



# Next Generation Sequencing Platform Price List



UNIVERSITÄT  
BERN

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

<b>-DNA Sequencing Libraries</b>	<b>Min. Input</b>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>~Mechanical DNA Fragmentation</b>				
<b>DNA PCR-free library</b> - Standard & no PCR	1 µg gDNA	LIBD01	225	269
<b>DNA PCR-free library</b> - Low Input & no PCR	250 ng gDNA	LIBD02	215	257
<b>DNA library</b> - Standard & with PCR	100 ng gDNA	LIBD03	230	275
<b>DNA library</b> - Low Input, with PCR & UMIs	500 pg gDNA	LIBD04	225	269
<b>DNA library for FFPE &amp; cfDNA</b> - Low Input, with PCR & UMIs	10 ng DNA	LIBD05	240	287
<b>ssDNA library</b> - precious, damaged, degraded ds & ssDNA	10 pg DNA	LIBD06	240	287
<b>~Enzymatic DNA Fragmentation</b>				
<b>DNA PCR-free library</b> - no PCR	50 ng gDNA	LIBD07	170	203
<b>DNA library</b> - Standard & PCR	1 ng small genome or 100 ng large genome	LIBD08	150	179
<b>DNA library</b> - Low Input, with PCR & UMIs	100 pg DNA	LIBD09	175	209
<b>DNA library for FFPE</b> - Low Input, with PCR & UMIs	10 ng FFPE DNA	LIBD10	220	263
<b>PlexWell service HTP DNA-Seq 96 samples</b> Examples for use: Microbial WGS, low depth WGS, metagenomics	3-30ng DNA	LIBD011	2'960	3'540
<b>Hi-C Arima Genomics</b> (30% discount samples 2-8)	Blood, tissue, cells etc.	LIBD012a	1'300	1'555
<b>Omni-C Dovetail Genomics</b> (30% discount samples 2-8)		LIBD012b	1'400	1'675
<b>Hi-C Phase Genomics</b> (50% discount for sample 2)		LIBD012c	1'300	1'555

UMI = Unique Molecular Identifier

<b>-Amplicon libraries</b>	<b>Input</b>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Amplicon PCR indexing service/12 samples</b> Incl. PCR amplicon clean-up, unique dual indexing step, 2 <sup>nd</sup> PCR step clean-up and QC PCR products with illumina compatible overhangs only	10 µL of 1 <sup>st</sup> step PCR	LIBA01a	214	256
<b>Amplicon PCR service/12 samples</b> Bring your own primers, incl., clean-up and quantification	DNA; protocol specific	LIBA01b	145	173
<b>Large amplicons</b> Illumina compatible overhangs are not necessary.	1 ng (≥300 bp)	LIBA02	145	173

<b>-Epigenomics</b>	<b>Input</b>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Chromatin Immunoprecipitation sequencing library</b> (ChIP-Seq)	10 pg ChIP'ed DNA	LIBE01	225	269
<b>CUT &amp; RUN library</b>	10 pg DNA fragments	LIBE02	190	227
<b>Assay for Transposase-Accessible Chromatin sequencing library</b> (ATAC-Seq)	nuclei prep. from 50'000 cells	LIBE03	260	311
<b>Whole Genome bisulfite sequencing library</b> (WGBS)	100 pg-50 ng gDNA ≥5 ng FFPE or cfDNA	LIBE04	335	401
<b>Enzymatic Methyl-Seq</b> (EM-Seq)	10 -200 ng gDNA	LIBE05	325	378
<b>Reduced Representation Bisulfite Sequencing library</b> (RRBS)	10-500 ng gDNA	LIBE06	240	287

<b>-Microbiomics</b>	<b>Input</b>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Amplicon libraries for 16S (V3-V4) or ITS</b> Including community standards & NTC	Microbial DNA: 10 ng/ µL	LIBM01a 16S LIBM01b ITS	25	30
<b>Amplicon library for full-length 16S (V1-9)- ITS</b> Including community standards & NTC	1 ng/ µL	LIBM02	40	48
<b>Shotgun metagenomic sequencing library - Standard &amp; PCR</b>	1 ng DNA	LIBM03	150	179
<b>Shotgun metagenomic sequencing library - Low Input, with PCR &amp; UMIs</b>	100 pg DNA	LIBM04	175	209

<b>-RNA libraries</b>	<b>Min. Input</b>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Small RNA</b> Size selected libraries according to project	100 ng total RNA 50 pg enriched small RNA	LIBR01	390	466
<b>miRNA-Seq</b> Price includes miRNA spike-in at point of extraction	100 ng total RNA 5uL of RNA from 200 uL serum/plasma	LIBR02	370	443
<b>Quant-Seq 3'mRNA-Seq/24 samples</b>	100 ng total RNA (RNA with polyA mRNA)	LIBR03	1'560	1'866
Stranded mRNA -standard	200 ng	LIBR04	255	305
Stranded mRNA – no fragmentation, low input & with UMIs	1 ng total RNA	LIBR05	225	269
Stranded mRNA - Ultra-low input	1-1'000 cells 10 pg of total RNA	LIBR06	340	407
Stranded <b>Total RNA</b> – standard - human, blood, rat, mouse & Plant	100 ng	LIBR07	350	419
Stranded <b>Total RNA</b> – no fragmentation, low input & with UMIs Compatible with diverse species for tailored rRNA depletion incl. bacteria	1 ng	LIBR08	325	389
Stranded <b>Total RNA</b> – Ultra Low input -mammalian RNA	10 ng total RNA	LIBR09	355	425
<b>FFPE RNA</b>	10 ng FFPE RNA	LIBR10	355	425
<b>Spike-In RNA Control</b>		LIBR11	12	14
<b>BRB-Seq 48 samples</b> , NextSeq 1000 sequencing, 90-100bp reads, 8M/sample	50 ng total RNA (RNA with polyA mRNA)	LIBR12	3'560	4'258
<b>BRB-Seq 96 samples</b> - NovaSeq 6000 sequencing, 90-100 bp reads, 8M/sample		LIBR13	6'200	7'416
<b>Stranded mRNA library package deal/8 samples</b>	50 ng total RNA (RNA with polyA mRNA)	LIBR14	800	957
<b>24 x stranded mRNA-Seq libraries, 25 M reads, at 2 x 50bp or 1 x 100bp</b>		LIBR15	5'400	6'459

Volume discounts on illumina sequencing libraries:

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

<b>-10 x Genomics - Chromium single cell/nuclei services</b>	<b>Target recovery</b>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Chromium Single Cell Gene Expression (3') v3.1</b> Cells to 3' gene expression library + Feature barcode library for cell surface protein <b>20% reduction in price for samples 2- 8</b>	500-10'000 cells	LIBSC01a LIBSC01b	2'600 165	3'110 197
<b>Chromium Single Cell ATAC v2</b> Nuclei to ATAC library <b>15% reduction in price for samples 2- 8</b>	500-10'000 nuclei	LIBSC02	2'300	2'751
<b>Chromium Single Cell Multiome ATAC + Gene Expression (3')</b> Nuclei to ATAC library and gene expression library <b>15% reduction in price for samples 2- 8</b>	500-10'000 nuclei	LIBSC03	4'100	4'904
<b>Chromium Single Cell Immune Profiling -cells to ds cDNA v2</b> + 5' gene expression library + VDJ enrichment library + Feature barcode library for cell surface protein <b>20% reduction in price for samples 2- 8</b>	500-10'000 cells	LIBSC04a LIBSC04b LIBSC04c LIBSC04d	2'300 320 450 165	2'751 383 538 197

<b>Single cell/nuclei services continued</b>				
<b>Chromium Single Cell Gene Expression (3') v3.1 bundle</b> 8 x Cells to 3' gene expression library ( <i>one batch of 8 samples</i> )	500-10'000 cells	LIBSC05	16'000	19'138
<b>Chromium Single Cell Immune Profiling -cells to ds cDNA v2 bundle</b> 8 x 5' gene expression library ( <i>one batch of 8 samples</i> ) 8 x VDJ enrichment library 8 x Cell surface protein library	500-10'000 cells	LIBSC06a LIBSC06b LIBSC06c	14'400 1'600 1'400	17'224 1'914 1'675
<b>Chromium Single Cell Gene Expression (3') v3.1 HT*</b> Cells to 3' gene expression library	2'000-20'000 cells	LIBSC07	2'200	2'631
<b>Chromium Single Cell Immune Profiling -cells to ds cDNA v2 HT*</b> + 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	2'000 320 450 165 165	2'392 383 538 197 197
<b>Single Cell Gene Expression Flex</b> Chromium Fixed RNA Kit, Human/Mouse Transcriptome Chromium Fixed RNA Kit, Human/Mouse Transcriptome Chromium Fixed RNA Kit, Human/Mouse Transcriptome	4Rxns, 1 barcode 4Rxns, 4 barcodes 4Rxns, 16 barcodes	LIBSC09a LIBSC09b LIBSC09c	8'300 16'400 Enquire	9'928 19'616 Enquire
<b>BD Rhapsody single cell 3' Whole Transcriptome Analysis</b> Single-cell capture, bead-based mRNA isolation and bead retrieval <b>20% reduction in price for samples 2- 8</b>	Up to 55'000 cells	LIBSC010a	2'400	2'871

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

<b>-10 x Genomics - Visium Spatial Transcriptomics Services</b>	<b>Capture Area</b>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Visium Spatial Gene Expression - 4 samples</b> <b>Fresh Frozen - 16 samples</b>	125M read-pairs /fully covered capture area	LIBSC11a LIBSC11b	7'200 Enquire	8'612 Enquire
<b>Visium Spatial Gene Expression FFPE CytAssist human/mouse 6.5 mm<sup>2</sup></b> <b>-4 samples</b> <b>-16 samples</b>	125M read-pairs /fully covered capture area	LIBSC12a LIBSC12b	7'800 27'000	9'330 32'295
<b>Visium Spatial Gene Expression FFPE CytAssist human/mouse 11 mm<sup>2</sup></b> <b>-2 samples</b> <b>-8 samples</b>	375M read-pairs /fully covered capture area	LIBSC13a LIBSC13b	7'900 Enquire	9'449 Enquire
<b>Visium Spatial Gene Expression HD FFPE CytAssist human/mouse 6.5 mm<sup>2</sup></b> <b>-4 samples</b> <b>-16 samples</b>	275M read-pairs /fully covered capture area	LIBSC014a LIBSC014b	13'500 Enquire	16'147 Enquire
<b>~Other spatial transcriptomics methods</b>	<b>Target recovery</b>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>CURIO Biosciences Trekker</b> Whole transcriptome, spatial mapping of fresh frozen tissues 2Rxn, <b>3 mm<sup>2</sup></b> 8Rxn, <b>3 mm<sup>2</sup></b> 4Rxn, <b>10 mm<sup>2</sup></b>	~400 M read-pairs ~400M read-pairs ~2B read-pairs	LIBSC15a LIBSC15b LIBSC15c	6'500 14'900 19'200	7'775 17'822 22'965
<b>CURIO Biosciences Seeker</b> -single-cell mapping kit- works with a single cell workflow (LIBSC01, 03, 04 & 10) to uncover the precise spatial locations of each single cell. 4Rxn, <b>10 mm<sup>2</sup></b> 6Rxn, <b>6 mm<sup>2</sup></b>	Enquire for more details	LIBSC16a LIBSC16b	Early access possible -enquire	

scSMRT-Seq, PIP-Seq & HIVE scRNA-Seq also available-please ask.

## Sequencing libraries compatible with the Pacific Bioscience Platforms

~PacBio DNA Sequencing Libraries*		Min. Input	Cat. No.	Tariff 1	Tariff 2
HiFi SMRTbell Library -standard & metagenome		300ng-10 µg – <i>project dependent</i>	LIBP01	400	478
HiFi SMRTbell Library - Low input		300 ng	LIBP02	420	502
HiFi SMRTbell Library – Ultra Low input <i>Size selections are not included in the price</i>		5 ng	LIBP03	550	658
HiFi Microbial multiplexed library (total 200-300 Mb/SMRTcell)		300ng-2 µg/microbe			
≤ 48			LIBP04a	140	167
≥ 48			LIBP04b	130	155
~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	359
ADAPTER BARCODED SAMPLES 1 amplicon/barcoded SMRTbell library			LIBP06	330	395
~PacBio RNA Sequencing Libraries			Cat. No.	Tariff 1	Tariff 2
Iso-Seq Library (full-length (FL) transcripts)		300 ng total RNA, High quality	LIBP07a	400	478
Barcoded FL cDNA 1 <sup>st</sup> sample		300 ng total RNA, High quality	LIBP08a	400	478
Samples 2-12, same batch			LIBP08b	200	239
Kinnex PCR & Array formation FL RNA-Seq 1 <sup>st</sup> sample		Requires 55 ng cDNA (LIBP08)	LIBP09a	800	957
Samples 2-4, same batch			LIBP09b	600	718
~PacBio single cell RNA Sequencing Libraries			Cat. No.	Tariff 1	Tariff 2
MAS-Seq for 10 x Genomics Single Cell 3'kit 1 <sup>st</sup> sample		Requires 15-75 ng 10 x Genomics 3' cDNA	LIBP10a	950	1'136
Samples 2-4, same batch			LIBP10b	600	718
Kinnex single cell RNA-Seq 1 <sup>st</sup> sample		Requires 15-75 ng 10 x Genomics 3' or 5' cDNA	LIBP11a	950	1'136
Samples 2-4, same batch			LIBP11b	600	718

\* 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- <i>cells or blood samples</i>		LIBPS01	400	478
HMW DNA extraction/sample 1-4 samples - <i>plant, tissue, insect samples etc.</i>		LIBPS02	650	777
HMW DNA extraction manual/16 samples – <i>microbial</i>		LIBPS03a	430	514
HMW DNA extraction on robot/48 samples – <i>microbial</i>		LIBPS03b	840	1'005
HMW DNA extraction on robot/96 samples – <i>microbial</i>		LIBPS03c	1'500	1'794
RNA extraction/sample - <i>cells or blood samples</i>		LIBPS04	30	36
RNA extraction/sample - <i>bacteria, plant, tissue samples</i>		LIBPS05	52	62
PacBio short read eliminator service/sample		LIBPS06	46	55
~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		LIBPS07a	20	24
≥ 96		LIBPS07b	10	12
Kinnex 16S rRNA V1-V9 (batches of ≥ 96, max 384 barcodes)		LIBPS08	15	18
1-2 ng input DNA				
One step PCR & including community standards & NTCs				
<i>Followed by Kinnex PCR &amp; Array formation (LIBP08)</i>				

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

## -Accessory DNA/RNA Services

<i>-DNA Fragmentation services</i>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Covaris E220evolution Focused Ultrasonicator</b> Shearing gDNA (50-130 µL) in the 100-1'000 bp range; microTUBE & service incl. QC/8 Rxn	AD01	152	182
<b>Covaris g-TUBE DNA shearing</b> Shearing of gDNA in the 6-20 kb range using centrifugal force; g-TUBE service incl. QC /sample	AD02	76	91
<b>Diagenode Megaruptor 2</b> DNA fragmentation in the 3-75 kb range; Hydropore devices & service, incl. QC /sample	AD03	48	57
<i>-DNA Size Selection</i>			
<b>Sage Science Blue Pippin</b> 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	250 250 250	299 299 299
<i>-Purify and concentrating services</i>			
<b>DNA concentrating service</b> - speed vac	AD05	3	4
<b>Clean, concentrate &amp; DNase I treatment for RNA samples</b> – column based ≤ 24	AD06a	20	24
≥ 24	AD06b	10	12
<b>Clean, concentrate treatment for DNA samples</b> – column based ≤ 24	AD07a	18	22
≥ 24	AD07b	8	10
<b>Clean, concentrate treatment for genomic DNA samples</b> – column based ≤ 24	AD08a	21	25
≥ 24	AD08b	9	11
<b>bead-based DNA clean-up service with quantification /12 samples</b>	AD09	76	91
<i>-DNA &amp; RNA QC services</i>			
<b>Spectrophotometric analysis</b>	AD010	1	1
<b>Advanced Analytics Fragment Analyzer CE12 - capillary gel electrophoresis</b> QC for libraries, RNA & DNA; reagents & service/1 lane (11 samples & ladder)	AD011	82	98
<b>Advanced Analytics FEMTO Pulse CE - pulsed field capillary gel electrophoresis</b> QC for libraries, RNA & HMW DNA; reagents & use/1 lane (11 samples & ladder)	AD012	123	147
<b>LifeTechnologies Qubit Fluorimetry</b> - Accurate quantitation for RNA or DNA; reagents/sample	AD013	3	3
<b>qPCR based illumina NGS Library Quantification/8 samples</b>	AD014	136	163
<b>Sample equimolar pooling service/24 samples</b>	AD015	80	96

## -Ready-to-Load Library Services

<i>- Ready-to-Load Library (RTL) services</i>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Custom-made library extra light service</b> RTL projects handling only	LIBRTL01	56	67
<b>Custom-made library light service</b> RTL quantitation (concentration) & pooling service/8 samples	LIBRTL02	80	96
<b>Custom-made library standard service</b> RTL quantitation (size and concentration) & pooling service/11 samples	LIBRTL03	140	167
<b>Custom-made standard service for low concentrated libraries</b> RTL quantitation (size and concentration) & pooling service/11 samples	LIBRTL04	180	215
<b>Custom-made library full service</b> RTL quantitation (size and concentration), purification & pooling service/11 samples	LIBRTL05	215	257

## -Sequencing Services

### illumina sequencing service

<b>illumina iSeq 100</b>	Cycles	No. reads	Output	Cat. No.	Tariff 1	Tariff 2
i1 Reagent v2	300	4 M	1.2 Gb	SEQi01	710	849
i1 Reagent v2 QC run	300	4 M	1.2 Gb	SEQi02	690	825
Custom sequencing i				SEQi03	Enquire	Enquire

<b>illumina MiSeq</b>	Cycles	No. reads	Output	Cat. No.	Tariff 1	Tariff 2
v2 nano flow cell	300	1 M	300 Mb	SEQM01	580	694
v2 nano flow cell	500	1 M	500 Mb	SEQM02	670	801
v2 standard flow cell	50	12 M	750 Mb	SEQM03	1'360	1'627
v2 standard flow cell	300	12 M	4.5 Gb	SEQM04	1'700	2'033
v2 standard flow cell	500	12 M	7.5 Gb	SEQM05	1'900	2'273
v3 flow cell	150	22 M	3.3 Gb	SEQM06	1'500	1'794
v3 flow cell	600	22 M	13.2 Gb	SEQM07	2'450	2'930
Custom sequencing M				SEQM08	62	74

<b>illumina NextSeq 1000</b>	Cycles	No. reads	Output	Cat. No.	Tariff 1	Tariff 2
P1 100 cycles	100	100 M	10 Gb	SEQNX01	1'150	1'376
P1 300 cycles	300	100 M	30 Gb	SEQNX02	1'560	1'866
P1 600 cycles	600	100 M	60 Gb	SEQNX03	2'320	2'775
P2 100 cycles	100	400 M	40 Gb	SEQNX04	1'800	2'153
P2 200 cycles	200	400 M	80 Gb	SEQNX05	3'280	3'93
P2 300 cycles	300	400 M	120 Gb	SEQNX06	4'320	5'167
P2 600 cycles	600	300 M	180 Gb	SEQNX07	4'720	5'646
Custom sequencing NX				SEQNX08	90	108

<b>illumina NovaSeq 6000<sup>3</sup></b>	Cycles	No. reads	Output	Cat. No.	Tariff 1	Tariff 2
SP flow cell	100	650 M	65 Gb	SEQN01	3'000	3'588
SP flow cell	200	650 M	134 Gb	SEQN02	3'900	4'665
SP flow cell	300	650 M	200 Gb	SEQN03	4'300	5'143
SP flow cell	500	650 M	325 Gb	SEQN04	5'900	7'057
S1 flow cell	100	1.3 B	134 Gb	SEQN05	5'400	6'459
S1 flow cell	200	1.3 B	266 Gb	SEQN06	6'800	8'134
S1 flow cell	300	1.3 B	400 Gb	SEQN07	7'350	8'791
S2 flow cell	100	3.3 B	333 Gb	SEQN08	10'000	11'961
S2 flow cell	200	3.3 B	667 Gb	SEQN09	12'400	14'832
S2 flow cell	300	3.3 B	1'000 Gb	SEQN10	13'300	15'908
SP, S1, S2 flow cell XP workflow				SEQN11	560	670
S4 flow cell	200	8.0 B	1'600 Gb	SEQN12	17'450	20'872
S4 flow cell	300	8.0 B	2'400 Gb	SEQN13	19'600	23'444
S4 flow cell XP workflow				SEQN14	950	1'136
Custom sequencing N				SEQN15	124	148

**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>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
1 SMRT cell 8M	SEQP01	2'100	2'512
<u>PacBio Revo System</u>			
1 SMRT cell 25M	SEQP02	1'440	1'722

### 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 (8.1%) will be added to the final invoice destined for non-university-based addresses (outside Switzerland exempt), as well as an overhead charge from the University of Bern (20%) for invoices destined to commercial customers.

**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](mailto: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

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**Tel:** 031 684 22 85

### **-Miscellaneous Services**

<u>Miscellaneous</u>	<b>Cat. No.</b>	<b>Tariff 1</b>	<b>Tariff 2</b>
<b>Additional Data Handling or consumable use in NGSP lab</b>	MISC01	56	59
<b>Urgent Project Service</b> Priority samples QC & library prep.	MISC02	10%	15%

*Prices and conditions are subject to change without notice.*