

Thomas BrÃ¼ls

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8868764/publications.pdf>

Version: 2024-02-01

24
papers

6,726
citations

623734

14
h-index

642732

23
g-index

27
all docs

27
docs citations

27
times ranked

11186
citing authors

#	ARTICLE	IF	CITATIONS
1	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
2	A placenta-specific receptor for the fusogenic, endogenous retrovirus-derived, human syncytin-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17532-17537.	7.1	185
3	Endogeic earthworms shape bacterial functional communities and affect organic matter mineralization in a tropical soil. <i>ISME Journal</i> , 2012, 6, 213-222.	9.8	169
4	Fermentative Spirochaetes mediate necromass recycling in anoxic hydrocarbon-contaminated habitats. <i>ISME Journal</i> , 2018, 12, 2039-2050.	9.8	74
5	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. <i>Scientific Reports</i> , 2017, 7, 44103.	3.3	67
6	An unusual strategy for the anoxic biodegradation of phthalate. <i>ISME Journal</i> , 2017, 11, 224-236.	9.8	61
7	Screening and Characterization of Novel Polyesterases from Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. <i>Environmental Science & Technology</i> , 2018, 52, 12388-12401.	10.0	56
8	Microbial Degradation of a Recalcitrant Pesticide: Chlordecone. <i>Frontiers in Microbiology</i> , 2016, 7, 2025.	3.5	55
9	Anaerobic degradation of phenanthrene by a sulfate-reducing enrichment culture. <i>Environmental Microbiology</i> , 2018, 20, 3589-3600.	3.8	45
10	Functional soil metagenomics: elucidation of polycyclic aromatic hydrocarbon degradation potential following 12 years of <i>in situ</i> bioremediation. <i>Environmental Microbiology</i> , 2017, 19, 2992-3011.	3.8	39
11	The human metagenome: our other genome?. <i>Human Molecular Genetics</i> , 2011, 20, R142-R148.	2.9	33
12	Metabolic reconstruction of the genome of candidate <i>Desulfatiglans</i> TRIP_1 and identification of key candidate enzymes for anaerobic phenanthrene degradation. <i>Environmental Microbiology</i> , 2019, 21, 1267-1286.	3.8	31
13	A patchwork pathway for oxygenase-independent degradation of side chain containing steroids. <i>Environmental Microbiology</i> , 2017, 19, 4684-4699.	3.8	28
14	Microbial communities in pyrene amended soil-compost mixture and fertilized soil. <i>AMB Express</i> , 2017, 7, 7.	3.0	17
15	A scalable assembly-free variable selection algorithm for biomarker discovery from metagenomes. <i>BMC Bioinformatics</i> , 2016, 17, 311.	2.6	10
16	The class II benzoyl-coenzyme A reductase complex from the sulfate-reducing <i>Desulfosarcina cetonica</i> . <i>Environmental Microbiology</i> , 2019, 21, 4241-4252.	3.8	10
17	A zero inflated log-normal model for inference of sparse microbial association networks. <i>PLoS Computational Biology</i> , 2021, 17, e1009089.	3.2	10
18	Channeling C1 Metabolism toward S-Adenosylmethionine-Dependent Conversion of Estrogens to Androgens in Estrogen-Degrading Bacteria. <i>MBio</i> , 2020, 11, .	4.1	8

#	ARTICLE	IF	CITATIONS
19	A spectral algorithm for fast <i>de novo</i> layout of uncorrected long nanopore reads. <i>Bioinformatics</i> , 2017, 33, 3188-3194.	4.1	7
20	Binning unassembled short reads based on k-mer abundance covariance using sparse coding. <i>GigaScience</i> , 2020, 9, .	6.4	7
21	Shared Nearest Neighbor Clustering in a Locality Sensitive Hashing Framework. <i>Journal of Computational Biology</i> , 2018, 25, 236-250.	1.6	6
22	An assessment of the amount of untapped fold level novelty in under-sampled areas of the tree of life. <i>Scientific Reports</i> , 2015, 5, 14717.	3.3	4
23	The enzymatic nature of an anonymous protein sequence cannot reliably be inferred from superfamily level structural information alone. <i>Protein Science</i> , 2015, 24, 643-650.	7.6	3
24	Sparse Non-negative Matrix Factorization for Retrieving Genomes Across Metagenomes. <i>Communications in Computer and Information Science</i> , 2020, , 97-105.	0.5	0