

PN Description EUR

Library preparation (Includes sample QC, library preparation and pooling)

Illumina technology		
LP-050	DNA library	218
	DNA library - at least 16 libraries	179
LP-060	Total RNA or mRNA (polyA-selected) library	294
	Total RNA or mRNA (polyA-selected) library - at least 16 libraries	247
LP-070	RNA library including rRNA depletion	351
	RNA library including rRNA depletion - at least 16 libraries	311
LP-170	miRNA library	297
	miRNA library - at least 16 libraries	249
Other sequencing technologies		
LP-110	gDNA library (size selection included) - PacBio	827
LP-190	cDNA/amplicon library - PacBio	450
LP-130	DNA Library - 10xGenomics	1 387
LP-160	Single Cell RNA Library (at least 2 samples, each) - 10xGenomics	2 758
LP-140	Size selection (>50 kb) - 10xGenomics, Oxford Nanopore	179
LP-150	DNA/RNA library - Oxford Nanopore	770
LP-180	cDNA library - Oxford Nanopore	654

Quality control of libraries prepared by customers

Illumina technology		
QC-080	Library QC, customer-prepared	97
<i>If customer-provided libraries do not pass our quality control, the libraries will not be sequenced and only the costs for steps performed are invoiced.</i>		

Sequencing services à la carte - Price per lane/chip

Illumina technology		
DS-020	MiSeq, paired-end, 250 b, 0,5-1 million reads	1 444
DS-030	MiSeq, paired-end, 250 b, 10-30 million reads	2 134
DS-080	NovaSeq6000 SP, single-end, 50 b, 300-400 million reads per lane	2 448
DS-090	NovaSeq6000 SP, single-end, 100 b, 300-400 million reads per lane	2 734
DS-220	NovaSeq6000 S2, single-end, 100 b, 1200-1600 million reads per lane	9 493
DS-150	NovaSeq6000 SP, paired-end, 150 b, 600-800 million reads per lane	3 996
DS-240	NovaSeq6000 S4, paired-end, 150 b, 4500-5000 million reads per lane	12 597
DS-130	NovaSeq6000 SP, paired-end, 250 b, 600-800 million reads per lane	5 437
Other sequencing technologies		
DS-200	PacBio, Sequel SMRT Cell 1M v3 LR (20 hrs movie), 500-600 thousand reads	2 825
DS-250	PacBio, Sequel SMRT Cell 1M v3 (10 hrs movie), 500-600 thousand reads	2 303
DS-210	Oxford Nanopore, single-end, 1-200 kb reads, 5-10 Gb	1 284



ShareSeq Sequencing services - Price per data package

Illumina technology		
DS-090S	Illumina, single-end, 100 b, 10 million reads (at least 30 million reads per order)	300
DS-150S	Illumina, paired-end, 150 b, 20 million reads (at least 60 million reads per order)	400
DS-030S	Illumina, paired-end, 250 b, 1 million reads	430

PN	Description	EUR
Metagenome / Microbiome analysis		
Sequencing (taxonomic) analysis includes: Sample QC, Amplicon generation using a single primer set, Double indexing, Library prep, 250 b paired-end read sequencing 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 *For selected primer sets this service is available starting from a single sample, see the order form on our website.		
SO-024	Metagenomic profiling, up to 24 samples	2 160
SO-048	Metagenomic profiling, up to 48 samples	3 120
SO-096	Metagenomic profiling, up to 96 samples	4 320
SO-192	Metagenomic profiling, up to 192 samples	5 760
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	1 560
SO-048B	Metagenome data analysis, up to 48 samples	2 160
SO-096B	Metagenome data analysis, up to 96 samples	2 880
SO-192B	Metagenome data analysis, up to 192 samples	4 800

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 in Euro without VAT and costs of sample shipment. This pricelist is valid since June 1, 2019. Subject to change at any time.
 For General terms and conditions and additional information please see www.seqme.eu