

Christian Quast

List of Publications by Year in descending order

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Version: 2024-02-01

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	The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. <i>Nucleic Acids Research</i> , 2012, 41, D590-D596.	6.5	21,425
2	Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. <i>Nucleic Acids Research</i> , 2013, 41, e1-e1.	6.5	6,268
3	SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. <i>Nucleic Acids Research</i> , 2007, 35, 7188-7196.	6.5	5,788
4	The SILVA and "All-species Living Tree Project (LTP)" taxonomic frameworks. <i>Nucleic Acids Research</i> , 2014, 42, D643-D648.	6.5	2,667
5	25 years of serving the community with ribosomal RNA gene reference databases and tools. <i>Journal of Biotechnology</i> , 2017, 261, 169-176.	1.9	679
6	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
7	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. <i>ELife</i> , 2016, 5, e11888.	2.8	414
8	Whole genome analysis of the marine Bacteroidetes 'Gramella forsetii' reveals adaptations to degradation of polymeric organic matter. <i>Environmental Microbiology</i> , 2006, 8, 2201-2213.	1.8	334
9	Microbial and Chemical Characterization of Underwater Fresh Water Springs in the Dead Sea. <i>PLoS ONE</i> , 2012, 7, e38319.	1.1	161
10	Characterization of a marine gammaproteobacterium capable of aerobic anoxygenic photosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2891-2896.	3.3	120
11	Diversity and activity of marine bacterioplankton during a diatom bloom in the North Sea assessed by total RNA and pyrotag sequencing. <i>Marine Genomics</i> , 2014, 18, 185-192.	0.4	84
12	<i>UniEuk</i>: Time to Speak a Common Language in Protistology!. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 407-411.	0.8	74
13	Transcriptional response of the model planctomycete <i>Rhodopirellula baltica</i> SH1T to changing environmental conditions. <i>BMC Genomics</i> , 2009, 10, 410.	1.2	49
14	Succession and dynamics of <i>Pristionchus</i> nematodes and their microbiome during decomposition of <i>Oryctes borbonicus</i> on La R�union Island. <i>Environmental Microbiology</i> , 2017, 19, 1476-1489.	1.8	40
15	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>. <i>Environmental Microbiology</i> , 2021, 23, 1379-1396.	1.8	35
16	Megx.net--database resources for marine ecological genomics. <i>Nucleic Acids Research</i> , 2006, 34, D390-D393.	6.5	34
17	Analysis of Bacterial Communities on North Sea Macroalgae and Characterization of the Isolated Planctomycetes <i>Adhaeritor mobilis</i> gen. nov., sp. nov., <i>Roseimaritima multifibrata</i> sp. nov., <i>Rosistilla ulvae</i> sp. nov. and <i>Rubripirellula lacrimiformis</i> sp. nov.. <i>Microorganisms</i> , 2021, 9, 1494.	1.6	34
18	On-Site Analysis of Bacterial Communities of the Ultraoligotrophic South Pacific Gyre. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	27

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19	Ecological structuring of bacterial and archaeal taxa in surface ocean waters. FEMS Microbiology Ecology, 2012, 81, 373-385.	1.3	22
20	SILVA tree viewer: interactive web browsing of the SILVA phylogenetic guide trees. BMC Bioinformatics, 2017, 18, 433.	1.2	18
21	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
22	Analysis of 23S rRNA genes in metagenomes – A case study from the Global Ocean Sampling Expedition. Systematic and Applied Microbiology, 2011, 34, 462-469.	1.2	14
23	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
24	Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR. F1000Research, 0, 10, 1238.	0.8	3
25	Going Molecular: Sequence-based spatiotemporal biodiversity evidence in GBIF. Biodiversity Information Science and Standards, 0, 3, .	0.0	2
26	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