

James U Bowie

List of Publications by Year in descending order

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123
papers

12,184
citations

32410

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107
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all docs

124
docs citations

124
times ranked

14156
citing authors

#	ARTICLE	IF	CITATIONS
1	How physical forces drive the process of helical membrane protein folding. <i>EMBO Reports</i> , 2022, 23, e53025.	2.0	13
2	Expanding the use of ethanol as a feedstock for cell-free synthetic biochemistry by implementing acetyl-CoA and ATP generating pathways. <i>Scientific Reports</i> , 2022, 12, 7700.	1.6	6
3	Crystal structure of mevalonate 3,5-bisphosphate decarboxylase reveals insight into the evolution of decarboxylases in the mevalonate metabolic pathways. <i>Journal of Biological Chemistry</i> , 2022, 298, 102111.	1.6	3
4	Cell-free synthetic biochemistry upgrading of ethanol to 1,3 butanediol. <i>Scientific Reports</i> , 2021, 11, 9449.	1.6	5
5	How bilayer properties influence membrane protein folding. <i>Protein Science</i> , 2020, 29, 2348-2362.	3.1	25
6	A bio-inspired cell-free system for cannabinoid production from inexpensive inputs. <i>Nature Chemical Biology</i> , 2020, 16, 1427-1433.	3.9	32
7	Isobutanol production freed from biological limits using synthetic biochemistry. <i>Nature Communications</i> , 2020, 11, 4292.	5.8	46
8	Synthetic Biochemistry: The Bio-inspired Cell-Free Approach to Commodity Chemical Production. <i>Trends in Biotechnology</i> , 2020, 38, 766-778.	4.9	92
9	A cell-free platform for the prenylation of natural products and application to cannabinoid production. <i>Nature Communications</i> , 2019, 10, 565.	5.8	82
10	Watching helical membrane proteins fold reveals a common N-to-C-terminal folding pathway. <i>Science</i> , 2019, 366, 1150-1156.	6.0	59
11	Accurate computational design of multipass transmembrane proteins. <i>Science</i> , 2018, 359, 1042-1046.	6.0	149
12	Crystal Structure of Bicc1 SAM Polymer and Mapping of Interactions between the Ciliopathy-Associated Proteins Bicc1, ANKS3, and ANKS6. <i>Structure</i> , 2018, 26, 209-224.e6.	1.6	18
13	Unfolding of a ClC chloride transporter retains memory of its evolutionary history. <i>Nature Chemical Biology</i> , 2018, 14, 489-496.	3.9	39
14	Applications of Single-Molecule Methods to Membrane Protein Folding Studies. <i>Journal of Molecular Biology</i> , 2018, 430, 424-437.	2.0	30
15	Complete topology inversion can be part of normal membrane protein biogenesis. <i>Protein Science</i> , 2017, 26, 824-833.	3.1	27
16	A synthetic biochemistry platform for cell free production of monoterpenes from glucose. <i>Nature Communications</i> , 2017, 8, 15526.	5.8	169
17	Backbone Hydrogen Bond Strengths Can Vary Widely in Transmembrane Helices. <i>Journal of the American Chemical Society</i> , 2017, 139, 10742-10749.	6.6	36
18	A molecular rheostat maintains ATP levels to drive a synthetic biochemistry system. <i>Nature Chemical Biology</i> , 2017, 13, 938-942.	3.9	58

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19	A simple DNA handle attachment method for single molecule mechanical manipulation experiments. <i>Protein Science</i> , 2016, 25, 1535-1544.	3.1	39
20	An Adaptation To Life In Acid Through A Novel Mevalonate Pathway. <i>Scientific Reports</i> , 2016, 6, 39737.	1.6	29
21	Production of FAME biodiesel in <i>E. coli</i> by direct methylation with an insect enzyme. <i>Scientific Reports</i> , 2016, 6, 24239.	1.6	31
22	A synthetic biochemistry module for production of bio-based chemicals from glucose. <i>Nature Chemical Biology</i> , 2016, 12, 393-395.	3.9	113
23	Molecular dynamics simulation strategies for protein-micelle complexes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 1566-1572.	1.4	19
24	Exome sequencing and CRISPR/Cas genome editing identify mutations of <i>ZAK</i> as a cause of limb defects in humans and mice. <i>Genome Research</i> , 2016, 26, 183-191.	2.4	52
25	Metazoans evolved by taking domains from soluble proteins to expand intercellular communication network. <i>Scientific Reports</i> , 2015, 5, 9576.	1.6	8
26	Mapping the energy landscape for second-stage folding of a single membrane protein. <i>Nature Chemical Biology</i> , 2015, 11, 981-987.	3.9	78
27	Dual-topology insertion of a dual-topology membrane protein. <i>Nature Communications</i> , 2015, 6, 8099.	5.8	46
28	Structural analysis of mevalonate-3-kinase provides insight into the mechanisms of isoprenoid pathway decarboxylases. <i>Protein Science</i> , 2015, 24, 212-220.	3.1	16
29	Bacteriorhodopsin Folds through a Poorly Organized Transition State. <i>Journal of the American Chemical Society</i> , 2014, 136, 16574-16581.	6.6	28
30	An energetic scale for equilibrium H/D fractionation factors illuminates hydrogen bond free energies in proteins. <i>Protein Science</i> , 2014, 23, 566-575.	3.1	19
31	Characterization of the SAM domain of the PKD-related protein ANKS6 and its interaction with ANKS3. <i>BMC Structural Biology</i> , 2014, 14, 17.	2.3	37
32	A synthetic biochemistry system for the <i>in vitro</i> production of isoprene from glycolysis intermediates. <i>Protein Science</i> , 2014, 23, 576-585.	3.1	61
33	Measuring membrane protein stability under native conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 219-224.	3.3	58
34	Evidence of a Novel Mevalonate Pathway in Archaea. <i>Biochemistry</i> , 2014, 53, 4161-4168.	1.2	46
35	Improving the tolerance of <i>Escherichia coli</i> to medium-chain fatty acid production. <i>Metabolic Engineering</i> , 2014, 25, 1-7.	3.6	67
36	A synthetic biochemistry molecular purge valve module that maintains redox balance. <i>Nature Communications</i> , 2014, 5, 4113.	5.8	93

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37	Dieselzymes: development of a stable and methanol tolerant lipase for biodiesel production by directed evolution. <i>Biotechnology for Biofuels</i> , 2013, 6, 70.	6.2	107
38	Measuring Transmembrane Helix Interaction Strengths in Lipid Bilayers Using Steric Trapping. <i>Methods in Molecular Biology</i> , 2013, 1063, 37-56.	0.4	20
39	Membrane Proteins Can Have High Kinetic Stability. <i>Journal of the American Chemical Society</i> , 2013, 135, 15183-15190.	6.6	42
40	Rampant Exchange of the Structure and Function of Extramembrane Domains between Membrane and Water Soluble Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1002997.	1.5	9
41	Membrane Protein Twists and Turns. <i>Science</i> , 2013, 339, 398-399.	6.0	32
42	Structural differences between thermophilic and mesophilic membrane proteins. <i>Protein Science</i> , 2012, 21, 1746-1753.	3.1	45
43	Shifting hydrogen bonds may produce flexible transmembrane helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8121-8126.	3.3	64
44	Thermodynamic stability of bacteriorhodopsin mutants measured relative to the bacterioopsin unfolded state. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1049-1054.	1.4	18
45	Crystal Structure of <i>Proteus mirabilis</i> Lipase, a Novel Lipase from the <i>Proteus</i> /Psychrophilic Subfamily of Lipase Family I.1. <i>PLoS ONE</i> , 2012, 7, e52890.	1.1	22
46	Revisiting the folding kinetics of bacteriorhodopsin. <i>Protein Science</i> , 2012, 21, 97-106.	3.1	33
47	Crystal Structure of the Central Coiled-Coil Domain from Human Liprin- $\hat{2}$. <i>Biochemistry</i> , 2011, 50, 3807-3815.	1.2	5
48	Dramatic Destabilization of Transmembrane Helix Interactions by Features of Natural Membrane Environments. <i>Journal of the American Chemical Society</i> , 2011, 133, 11389-11398.	6.6	85
49	Probing Membrane Protein Unfolding with Pulse Proteolysis. <i>Journal of Molecular Biology</i> , 2011, 406, 545-551.	2.0	31
50	Crystallizing membrane proteins using lipidic bicelles. <i>Methods</i> , 2011, 55, 337-341.	1.9	112
51	Tandem SAM Domain Structure of Human Caskin1: A Presynaptic, Self-Assembling Scaffold for CASK. <i>Structure</i> , 2011, 19, 1826-1836.	1.6	28
52	Membrane protein folding: how important are hydrogen bonds?. <i>Current Opinion in Structural Biology</i> , 2011, 21, 42-49.	2.6	151
53	TMKink: A method to predict transmembrane helix kinks. <i>Protein Science</i> , 2011, 20, 1256-1264.	3.1	37
54	A human sterile alpha motif domain polymerizome. <i>Protein Science</i> , 2011, 20, 1697-1706.	3.1	77

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55	Regulation of clathrin adaptor function in endocytosis: novel role for the SAM domain. <i>EMBO Journal</i> , 2010, 29, 1033-1044.	3.5	38
56	Method to measure strong protein-protein interactions in lipid bilayers using a steric trap. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19802-19807.	3.3	92
57	Zinc Binding Drives Sheet Formation by the SAM Domain of Diacylglycerol Kinase β . <i>Biochemistry</i> , 2010, 49, 9667-9676.	1.2	22
58	Structural imperatives impose diverse evolutionary constraints on helical membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17747-17750.	3.3	59
59	Chapter 5 Practical Aspects of Membrane Proteins Crystallization in Bicelles. <i>Current Topics in Membranes</i> , 2009, 63, 109-125.	0.5	12
60	Identifying polymer-forming SAM domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 1-5.	1.5	42
61	G-protein-coupled receptor structures were not built in a day. <i>Protein Science</i> , 2009, 18, 1335-1342.	3.1	27
62	Genetic selection system for improving recombinant membrane protein expression in <i>E. coli</i> . <i>Protein Science</i> , 2009, 18, 372-383.	3.1	55
63	Chapter 8 Methods for Measuring the Thermodynamic Stability of Membrane Proteins. <i>Methods in Enzymology</i> , 2009, 455, 213-236.	0.4	68
64	Protein Unfolding with a Steric Trap. <i>Journal of the American Chemical Society</i> , 2009, 131, 13914-13915.	6.6	24
65	Similar Energetic Contributions of Packing in the Core of Membrane and Water-Soluble Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 10846-10847.	6.6	67
66	Modest stabilization by most hydrogen-bonded side-chain interactions in membrane proteins. <i>Nature</i> , 2008, 453, 1266-1270.	13.7	238
67	Dimerization of the transmembrane domain of amyloid precursor proteins and familial Alzheimer's disease mutants. <i>BMC Neuroscience</i> , 2008, 9, 17.	0.8	73
68	Regulation of Enzyme Localization by Polymerization: Polymer Formation by the SAM Domain of Diacylglycerol Kinase β . <i>Structure</i> , 2008, 16, 380-387.	1.6	56
69	Point Mutations in Membrane Proteins Reshape Energy Landscape and Populate Different Unfolding Pathways. <i>Journal of Molecular Biology</i> , 2008, 376, 1076-1090.	2.0	52
70	HotPatch: A Statistical Approach to Finding Biologically Relevant Features on Protein Surfaces. <i>Journal of Molecular Biology</i> , 2007, 369, 863-879.	2.0	73
71	Transmembrane Domain of Myelin Protein Zero Can Form Dimers: Possible Implications for Myelin Construction. <i>Biochemistry</i> , 2007, 46, 12164-12173.	1.2	36
72	Polymer-driven crystallization. <i>Protein Science</i> , 2007, 16, 2542-2551.	3.1	34

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73	Flip-flopping membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 94-96.	3.6	31
74	Mae inhibits Pointed-P2 transcriptional activity by blocking its MAPK docking site. <i>EMBO Journal</i> , 2006, 25, 70-79.	3.5	35
75	A limited universe of membrane protein families and folds. <i>Protein Science</i> , 2006, 15, 1723-1734.	3.1	77
76	A role for zinc in postsynaptic density assembly and plasticity?. <i>Trends in Biochemical Sciences</i> , 2006, 31, 366-373.	3.7	91
77	An Architectural Framework That May Lie at the Core of the Postsynaptic Density. <i>Science</i> , 2006, 311, 531-535.	6.0	261
78	Refolding the integral membrane protein bacteriorhodopsin. <i>FASEB Journal</i> , 2006, 20, .	0.2	1
79	Pivotal role of the glycine-rich TM3 helix in gating the MscS mechanosensitive channel. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 113-119.	3.6	125
80	Solving the membrane protein folding problem. <i>Nature</i> , 2005, 438, 581-589.	13.7	397
81	Transmembrane glycine zippers: Physiological and pathological roles in membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14278-14283.	3.3	240
82	Structural Organization of a Sex-comb-on-midleg/Polyhomeotic Copolymer. <i>Journal of Biological Chemistry</i> , 2005, 280, 27769-27775.	1.6	77
83	Transmembrane Domain Helix Packing Stabilizes Integrin β 3 in the Low Affinity State. <i>Journal of Biological Chemistry</i> , 2005, 280, 7294-7300.	1.6	131
84	The Many Faces of SAM. <i>Science Signaling</i> , 2005, 2005, re7-re7.	1.6	246
85	Crystallization of bacteriorhodopsin from bicelle formulations at room temperature. <i>Protein Science</i> , 2005, 14, 836-840.	3.1	85
86	Membrane proteins: A new method enters the fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3995-3996.	3.3	31
87	Membrane channel structure of <i>Helicobacter pylori</i> vacuolating toxin: Role of multiple GXXXG motifs in cylindrical channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5988-5991.	3.3	77
88	The Affinity of GXXXG Motifs in Transmembrane Helix-Helix Interactions Is Modulated by Long-range Communication. <i>Journal of Biological Chemistry</i> , 2004, 279, 16591-16597.	1.6	103
89	A C-H \cdots H \cdots O Hydrogen Bond in a Membrane Protein Is Not Stabilizing. <i>Journal of the American Chemical Society</i> , 2004, 126, 2284-2285.	6.6	78
90	Asymmetric amino acid compositions of transmembrane β -strands. <i>Protein Science</i> , 2004, 13, 2270-2274.	3.1	19

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91	A Model of the Closed Form of the Nicotinic Acetylcholine Receptor M2 Channel Pore. <i>Biophysical Journal</i> , 2004, 87, 792-799.	0.2	20
92	Analysis of Side-Chain Rotamers in Transmembrane Proteins. <i>Biophysical Journal</i> , 2004, 87, 3460-3469.	0.2	49
93	Derepression by Depolymerization. <i>Cell</i> , 2004, 118, 163-173.	13.5	89
94	Side-chain Contributions to Membrane Protein Structure and Stability. <i>Journal of Molecular Biology</i> , 2004, 335, 297-305.	2.0	190
95	Snorkeling Preferences Foster an Amino Acid Composition Bias in Transmembrane Helices. <i>Journal of Molecular Biology</i> , 2004, 339, 471-479.	2.0	74
96	Proline Substitutions are not Easily Accommodated in a Membrane Protein. <i>Journal of Molecular Biology</i> , 2004, 341, 1-6.	2.0	70
97	SAM Domains Can Utilize Similar Surfaces for the Formation of Polymers and Closed Oligomers. <i>Journal of Molecular Biology</i> , 2004, 342, 1353-1358.	2.0	23
98	The evolution of transmembrane helix kinks and the structural diversity of G protein-coupled receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 959-963.	3.3	203
99	SAM domains: uniform structure, diversity of function. <i>Trends in Biochemical Sciences</i> , 2003, 28, 625-628.	3.7	240
100	A Simple Method for Modeling Transmembrane Helix Oligomers. <i>Journal of Molecular Biology</i> , 2003, 329, 831-840.	2.0	73
101	Construction of helix-bundle membrane proteins. <i>Advances in Protein Chemistry</i> , 2003, 63, 19-46.	4.4	39
102	Oligomerization-dependent Association of the SAM Domains from <i>Schizosaccharomyces pombe</i> Byr2 and Ste4. <i>Journal of Biological Chemistry</i> , 2002, 277, 39585-39593.	1.6	41
103	Bicelle crystallization: a new method for crystallizing membrane proteins yields a monomeric bacteriorhodopsin structure. <i>Journal of Molecular Biology</i> , 2002, 316, 1-6.	2.0	311
104	Evaluation of C α -H \cdots O Hydrogen Bonds in Native and Misfolded Proteins. <i>Journal of Molecular Biology</i> , 2002, 322, 497-503.	2.0	24
105	Native interface of the SAM domain polymer of TEL. <i>BMC Structural Biology</i> , 2002, 2, 5.	2.3	35
106	The SAM domain of polyhomeotic forms a helical polymer. <i>Nature Structural Biology</i> , 2002, 9, 453-7.	9.7	131
107	Inactivation mechanism of the membrane protein diacylglycerol kinase in detergent solution. <i>Protein Science</i> , 2001, 10, 378-383.	3.1	40
108	Stabilizing membrane proteins. <i>Current Opinion in Structural Biology</i> , 2001, 11, 397-402.	2.6	232

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109	Understanding membrane protein structure by design. , 2000, 7, 91-94.		35
110	Membrane proteins Are we destined to repeat history?. Current Opinion in Structural Biology, 2000, 10, 435-437.	2.6	24
111	Building a Thermostable Membrane Protein. Journal of Biological Chemistry, 2000, 275, 6975-6979.	1.6	129
112	p53 Family members p63 and p73 are SAM domain-containing proteins. Protein Science, 1999, 8, 1708-1710.	3.1	136
113	Oligomeric Structure of the Human EphB2 Receptor SAM Domain. Science, 1999, 283, 833-836.	6.0	222
114	Active Sites of Diacylglycerol Kinase from Escherichia coli Are Shared between Subunits. Biochemistry, 1999, 38, 5521-5527.	1.2	52
115	Changing single side-chains can greatly enhance the resistance of a membrane protein to irreversible inactivation. Journal of Molecular Biology, 1999, 290, 559-564.	2.0	58
116	Helix bundle membrane protein fold templates. Protein Science, 1999, 8, 2711-2719.	3.1	39
117	A Method for Assessing the Stability of a Membrane Protein. Biochemistry, 1997, 36, 5884-5892.	1.2	239
118	Helix packing in membrane proteins. Journal of Molecular Biology, 1997, 272, 780-789.	2.0	311
119	Helix packing angle preferences. Nature Structural and Molecular Biology, 1997, 4, 915-917.	3.6	76
120	A passive transmembrane helix. Nature Structural Biology, 1997, 4, 986-990.	9.7	23
121	Assigning amino acid sequences to 3-dimensional protein folds. FASEB Journal, 1996, 10, 126-136.	0.2	101
122	Inverted protein structure prediction. Current Opinion in Structural Biology, 1993, 3, 437-444.	2.6	73
123	Assessment of protein models with three-dimensional profiles. Nature, 1992, 356, 83-85.	13.7	2,958