

PN	Description	CZK	EUR	PLN
Library preparation (Includes sample QC, library preparation and pooling)				
Illumina				
LP-050	DNA library (PCR-free on request)	5 500	200	920
	DNA library (PCR-free on request) - at least 16 libraries	4 500	164	750
LP-060	Total RNA or mRNA (polyA-selected) library	7 400	270	1 240
	Total RNA or mRNA (polyA-selected) library - at least 16 libraries	6 300	230	1 050
LP-070	RNA library including rRNA depletion (H/M/R/Bacteria)	8 700	317	1 450
	RNA library including rRNA depletion (H/M/R/Bacteria) - at least 16 libraries	7 600	277	1 270
LP-170	miRNA library	7 900	288	1 320
	miRNA library - at least 16 libraries	7 000	255	1 170
LP-200	3' mRNA library (QuantSeq/UMI)	5 100	186	850
	3' mRNA library (QuantSeq/UMI) - at least 16 libraries	3 700	135	620
TA-024	Tailed Amplicon library, up to 24 samples	30 000	1 091	5 000
TA-048	Tailed Amplicon library, up to 48 samples	38 400	1 397	6 400
TA-096	Tailed Amplicon library, up to 94 samples	52 800	1 920	8 800
TA-192	Tailed Amplicon library, up to 190 samples	76 800	2 793	12 800
Pacific Biosciences and Oxford Nanopore Technologies				
LP-110	DNA library - PacBio		Inquire	
LP-150	DNA library - Oxford Nanopore	9 500	346	1 590
Quality control of libraries prepared by customers				
Illumina				
QC-080	Library QC, customer-prepared	2 600	95	440
Sequencing services à la carte - Price per lane/chip				
Illumina				
DS-030	MiSeq, paired-end, 250 b, 10-30 million reads	55 200	2 008	9 200
DS-040	MiSeq, paired-end, 300 b (QC specs invalid - see www.seqme.eu/magazine)	68 400	2 488	11 400
DS-270	NovaSeq6000 SP lane, single-end, 50 b, 350-400 million reads per lane	65 100	2 368	10 850
DS-090	NovaSeq6000 SP lane, single-end, 100 b, 350-400 million reads per lane	65 100	2 368	10 850
DS-150	NovaSeq6000 SP lane, paired-end, 150 b, 700-800 million reads per lane	69 100	2 513	11 520
DS-240	NovaSeq6000 S4 lane, paired-end, 150 b, 5000-6000 million reads per lane	268 000	9 746	44 670
Pacific Biosciences and Oxford Nanopore Technologies				
DS-200	PacBio Sequel I / Sequel II, 10-30 hrs movie, upto 5 million reads		Inquire	
DS-210	Oxford Nanopore MinION FC, single-end, 1-200 kb reads, 5-10 Gb	35 300	1 284	5 890
DS-280	Oxford Nanopore Flongle FC, single-end, 1-200 kb reads, 1-2 Gb	14 600	531	2 440
ShareSeq Sequencing services - Price per data package				
Illumina				
DS-270S	Illumina, single-end, 50 b, 10 million reads (at least 30 million reads per order)	3 100	120	520
DS-150S	Illumina, paired-end, 150 b, 10 million reads (at least 30 million reads per order)	2 200	80	370
DS-030S	Illumina, paired-end, 250 b, 1 million reads	7 900	290	1 320
For all ShareSeq sequencing services, a one-time fee is applied to every order.		3000	110	500

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Metagenome / Microbiome analysis (Illumina)

Sequencing (taxonomic) analysis includes: Sample QC, amplicon generation using a single primer set, double indexing, library prep, 250 b paired-end read sequencing (Illumina) with output >20K reads/sample, demultiplexing, analysis report				
For taxonomic analysis you can order amplification of hypervariable regions by using the following primer sets: Bacteria, 16S rRNA - V4 region: 515F+806R, V3-V4 region: F357+R805, V3-V5 region: F357+R926, V4-V5 region: 515F+R926 Archaea, 16S rRNA - 349-806 region: Arch349F+Arch806R Eukaryotes, 18S rRNA - ITS1 and ITS2 regions: ITS1F+ITS4R, ITS2 region: ITS3F+ITS4R, 1391-3' end region: Euk_1391F + EukBr-7R				
SO-024	Metagenomic profiling, up to 24 samples	45 600	1 659	7 600
SO-048	Metagenomic profiling, up to 48 samples	67 200	2 444	11 200
SO-096	Metagenomic profiling, up to 94 samples	96 000	3 491	16 000
SO-192	Metagenomic profiling, up to 190 samples	134 400	4 888	22 400

Data analysis includes: Data QC, paired end read merging, dereplication (clustering), FASTQ to FASTA conversion, taxonomy analysis + visualization, analysis report				
SO-024B	Metagenome data analysis, up to 24 samples	38 400	1 397	6 400
SO-048B	Metagenome data analysis, up to 48 samples	52 800	1 920	8 800
SO-096B	Metagenome data analysis, up to 94 samples	67 200	2 444	11 200
SO-192B	Metagenome data analysis, up to 190 samples	115 200	4 190	19 200

Whole-exome human sequencing (Illumina)

Sequencing analysis includes: Sample QC, library prep, 150 b paired-end read sequencing (Illumina), analysis report				
SO-006	WES - human, Agilent V6 (58Mb), 6 Gb	6 100	222	1 020
SO-012	WES - human, Agilent V6 (58Mb), 12 Gb	8 800	320	1 470
For all WES services, a one-time fee is applied to every order.		1800	66	300

Data analysis includes: WES - Alignment and summary, variant calling (SNP, INDELs), variant annotation, analysis report				
SO-006B	WES - data analysis/sample	1 500	55	250

Notice

This is a shortened pricelist of our services. If you require additional information please contact us.
 If customer-provided samples do not pass the quality control and library preparation cannot be performed, costs for steps taken may be charged.
 Please be aware that depending on the supplied samples there is always a risk that even when they pass QC the technical specifications quoted (namely read length and number of reads) may not be achieved (especially but not limited to sequencing of highly homogeneous templates, for example amplicons).

Orders and inquiries: ngs@seqme.eu

All prices quoted without VAT and costs of sample shipment. This pricelist is valid since September 24, 2020. Subject to change at any time.
 General terms and conditions and additional information available at www.seqme.eu apply.