

Pelâ'n Yılmaz

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

32,556
citations

201674

27
h-index

214800

47
g-index

51
all docs

51
docs citations

51
times ranked

37858
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.	14.5	21,425
2	The SILVA and "All-species Living Tree Project (LTP)" taxonomic frameworks. <i>Nucleic Acids Research</i> , 2014, 42, D643-D648.	14.5	2,667
3	Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. <i>Nature Reviews Microbiology</i> , 2014, 12, 635-645.	28.6	2,000
4	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
5	Proposal to reclassify the proteobacterial classes Deltaproteobacteria and Oligoflexia, and the phylum Thermodesulfobacteria into four phyla reflecting major functional capabilities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5972-6016.	1.7	830
6	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015, 11, 625-631.	8.0	715
7	25 years of serving the community with ribosomal RNA gene reference databases and tools. <i>Journal of Biotechnology</i> , 2017, 261, 169-176.	3.8	679
8	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	17.5	608
9	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
10	The small unicellular diazotrophic symbiont, UCYN-A, is a key player in the marine nitrogen cycle. <i>Nature Microbiology</i> , 2016, 1, 16163.	13.3	194
11	The importance of designating type material for uncultured taxa. <i>Systematic and Applied Microbiology</i> , 2019, 42, 15-21.	2.8	149
12	MlxS-BE: a MlxS extension defining a minimum information standard for sequence data from the built environment. <i>ISME Journal</i> , 2014, 8, 1-3.	9.8	127
13	Expanding the World of Marine Bacterial and Archaeal Clades. <i>Frontiers in Microbiology</i> , 2015, 6, 1524.	3.5	122
14	Refining the taxonomic structure of the phylum Acidobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3796-3806.	1.7	101
15	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5022-5033.	14.5	97
16	Improved taxonomic assignment of rumen bacterial 16S rRNA sequences using a revised SILVA taxonomic framework. <i>PeerJ</i> , 2019, 7, e6496.	2.0	82
17	<i>UniEuk</i>: Time to Speak a Common Language in Protistology!. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 407-411.	1.7	74
18	Adaptability as the key to success for the ubiquitous marine nitrite oxidizer <i>Nitrocooccus</i>. <i>Science Advances</i> , 2017, 3, e1700807.	10.3	74

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19	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.	2.5	62
20	The genomic standards consortium: bringing standards to life for microbial ecology. <i>ISME Journal</i> , 2011, 5, 1565-1567.	9.8	59
21	Terrestrial-type nitrogen-fixing symbiosis between seagrass and a marine bacterium. <i>Nature</i> , 2021, 600, 105-109.	27.8	48
22	A phylogenetic framework for the kingdom Fungi based on 18S rRNA gene sequences. <i>Marine Genomics</i> , 2017, 36, 33-39.	1.1	47
23	Hydrogen sulfide can inhibit and enhance oxygenic photosynthesis in a cyanobacterium from sulfidic springs. <i>Environmental Microbiology</i> , 2015, 17, 3301-3313.	3.8	45
24	BioVeL: a virtual laboratory for data analysis and modelling in biodiversity science and ecology. <i>BMC Ecology</i> , 2016, 16, 49.	3.0	45
25	Anoxygenic Photosynthesis Controls Oxygenic Photosynthesis in a Cyanobacterium from a Sulfidic Spring. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2025-2031.	3.1	41
26	Megx.net: integrated database resource for marine ecological genomics. <i>Nucleic Acids Research</i> , 2010, 38, D391-D395.	14.5	35
27	Sulfur cycling in oceanic oxygen minimum zones. <i>Limnology and Oceanography</i> , 2021, 66, 2360-2392.	3.1	34
28	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	29
29	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	26
30	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , 2015, 7, 1988-1999.	2.5	25
31	Ecological structuring of bacterial and archaeal taxa in surface ocean waters. <i>FEMS Microbiology Ecology</i> , 2012, 81, 373-385.	2.7	22
32	SILVA tree viewer: interactive web browsing of the SILVA phylogenetic guide trees. <i>BMC Bioinformatics</i> , 2017, 18, 433.	2.6	18
33	A Metagenomics Portal for a Democratized Sequencing World. <i>Methods in Enzymology</i> , 2013, 531, 487-523.	1.0	16
34	Analysis of 23S rRNA genes in metagenomes – A case study from the Global Ocean Sampling Expedition. <i>Systematic and Applied Microbiology</i> , 2011, 34, 462-469.	2.8	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, .	3.0	14
36	Versatile cyanobacteria control the timing and extent of sulfide production in a Proterozoic analog microbial mat. <i>ISME Journal</i> , 2020, 14, 3024-3037.	9.8	14

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37	Ecogenomic Perspectives on Domains of Unknown Function: Correlation-Based Exploration of Marine Metagenomes. PLoS ONE, 2013, 8, e50869.	2.5	11
38	MetaBar - a tool for consistent contextual data acquisition and standards compliant submission. BMC Bioinformatics, 2010, 11, 358.	2.6	10
39	Meeting Report: Hackathon-Workshop on Darwin Core and MlxS Standards Alignment (February 2012). Standards in Genomic Sciences, 2012, 7, 166-170.	1.5	8
40	Meeting Report: GBIF hackathon-workshop on Darwin Core and sample data (22-24 May 2013). Standards in Genomic Sciences, 2014, 9, 585-598.	1.5	8
41	Plant specimen contextual data consensus. GigaScience, 2016, 5, 1-4.	6.4	8
42	Meeting report: GSC M5 roundtable at the 13th International Society for Microbial Ecology meeting in Seattle, WA, USA August 22-27, 2010. Standards in Genomic Sciences, 2010, 3, 235-239.	1.5	7
43	CDinFusion – Submission-Ready, On-Line Integration of Sequence and Contextual Data. PLoS ONE, 2011, 6, e24797.	2.5	7
44	Data shopping in an open marketplace: Introducing the Ontogrator web application for marking up data using ontologies and browsing using facets. Standards in Genomic Sciences, 2011, 4, 286-292.	1.5	4
45	MlxS-HCR: a MlxS extension defining a minimal information standard for sequence data from environments pertaining to hydrocarbon resources. Standards in Genomic Sciences, 2016, 11, 78.	1.5	2
46	Metagenomes: 23S Sequences. , 2012, , 1-8.		0
47	Metadata Standards for Genomic Sequence Data: Past and Future of MlxS Standards Family. Biodiversity Information Science and Standards, 0, 1, e20423.	0.0	0