

David A C Beck

List of Publications by Year in descending order

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53
papers

3,139
citations

136950

32
h-index

168389

53
g-index

53
all docs

53
docs citations

53
times ranked

3269
citing authors

#	ARTICLE	IF	CITATIONS
1	Water-Accelerated Photooxidation of CH ₃ NH ₃ Pb ₃ Perovskite. <i>Journal of the American Chemical Society</i> , 2022, 144, 5552-5561.	13.7	40
2	Attention-based generative models for <i>de novo</i> molecular design. <i>Chemical Science</i> , 2021, 12, 8362-8372.	7.4	34
3	A Computational Framework for Identifying Promoter Sequences in Nonmodel Organisms Using RNA-seq Data Sets. <i>ACS Synthetic Biology</i> , 2021, 10, 1394-1405.	3.8	15
4	Data Science in Chemical Engineering: Applications to Molecular Science. <i>Annual Review of Chemical and Biomolecular Engineering</i> , 2021, 12, 15-37.	6.8	9
5	An automated multiplexed turbidometric and data collection system for measuring growth kinetics of anaerobes dependent on gaseous substrates. <i>Journal of Microbiological Methods</i> , 2021, 188, 106294.	1.6	1
6	Continuous Molecular Representations of Ionic Liquids. <i>Journal of Physical Chemistry B</i> , 2020, 124, 8347-8357.	2.6	12
7	Core Metabolism Shifts during Growth on Methanol versus Methane in the Methanotroph <i>Methylomicrobium buryatense</i> 5GB1. <i>MBio</i> , 2019, 10, .	4.1	31
8	Mosaic plasmids are abundant and unevenly distributed across prokaryotic taxa. <i>Plasmid</i> , 2019, 102, 10-18.	1.4	70
9	DNA-SIP based genome-centric metagenomics identifies key long-chain fatty acid-degrading populations in anaerobic digesters with different feeding frequencies. <i>ISME Journal</i> , 2018, 12, 112-123.	9.8	88
10	Long-chain fatty acid feeding frequency in anaerobic codigestion impacts syntrophic community structure and biokinetics. <i>Water Research</i> , 2017, 117, 218-229.	11.3	81
11	Quorum Sensing in a Methane-Oxidizing Bacterium. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	29
12	Lanthanide-dependent cross-feeding of methane-derived carbon is linked by microbial community interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 358-363.	7.1	156
13	Metabolic crosstalk regulates <i>Porphyromonas gingivalis</i> colonization and virulence during oral polymicrobial infection. <i>Nature Microbiology</i> , 2017, 2, 1493-1499.	13.3	100
14	Natural Selection in Synthetic Communities Highlights the Roles of <i>Methylococcaceae</i> and <i>Methylophilaceae</i> and Suggests Differential Roles for Alternative Methanol Dehydrogenases in Methane Consumption. <i>Frontiers in Microbiology</i> , 2017, 8, 2392.	3.5	51
15	Oxygen-limited metabolism in the methanotroph <i>Methylomicrobium buryatense</i> 5GB1C. <i>PeerJ</i> , 2017, 5, e3945.	2.0	81
16	A Synthetic Ecology Perspective: How Well Does Behavior of Model Organisms in the Laboratory Predict Microbial Activities in Natural Habitats?. <i>Frontiers in Microbiology</i> , 2016, 7, 946.	3.5	25
17	Data science: Accelerating innovation and discovery in chemical engineering. <i>AIChE Journal</i> , 2016, 62, 1402-1416.	3.6	63
18	Microbial community adaptation influences long-chain fatty acid conversion during anaerobic codigestion of fats, oils, and grease with municipal sludge. <i>Water Research</i> , 2016, 103, 372-382.	11.3	105

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19	Difference in C3â€C4 metabolism underlies tradeoff between growth rate and biomass yield in <i>Methylobacterium extorquens</i> AM1. <i>BMC Microbiology</i> , 2016, 16, 156.	3.3	10
20	Comprehensive molecular characterization of <i>Methylobacterium extorquens</i> AM1 adapted for 1-butanol tolerance. <i>Biotechnology for Biofuels</i> , 2016, 9, 84.	6.2	42
21	MxaY regulates the lanthanide-mediated methanol dehydrogenase switch in <i>Methylobacterium buryatense</i> . <i>PeerJ</i> , 2016, 4, e2435.	2.0	59
22	Multiphyletic origins of methylotrophy in <i>Alphaproteobacteria</i> , exemplified by comparative genomics of <i>Leishmania</i> and <i>Wolbachia</i> Washington isolates. <i>Environmental Microbiology</i> , 2015, 17, 547-554.	3.8	38
23	Genome-scale metabolic reconstructions and theoretical investigation of methane conversion in <i>Methylobacterium buryatense</i> strain 5G(B1). <i>Microbial Cell Factories</i> , 2015, 14, 188.	4.0	117
24	Genomics of Methylotrophy in Gram-Positive Methylamine-Utilizing Bacteria. <i>Microorganisms</i> , 2015, 3, 94-112.	3.6	19
25	C1-Pathways in <i>Methylobacterium extorquens</i> FAM5: Genome Wide Gene Expression and Mutagenesis Studies. <i>Microorganisms</i> , 2015, 3, 175-197.	3.6	14
26	Monitoring the dynamics of syntrophic H_2 -oxidizing bacteria during anaerobic degradation of oleic acid by quantitative PCR. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	2.7	41
27	Ethylmalonyl Coenzyme A Mutase Operates as a Metabolic Control Point in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2015, 197, 727-735.	2.2	15
28	Genetic Tools for the Industrially Promising Methanotroph <i>Methylobacterium buryatense</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 1775-1781.	3.1	144
29	Systems Biology Tools for Methylotrophs. <i>Springer Protocols</i> , 2015, , 97-118.	0.3	4
30	Methane-fed microbial microcosms show differential community dynamics and pinpoint taxa involved in communal response. <i>ISME Journal</i> , 2015, 9, 1119-1129.	9.8	118
31	Oxygen availability is a major factor in determining the composition of microbial communities involved in methane oxidation. <i>PeerJ</i> , 2015, 3, e801.	2.0	104
32	The Expanded Diversity of Methylophilaceae from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. <i>PLoS ONE</i> , 2014, 9, e102458.	2.5	62
33	Dynameomics: Data-driven methods and models for utilizing large-scale protein structure repositories for improving fragment-based loop prediction. <i>Protein Science</i> , 2014, 23, 1584-1595.	7.6	8
34	Membrane protein complex of APS reductase and Qmo is present in <i>Desulfovibrio vulgaris</i> and <i>Desulfovibrio alaskensis</i> . <i>Microbiology (United Kingdom)</i> , 2013, 159, 2162-2168.	1.8	14
35	Draft Genome Sequence of <i>Methylobacterium buryatense</i> Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. <i>Genome Announcements</i> , 2013, 1, .	0.8	36
36	Promiscuous contacts and heightened dynamics increase thermostability in an engineered variant of the engrailed homeodomain. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 35-45.	2.1	11

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37	Comparative transcriptomics in three <i>Methylophilaceae</i> species uncover different strategies for environmental adaptation. PeerJ, 2013, 1, e115.	2.0	20
38	A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the <i>Methylococcaceae</i> and the <i>Methylophilaceae</i> . PeerJ, 2013, 1, e23.	2.0	139
39	Deep Sequencing of <i>Porphyromonas gingivalis</i> and Comparative Transcriptome Analysis of a LuxS Mutant. Frontiers in Cellular and Infection Microbiology, 2012, 2, 79.	3.9	27
40	Novel methylophilic isolates from lake sediment, description of <i>Methylotenera versatilis</i> sp. nov. and emended description of the genus <i>Methylotenera</i> . International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 106-111.	1.7	89
41	Genetic Systems for Moderately Halo(alkali)philic Bacteria of the Genus <i>Methylomicrobium</i> . Methods in Enzymology, 2011, 495, 99-118.	1.0	51
42	Implementation of 3D spatial indexing and compression in a large-scale molecular dynamics simulation database for rapid atomic contact detection. BMC Bioinformatics, 2011, 12, 334.	2.6	4
43	Genomes of Three Methylophilic Bacteria from a Single Niche Reveal the Genetic and Metabolic Divergence of the <i>Methylophilaceae</i> . Journal of Bacteriology, 2011, 193, 3757-3764.	2.2	66
44	An Integrated Proteomics/Transcriptomics Approach Points to Oxygen as the Main Electron Sink for Methanol Metabolism in <i>Methylotenera mobilis</i> . Journal of Bacteriology, 2011, 193, 4758-4765.	2.2	22
45	Dynameomics: A Comprehensive Database of Protein Dynamics. Structure, 2010, 18, 423-435.	3.3	131
46	Functioning <i>in situ</i> : gene expression in <i>Methylotenera mobilis</i> in its native environment as assessed through transcriptomics. ISME Journal, 2010, 4, 388-398.	9.8	38
47	A consensus view of fold space: Combining SCOP, CATH, and the Dali Domain Dictionary. Protein Science, 2009, 12, 2150-2160.	7.6	121
48	Microscopic Reversibility of Protein Folding in Molecular Dynamics Simulations of the Engrailed Homeodomain. Biochemistry, 2008, 47, 7079-7089.	2.5	55
49	Dynameomics: mass annotation of protein dynamics and unfolding in water by high-throughput atomistic molecular dynamics simulations. Protein Engineering, Design and Selection, 2008, 21, 353-368.	2.1	60
50	The intrinsic conformational propensities of the 20 naturally occurring amino acids and reflection of these propensities in proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12259-12264.	7.1	120
51	A One-Dimensional Reaction Coordinate for Identification of Transition States from Explicit Solvent Pfold-Like Calculations. Biophysical Journal, 2007, 93, 3382-3391.	0.5	25
52	Cutoff Size Need Not Strongly Influence Molecular Dynamics Results for Solvated Polypeptides. Biochemistry, 2005, 44, 609-616.	2.5	140
53	Methods for molecular dynamics simulations of protein folding/unfolding in solution. Methods, 2004, 34, 112-120.	3.8	184