JÃ¶rg Peplies

List of Publications by Year
in descending order

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Version: 2024-02-01

35 papers	44,330 citations	201674 27 h-index	361022 35 g-index
38 all docs	38 docs citations	38 times ranked	45786 citing authors

#	Article	IF	Citations
1	The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Nucleic Acids Research, 2012, 41, D590-D596.	14.5	21,425
2	Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. Nucleic Acids Research, 2013, 41, e1-e1.	14.5	6,268
3	SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. Nucleic Acids Research, 2007, 35, 7188-7196.	14.5	5,788
4	SINA: Accurate high-throughput multiple sequence alignment of ribosomal RNA genes. Bioinformatics, 2012, 28, 1823-1829.	4.1	2,826
5	The SILVA and â€œAll-species Living Tree Project (LTP)â€•taxonomic frameworks. Nucleic Acids Research, 2014, 42, D643-D648.	14.5	2,667
6	Substrate-Controlled Succession of Marine Bacterioplankton Populations Induced by a Phytoplankton Bloom. Science, 2012, 336, 608-611.	12.6	1,304
7	The All-Species Living Tree project: A 16S rRNA-based phylogenetic tree of all sequenced type strains. Systematic and Applied Microbiology, 2008, 31, 241-250.	2.8	884
8	25 years of serving the community with ribosomal RNA gene reference databases and tools. Journal of Biotechnology, 2017, 261, 169-176.	3.8	679
9	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
10	Covalent DNA-Streptavidin Conjugates as Building Blocks for Novel Biometallic Nanostructures. Angewandte Chemie - International Edition, 1998, 37, 2265-2268.	13.8	209
11	Diverse sulfate-reducing bacteria of the Desulfosarcina/Desulfococcus clade are the key alkane degraders at marine seeps. ISME Journal, 2014, 8, 2029-2044.	9.8	182
12	Optimization Strategies for DNA Microarray-Based Detection of Bacteria with 16S rRNA-Targeting Oligonucleotide Probes. Applied and Environmental Microbiology, 2003, 69, 1397-1407.	3.1	179
13	Microbial and Chemical Characterization of Underwater Fresh Water Springs in the Dead Sea. PLoS ONE, 2012, 7, e38319.	2.5	161
14	Combined Approach for Characterization of Uncultivated Magnetotactic Bacteria from Various Aquatic Environments. Applied and Environmental Microbiology, 2005, 71, 2723-2731.	3.1	125
15	Statin therapy causes gut dysbiosis in mice through a PXR-dependent mechanism. Microbiome, 2017, 5, 95.	11.1	124
16	Singleâ€cell analysis reveals a novel uncultivated magnetotactic bacterium within the candidate division OP3. Environmental Microbiology, 2012, 14, 1709-1721.	3.8	121
17	Bacterial communities associated with four ctenophore genera from the German Bight (North Sea). FEMS Microbiology Ecology, 2015, 91, 1-11.	2.7	108
18	A standard operating procedure for phylogenetic inference (SOPPI) using (rRNA) marker genes. Systematic and Applied Microbiology, 2008, 31, 251-257.	2.8	77

#	Article	IF	Citations
19	Transcriptional Organization and Regulation of Magnetosome Operons in Magnetospirillum gryphiswaldense. Applied and Environmental Microbiology, 2006, 72, 5757-5765.	3.1	71
20	Application and validation of DNA microarrays for the 16S rRNA-based analysis of marine bacterioplankton. Environmental Microbiology, 2004, 6, 638-645.	3.8	63
21	JCoast â€“ A biologist-centric software tool for data mining and comparison of prokaryotic (meta)genomes. BMC Bioinformatics, 2008, 9, 177.	2.6	58
22	Bacterial community dynamics in a cooling tower with emphasis on pathogenic bacteria and Legionella species using universal and genus-specific deep sequencing. Water Research, 2017, 122, 363-376.	11.3	48
23	Diversity and Taxonomy of Magnetotactic Bacteria. , 2006, , 25-36.		44
24	Microbial lipids reveal carbon assimilation patterns on hydrothermal sulfide chimneys. Environmental Microbiology, 2014, 16, 3515-3532.	3.8	44
25	A DNA Microarray Platform Based on Direct Detection of rRNA for Characterization of Freshwater Sediment-Related Prokaryotic Communities. Applied and Environmental Microbiology, 2006, 72, 4829-4838.	3.1	38
26	Development of a genus-specific next generation sequencing approach for sensitive and quantitative determination of the Legionella microbiome in freshwater systems. BMC Microbiology, 2017, 17, 79.	3.3	32
27	Close association of active nitrifiers with <scp>B</scp>eggiatoa mats covering deepâ€sea hydrothermal sediments. Environmental Microbiology, 2014, 16, 1612-1626.	3.8	29
28	Microbial changes in periodontitis successfully treated by mechanical plaque removal and systemic amoxicillin and metronidazole. International Journal of Medical Microbiology, 2009, 299, 427-438.	3.6	28
29	Hydrobacter penzbergensis gen. nov., sp. nov., isolated from purified water. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 920-926.	1.7	25
30	Gene Sets for Utilization of Primary and Secondary Nutrition Supplies in the Distal Gut of Endangered Iberian Lynx. PLoS ONE, 2012, 7, e51521.	2.5	23
31	Comparative Sequence Analysis and Oligonucleotide Probe Design Based on 23S rRNA Genes of Alphaproteobacteria from North Sea Bacterioplankton. Systematic and Applied Microbiology, 2004, 27, 573-580.	2.8	17
32	Pseudomonas-Specific NGS Assay Provides Insight Into Abundance and Dynamics of Pseudomonas Species Including P. aeruginosa in a Cooling Tower. Frontiers in Microbiology, 2018, 9, 1958.	3.5	17
33	Bile Acid Signal Molecules Associate Temporally with Respiratory Inflammation and Microbiome Signatures in Clinically Stable Cystic Fibrosis Patients. Microorganisms, 2020, 8, 1741.	3.6	13
34	Evaluation of gene expression analysis using RNA-targeted partial genome arrays. Systematic and Applied Microbiology, 2006, 29, 349-357.	2.8	10
35	Recognition of the unsuitability of DSM 12173 as the deposited type strain of Thermocrinis ruber Huber et al. 1999, recognition of DSM 23557 as an authentic sub-culture of strain OC 1/4, the nomenclatural type of Thermocrinis ruber Huber et al. 1999 and an emended description of Thermocrinis ruber Huber et al. 1999. Archives of Microbiology, 2020, 202, 1559-1562.	2.2	4