

James U Bowie

List of Publications by Year in descending order

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123
papers

12,184
citations

28274

55
h-index

26613

107
g-index

124
all docs

124
docs citations

124
times ranked

12536
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessment of protein models with three-dimensional profiles. <i>Nature</i> , 1992, 356, 83-85.	27.8	2,958
2	Solving the membrane protein folding problem. <i>Nature</i> , 2005, 438, 581-589.	27.8	397
3	Helix packing in membrane proteins. <i>Journal of Molecular Biology</i> , 1997, 272, 780-789.	4.2	311
4	Bicelle crystallization: a new method for crystallizing membrane proteins yields a monomeric bacteriorhodopsin structure. <i>Journal of Molecular Biology</i> , 2002, 316, 1-6.	4.2	311
5	An Architectural Framework That May Lie at the Core of the Postsynaptic Density. <i>Science</i> , 2006, 311, 531-535.	12.6	261
6	The Many Faces of SAM. <i>Science Signaling</i> , 2005, 2005, re7-re7.	3.6	246
7	SAM domains: uniform structure, diversity of function. <i>Trends in Biochemical Sciences</i> , 2003, 28, 625-628.	7.5	240
8	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.	7.1	240
9	A Method for Assessing the Stability of a Membrane Protein. <i>Biochemistry</i> , 1997, 36, 5884-5892.	2.5	239
10	Modest stabilization by most hydrogen-bonded side-chain interactions in membrane proteins. <i>Nature</i> , 2008, 453, 1266-1270.	27.8	238
11	Stabilizing membrane proteins. <i>Current Opinion in Structural Biology</i> , 2001, 11, 397-402.	5.7	232
12	Oligomeric Structure of the Human EphB2 Receptor SAM Domain. <i>Science</i> , 1999, 283, 833-836.	12.6	222
13	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.	7.1	203
14	Side-chain Contributions to Membrane Protein Structure and Stability. <i>Journal of Molecular Biology</i> , 2004, 335, 297-305.	4.2	190
15	A synthetic biochemistry platform for cell free production of monoterpenes from glucose. <i>Nature Communications</i> , 2017, 8, 15526.	12.8	169
16	Membrane protein folding: how important are hydrogen bonds?. <i>Current Opinion in Structural Biology</i> , 2011, 21, 42-49.	5.7	151
17	Accurate computational design of multipass transmembrane proteins. <i>Science</i> , 2018, 359, 1042-1046.	12.6	149
18	p53 Family members p63 and p73 are SAM domain-containing proteins. <i>Protein Science</i> , 1999, 8, 1708-1710.	7.6	136

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19	Transmembrane Domain Helix Packing Stabilizes Integrin $\alpha 5 \beta 1$ in the Low Affinity State. <i>Journal of Biological Chemistry</i> , 2005, 280, 7294-7300.	3.4	131
20	The SAM domain of polyhomeotic forms a helical polymer. <i>Nature Structural Biology</i> , 2002, 9, 453-7.	9.7	131
21	Building a Thermostable Membrane Protein. <i>Journal of Biological Chemistry</i> , 2000, 275, 6975-6979.	3.4	129
22	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.	8.2	125
23	A synthetic biochemistry module for production of bio-based chemicals from glucose. <i>Nature Chemical Biology</i> , 2016, 12, 393-395.	8.0	113
24	Crystallizing membrane proteins using lipidic bicelles. <i>Methods</i> , 2011, 55, 337-341.	3.8	112
25	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
26	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.	3.4	103
27	Assigning amino acid sequences to 3-dimensional protein folds. <i>FASEB Journal</i> , 1996, 10, 126-136.	0.5	101
28	A synthetic biochemistry molecular purge valve module that maintains redox balance. <i>Nature Communications</i> , 2014, 5, 4113.	12.8	93
29	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.	7.1	92
30	Synthetic Biochemistry: The Bio-inspired Cell-Free Approach to Commodity Chemical Production. <i>Trends in Biotechnology</i> , 2020, 38, 766-778.	9.3	92
31	A role for zinc in postsynaptic density assembly and plasticity?. <i>Trends in Biochemical Sciences</i> , 2006, 31, 366-373.	7.5	91
32	Derepression by Depolymerization. <i>Cell</i> , 2004, 118, 163-173.	28.9	89
33	Crystallization of bacteriorhodopsin from bicelle formulations at room temperature. <i>Protein Science</i> , 2005, 14, 836-840.	7.6	85
34	Dramatic Destabilization of Transmembrane Helix Interactions by Features of Natural Membrane Environments. <i>Journal of the American Chemical Society</i> , 2011, 133, 11389-11398.	13.7	85
35	A cell-free platform for the prenylation of natural products and application to cannabinoid production. <i>Nature Communications</i> , 2019, 10, 565.	12.8	82
36	A C-H...O Hydrogen Bond in a Membrane Protein Is Not Stabilizing. <i>Journal of the American Chemical Society</i> , 2004, 126, 2284-2285.	13.7	78

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37	Mapping the energy landscape for second-stage folding of a single membrane protein. <i>Nature Chemical Biology</i> , 2015, 11, 981-987.	8.0	78
38	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.	7.1	77
39	Structural Organization of a Sex-comb-on-midleg/Polyhomeotic Copolymer. <i>Journal of Biological Chemistry</i> , 2005, 280, 27769-27775.	3.4	77
40	A limited universe of membrane protein families and folds. <i>Protein Science</i> , 2006, 15, 1723-1734.	7.6	77
41	A human sterile alpha motif domain polymerizome. <i>Protein Science</i> , 2011, 20, 1697-1706.	7.6	77
42	Helix packing angle preferences. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 915-917.	8.2	76
43	Snorkeling Preferences Foster an Amino Acid Composition Bias in Transmembrane Helices. <i>Journal of Molecular Biology</i> , 2004, 339, 471-479.	4.2	74
44	Inverted protein structure prediction. <i>Current Opinion in Structural Biology</i> , 1993, 3, 437-444.	5.7	73
45	A Simple Method for Modeling Transmembrane Helix Oligomers. <i>Journal of Molecular Biology</i> , 2003, 329, 831-840.	4.2	73
46	HotPatch: A Statistical Approach to Finding Biologically Relevant Features on Protein Surfaces. <i>Journal of Molecular Biology</i> , 2007, 369, 863-879.	4.2	73
47	Dimerization of the transmembrane domain of amyloid precursor proteins and familial Alzheimer's disease mutants. <i>BMC Neuroscience</i> , 2008, 9, 17.	1.9	73
48	Proline Substitutions are not Easily Accommodated in a Membrane Protein. <i>Journal of Molecular Biology</i> , 2004, 341, 1-6.	4.2	70
49	Chapter 8 Methods for Measuring the Thermodynamic Stability of Membrane Proteins. <i>Methods in Enzymology</i> , 2009, 455, 213-236.	1.0	68
50	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.	13.7	67
51	Improving the tolerance of <i>Escherichia coli</i> to medium-chain fatty acid production. <i>Metabolic Engineering</i> , 2014, 25, 1-7.	7.0	67
52	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.	7.1	64
53	A synthetic biochemistry system for the <i>in vitro</i> production of isoprene from glycolysis intermediates. <i>Protein Science</i> , 2014, 23, 576-585.	7.6	61
54	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.	7.1	59

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55	Watching helical membrane proteins fold reveals a common N-to-C-terminal folding pathway. <i>Science</i> , 2019, 366, 1150-1156.	12.6	59
56	Changing single side-chains can greatly enhance the resistance of a membrane protein to irreversible inactivation. <i>Journal of Molecular Biology</i> , 1999, 290, 559-564.	4.2	58
57	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.	7.1	58
58	A molecular rheostat maintains ATP levels to drive a synthetic biochemistry system. <i>Nature Chemical Biology</i> , 2017, 13, 938-942.	8.0	58
59	Regulation of Enzyme Localization by Polymerization: Polymer Formation by the SAM Domain of Diacylglycerol Kinase 1. <i>Structure</i> , 2008, 16, 380-387.	3.3	56
60	Genetic selection system for improving recombinant membrane protein expression in <i>E. coli</i> . <i>Protein Science</i> , 2009, 18, 372-383.	7.6	55
61	Active Sites of Diacylglycerol Kinase from <i>Escherichia coli</i> Are Shared between Subunits. <i>Biochemistry</i> , 1999, 38, 5521-5527.	2.5	52
62	Point Mutations in Membrane Proteins Reshape Energy Landscape and Populate Different Unfolding Pathways. <i>Journal of Molecular Biology</i> , 2008, 376, 1076-1090.	4.2	52
63	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.	5.5	52
64	Analysis of Side-Chain Rotamers in Transmembrane Proteins. <i>Biophysical Journal</i> , 2004, 87, 3460-3469.	0.5	49
65	Evidence of a Novel Mevalonate Pathway in Archaea. <i>Biochemistry</i> , 2014, 53, 4161-4168.	2.5	46
66	Dual-topology insertion of a dual-topology membrane protein. <i>Nature Communications</i> , 2015, 6, 8099.	12.8	46
67	Isobutanol production freed from biological limits using synthetic biochemistry. <i>Nature Communications</i> , 2020, 11, 4292.	12.8	46
68	Structural differences between thermophilic and mesophilic membrane proteins. <i>Protein Science</i> , 2012, 21, 1746-1753.	7.6	45
69	Identifying polymer-forming SAM domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 1-5.	2.6	42
70	Membrane Proteins Can Have High Kinetic Stability. <i>Journal of the American Chemical Society</i> , 2013, 135, 15183-15190.	18.7	42
71	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.	3.4	41
72	Inactivation mechanism of the membrane protein diacylglycerol kinase in detergent solution. <i>Protein Science</i> , 2001, 10, 378-383.	7.6	40

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73	Construction of helix-bundle membrane proteins. <i>Advances in Protein Chemistry</i> , 2003, 63, 19-46.	4.4	39
74	Helix-bundle membrane protein fold templates. <i>Protein Science</i> , 1999, 8, 2711-2719.	7.6	39
75	A simple DNA handle attachment method for single molecule mechanical manipulation experiments. <i>Protein Science</i> , 2016, 25, 1535-1544.	7.6	39
76	Unfolding of a ClC chloride transporter retains memory of its evolutionary history. <i>Nature Chemical Biology</i> , 2018, 14, 489-496.	8.0	39
77	Regulation of clathrin adaptor function in endocytosis: novel role for the SAM domain. <i>EMBO Journal</i> , 2010, 29, 1033-1044.	7.8	38
78	TMKink: A method to predict transmembrane helix kinks. <i>Protein Science</i> , 2011, 20, 1256-1264.	7.6	37
79	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
80	Transmembrane Domain of Myelin Protein Zero Can Form Dimers: Possible Implications for Myelin Construction. <i>Biochemistry</i> , 2007, 46, 12164-12173.	2.5	36
81	Backbone Hydrogen Bond Strengths Can Vary Widely in Transmembrane Helices. <i>Journal of the American Chemical Society</i> , 2017, 139, 10742-10749.	13.7	36
82	Understanding membrane protein structure by design. , 2000, 7, 91-94.		35
83	Native interface of the SAM domain polymer of TEL. <i>BMC Structural Biology</i> , 2002, 2, 5.	2.3	35
84	Mae inhibits Pointed-P2 transcriptional activity by blocking its MAPK docking site. <i>EMBO Journal</i> , 2006, 25, 70-79.	7.8	35
85	Polymer-driven crystallization. <i>Protein Science</i> , 2007, 16, 2542-2551.	7.6	34
86	Revisiting the folding kinetics of bacteriorhodopsin. <i>Protein Science</i> , 2012, 21, 97-106.	7.6	33
87	Membrane Protein Twists and Turns. <i>Science</i> , 2013, 339, 398-399.	12.6	32
88	A bio-inspired cell-free system for cannabinoid production from inexpensive inputs. <i>Nature Chemical Biology</i> , 2020, 16, 1427-1433.	8.0	32
89	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.	7.1	31
90	Flip-flopping membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 94-96.	8.2	31

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91	Probing Membrane Protein Unfolding with Pulse Proteolysis. <i>Journal of Molecular Biology</i> , 2011, 406, 545-551.	4.2	31
92	Production of FAME biodiesel in <i>E. coli</i> by direct methylation with an insect enzyme. <i>Scientific Reports</i> , 2016, 6, 24239.	3.3	31
93	Applications of Single-Molecule Methods to Membrane Protein Folding Studies. <i>Journal of Molecular Biology</i> , 2018, 430, 424-437.	4.2	30
94	An Adaptation To Life In Acid Through A Novel Mevalonate Pathway. <i>Scientific Reports</i> , 2016, 6, 39737.	3.3	29
95	Tandem SAM Domain Structure of Human Caskin1: A Presynaptic, Self-Assembling Scaffold for CASK. <i>Structure</i> , 2011, 19, 1826-1836.	3.3	28
96	Bacteriorhodopsin Folds through a Poorly Organized Transition State. <i>Journal of the American Chemical Society</i> , 2014, 136, 16574-16581.	13.7	28
97	G α protein-coupled receptor structures were not built in a day. <i>Protein Science</i> , 2009, 18, 1335-1342.	7.6	27
98	Complete topology inversion can be part of normal membrane protein biogenesis. <i>Protein Science</i> , 2017, 26, 824-833.	7.6	27
99	How bilayer properties influence membrane protein folding. <i>Protein Science</i> , 2020, 29, 2348-2362.	7.6	25
100	Membrane proteins Are we destined to repeat history?. <i>Current Opinion in Structural Biology</i> , 2000, 10, 435-437.	5.7	24
101	Evaluation of C-H \cdots O Hydrogen Bonds in Native and Misfolded Proteins. <i>Journal of Molecular Biology</i> , 2002, 322, 497-503.	4.2	24
102	Protein Unfolding with a Steric Trap. <i>Journal of the American Chemical Society</i> , 2009, 131, 13914-13915.	13.7	24
103	A passive transmembrane helix. <i>Nature Structural Biology</i> , 1997, 4, 986-990.	9.7	23
104	SAM Domains Can Utilize Similar Surfaces for the Formation of Polymers and Closed Oligomers. <i>Journal of Molecular Biology</i> , 2004, 342, 1353-1358.	4.2	23
105	Zinc Binding Drives Sheet Formation by the SAM Domain of Diacylglycerol Kinase β . <i>Biochemistry</i> , 2010, 49, 9667-9676.	2.5	22
106	Crystal Structure of <i>Proteus mirabilis</i> Lipase, a Novel Lipase from the Proteus/Psychrophilic Subfamily of Lipase Family I.1. <i>PLoS ONE</i> , 2012, 7, e52890.	2.5	22
107	A Model of the Closed Form of the Nicotinic Acetylcholine Receptor M2 Channel Pore. <i>Biophysical Journal</i> , 2004, 87, 792-799.	0.5	20
108	Measuring Transmembrane Helix Interaction Strengths in Lipid Bilayers Using Steric Trapping. <i>Methods in Molecular Biology</i> , 2013, 1063, 37-56.	0.9	20

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109	Asymmetric amino acid compositions of transmembrane β^2 -strands. <i>Protein Science</i> , 2004, 13, 2270-2274.	7.6	19
110	An energetic scale for equilibrium H/D fractionation factors illuminates hydrogen bond free energies in proteins. <i>Protein Science</i> , 2014, 23, 566-575.	7.6	19
111	Molecular dynamics simulation strategies for protein-micelle complexes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 1566-1572.	2.6	19
112	Thermodynamic stability of bacteriorhodopsin mutants measured relative to the bacterioopsin unfolded state. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1049-1054.	2.6	18
113	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.	3.3	18
114	Structural analysis of mevalonate-3-kinase provides insight into the mechanisms of isoprenoid pathway decarboxylases. <i>Protein Science</i> , 2015, 24, 212-220.	7.6	16
115	How physical forces drive the process of helical membrane protein folding. <i>EMBO Reports</i> , 2022, 23, e53025.	4.5	13
116	Chapter 5 Practical Aspects of Membrane Proteins Crystallization in Bicelles. <i>Current Topics in Membranes</i> , 2009, 63, 109-125.	0.9	12
117	Rampant Exchange of the Structure and Function of Extramembrane Domains between Membrane and Water Soluble Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1002997.	3.2	9
118	Metazoans evolved by taking domains from soluble proteins to expand intercellular communication network. <i>Scientific Reports</i> , 2015, 5, 9576.	3.3	8
119	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.	3.3	6
120	Crystal Structure of the Central Coiled-Coil Domain from Human Liprin- β^2 . <i>Biochemistry</i> , 2011, 50, 3807-3815.	2.5	5
121	Cell-free synthetic biochemistry upgrading of ethanol to 1,3 butanediol. <i>Scientific Reports</i> , 2021, 11, 9449.	3.3	5
122	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.	3.4	3
123	Refolding the integral membrane protein bacteriorhodopsin. <i>FASEB Journal</i> , 2006, 20, .	0.5	1