

# Daan R Speth

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3526204/publications.pdf>

Version: 2024-02-01

21  
papers

3,601  
citations

516710

16  
h-index

713466

21  
g-index

25  
all docs

25  
docs citations

25  
times ranked

4901  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	5.6	62
2	Unique mobile elements and scalable gene flow at the prokaryote–eukaryote boundary revealed by circularized Asgard archaea genomes. <i>Nature Microbiology</i> , 2022, 7, 200-212.	13.3	29
3	Microbial communities of Auka hydrothermal sediments shed light on vent biogeography and the evolutionary history of thermophily. <i>ISME Journal</i> , 2022, 16, 1750-1764.	9.8	16
4	Community Structure and Microbial Associations in Sediment-Free Methanotrophic Enrichment Cultures from a Marine Methane Seep. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	8
5	Microbial succession and dynamics in meromictic Mono Lake, California. <i>Geobiology</i> , 2021, 19, 376-393.	2.4	15
6	A Novel Laboratory-Scale Mesocosm Setup to Study Methane Emission Mitigation by Sphagnum Mosses and Associated Methanotrophs. <i>Frontiers in Microbiology</i> , 2021, 12, 652486.	3.5	3
7	<i>Methylotetracoccus oryzae</i> Strain C50C1 Is a Novel Type Ib Gammaproteobacterial Methanotroph Adapted to Freshwater Environments. <i>MSphere</i> , 2019, 4, .	2.9	14
8	Comparative Genomics of Candidatus <i>Methylomirabilis</i> Species and Description of Ca. <i>Methylomirabilis</i> <i>Lanthanidiphila</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1672.	3.5	67
9	Metabolic marker gene mining provides insight in global <i>mcrA</i> diversity and, coupled with targeted genome reconstruction, sheds further light on metabolic potential of the <i>Methanomassiliicoccales</i> . <i>PeerJ</i> , 2018, 6, e5614.	2.0	34
10	Draft Genome of <i>Scalindua rubra</i> , Obtained from the Interface Above the Discovery Deep Brine in the Red Sea, Sheds Light on Potential Salt Adaptation Strategies in Anammox Bacteria. <i>Microbial Ecology</i> , 2017, 74, 1-5.	2.8	73
11	Metagenomic analysis of nitrogen and methane cycling in the Arabian Sea oxygen minimum zone. <i>PeerJ</i> , 2016, 4, e1924.	2.0	77
12	Genome Characteristics of Two Novel Type I Methanotrophs Enriched from North Sea Sediments Containing Exclusively a Lanthanide-Dependent XoxF5-Type Methanol Dehydrogenase. <i>Microbial Ecology</i> , 2016, 72, 503-509.	2.8	39
13	Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. <i>Nature Communications</i> , 2016, 7, 11172.	12.8	373
14	Archaea catalyze iron-dependent anaerobic oxidation of methane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12792-12796.	7.1	470
15	A Metagenomics-Based Metabolic Model of Nitrate-Dependent Anaerobic Oxidation of Methane by <i>Methanoperedens</i> -Like Archaea. <i>Frontiers in Microbiology</i> , 2015, 6, 1423.	3.5	170
16	Draft Genome Sequence of Anammox Bacterium –Candidatus <i>Scalindua brodae</i> – Obtained Using Differential Coverage Binning of Sequencing Data from Two Reactor Enrichments. <i>Genome Announcements</i> , 2015, 3, .	0.8	46
17	Complete nitrification by a single microorganism. <i>Nature</i> , 2015, 528, 555-559.	27.8	1,336
18	Shotgun metagenomic data reveals significant abundance but low diversity of –Candidatus <i>Scalindua</i> – marine anammox bacteria in the Arabian Sea oxygen minimum zone. <i>Frontiers in Microbiology</i> , 2014, 5, 31.	3.5	41

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19	A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. <i>Nature Communications</i> , 2014, 5, 4498.	12.8	617
20	Genomic Analysis Indicates the Presence of an Asymmetric Bilayer Outer Membrane in Planctomycetes and Verrucomicrobia. <i>Frontiers in Microbiology</i> , 2012, 3, 304.	3.5	51
21	Comparative Genomics of Two Independently Enriched "Candidatus Kuenenia Stutgartiensis" Anammox Bacteria. <i>Frontiers in Microbiology</i> , 2012, 3, 307.	3.5	51