

Frank Oliver Glöckner

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

38,338
citations

201575

27
h-index

223716

46
g-index

56
all docs

56
docs citations

56
times ranked

41957
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	SINA: Accurate high-throughput multiple sequence alignment of ribosomal RNA genes. <i>Bioinformatics</i> , 2012, 28, 1823-1829.	1.8	2,826
3	The SILVA and "All-species Living Tree Project (LTP)" taxonomic frameworks. <i>Nucleic Acids Research</i> , 2014, 42, D643-D648.	6.5	2,667
4	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. <i>Nucleic Acids Research</i> , 2019, 47, D259-D264.	6.5	2,072
5	JSpeciesWS: a web server for prokaryotic species circumscription based on pairwise genome comparison. <i>Bioinformatics</i> , 2016, 32, 929-931.	1.8	2,023
6	Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. <i>Nature Reviews Microbiology</i> , 2014, 12, 635-645.	13.6	2,000
7	The All-Species Living Tree project: A 16S rRNA-based phylogenetic tree of all sequenced type strains. <i>Systematic and Applied Microbiology</i> , 2008, 31, 241-250.	1.2	884
8	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015, 11, 625-631.	3.9	715
9	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
10	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
11	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. <i>ELife</i> , 2016, 5, e11888.	2.8	414
12	Genomics in marine monitoring: New opportunities for assessing marine health status. <i>Marine Pollution Bulletin</i> , 2013, 74, 19-31.	2.3	196
13	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
14	The ocean sampling day consortium. <i>GigaScience</i> , 2015, 4, 27.	3.3	185
15	Niches of two polysaccharide-degrading <i>Polaribacter</i> isolates from the North Sea during a spring diatom bloom. <i>ISME Journal</i> , 2015, 9, 1410-1422.	4.4	182
16	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algae-associated bacterium <i>Zobellia galactanivorans</i> Dsij ^T . <i>Environmental Microbiology</i> , 2016, 18, 4610-4627.	1.8	131
17	<i>Candidatus</i> <i>Desulfofervidus auxilii</i> , a hydrogenotrophic sulfate-reducing bacterium involved in the thermophilic anaerobic oxidation of methane. <i>Environmental Microbiology</i> , 2016, 18, 3073-3091.	1.8	115
18	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5022-5033.	6.5	97

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19	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
20	A comprehensive fungi-specific 18S rRNA gene sequence primer toolkit suited for diverse research issues and sequencing platforms. <i>BMC Microbiology</i> , 2018, 18, 190.	1.3	84
21	<i>UniEuk</i>: Time to Speak a Common Language in Protistology!. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 407-411.	0.8	74
22	Ecogenomics and genome landscapes of marine Pseudoalteromonas phage H105/1. <i>ISME Journal</i> , 2011, 5, 107-121.	4.4	62
23	Identification of Habitat-Specific Biomes of Aquatic Fungal Communities Using a Comprehensive Nearly Full-Length 18S rRNA Dataset Enriched with Contextual Data. <i>PLoS ONE</i> , 2015, 10, e0134377.	1.1	62
24	The founding charter of the Genomic Observatories Network. <i>GigaScience</i> , 2014, 3, 2.	3.3	51
25	A phylogenetic framework for the kingdom Fungi based on 18S rRNA gene sequences. <i>Marine Genomics</i> , 2017, 36, 33-39.	0.4	47
26	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020, 36, 2636-2642.	1.8	47
27	Marine microbial genomics in Europe: current status and perspectives. <i>Microbial Biotechnology</i> , 2010, 3, 523-530.	2.0	28
28	On-Site Analysis of Bacterial Communities of the Ultraoligotrophic South Pacific Gyre. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	27
29	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	26
30	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
31	The North Sea goes viral: Occurrence and distribution of North Sea bacteriophages. <i>Marine Genomics</i> , 2018, 41, 31-41.	0.4	17
32	Taxonomic and functional diversity of a coastal planktonic bacterial community in a river-influenced marine area. <i>Marine Genomics</i> , 2017, 32, 61-69.	0.4	15
33	Fast and accurate average genome size and 16S rRNA gene average copy number computation in metagenomic data. <i>BMC Bioinformatics</i> , 2019, 20, 453.	1.2	15
34	Metatranscriptome of marine bacterioplankton during winter time in the North Sea assessed by total RNA sequencing. <i>Marine Genomics</i> , 2015, 19, 45-46.	0.4	14
35	Meta-omics data and collection objects (MOD-CO): a conceptual schema and data model for processing sample data in meta-omics research. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	14
36	The SILVA Database Project: An ELIXIR core data resource for high-quality ribosomal RNA sequences. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	11

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37	Genomic characterization of filamentous phage vB_Vpal_VP-3218, an inducible prophage of <i>Vibrio parahaemolyticus</i> . <i>Marine Genomics</i> , 2020, 53, 100767.	0.4	10
38	Permanent draft genome of <i>Rhodopirellula rubra</i> SWK7. <i>Marine Genomics</i> , 2014, 13, 11-12.	0.4	6
39	MyOSD 2014: Evaluating Oceanographic Measurements Contributed by Citizen Scientists in Support of Ocean Sampling Day. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 163-171.	0.5	6
40	Permanent draft genome of <i>Rhodopirellula sallentina</i> SM41. <i>Marine Genomics</i> , 2014, 13, 17-18.	0.4	5
41	Permanent draft genomes of the <i>Rhodopirellula maiorica</i> strain SM1. <i>Marine Genomics</i> , 2014, 13, 19-20.	0.4	5
42	Permanent draft genomes of the two <i>Rhodopirellula europaea</i> strains 6C and SH398. <i>Marine Genomics</i> , 2014, 13, 15-16.	0.4	4
43	Permanent draft genomes of the three <i>Rhodopirellula baltica</i> strains SH28, SWK14 and WH47. <i>Marine Genomics</i> , 2014, 13, 13-14.	0.4	3
44	FAIR data in meta-omics research: Using the MOD-CO schema to describe structural and operational elements of workflows from field to publication. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	3
45	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , 2019, 8, 1877.	0.8	3
46	Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR. <i>F1000Research</i> , 0, 10, 1238.	0.8	3
47	FastaValidator: an open-source Java library to parse and validate FASTA formatted sequences. <i>BMC Research Notes</i> , 2014, 7, 365.	0.6	2
48	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , 2019, 8, 1877.	0.8	1
49	NFDI4BioDiversity: Biodiversity, ecology and environmental data. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	1
50	Mg-Traits pipeline: advancing functional trait-based approaches in metagenomics. <i>ARPHA Conference Abstracts</i> , 0, 4, .	0.0	0
51	Mainstreaming Molecular Biodiversity: A call for a unified and interoperable framework. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	0