Christian Quast

List of Publications by Year
in descending order

26 papers	38,938 citations	394286 19 h-index	610775 24 g-index
28 all docs	28 docs citations	28 times ranked	43244 citing authors

#	Article	IF	Citations
1	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. Briefings in Bioinformatics, 2021, 22, .	3.2	18
2	Analysis of Bacterial Communities on North Sea Macroalgae and Characterization of the Isolated Planctomycetes Adhaeretor mobilis gen. nov., sp. nov., Roseimaritima multifibrata sp. nov., Rosistilla ulvae sp. nov. and Rubripirellula lacrimiformis sp. nov.. Microorganisms, 2021, 9, 1494.	1.6	34
3	Analysis of bacterial communities in a municipal duck pond during a phytoplankton bloom and isolation of <i>Anatilimnocola aggregata</i> gen. nov., sp. nov., <i>Lacipirellula limnantheis</i> sp. nov. and <i>Urbifossiella limnaea</i> gen. nov., sp. nov. belonging to the phylum <i>Planctomycetes</i>. Environmental Microbiology, 2021, 23, 1379-1396.	1.8	35
4	On-Site Analysis of Bacterial Communities of the Ultraoligotrophic South Pacific Gyre. Applied and Environmental Microbiology, 2019, 85, .	1.4	27
5	A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects. Briefings in Bioinformatics, 2019, 20, 1215-1221.	3.2	1
6	Succession and dynamics of <i>Pristionchus</i> nematodes and their microbiome during decomposition of <i>Oryctes borbonicus</i> on La RÃ©union Island. Environmental Microbiology, 2017, 19, 1476-1489.	1.8	40
7	<i>UniEuk</i>: Time to Speak a Common Language in Protistology!. Journal of Eukaryotic Microbiology, 2017, 64, 407-411.	0.8	74
8	25 years of serving the community with ribosomal RNA gene reference databases and tools. Journal of Biotechnology, 2017, 261, 169-176.	1.9	679
9	SILVA tree viewer: interactive web browsing of the SILVA phylogenetic guide trees. BMC Bioinformatics, 2017, 18, 433.	1.2	18
10	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. ELife, 2016, 5, e11888.	2.8	414
11	Metatranscriptome of marine bacterioplankton during winter time in the North Sea assessed by total RNA sequencing. Marine Genomics, 2015, 19, 45-46.	0.4	14
12	The SILVA and â€œAll-species Living Tree Project (LTP)â€•taxonomic frameworks. Nucleic Acids Research, 2014, 42, D643-D648.	6.5	2,667
13	Diversity and activity of marine bacterioplankton during a diatom bloom in the North Sea assessed by total RNA and pyrotag sequencing. Marine Genomics, 2014, 18, 185-192.	0.4	84
14	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.	6.5	6,268
15	The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Nucleic Acids Research, 2012, 41, D590-D596.	6.5	21,425
16	Ecological structuring of bacterial and archaeal taxa in surface ocean waters. FEMS Microbiology Ecology, 2012, 81, 373-385.	1.3	22
17	Microbial and Chemical Characterization of Underwater Fresh Water Springs in the Dead Sea. PLoS ONE, 2012, 7, e38319.	1.1	161
18	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	9.4	608

#	Article	IF	Citations
19	Analysis of 23S rRNA genes in metagenomes â€" A case study from the Global Ocean Sampling Expedition. Systematic and Applied Microbiology, 2011, 34, 462-469.	1.2	14
20	Transcriptional response of the model planctomycete Rhodopirellula baltica SH1T to changing environmental conditions. BMC Genomics, 2009, 10, 410.	1.2	49
21	Characterization of a marine gammaproteobacterium capable of aerobic anoxygenic photosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2891-2896.	3.3	120
22	SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. Nucleic Acids Research, 2007, 35, 7188-7196.	6.5	5,788
23	Whole genome analysis of the marine Bacteroidetes 'Gramella forsetii' reveals adaptations to degradation of polymeric organic matter. Environmental Microbiology, 2006, 8, 2201-2213.	1.8	334
24	Megx.net--database resources for marine ecological genomics. Nucleic Acids Research, 2006, 34, D390-D393.	6.5	34
25	Going Molecular: Sequence-based spatiotemporal biodiversity evidence in GBIF. Biodiversity Information Science and Standards, 0, 3, .	0.0	2
26	Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR. F1000Research, 0, 10, 1238.	0.8	3