David A C Beck

List of Publications by Year
in descending order

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	Methods for molecular dynamics simulations of protein folding/unfolding in solution. Methods, 2004, 34, 112-120.	3.8	184
2	Lanthanide-dependent cross-feeding of methane-derived carbon is linked by microbial community interactions. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 358-363.	7.1	156
3	Genetic Tools for the Industrially Promising Methanotroph Methylomicrobium buryatense. Applied and Environmental Microbiology, 2015, 81, 1775-1781.	3.1	144
4	Cutoff Size Need Not Strongly Influence Molecular Dynamics Results for Solvated Polypeptides. Biochemistry, 2005, 44, 609-616.	2.5	140
5	A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the *Methylococcaceae* and the *Methylophilaceae*. PeerJ, 2013, 1, e23.	2.0	139
6	Dynameomics: A Comprehensive Database of Protein Dynamics. Structure, 2010, 18, 423-435.	3.3	131
7	A consensus view of fold space: Combining SCOP, CATH, and the Dali Domain Dictionary. Protein Science, 2009, 12, 2150-2160.	7.6	121
8	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
9	Methane-fed microbial microcosms show differential community dynamics and pinpoint taxa involved in communal response. ISME Journal, 2015, 9, 1119-1129.	9.8	118
10	Genome-scale metabolic reconstructions and theoretical investigation of methane conversion in Methylomicrobium buryatense strain 5G(B1). Microbial Cell Factories, 2015, 14, 188.	4.0	117
11	Microbial community adaptation influences long-chain fatty acid conversion during anaerobic codigestion of fats, oils, and grease with municipal sludge. Water Research, 2016, 103, 372-382.	11.3	105
12	Oxygen availability is a major factor in determining the composition of microbial communities involved in methane oxidation. PeerJ, 2015, 3, e801.	2.0	104
13	Metabolic crosstalk regulates Porphyromonas gingivalis colonization and virulence during oral polymicrobial infection. Nature Microbiology, 2017, 2, 1493-1499.	13.3	100
14	Novel methylotrophic isolates from lake sediment, description of Methylotenera versatilis sp. nov. and emended description of the genus Methylotenera. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 106-111.	1.7	89
15	DNA-SIP based genome-centric metagenomics identifies key long-chain fatty acid-degrading populations in anaerobic digesters with different feeding frequencies. ISME Journal, 2018, 12, 112-123.	9.8	88
16	Long-chain fatty acid feeding frequency in anaerobic codigestion impacts syntrophic community structure and biokinetics. Water Research, 2017, 117, 218-229.	11.3	81
17	Oxygen-limited metabolism in the methanotroph *Methylomicrobium buryatense* 5GB1C. PeerJ, 2017, 5, e3945.	2.0	81
18	Mosaic plasmids are abundant and unevenly distributed across prokaryotic taxa. Plasmid, 2019, 102, 10-18.	1.4	70

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19	Genomes of Three Methylotrophs from a Single Niche Reveal the Genetic and Metabolic Divergence of the Methylophilaceae. Journal of Bacteriology, 2011, 193, 3757-3764.	2.2	66
20	Data science: Accelerating innovation and discovery in chemical engineering. AICHE Journal, 2016, 62, 1402-1416.	3.6	63
21	The Expanded Diversity of Methylophilaceae from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. PLoS ONE, 2014, 9, e102458.	2.5	62
22	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
23	MxaY regulates the lanthanide-mediated methanol dehydrogenase switch in *Methylomicrobium buryatense*. PeerJ, 2016, 4, e2435.	2.0	59
24	Microscopic Reversibility of Protein Folding in Molecular Dynamics Simulations of the Engrailed Homeodomain. Biochemistry, 2008, 47, 7079-7089.	2.5	55
25	Genetic Systems for Moderately Halo(alkali)philic Bacteria of the Genus Methylomicrobium. Methods in Enzymology, 2011, 495, 99-118.	1.0	51
26	Natural Selection in Synthetic Communities Highlights the Roles of Methylococcaceae and Methylophilaceae and Suggests Differential Roles for Alternative Methanol Dehydrogenases in Methane Consumption. Frontiers in Microbiology, 2017, 8, 2392.	3.5	51
27	Comprehensive molecular characterization of Methylobacterium extorquens AM1 adapted for 1-butanol tolerance. Biotechnology for Biofuels, 2016, 9, 84.	6.2	42
28	Monitoring the dynamics of syntrophic β-oxidizing bacteria during anaerobic degradation of oleic acid by quantitative PCR. FEMS Microbiology Ecology, 2015, 91, .	2.7	41
29	Water-Accelerated Photooxidation of $CH_3NH_3PbI_3$ Perovskite. Journal of the American Chemical Society, 2022, 144, 5552-5561.	13.7	40
30	Functioning *in situ*: gene expression in *Methylotenera mobilis* in its native environment as assessed through transcriptomics. ISME Journal, 2010, 4, 388-398.	9.8	38
31	Multiphyletic origins of methylotrophy in *A*lphaproteobacteria, exemplified by comparative genomics of *L*ake *W*ashington isolates. Environmental Microbiology, 2015, 17, 547-554.	3.8	38
32	Draft Genome Sequence of Methylomicrobium buryatense Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. Genome Announcements, 2013, 1, .	0.8	36
33	Attention-based generative models for *de novo* molecular design. Chemical Science, 2021, 12, 8362-8372.	7.4	34
34	Core Metabolism Shifts during Growth on Methanol versus Methane in the Methanotroph *Methylomicrobium buryatense* 5GB1. MBio, 2019, 10, .	4.1	31
35	Quorum Sensing in a Methane-Oxidizing Bacterium. Journal of Bacteriology, 2017, 199, .	2.2	29
36	Deep Sequencing of Porphyromonas gingivalis and Comparative Transcriptome Analysis of a LuxS Mutant. Frontiers in Cellular and Infection Microbiology, 2012, 2, 79.	3.9	27

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37	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
38	A Synthetic Ecology Perspective: How Well Does Behavior of Model Organisms in the Laboratory Predict Microbial Activities in Natural Habitats?. Frontiers in Microbiology, 2016, 7, 946.	3.5	25
39	An Integrated Proteomics/Transcriptomics Approach Points to Oxygen as the Main Electron Sink for Methanol Metabolism in Methylotenera mobilis. Journal of Bacteriology, 2011, 193, 4758-4765.	2.2	22
40	Comparative transcriptomics in three <i>Methylophilaceae</i> species uncover different strategies for environmental adaptation. PeerJ, 2013, 1, e115.	2.0	20
41	Genomics of Methylotrophy in Gram-Positive Methylamine-Utilizing Bacteria. Microorganisms, 2015, 3, 94-112.	3.6	19
42	Ethylmalonyl Coenzyme A Mutase Operates as a Metabolic Control Point in Methylobacterium extorquens AM1. Journal of Bacteriology, 2015, 197, 727-735.	2.2	15
43	A Computational Framework for Identifying Promoter Sequences in Nonmodel Organisms Using RNA-seq Data Sets. ACS Synthetic Biology, 2021, 10, 1394-1405.	3.8	15
44	Membrane protein complex of APS reductase and Qmo is present in Desulfovibrio vulgaris and Desulfovibrio alaskensis. Microbiology (United Kingdom), 2013, 159, 2162-2168.	1.8	14
45	C1-Pathways in Methyloversatilis universalis FAM5: Genome Wide Gene Expression and Mutagenesis Studies. Microorganisms, 2015, 3, 175-197.	3.6	14
46	Continuous Molecular Representations of Ionic Liquids. Journal of Physical Chemistry B, 2020, 124, 8347-8357.	2.6	12
47	Promiscuous contacts and heightened dynamics increase thermostability in an engineered variant of the engrailed homeodomain. Protein Engineering, Design and Selection, 2013, 26, 35-45.	2.1	11
48	Difference in C3â€"C4 metabolism underlies tradeoff between growth rate and biomass yield in Methylobacterium extorquens AM1. BMC Microbiology, 2016, 16, 156.	3.3	10
49	Data Science in Chemical Engineering: Applications to Molecular Science. Annual Review of Chemical and Biomolecular Engineering, 2021, 12, 15-37.	6.8	9
50	Dynameomics: Dataâ€driven methods and models for utilizing largeâ€scale protein structure repositories for improving fragmentâ€based loop prediction. Protein Science, 2014, 23, 1584-1595.	7.6	8
51	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
52	Systems Biology Tools for Methylotrophs. Springer Protocols, 2015, , 97-118.	0.3	4
53	An automated multiplexed turbidometric and data collection system for measuring growth kinetics of anaerobes dependent on gaseous substrates. Journal of Microbiological Methods, 2021, 188, 106294.	1.6	1