Thijs Ettema

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5697286/publications.pdf

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25 papers	1,647 citations	471509 17 h-index	552781 26 g-index
32 all docs	32 docs citations	32 times ranked	2082 citing authors

#	Article	IF	Citations
1	Spatial separation of ribosomes and DNA in Asgard archaeal cells. ISME Journal, 2022, 16, 606-610.	9.8	17
2	The human archaeome in focus. Nature Microbiology, 2022, 7, 10-11.	13.3	8
3	A closed Candidatus Odinarchaeum chromosome exposes Asgard archaeal viruses. Nature Microbiology, 2022, 7, 948-952.	13.3	18
4	The evolutionary origin of host association in the Rickettsiales. Nature Microbiology, 2022, 7, 1189-1199.	13.3	29
5	Innovations to culturing the uncultured microbial majority. Nature Reviews Microbiology, 2021, 19, 225-240.	28.6	254
6	Expanding Archaeal Diversity and Phylogeny: Past, Present, and Future. Annual Review of Microbiology, 2021, 75, 359-381.	7.3	34
7	Single cell genomics reveals plastid-lacking Picozoa are close relatives of red algae. Nature Communications, 2021, 12, 6651.	12.8	40
8	Chlamydial contribution to anaerobic metabolism during eukaryotic evolution. Science Advances, 2020, 6, eabb7258.	10.3	18
9	Hikarchaeia demonstrate an intermediate stage in the methanogen-to-halophile transition. Nature Communications, 2020, 11, 5490.	12.8	39
10	The Archaeal Roots of the Eukaryotic Dynamic Actin Cytoskeleton. Current Biology, 2020, 30, R521-R526.	3.9	31
11	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	13.3	115
12	An efficient single-cell transcriptomics workflow for microbial eukaryotes benchmarked on Giardia intestinalis cells. BMC Genomics, 2020, 21, 448.	2.8	8
13	Culturing the uncultured. Nature Biotechnology, 2019, 37, 1278-1279.	17.5	8
14	Asgard archaea capable of anaerobic hydrocarbon cycling. Nature Communications, 2019, 10, 1822.	12.8	165
15	Confident phylogenetic identification of uncultured prokaryotes through long read amplicon sequencing of the 16Sâ€ITSâ€23S rRNA operon. Environmental Microbiology, 2019, 21, 2485-2498.	3.8	46
16	Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism. Nature Microbiology, 2019, 4, 1138-1148.	13.3	143
17	Genomes of two archaeal endosymbionts show convergent adaptations to an intracellular lifestyle. ISME Journal, 2018, 12, 2655-2667.	9.8	26
18	Asgard archaea are the closest prokaryotic relatives of eukaryotes. PLoS Genetics, 2018, 14, e1007080.	3.5	114

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19	Functional reconstruction of a eukaryotic-like E1/E2/(RING) E3 ubiquitylation cascade from an uncultured archaeon. Nature Communications, 2017, 8, 1120.	12.8	23
20	Genomic exploration of the diversity, ecology, and evolution of the archaeal domain of life. Science, 2017, 357, .	12.6	247
21	Genomic inference of the metabolism of cosmopolitan subsurface Archaea, Hadesarchaea. Nature Microbiology, 2016, 1, 16002.	13.3	118
22	<scp>R</scp>olf <scp>B</scp>ernander (1956â€“2014): pioneer of the archaeal cell cycle. Molecular Microbiology, 2014, 92, 903-909.	2.5	1
23	â€˜Geoarchaeote NAG1â€™ is a deeply rooting lineage of the archaeal order Thermoproteales rather than a new phylum. ISME Journal, 2014, 8, 1353-1357.	9.8	19
24	Identification and Functional Verification of Archaeal-Type Phosphoenolpyruvate Carboxylase, a Missing Link in Archaeal Central Carbohydrate Metabolism. Journal of Bacteriology, 2004, 186, 7754-7762.	2.2	33
25	TRASH: a novel metal-binding domain predicted to be involved in heavy-metal sensing, trafficking and resistance. Trends in Biochemical Sciences, 2003, 28, 170-173.	7.5	65