SCIENCE DOESN´T TAKE WINTER BREAKS- AND WE WON´T SLOW DOWN EITHER

Explore our exclusive deals and flexible 12-month voucher options.
Fast, precise, and ready for your next breakthrough - all season long.

****

1-Step 16S and ITS Microbiome analysis promotion and voucher option

---

1-Step Bacterial microbiome analysis or 1-Step Fungal 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]
ITS	ITS 1 region,	Primer combination: ITS1F – ITS2[2]

Price example:

Package A:	288 samples	only	26,52 €	per sample and one region
Package B:	192 samples	only	31,54 €	per sample and one region
Package C:	96 samples	only	47,08 €	per sample and one region
Package D:	48 samples	only	76,17 €	per sample and one region

Price examples, all other sample sizes are possible. We charge per sample. The price is a combination of a fixed price for the run and a variable price for the libraries depending on the number of samples.
No shared runs, customer samples are sequenced exclusively on one MiSeq run!

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 / NextSeq 2000™ sequencing package A-D: 2 x 300 nt paired-end sequencing with V3 chemistry
- Output package A-D: 20-30 M reads (including 25 % PhiX to balance the composition of bases)
- De-multiplexing of reads
- Data delivery via FTP server

2-Step 16S, 18S, ITS and Barcoding Microbiome analysis

Eukaryotes (microbial) analysis:

V4–V5 region, Primer combination: 574-f (5'-CGGTAAYTCCAGCTCYV-3') – 1132R (5'-CCGTCAATTHCTTYAART-3')

V8-V9 region, Primer combination: 18S-1422f (5'-ataacaggtctgtgatgccct-3') – 18S_1797R (5'-ccttcygcaggttcacctac-3')[5]

[1,2,3,4,5] Some Primer sequence references: Please see page 4!

StarSEQ

Prices without tax. Cannot be combined with other promotions or discounts. Valid until 31.03.2026.

SCIENCE DOESN´T TAKE WINTER BREAKS- AND WE WON´T SLOW DOWN EITHER

Explore our exclusive deals and flexible 12-month voucher options.
Fast, precise, and ready for your next breakthrough - all season long.

****

2-Step 16S, 18S, ITS and Barcoding Microbiome analysis

2-Step Bacterial and Archaea Microbiome analysis:

16S, V1-V2 region, Primer combination 27F (5'-AGAGTTTGATCMTGGCTCAG-3') – 338R (5'-TGCTGCCTCCCGTAGGAGT-3')

mcrA, Primer combination mlas-For (5'-GGTGGTGTMGGDTTCACMCARTA-3') – mcrA-Rev (5'-CGTTCATBGCGTAGTTVGGRTAGT-3')

2-Step Fungal (18S) microbiome analysis:

ITS, ITS 1/2 region, Primer combination: ITS-u2 (5'-GAAYCATCGARTCTTTGAACGC-3') – ITS-p4 (5'-CCGCTTAKTGATATGCTTAAA-3')

ITS, ITS 2 region, Primer combination: ITS3F (5'-GCATCGATGAAGAACGCAGC-3') – TS4R (5'-TCCTCCGCTTATTGATATGC-3')

ITS, ITS 2 region, Primer combination: 5.8S-Fun (5'-AACTTTYRRCAAYGGATCWCT-3') – ITS4-Fun (5'-AGCCTCCGCTTATTGATATGCTTAART-5')

SSU region, SSUfungiF (5'-TGGAGGGCAAGTCTGGTG-3') – SSUFungiR (5'-TCGGCATAGTTTATGGTTAAG-3')

LSU region, LSU Fungi LR0R_f (5'-ACCCGCTGAACTTAAGC-3') – LSU Fungi JH-LSU-369rc_r (5'-CTTCCCTTTCAACAATTTCAC-3')

2-Step Barcoding and Custom Amplicon analysis

2-Step Barcoding:

cytochrome b, cytb1 (5'-ccatccaacatctcagcatgatgaaa-3') – cytb2 (5'-gcccctcagaatgatatttgtcctca-3')

cytochrome oxidase I, CO I E (5'-ccagagattagagggaatcagtg-3') – CO 1 F (5'-cctgcaggaggaggagaycc-3')

or 2-Step Custom Amplicons:

design of custom primers with Illumina specific overhangs

Request for offer: microbiome@starseq.com

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

StarSEQ

Prices without tax. Cannot be combined with other promotions or discounts. Valid until 31.03.2026.

SCIENCE DOESN´T TAKE WINTER BREAKS- AND WE WON´T SLOW DOWN EITHER

Explore our exclusive deals and flexible 12-month voucher options.
Fast, precise, and ready for your next breakthrough - all season long.

* * *

eDNA - Metabarcoding

The term ‘environmental DNA’ (eDNA) refers to the free DNA released by all living organisms into their environment. Monitoring using eDNA in bodies of water is a minimally invasive method, as it does not require the target organisms to be caught or removed from the water. The premise of this method is that every organism releases DNA into its environment through cell abrasion, excreta or secretion of DNA.

StarSEQ offers you a complete service for the analysis of your environmental samples: from DNA isolation to the preparation of metabarcoding or snapshot metagenome libraries or a qPCR to the bioinformatic analysis of the data. StarSEQ has created its own curated database. Search via StarSEQ database using verified sequences. The Database can easily be extended with target sequences on customer request. ~130 fish (of which 55 species already identified in different projects), 30 amphibians and reptiles, 49 birds and 48 mammals are included.

Contact us to discuss your eDNA project:
eDNA@starseq.com

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 31.03.2026.

SCIENCE DOESN´T TAKE WINTER BREAKS- AND WE WON´T SLOW DOWN EITHER

Explore our exclusive deals and flexible 12-month voucher options.
Fast, precise, and ready for your next breakthrough - all season long.

****

16S and ITS Microbiome analysis

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 starting from 18 €.

Some 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

[5] Bradley, I. M., Pinto, A. J., & Guest, J. S. (2016). Design and Evaluation of Illumina MiSeq-Compatible, 18S rRNA Gene-Specific Primers for Improved Characterization of Mixed Phototrophic Communities. Applied and Environmental Microbiology, 82(19), 5878 LP-5891. https://doi.org/10.1128/AEM.01630-16

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 31.03.2026.