

Catalog No.	Description	EUR
Library preparation (Includes sample QC, library preparation and pooling)		
LP-050	DNA library - MiSeq/HiSeq/NovaSeq	208
	DNA library - MiSeq/HiSeq/NovaSeq, at least 24 libraries	170
	DNA library - MiSeq/HiSeq/NovaSeq, at least 48 libraries	154
LP-060	Total RNA or mRNA (polyA-selected) library - MiSeq/HiSeq/NovaSeq	277
	Total RNA or mRNA (polyA-selected) library - MiSeq/HiSeq/NovaSeq, at least 24 libraries	235
	Total RNA or mRNA (polyA-selected) library - MiSeq/HiSeq/NovaSeq, at least 48 libraries	220
LP-070	RNA library including rRNA depletion - MiSeq/HiSeq/NovaSeq	331
	RNA library including rRNA depletion - MiSeq/HiSeq/NovaSeq, at least 24 libraries	297
	RNA library including rRNA depletion - MiSeq/HiSeq/NovaSeq, at least 48 libraries	285
LP-010	DNA library - IonProton	208
	DNA library - IonProton, at least 24 libraries	170
	DNA library - IonProton, at least 48 libraries	154
LP-030	Total RNA or mRNA (polyA-selected) library - IonProton	335
	Total RNA or mRNA (polyA-selected) library - IonProton, at least 8 libraries	285
LP-040	RNA library including rRNA depletion - IonProton	397
	RNA library including rRNA depletion - IonProton, at least 8 libraries	347
LP-110	DNA library (hmw DNA, PCR products over 1 kb, cDNA) - PacBio (RS II / Sequel)	800
LP-120	Size selection (10-35 kb) and DNA damage repair - PacBio (RS II / Sequel)	635
LP-130	10X Library Construction (1-7 samples, each) - 10xGenomics (Chromium)	1 227
LP-160	10X Single Cell RNA Library (2-7 samples, each) - 10xGenomics (Chromium)	2 689
LP-140	Size selection (>50 kb) - 10xGenomics, Oxford Nanopore	177
LP-150	DNA/RNA library (hmw DNA, PCR products, cDNA, full transcripts) - Oxford Nanopore	616
Quality control of libraries prepared by customers		
QC-010	DNA samples QC, 1-10 samples	150
Quality control of libraries prepared by customers		
QC-060	Library quantification (MiSeq, IonProton), 1-10 libraries, customer-prepared	131
QC-070	Library QC on Bioanalyzer (MiSeq, HiSeq, NovaSeq, IonProton), 1-10 libraries, customer-prepared	189
<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. For PacBio, 10xGenomics and Oxford Nanopore we do not accept libraries prepared by customers. Library quantification for HiSeq is included in the price of sequencing.</i>		
Sequencing services - Ion Proton, MiSeq, HiSeq2500, HiSeq4000, PacBio RS II, PacBio Sequel, MinION		
DS-010	Ion Proton, single-end, 200 b, 60-80 million reads	1 608
DS-020	MiSeq, paired-end, 250 b, Nano v2 chemistry, 0,5-1 million reads	1 366
DS-030	MiSeq, paired-end, 250 b, v2 chemistry, 10-30 million reads	2 043
DS-040	MiSeq, paired-end, 300 b, v3 chemistry, 25-50 million reads	2 543
DS-080	HiSeq4000, single-end, 50 b, 300-400 million reads per lane	2 193
DS-090	HiSeq4000, single-end, 100 b, 300-400 million reads per lane	2 666
DS-220	NovaSeq6000 S2, single-end, 100 b, 1500 - 2000 million reads per lane	11 720
DS-130	HiSeq2500, paired-end, 250 b, 220-350 million reads per lane (Rapid run)	5 404
DS-140	HiSeq4000, paired-end, 100 b, 650-800 million reads per lane	3 758
DS-150	HiSeq4000, paired-end, 150 b, 650-800 million reads per lane	4 027
DS-240	NovaSeq6000 S4, paired-end, 150 b, 4500-5000 million reads per lane	14 258
DS-160	PacBio RSII, single-end, 1-60 kb, 80-100 thousand reads per SMRT cell	1 177
DS-200	SEQUEL, single-end, 1-60 kb, 250-300 thousand reads per SMRT cell	3 227
DS-210	GridION flowcell each, single-end, 1-200 kb reads, 5-10 Gb	1 254

Catalog No.	Description	EUR
Sequencing services - Special services		
Exome Sequencing		
SO-010	Trio whole exome sequencing (Includes Sample QC, Exome library prep for 3 samples, Ion Proton single end sequencing, 200 b, 60-80 million reads, vcf file + annotation)	2 839
SO-020	Duo whole exome sequencing (Includes Sample QC, Exome library prep for 2 samples, Ion Proton single end sequencing, 200 b, 60-80 million reads, vcf file + annotation)	2 500
Metagenomic analysis		
SO-040	Metagenomic library - 1 library of up to 48 pooled samples (Includes Sample QC, Amplicon generation for up to 48 samples using a single primer set, double indexing, 1x library prep + QC)	1 100
SO-050	Metagenome analysis, up to 48 samples (Includes Sample QC, Amplicon generation for up to 48 samples using a single primer set, double indexing, 1x library prep + QC, 1x MiSeq 250 b paired-end sequencing using V2 chemistry, 10-30 million reads, demultiplexing)	3 027
SO-060	Metagenome analysis, up to 96 samples (Includes Sample QC, Amplicon generation for up to 96 samples using a single primer set, double indexing, 2x library prep + QC, pooling, 1x MiSeq 250 b paired-end sequencing using V2 chemistry, 10-30 million reads, demultiplexing)	3 762
SO-070	Metagenome data analysis, up to 48 samples (Includes Data QC, Paired end read merging, Dereplication (Clustering), FASTQ to FASTA conversion, Taxonomy analysis + visualization, Data analysis report)	1 974

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.
 ShareSeq sequencing service not included in this pricelist, see www.shareseq.eu.

Orders and inquiries: ngs@seqme.eu

All prices quoted in Euro without VAT and costs of sample shipment. This pricelist is valid since May 16, 2018. Subject to change at any time.
 For General terms and conditions and additional information please see www.seqme.eu