

NEW SEASON, NEW DISCOUNTS!

Discover our exclusive spring offers with flexible voucher solutions.
Our all-in-one package and adaptable service are custom-fit for your project.

RNAseq promotion and voucher option

HIGH THROUGHPUT GENE EXPRESSION PROFILING

Service includes:



- mRNA isolation from total RNA starting from 6 samples
- NEBNext® Ultra™ II Directional RNA library preparation
- Quantification and QC of library
- Sequencing of 2 x 150 nt with Illumina NextSeq 2000™
- Data delivery of FASTQ files via download

Price example:

- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 168,75 €/sample, 48 samples*
- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 173,75 €/sample, 36 samples*
- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 178,75 €/sample, 24 samples*
- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 188,75 €/sample, 12 samples*
- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 193,75 €/sample, 6 samples*

- 50 mio PE reads¹ (2 x 150 nt, 7.5 Gb) for only 232,50 €/sample, 48 samples*
- 50 mio PE reads¹ (2 x 150 nt, 7.5 Gb) for only 237,50 €/sample, 36 samples*
- 50 mio PE reads¹ (2 x 150 nt, 7.5 Gb) for only 242,50 €/sample, 24 samples*
- 50 mio PE reads¹ (2 x 150 nt, 7.5 Gb) for only 252,50 €/sample, 12 samples*
- 50 mio PE reads¹ (2 x 150 nt, 7.5 Gb) for only 257,50 €/sample, 6 samples*



Prices without tax. Cannot be combined with other promotions or discounts. Valid until 30.06.2025.

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Additional services

Bioanalyzer check of RNA samples: Starting from 10 €/sample

Qubit™ check with RNA assay: Starting from 5 €/sample

rRNA depletion: Starting from 80 €/sample

Bioinformatic services

Bioinformatic data analysis 1:

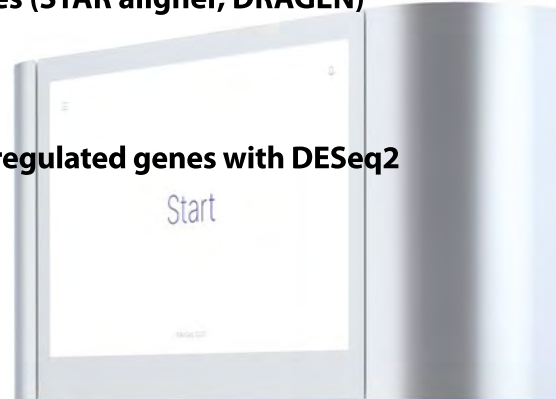
RNA-Seq Alignment to reference genomes² (STAR aligner, DRAGEN)
starting from 40 €/sample

Bioinformatic data analysis 1:

RNA-Seq Alignment to non-reference genomes (STAR aligner, DRAGEN)
starting from 50 €/sample

Bioinformatic data analysis 2:

Pairwise comparison to identify differentially regulated genes with DESeq2
or DRAGEN workflow
starting from 40 €/comparison



¹ Depending on the nature of starting material and according to Illumina specifications the data output can vary 5-10%.

² Available reference genomes include: *H. sapiens* hg19, *H. sapiens* GRCh38Decoy, *M. musculus* mm10, *M. musculus* UCSC mm9, *R. norvegicus* rn5, *D. melanogaster* dm3, *B. taurus* bosTau6, *S. scrofa* susScr3, *G. gallus* galGal4, *D. rerio* danRer7, *C. elegans* ce10, *Z. mays* AGPv3, *A. thaliana* TAIR10, *O. sativa japonica* IRGSP-1.0, *S. cerevisiae* R64-1-1

* Samples must be delivered as batch.

