offered services. Changes to service will be notified via our quarterly newsletter starting January 2021.

Storage of samples, libraries, and data: We guarantee the storage of your samples, any generated libraries and data for 3 months. You are free to collect your samples them at any point in these 3 months. Once your data has been released, you will receive an email informing that the data is ready for download. Please have a data management plan ready for your data.

Contact details: NGS Platform - University of Bern

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Prices and conditions are subject to change without notice.