

Jonathan D Todd

List of Publications by Year in descending order

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70
papers

4,365
citations

117625

34
h-index

114465

63
g-index

75
all docs

75
docs citations

75
times ranked

3142
citing authors

#	ARTICLE	IF	CITATIONS
1	DMSP Production by Coral-Associated Bacteria. <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	17
2	Insights into methionine S-methylation in diverse organisms. <i>Nature Communications</i> , 2022, 13, .	12.8	9
3	Mechanistic insights into the key marine dimethylsulfoniopropionate synthesis enzyme DsyB/DSYB. , 2022, 1, 114-130.		5
4	Bacterial Dimethylsulfoniopropionate Biosynthesis in the East China Sea. <i>Microorganisms</i> , 2021, 9, 657.	3.6	12
5	A novel ATP dependent dimethylsulfoniopropionate lyase in bacteria that releases dimethyl sulfide and acryloyl-CoA. <i>ELife</i> , 2021, 10, .	6.0	38
6	DiTing: A Pipeline to Infer and Compare Biogeochemical Pathways From Metagenomic and Metatranscriptomic Data. <i>Frontiers in Microbiology</i> , 2021, 12, 698286.	3.5	21
7	Spatiotemporal distribution of bacterial dimethylsulfoniopropionate producing and catabolic genes in the Changjiang Estuary. <i>Environmental Microbiology</i> , 2021, 23, 7073-7092.	3.8	11
8	Dimethylsulfoniopropionate Biosynthetic Bacteria in the Subseafloor Sediments of the South China Sea. <i>Frontiers in Microbiology</i> , 2021, 12, 731524.	3.5	4
9	Bacteria are important dimethylsulfoniopropionate producers in marine aphotic and high-pressure environments. <i>Nature Communications</i> , 2020, 11, 4658.	12.8	62
10	Metagenomic Insights Into the Cycling of Dimethylsulfoniopropionate and Related Molecules in the Eastern China Marginal Seas. <i>Frontiers in Microbiology</i> , 2020, 11, 157.	3.5	22
11	DMSP-Producing Bacteria Are More Abundant in the Surface Microlayer than Subsurface Seawater of the East China Sea. <i>Microbial Ecology</i> , 2020, 80, 350-365.	2.8	28
12	Biosynthesis of CdS Quantum Dots Mediated by Volatile Sulfur Compounds Released by Antarctic <i>Pseudomonas fragi</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1866.	3.5	38
13	Bacteria are important dimethylsulfoniopropionate producers in coastal sediments. <i>Nature Microbiology</i> , 2019, 4, 1815-1825.	13.3	67
14	Biogenic production of DMSP and its degradation to DMSâ€”their roles in the global sulfur cycle. <i>Science China Life Sciences</i> , 2019, 62, 1296-1319.	4.9	68
15	The Production and Fate of Volatile Organosulfur Compounds in Sulfidic and Ferruginous Sediment. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 3390-3402.	3.0	14
16	A day in the life of marine sulfonates. <i>Nature Microbiology</i> , 2019, 4, 1610-1611.	13.3	7
17	Mechanistic insight into 3â€”methylmercaptopropionate metabolism and kinetical regulation of demethylation pathway in marine dimethylsulfoniopropionateâ€”catabolizing bacteria. <i>Molecular Microbiology</i> , 2019, 111, 1057-1073.	2.5	18
18	Methanethiol and Dimethylsulfide Cycling in Stiffkey Saltmarsh. <i>Frontiers in Microbiology</i> , 2019, 10, 1040.	3.5	23

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19	Proliferation of hydrocarbon-degrading microbes at the bottom of the Mariana Trench. <i>Microbiome</i> , 2019, 7, 47.	11.1	128
20	Structure-Function Analysis Indicates that an Active-Site Water Molecule Participates in Dimethylsulfoniopropionate Cleavage by DddK. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	12
21	Mechanisms of iron- and O ₂ -sensing by the [4Fe-4S] cluster of the global iron regulator RirA. <i>ELife</i> , 2019, 8, .	6.0	27
22	DSYB catalyses the key step of dimethylsulfoniopropionate biosynthesis in many phytoplankton. <i>Nature Microbiology</i> , 2018, 3, 430-439.	13.3	116
23	Bacterial SBP56 identified as a Cu-dependent methanethiol oxidase widely distributed in the biosphere. <i>ISME Journal</i> , 2018, 12, 145-160.	9.8	62
24	Novel Insights Into Bacterial Dimethylsulfoniopropionate Catabolism in the East China Sea. <i>Frontiers in Microbiology</i> , 2018, 9, 3206.	3.5	35
25	Comparative Genomics and Mutational Analysis Reveals a Novel XoxF-Utilizing Methylotroph in the Roseobacter Group Isolated From the Marine Environment. <i>Frontiers in Microbiology</i> , 2018, 9, 766.	3.5	13
26	Dimethylsulfoniopropionate biosynthesis in marine bacteria and identification of the key gene in this process. <i>Nature Microbiology</i> , 2017, 2, 17009.	13.3	222
27	Structural and Biochemical Insights into Dimethylsulfoniopropionate Cleavage by Cofactor-Bound DddK from the Prolific Marine Bacterium <i>Pelagibacter</i> . <i>Biochemistry</i> , 2017, 56, 2873-2885.	2.5	26
28	Mechanistic insight into acrylate metabolism and detoxification in marine dimethylsulfoniopropionate-catabolizing bacteria. <i>Molecular Microbiology</i> , 2017, 105, 674-688.	2.5	16
29	Sensing iron availability via the fragile [4Fe-4S] cluster of the bacterial transcriptional repressor RirA. <i>Chemical Science</i> , 2017, 8, 8451-8463.	7.4	27
30	Methanethiol-dependent dimethylsulfide production in soil environments. <i>ISME Journal</i> , 2017, 11, 2379-2390.	9.8	54
31	Mechanistic Insights into Dimethylsulfoniopropionate Lyase DddY, a New Member of the Cupin Superfamily. <i>Journal of Molecular Biology</i> , 2017, 429, 3850-3862.	4.2	22
32	Recumbent Stepper Submaximal Test response is reliable in adults with and without stroke. <i>PLoS ONE</i> , 2017, 12, e0172294.	2.5	13
33	The abundant marine bacterium <i>Pelagibacter</i> simultaneously catabolizes dimethylsulfoniopropionate to the gases dimethyl sulfide and methanethiol. <i>Nature Microbiology</i> , 2016, 1, 16065.	13.3	110
34	Enzymatic breakage of dimethylsulfoniopropionate – a signature molecule for life at sea. <i>Current Opinion in Chemical Biology</i> , 2016, 31, 58-65.	6.1	62
35	Biochemical, Kinetic, and Spectroscopic Characterization of <i>Ruegeria pomeroyi</i> DddW – A Mononuclear Iron-Dependent DMSP Lyase. <i>PLoS ONE</i> , 2015, 10, e0127288.	2.5	40
36	A novel pathway producing dimethylsulphide in bacteria is widespread in soil environments. <i>Nature Communications</i> , 2015, 6, 6579.	12.8	82

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37	Screening of Metagenomic and Genomic Libraries Reveals Three Classes of Bacterial Enzymes That Overcome the Toxicity of Acrylate. <i>PLoS ONE</i> , 2014, 9, e97660.	2.5	20
38	Manganese uptake in marine bacteria; the novel MntX transporter is widespread in Roseobacters, Vibrrios, Alteromonadales and the SAR11 and SAR116 clades. <i>ISME Journal</i> , 2013, 7, 581-591.	9.8	23
39	DddW, a third DMSP lyase in a model Roseobacter marine bacterium, <i>Ruegeria pomeroyi</i> DSS-3. <i>ISME Journal</i> , 2012, 6, 223-226.	9.8	88
40	Multiple DMSP lyases in the β -proteobacterium <i>Oceanimonas doudoroffii</i> . <i>Biogeochemistry</i> , 2012, 110, 109-119.	3.5	18
41	Diversity of DMSP transport in marine bacteria, revealed by genetic analyses. <i>Biogeochemistry</i> , 2012, 110, 121-130.	3.5	21
42	Phylogenetic diversity of the <i>dddP</i> gene for dimethylsulfoniopropionate-dependent dimethyl sulfide synthesis in mangrove soils. <i>Canadian Journal of Microbiology</i> , 2012, 58, 523-530.	1.7	16
43	Microbial Origins and Consequences of Dimethyl Sulfide. <i>Microbe Magazine</i> , 2012, 7, 181-185.	0.4	6
44	The <i>Ruegeria pomeroyi</i> acul Gene Has a Role in DMSP Catabolism and Resembles yhdH of <i>E. coli</i> and Other Bacteria in Conferring Resistance to Acrylate. <i>PLoS ONE</i> , 2012, 7, e35947.	2.5	43
45	Catabolism of dimethylsulphoniopropionate: microorganisms, enzymes and genes. <i>Nature Reviews Microbiology</i> , 2011, 9, 849-859.	28.6	314
46	DddQ, a novel, cupin-containing, dimethylsulfoniopropionate lyase in marine roseobacters and in uncultured marine bacteria. <i>Environmental Microbiology</i> , 2011, 13, 427-438.	3.8	111
47	Heme binding to the second, lower-affinity site of the global iron regulator <i>Irr</i> from <i>Rhizobium leguminosarum</i> promotes oligomerization. <i>FEBS Journal</i> , 2011, 278, 2011-2021.	4.7	13
48	DddY, a periplasmic dimethylsulfoniopropionate lyase found in taxonomically diverse species of Proteobacteria. <i>ISME Journal</i> , 2011, 5, 1191-1200.	9.8	78
49	Unusual Regulation of a Leaderless Operon Involved in the Catabolism of Dimethylsulfoniopropionate in <i>Rhodobacter sphaeroides</i> . <i>PLoS ONE</i> , 2011, 6, e15972.	2.5	33
50	The opportunistic coral pathogen <i>Aspergillus sydowii</i> contains <i>dddP</i> and makes dimethyl sulfide from dimethylsulfoniopropionate. <i>ISME Journal</i> , 2010, 4, 147-150.	9.8	33
51	Identification of genes for dimethyl sulfide production in bacteria in the gut of Atlantic Herring (<i>Clupea harengus</i>). <i>ISME Journal</i> , 2010, 4, 144-146.	9.8	38
52	Molecular dissection of bacterial acrylate catabolism – unexpected links with dimethylsulfoniopropionate catabolism and dimethyl sulfide production. <i>Environmental Microbiology</i> , 2010, 12, 327-343.	3.8	116
53	Heme-responsive DNA Binding by the Global Iron Regulator <i>Irr</i> from <i>Rhizobium leguminosarum</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 16023-16031.	3.4	44
54	The <i>dddP</i> gene of <i>Roseovarius nubinhibens</i> encodes a novel lyase that cleaves dimethylsulfoniopropionate into acrylate plus dimethyl sulfide. <i>Microbiology (United Kingdom)</i> , 2010, 156, 1900-1906.	1.8	49

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55	The <i>dddP</i> gene, encoding a novel enzyme that converts dimethylsulfoniopropionate into dimethyl sulfide, is widespread in ocean metagenomes and marine bacteria and also occurs in some Ascomycete fungi. <i>Environmental Microbiology</i> , 2009, 11, 1376-1385.	3.8	145
56	The <i>dddP</i> gene, encoding a novel enzyme that converts dimethylsulfoniopropionate into dimethyl sulfide, is widespread in ocean metagenomes and marine bacteria and also occurs in some Ascomycete fungi. <i>Environmental Microbiology</i> , 2009, 11, 1624-1625.	3.8	9
57	Molecular genetic analysis of a dimethylsulfoniopropionate lyase that liberates the climate-changing gas dimethylsulfide in several marine α -proteobacteria and <i>Rhodobacter sphaeroides</i> .	3.8	156
58	Molecular genetic analysis of a dimethylsulfoniopropionate lyase that liberates the climate-changing gas dimethylsulfide in several marine α -proteobacteria and <i>Rhodobacter sphaeroides</i> .	3.8	5
59	Molecular diversity of bacterial production of the climate-changing gas, dimethyl sulphide, a molecule that impinges on local and global symbioses. <i>Journal of Experimental Botany</i> , 2008, 59, 1059-1067.	4.8	36
60	Structural and Regulatory Genes Required to Make the Gas Dimethyl Sulfide in Bacteria. <i>Science</i> , 2007, 315, 666-669.	12.6	256
61	Living without Fur: the subtlety and complexity of iron-responsive gene regulation in the symbiotic bacterium <i>Rhizobium</i> and other α -proteobacteria. <i>BioMetals</i> , 2007, 20, 501-511.	4.1	92
62	The genome of <i>Rhizobium leguminosarum</i> has recognizable core and accessory components. <i>Genome Biology</i> , 2006, 7, R34.	9.6	489
63	The <i>Rhizobium leguminosarum</i> regulator <i>IrrA</i> affects the transcription of a wide range of genes in response to Fe availability. <i>Molecular Genetics and Genomics</i> , 2006, 275, 564-577.	2.1	45
64	Computational Reconstruction of Iron- and Manganese-Responsive Transcriptional Networks in α -Proteobacteria. <i>PLoS Computational Biology</i> , 2006, 2, e163.	3.2	138
65	Proteomic analysis reveals the wide-ranging effects of the novel, iron-responsive regulator <i>RirA</i> in <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> . <i>Molecular Genetics and Genomics</i> , 2005, 273, 197-206.	2.1	40
66	The manganese-responsive repressor <i>Mur</i> of <i>Rhizobium leguminosarum</i> is a member of the Fur-superfamily that recognizes an unusual operator sequence. <i>Microbiology (United Kingdom)</i> , 2005, 151, 4071-4078.	1.8	32
67	Evidence that the <i>Rhizobium</i> regulatory protein <i>RirA</i> binds to cis-acting iron-responsive operators (IROs) at promoters of some Fe-regulated genes. <i>Microbiology (United Kingdom)</i> , 2004, 150, 4065-4074.	1.8	44
68	The Fur-like protein <i>Mur</i> of <i>Rhizobium leguminosarum</i> is a Mn ²⁺ -responsive transcriptional regulator. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1447-1456.	1.8	105
69	Fur is not the global regulator of iron uptake genes in <i>Rhizobium leguminosarum</i> . <i>Microbiology (United Kingdom)</i> , 2003, 149, 1357-1365.	1.8	56
70	<i>RirA</i> , an iron-responsive regulator in the symbiotic bacterium <i>Rhizobium leguminosarum</i> The GenBank accession number for the <i>RirA</i> sequence is CAC35510.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 4059-4071.	1.8	114