END OF YEAR PROMOTION 2020!

Flexible Voucher Option. Transfer your Funds and Budget to 2021!

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

****

16S and ITS Microbiome analysis promotion and voucher option

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[1]
16S V4-V5 region, Primer combination: 515F – 909R[1]
16S V3-V4 region, Primer combination: 341F – 806R[4]

Fungal microbiome analysis:

ITS ITS 1 region, Primer combination: ITS1F – ITS2[2]

Eukaryotes (microbial) analysis:

V9 region, Primer combination: Illumina_Euk_1391f - Illumina_EukBr_1510r, blocking primer optional[3]

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

[1,2,3,4] Primer sequence references: Please see page 3!

StarSEQ

Prices without tax. Cannot be combined with other promotions or discounts. Valid until 31.01.2021.

END OF YEAR PROMOTION 2020!

Flexible Voucher Option. Transfer your Funds and Budget to 2021!

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

****

16S and ITS Microbiome analysis promotion and voucher option

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 adaptoring of samples to reduce the bias caused during PCR.

StarSEQ

Prices without tax. Cannot be combined with other promotions or discounts. Valid until 31.01.2021.

END OF YEAR PROMOTION 2020!

Flexible Voucher Option. Transfer your Funds and Budget to 2021!

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

****

16S and ITS Microbiome analysis promotion and voucher option

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:

[1] 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.

[1] 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

[1] 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

[2] 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.

[3] 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

[4] 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

StarSEQ

Prices without tax. Cannot be combined with other promotions or discounts. Valid until 31.01.2021.