Ce–M–M–
Research Center for Molecular Medicine
of the Austrian Academy of Sciences

ÖAW

CeMM Biomedical Sequencing Facility
Services and Prices[1]

(the listed prices do not include value-added tax (i.e. VAT/USt/MwSt), which will be added when required by law)

All-inclusive RNA-seq (including quality control, library prep, sequencing, and initial bioinformatics)	**Unit**	
Stranded mRNA-seq (poly-A enrichment or low-input), 24 samples per 1x50bp HiSeq 3000/4000 lane (single-read)	sample	€ 209
Stranded mRNA-seq (poly-A enrichment or low-input), 16 samples per 1x50bp HiSeq 3000/4000 lane (single-read)	sample	€ 238
Stranded mRNA-seq (poly-A enrichment or low-input), 12 samples per 1x50bp HiSeq 3000/4000 lane (single-read)	sample	€ 266
Stranded mRNA-seq (poly-A enrichment or low-input), 8 samples per 1x50bp HiSeq 3000/4000 lane (single-read)	sample	€ 322
Stranded mRNA-seq (poly-A enrichment or low-input), 4 samples per 1x50bp HiSeq 3000/4000 lane (single-read)	sample	€ 492
Stranded mRNA-seq (poly-A enrichment or low-input), 4 samples per 2x75bp HiSeq 3000/4000 lane (paired-end)	sample	€ 689
Stranded total RNA-seq (Ribo-Zero depletion), 24 samples per 1x50bp HiSeq 3000/4000 lane (single-read)	sample	€ 282
Stranded total RNA-seq (Ribo-Zero depletion), 12 samples per 1x50bp HiSeq 3000/4000 lane (single-read)	sample	€ 339
Stranded total RNA-seq (Ribo-Zero depletion), 4 samples per 2x75bp HiSeq 3000/4000 lane (paired-end)	sample	€ 766
Stranded mRNA-seq (poly-A enrichment, low-input, or Ribo-Zero) with custom sequencing depth	sample	on request

Transcription fingerprinting 3' RNA-seq protocol ("QuantSeq"), 48 samples per 1x50bp HiSeq 3000/4000 lane (single-read), price per sample	sample	€ 68
Transcription fingerprinting 3' RNA-seq protocol ("QuantSeq"), 96 samples per 1x50bp HiSeq 3000/4000 lane (single-read), price per 96-well plate	96-well plate	€ 5.535
All-inclusive human exome sequencing (including library preparation, sequencing, and initial bioinformatics)	**Unit**	
Comprehensive human exome (37 Mb), 16 samples per 2x75bp HiSeq 3000/4000 lane (paired-end)	sample	€ 361
Comprehensive human exome (37 Mb), 8 samples per 2x75bp HiSeq 3000/4000 lane (paired-end)	sample	€ 532
Comprehensive human exome (37 Mb), 6 samples per 2x75bp HiSeq 3000/4000 lane (paired-end)	sample	€ 678
Comprehensive human exome (37 Mb), 3 samples per 2x75bp HiSeq 3000/4000 lane (paired-end)	sample	€ 1.108
Comprehensive human exome (37 Mb), FAST-TRACK WORKFLOW (target: 5 working days, requires prior approval)	sample	on request
Comprehensive human exome (37 Mb), COHORT SEQUENCING, 96 samples per 2x100bp NovaSeq S4 6000 (paired-end)	sample	€ 353
Comprehensive human exome (37 Mb), with custom sequencing depth	sample	on request
All-inclusive whole genome sequencing (including library preparation, sequencing and initial bioinformatics)	**Unit**	
Whole genome sequencing (human germline genome), 30 samples per 2x150bp NovaSeq S4 (paired-end)	sample	€ 660
Whole genome sequencing (human or mouse) with custom sequencing depth	sample	on request
All-inclusive epigenome sequencing (including library preparation, sequencing, and initial bioinformatics)	**Unit**	
Reduced representation bisulfite sequencing (moderate coverage)	sample	€ 250
Reduced representation bisulfite sequencing (high coverage)	sample	€ 400
Whole genome bisulfite sequencing, with custom sequencing depth	sample	on request
High-throughput chromatin profiling for open chromatin mapping	sample	€ 200

All-inclusive single-cell RNA-seq (including quality control, library prep, sequencing, and initial bioinformatics) Single-cell RNA-seq (10x Genomics, 3' sequencing protocol), 4 samples per 2x75bp HiSeq 3000/4000 lane (paired-end)	**Unit** sample	 € 2.662

Quality control & special protocols	Unit	
Handling & quality control		
Handling & quality control of client-provided libraries[3]	sample	€ 40
Custom genome library preparation[4] (excluding sequencing and initial bioinformatics)		
PCR-free, TruSeq nano, Nextera DNA Flex, NEBNext Ultra II or similar (batches of 12 samples)	sample	€ 65
Custom single-cell library preparation[4] (excluding sequencing and initial bioinformatics)		
Single-cell RNA-seq (Smart-seq2 for full-length transcripts, cDNA preparation only), price refers to a full 96-well plate	96-well plate	€ 1.380
Single-cell RNA-seq (Smart-seq2 for full-length transcripts, library preparation from cDNA), price refers to a full 96-well plate	96-well plate	€ 1.240
Single-cell RNA-seq (10x Genomics, 5' sequencing protocol)	sample	€ 2.157
Single-cell immune repertoire profiling (10x Genomics, BCR or TCR sequencing), as an add-on to the 5' sequencing protocol[5]	sample	€ 264
Single-cell chromatin profiling (10x Genomics, ATAC-seq protocol)	sample	€ 1.970

Next-generation sequencing	Unit	
HiSeq 3000/4000 sequencing (high throughput and cost efficiency for deep sequencing)	**Million reads[6]**	
HiSeq 3000/4000: Lane of 1x50bp (single-read)	312,5	€ 987
HiSeq 3000/4000: Lane of 2x75bp (paired-end)	312,5	€ 1.778
NovaSeq 6000 sequencing (highest throughput and cost efficiency for deep sequencing)	**Million reads[6]**	
NovaSeq SP: Flow cell 2x50bp (paired-end)	650	€ 2.500
NovaSeq SP: 1/2 flow cell 2x50bp (paired-end)	325	€ 1.450
NovaSeq SP: Flow cell 2x100bp (paired-end)	650	€ 3.250
NovaSeq SP: 1/2 flow cell 2x100bp (paired-end)	325	€ 1.800
NovaSeq SP: Flow cell 2x150bp (paired-end)	650	€ 3.550
NovaSeq SP: 1/2 flow cell 2x150bp (paired-end)	325	€ 1.950
NovaSeq SP: Flow cell 2x250bp (paired-end)	650	€ 4.900
NovaSeq SP: 1/2 flow cell 2x250bp (paired-end)	325	€ 2.600
NovaSeq S1: Flow cell 2x50bp (paired-end)	1.300	€ 4.500
NovaSeq S1: 1/2 flow cell 2x50bp (paired-end)	650	€ 2.400
NovaSeq S1: Flow cell 2x100bp (paired-end)	1.300	€ 5.650
NovaSeq S1: 1/2 flow cell 2x100bp (paired-end)	650	€ 3.000
NovaSeq S1: Flow cell 2x150bp (paired-end)	1.300	€ 6.100
NovaSeq S1: 1/2 flow cell 2x150bp (paired-end)	650	€ 3.200
NovaSeq S2: Flow cell 2x50bp (paired-end)	3.300	€ 8.350
NovaSeq S2: 1/2 flow cell 2x50bp (paired-end)	1.650	€ 4.350
NovaSeq S2: Flow cell 2x100bp (paired-end)	3.300	€ 10.350
NovaSeq S2: 1/2 flow cell 2x100bp (paired-end)	1.650	€ 5.350
NovaSeq S2: Flow cell 2x150bp (paired-end)	3.300	€ 11.050
NovaSeq S2: 1/2 flow cell 2x150bp (paired-end)	1.650	€ 5.700
NovaSeq S4: Flow cell 35bp (fragment counting)	8.000	€ 12.050
NovaSeq S4: 1/4 Flow cell 35bp (fragment counting)	2.000	€ 3.200
NovaSeq S4: Flow cell 2x100bp (paired-end)	8.000	€ 14.800

NovaSeq S4: 1/4 flow cell 2x100bp (paired-end)	2.000	€ 3.900
NovaSeq S4: Flow cell 2x150bp (paired-end)	8.000	€ 16.000
NovaSeq S4: 1/4 flow cell 2x150bp (paired-end)	2.000	€ 4.200
NextSeq sequencing (technology development and certain medium-scale applications)	**Million reads[6]**	
NextSeq 500/550 Mid Output: Flow cell 2x75bp (paired-end)	130	on request
NextSeq 500/550 Mid Output: Flow cell 2x150bp (paired-end)	130	on request
NextSeq 500/550 High Output: Flow cell 1x75bp (single-read)	400	on request
NextSeq 500/550 High Output: Flow cell 2x75bp (paired-end)	400	on request
NextSeq 500/550 High Output: Flow cell 2x150bp (paired-end)	400	on request
MiSeq sequencing (amplicon gene panels and other small-scale applications)	**Million reads[6]**	
MiSeq v2 nano: Flow cell 2x150bp (paired-end)	1	€ 436
MiSeq v2 nano: Flow cell 2x250bp (paired-end)	1	€ 513
MiSeq v2 micro: Flow cell 2x150bp (paired-end)	4	€ 617
MiSeq v2: Flow cell 1x50bp (single-read)	15	€ 1.054
MiSeq v2: Flow cell 2x150bp (paired-end)	15	€ 1.321
MiSeq v2: Flow cell 2x250bp (paired-end)	15	€ 1.469
MiSeq v3: Flow cell 2x75bp (paired-end)	25	€ 1.158
MiSeq v3: Flow cell 2x300bp (paired-end)	25	€ 1.884
Other sequencing platforms (long reads and special requirements)		
Oxford Nanopore long-read sequencing (per MinION flowcell including library preparation)		on request
Pacific Biosciences long-read sequencing (per Sequel flowcell including library preparation)		on request

Bioinformatics	Unit	
Bioinformatic data processing[7]	sequencing unit / lane	€ 120
Initial bioinformatic analysis (web-based report with genome browser tracks, clustering, differential genes, etc., as applicable)	experiment	€ 320
Additional bioinformatic services including data analyses, long-term archival, assistance with GEO submission, etc.	experiment	on request

Additional services		
The all-inclusive protocols are also available with custom sequencing depth - please inquire		on request
For large projects (>100 samples), please contact us early on, in order to plan in detail and reserve capacity		on request
Metagenome and metatranscriptome sequencing		on request
Small RNA-seq sequencing		on request
Additional protocols will be established if there is sufficient demand - please inquire		on request

Custom library preparation for genetic diseases and cancer[4] (excluding sequencing and initial bioinformatics)	Unit	
Nextera DNA Flex Exome 45Mb (batches of 6 samples)	sample	on request
Nextera DNA Flex TruSight Cancer 255Kb (batches of 6 samples)	sample	on request
Nextera DNA Flex TruSight One 12Mb (batches of 6 samples)	sample	on request
Nextera DNA Flex TruSight One Expanded 16.5Mb (batches of 6 samples)	sample	on request
Nextera DNA Flex TruSight Cardio 575Kb (batches of 6 samples)	sample	on request
Nextera DNA Flex TruSeq Neurodegeneration 8.7Mb (batches of 6 samples)	sample	on request

[1] The Biomedical Sequencing Facility (BSF) of CeMM and MedUni Vienna is an academic and non-profit sequencing technology platform. Prices are calculated to cover costs and do not contain any commercial profit margin.

[2] Sequencing for academic research is subsidized by the BSF and available only for academic research projects with no commercial interests. Unsubsidized prices for projects that do not fall under this definition are available upon request.

[3] The handling fee applies to client-provided libraries on a per-library basis for each library that is submitted to the BSF. To reduce costs, it is recommended to multiplex/pool libraries prior to submission.

[4] Sequencing and bioinformatics are charged separately for the custom library preparation services (in contrast to the all-inclusive protocols, where they are already included in the price)

[5] The 10x Genomics Immune Profiling (B-cell or T-cell) human or mouse (as an add-on to single-cell RNA-seq) can only be requested in combination with the single-cell RNA-seq 5' protocol

[6] The indicated read numbers are based on Illumina's specifications for each flowcell. These are conservative estimates, and the actual read numbers are often substantially higher. However, they may also be lower, e.g. in case of low-quality samples

[7] The bioinformatic data processing fee applies to client-provided libraries and is charged on a per-lane basis (HiSeq: 8 lanes; NovaSeq SP/S1/S2: 2 lanes; S4: 4 lanes; MiSeq nad NextSeq: 1 lane) for all sequencing that is not part of an "all-inclusive package"

[8] Further bioinformatic analyses and services can optionally be contributed on a collaborative basis. For large projects, it is critical to discuss requirements with BSF staff early on in order to allocate sufficient resources and capacity.