

# SPRING PROMOTION 2020!

## Flexible Voucher Option!

Buy now and perform this or any other project within 12 months.

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## 16S and ITS Microbiome analysis promotion and voucher option



(Leiopicus medius)

Package A: 192 samples only	32 € per sample and region
Package B: 96 samples only	50 € per sample and region
Package C: 48 samples only	75 € per sample and region
Package D: 10 samples only	199 € per sample*

(\*limited to V4 region)

### Bacterial microbiome analysis:

16S V4 region, Primer combination: 515F – 806R<sup>1</sup>

16S V4-V5 region, Primer combination: 515F – 909R<sup>1</sup>

16S V3-V4 region, Primer combination: 341F – 806R<sup>4</sup>

### Fungal microbiome analysis:

ITS ITS 1 region, Primer combination: ITS1F – ITS2<sup>2</sup>

### Eukaryotes (microbial) analysis:

V9 region, Primer combination: Illumina\_Euk\_1391f -

Illumina\_EukBr\_1510r, blocking primer optional<sup>3</sup>

V9 region samples need to be sequenced separately!

Send us your gDNA samples and make use of our "All in One" service:

- Quality control
- Single step amplicon generation with reduced bias
- Double indexing, quality check, quantification, normalization and pooling of amplicons
- Illumina MiSeq sequencing package A-C: 2 x 300 nt paired-end sequencing with V3 chemistry
- Illumina MiSeq sequencing package D: 2 x 250 nt paired-end sequencing with V2 chemistry nano flow cell
- Output package A-C: 20-30 M reads (including 25 % PhiX to balance the composition of bases)
- Output package D: 750 K reads (including 25 % PhiX to balance the composition of bases)
- De-multiplexing of reads
- Free 16S metagenomics analysis (Illumina App)
- Data delivery via FTP server



### **Optional: gold standard bioinformatic analysis of 16S/18S/ITS sequences (QIIME2)**

The bioinformatics analysis pipeline consists of quality control, pre-processing of reads, taxonomy identification and visualization, calculation of alpha and beta-diversity metrics.

**Request for offer: [microbiome@starseq.com](mailto:microbiome@starseq.com)**

<sup>1,2,3,4</sup> Primer sequence references: Please see page 3!



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### Sequencing of your ready to load 16S/ITS/18S libraries

- Illumina MiSeq sequencing: 2 x 300 nt paired-end sequencing with V3 chemistry
- Output 20-30 M reads (including 25 % PhiX to balance the composition of bases)
- De-multiplexing of reads
- Free 16S metagenomics analysis (Illumina App)
- Data delivery via FTP server



**Only 2600 €**

### Optimize your research with our 16S/ITS workflow solutions

From sample prep to library prep to sequencing and bioinformatics. StarSEQ offers a complete and comprehensive workflow for various 16S/ITS applications. Sequencing of the hypervariable regions of the 16S rRNA gene is the gold-standard for identification and classification of bacterial communities within a given sample.

StarSEQ is using established gold-standard primer sequences to target regions covering the hypervariable regions V3-V4, V4 and V4-V5. In contrast to common used methods, StarSEQ has designed its own single-step technique for simultaneous amplification, indexing and adapting of samples to reduce the bias caused during PCR.



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### Applications:

- Environmental Metagenomics (soil, water, air, biofilms, complex organic communities)
- Human or Animal Microbiome (skin, stool, gut, blood, swab)
- Monitoring of animal health (e.g. alternatively or supplementarily to FELASA-Test)
- Sterility Monitoring
- Detection of Contamination
- Monitoring of Biogas Plant
- Biosafety Monitoring
- Food Quality
- Clinical Samples

**You have no time/staff for routine preparation of gDNA from your collected samples?**

**As an additional service we offer also the purification of gDNA from various starting material.**

### Primer sequence references:

- <sup>1</sup> Apprill A, McNally S, Parsons R, Weber L. 2015. Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. *Aquat Microb Ecol* 75:129–137. Parada AE, Needham DM, Fuhrman JA. Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. *Environ Microbiol.* 2016;18: 1403-1414.
- <sup>1</sup> Parada, A. E., Needham, D. M., & Fuhrman, J. A. (2016). Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. *Environmental Microbiology*, 18(5), 1403–1414. <https://doi.org/10.1111/1462-2920.13023>
- <sup>1</sup> Walters, W., Hyde, E. R., Berg-Lyons, D., Ackermann, G., Humphrey, G., Parada, A., ... Knight, R. (2016). Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. *mSystems*, 1(1), e00009-15. <https://doi.org/10.1128/mSystems.00009-15>
- <sup>2</sup> White, T. J., T. Bruns, S. Lee, and J. W. Taylor. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. Pp. 315-322 In: PCR Protocols: A Guide to Methods and Applications. Academic Press, New York, NY. Gardes, M., and T. D. Bruns. 1993. ITS primers with enhanced specificity for basidiomycetes - application to the identification of mycorrhizae and rusts. *Mol. Ecol.* 2: 113-118.
- <sup>3</sup> Amaral-Zettler, L. A., McCliment, E. A., Ducklow, H. W., & Huse, S. M. (2009). A Method for Studying Protistan Diversity Using Massively Parallel Sequencing of V9 Hypervariable Regions of Small-Subunit Ribosomal RNA Genes. *PLOS ONE*, 4(7), e6372. Retrieved from <https://doi.org/10.1371/journal.pone.0006372>
- <sup>4</sup> Klindworth A., Pruesse E., Schweer T., Peplies J., Quast C., Horn M., et al. (2013). Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. *Nucleic Acids Res.* 41, 1–11. 10.1093/nar/gks808  
see also [https://support.illumina.com/downloads/16s\\_metagenomic\\_sequencing\\_library\\_preparation.html](https://support.illumina.com/downloads/16s_metagenomic_sequencing_library_preparation.html)



Prices without tax. Cannot be combined with other promotions or discounts. Valid until 31.05.2020.