James U Bowie

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8258160/publications.pdf

Version: 2024-02-01

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	How physical forces drive the process of helical membrane protein folding. EMBO Reports, 2022, 23, e53025.	4.5	13
2	Expanding the use of ethanol as a feedstock for cell-free synthetic biochemistry by implementing acetyl-CoA and ATP generating pathways. Scientific Reports, 2022, 12, 7700.	3.3	6
3	Crystal structure of mevalonate 3,5-bisphosphate decarboxylase reveals insight into the evolution of decarboxylases in the mevalonate metabolic pathways. Journal of Biological Chemistry, 2022, 298, 102111.	3.4	3
4	Cell-free synthetic biochemistry upgrading of ethanol to 1,3 butanediol. Scientific Reports, 2021, 11, 9449.	3.3	5
5	How bilayer properties influence membrane protein folding. Protein Science, 2020, 29, 2348-2362.	7.6	25
6	A bio-inspired cell-free system for cannabinoid production from inexpensive inputs. Nature Chemical Biology, 2020, 16, 1427-1433.	8.0	32
7	Isobutanol production freed from biological limits using synthetic biochemistry. Nature Communications, 2020, 11, 4292.	12.8	46
8	Synthetic Biochemistry: The Bio-inspired Cell-Free Approach to Commodity Chemical Production. Trends in Biotechnology, 2020, 38, 766-778.	9.3	92
9	A cell-free platform for the prenylation of natural products and application to cannabinoid production. Nature Communications, 2019, 10, 565.	12.8	82
10	Watching helical membrane proteins fold reveals a common N-to-C-terminal folding pathway. Science, 2019, 366, 1150-1156.	12.6	59
11	Accurate computational design of multipass transmembrane proteins. Science, 2018, 359, 1042-1046.	12.6	149
12	Crystal Structure of Bicc1 SAM Polymer and Mapping of Interactions between the Ciliopathy-Associated Proteins Bicc1, ANKS3, and ANKS6. Structure, 2018, 26, 209-224.e6.	3.3	18
13	Unfolding of a ClC chloride transporter retains memory of its evolutionary history. Nature Chemical Biology, 2018, 14, 489-496.	8.0	39
14	Applications of Single-Molecule Methods to Membrane Protein Folding Studies. Journal of Molecular Biology, 2018, 430, 424-437.	4.2	30
15	Complete topology inversion can be part of normal membrane protein biogenesis. Protein Science, 2017, 26, 824-833.	7.6	27
16	A synthetic biochemistry platform for cell free production of monoterpenes from glucose. Nature Communications, 2017, 8, 15526.	12.8	169
17	Backbone Hydrogen Bond Strengths Can Vary Widely in Transmembrane Helices. Journal of the American Chemical Society, 2017, 139, 10742-10749.	13.7	36
18	A molecular rheostat maintains ATP levels to drive a synthetic biochemistry system. Nature Chemical Biology, 2017, 13, 938-942.	8.0	58

#	ARTICLE	IF	CITATIONS
19	A simple DNA handle attachment method for single molecule mechanical manipulation experiments. Protein Science, 2016, 25, 1535-1544.	7.6	39
20	An Adaptation To Life In Acid Through A Novel Mevalonate Pathway. Scientific Reports, 2016, 6, 39737.	3.3	29
21	Production of FAME biodiesel in E. coli by direct methylation with an insect enzyme. Scientific Reports, 2016, 6, 24239.	3.3	31
22	A synthetic biochemistry module for production of bio-based chemicals from glucose. Nature Chemical Biology, 2016, 12, 393-395.	8.0	113
23	Molecular dynamics simulation strategies for proteinâ€"micelle complexes. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 1566-1572.	2.6	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. Genome Research, 2016, 26, 183-191.	5.5	52
25	Metazoans evolved by taking domains from soluble proteins to expand intercellular communication network. Scientific Reports, 2015, 5, 9576.	3.3	8
26	Mapping the energy landscape for second-stage folding of a single membrane protein. Nature Chemical Biology, 2015, 11, 981-987.	8.0	78
27	Dual-topology insertion of a dual-topology membrane protein. Nature Communications, 2015, 6, 8099.	12.8	46
28	Structural analysis of mevalonate-3-kinase provides insight into the mechanisms of isoprenoid pathway decarboxylases. Protein Science, 2015, 24, 212-220.	7.6	16
29	Bacteriorhodopsin Folds through a Poorly Organized Transition State. Journal of the American Chemical Society, 2014, 136, 16574-16581.	13.7	28
30	An energetic scale for equilibrium H/D fractionation factors illuminates hydrogen bond free energies in proteins. Protein Science, 2014, 23, 566-575.	7.6	19
31	Characterization of the SAM domain of the PKD-related protein ANKS6 and its interaction with ANKS3. BMC Structural Biology, 2014, 14, 17.	2.3	37
32	A synthetic biochemistry system for the <i>in vitro</i> production of isoprene from glycolysis intermediates. Protein Science, 2014, 23, 576-585.	7.6	61
33	Measuring membrane protein stability under native conditions. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 219-224.	7.1	58
34	Evidence of a Novel Mevalonate Pathway in Archaea. Biochemistry, 2014, 53, 4161-4168.	2.5	46
35	Improving the tolerance of Escherichia coli to medium-chain fatty acid production. Metabolic Engineering, 2014, 25, 1-7.	7.0	67
36	A synthetic biochemistry molecular purge valve module that maintains redox balance. Nature Communications, 2014, 5, 4113.	12.8	93

#	ARTICLE	IF	CITATIONS
37	Dieselzymes: development of a stable and methanol tolerant lipase for biodiesel production by directed evolution. Biotechnology for Biofuels, 2013, 6, 70.	6.2	107
38	Measuring Transmembrane Helix Interaction Strengths in Lipid Bilayers Using Steric Trapping. Methods in Molecular Biology, 2013, 1063, 37-56.	0.9	20
39	Membrane Proteins Can Have High Kinetic Stability. Journal of the American Chemical Society, 2013, 135, 15183-15190.	13.7	42
40	Rampant Exchange of the Structure and Function of Extramembrane Domains between Membrane and Water Soluble Proteins. PLoS Computational Biology, 2013, 9, e1002997.	3.2	9
41	Membrane Protein Twists and Turns. Science, 2013, 339, 398-399.	12.6	32
42	Structural differences between thermophilic and mesophilic membrane proteins. Protein Science, 2012, 21, 1746-1753.	7.6	45
43	Shifting hydrogen bonds may produce flexible transmembrane helices. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8121-8126.	7.1	64
44	Thermodynamic stability of bacteriorhodopsin mutants measured relative to the bacterioopsin unfolded state. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1049-1054.	2.6	18
45	Crystal Structure of Proteus mirabilis Lipase, a Novel Lipase from the Proteus/Psychrophilic Subfamily of Lipase Family I.1. PLoS ONE, 2012, 7, e52890.	2.5	22
46	Revisiting the folding kinetics of bacteriorhodopsin. Protein Science, 2012, 21, 97-106.	7.6	33
47	Crystal Structure of the Central Coiled-Coil Domain from Human Liprin-Î²2. Biochemistry, 2011, 50, 3807-3815.	2.5	5
48	Dramatic Destabilization of Transmembrane Helix Interactions by Features of Natural Membrane Environments. Journal of the American Chemical Society, 2011, 133, 11389-11398.	13.7	85
49	Probing Membrane Protein Unfolding with Pulse Proteolysis. Journal of Molecular Biology, 2011, 406, 545-551.	4.2	31
50	Crystallizing membrane proteins using lipidic bicelles. Methods, 2011, 55, 337-341.	3.8	112
51	Tandem SAM Domain Structure of Human Caskin1: A Presynaptic, Self-Assembling Scaffold for CASK. Structure, 2011, 19, 1826-1836.	3.3	28
52	Membrane protein folding: how important are hydrogen bonds?. Current Opinion in Structural Biology, 2011, 21, 42-49.	5.7	151
53	TMKink: A method to predict transmembrane helix kinks. Protein Science, 2011, 20, 1256-1264.	7.6	37
54	A human sterile alpha motif domain polymerizome. Protein Science, 2011, 20, 1697-1706.	7.6	77

#	Article	IF	Citations
55	Regulation of clathrin adaptor function in endocytosis: novel role for the SAM domain. EMBO Journal, 2010, 29, 1033-1044.	7.8	38
56	Method to measure strong proteinâ€"protein interactions in lipid bilayers using a steric trap. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19802-19807.	7.1	92
57	Zinc Binding Drives Sheet Formation by the SAM Domain of Diacylglycerol Kinase Î´. Biochemistry, 2010, 49, 9667-9676.	2.5	22
58	Structural imperatives impose diverse evolutionary constraints on helical membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17747-17750.	7.1	59
59	Chapter 5 Practical Aspects of Membrane Proteins Crystallization in Bicelles. Current Topics in Membranes, 2009, 63, 109-125.	0.9	12
60	Identifying polymerâ€forming SAM domains. Proteins: Structure, Function and Bioinformatics, 2009, 74, 1-5.	2.6	42
61	Gâ€proteinâ€coupled receptor structures were not built in a day. Protein Science, 2009, 18, 1335-1342.	7.6	27
62	Genetic selection system for improving recombinant membrane protein expression in <i>E. coli</i>. Protein Science, 2009, 18, 372-383.	7.6	55
63	Chapter 8 Methods for Measuring the Thermodynamic Stability of Membrane Proteins. Methods in Enzymology, 2009, 455, 213-236.	1.0	68
64	Protein Unfolding with a Steric Trap. Journal of the American Chemical Society, 2009, 131, 13914-13915.	13.7	24
65	Similar Energetic Contributions of Packing in the Core of Membrane and Water-Soluble Proteins. Journal of the American Chemical Society, 2009, 131, 10846-10847.	13.7	67
66	Modest stabilization by most hydrogen-bonded side-chain interactions in membrane proteins. Nature, 2008, 453, 1266-1270.	27.8	238
67	Dimerization of the transmembrane domain of amyloid precursor proteins and familial Alzheimer's disease mutants. BMC Neuroscience, 2008, 9, 17.	1.9	73
68	Regulation of Enzyme Localization by Polymerization: Polymer Formation by the SAM Domain of Diacylglycerol Kinase Î´1. Structure, 2008, 16, 380-387.	3.3	56
69	Point Mutations in Membrane Proteins Reshape Energy Landscape and Populate Different Unfolding Pathways. Journal of Molecular Biology, 2008, 376, 1076-1090.	4.2	52
70	HotPatch: A Statistical A pproach to Finding Biologically Relevant Features on Protein Surfaces. Journal of Molecular Biology, 2007, 369, 863-879.	4.2	73
71	Transmembrane Domain of Myelin Protein Zero Can Form Dimers:â€‰ Possible Implications for Myelin Construction. Biochemistry, 2007, 46, 12164-12173.	2.5	36
72	Polymerâ€driven crystallization. Protein Science, 2007, 16, 2542-2551.	7.6	34

#	ARTICLE	IF	CITATIONS
73	Flip-flopping membrane proteins. Nature Structural and Molecular Biology, 2006, 13, 94-96.	8.2	31
74	Mae inhibits Pointed-P2 transcriptional activity by blocking its MAPK docking site. EMBO Journal, 2006, 25, 70-79.	7.8	35
75	A limited universe of membrane protein families and folds. Protein Science, 2006, 15, 1723-1734.	7.6	77
76	A role for zinc in postsynaptic density asSAMbly and plasticity?. Trends in Biochemical Sciences, 2006, 31, 366-373.	7.5	91
77	An Architectural Framework That May Lie at the Core of the Postsynaptic Density. Science, 2006, 311, 531-535.	12.6	261
78	Refolding the integral membrane protein bacteriorhodopsin. FASEB Journal, 2006, 20, .	0.5	1
79	Pivotal role of the glycine-rich TM3 helix in gating the MscS mechanosensitive channel. Nature Structural and Molecular Biology, 2005, 12, 113-119.	8.2	125
80	Solving the membrane protein folding problem. Nature, 2005, 438, 581-589.	27.8	397
81	Transmembrane glycine zippers: Physiological and pathological roles in membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14278-14283.	7.1	240
82	Structural Organization of a Sex-comb-on-midleg/Polyhomeotic Copolymer. Journal of Biological Chemistry, 2005, 280, 27769-27775.	3.4	77
83	Transmembrane Domain Helix Packing Stabilizes Integrin Î±IIbÎ²3 in the Low Affinity State. Journal of Biological Chemistry, 2005, 280, 7294-7300.	3.4	131
84	The Many Faces of SAM. Science Signaling, 2005, 2005, re7-re7.	3.6	246
85	Crystallization of bacteriorhodopsin from bicelle formulations at room temperature. Protein Science, 2005, 14, 836-840.	7.6	85
86	Membrane proteins: A new method enters the fold. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3995-3996.	7.1	31
87	Membrane channel structure of Helicobacter pylori vacuolating toxin: Role of multiple GXXXG motifs in cylindrical channels. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5988-5991.	7.1	77
88	The Affinity of GXXXG Motifs in Transmembrane Helix-Helix Interactions Is Modulated by Long-range Communication. Journal of Biological Chemistry, 2004, 279, 16591-16597.	3.4	103
89	A CÎ±âˆ’HÂ·Â·Â·O Hydrogen Bond in a Membrane Protein Is Not Stabilizing. Journal of the American Chemical Society, 2004, 126, 2284-2285.	13.7	78
90	Asymmetric amino acid compositions of transmembrane Î²-strands. Protein Science, 2004, 13, 2270-2274.	7.6	19

#	ARTICLE	IF	CITATIONS
91	A Model of the Closed Form of the Nicotinic Acetylcholine Receptor M2 Channel Pore. Biophysical Journal, 2004, 87, 792-799.	0.5	20
92	Analysis of Side-Chain Rotamers in Transmembrane Proteins. Biophysical Journal, 2004, 87, 3460-3469.	0.5	49
93	Derepression by Depolymerization. Cell, 2004, 118, 163-173.	28.9	89
94	Side-chain Contributions to Membrane Protein Structure and Stability. Journal of Molecular Biology, 2004, 335, 297-305.	4.2	190
95	Snorkeling Preferences Foster an Amino Acid Composition Bias in Transmembrane Helices. Journal of Molecular Biology, 2004, 339, 471-479.	4.2	74
96	Proline Substitutions are not Easily Accommodated in a Membrane Protein. Journal of Molecular Biology, 2004, 341, 1-6.	4.2	70
97	SAM Domains Can Utilize Similar Surfaces for the Formation of Polymers and Closed Oligomers. Journal of Molecular Biology, 2004, 342, 1353-1358.	4.2	23
98	The evolution of transmembrane helix kinks and the structural diversity of G protein-coupled receptors. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 959-963.	7.1	203
99	SAM domains: uniform structure, diversity of function. Trends in Biochemical Sciences, 2003, 28, 625-628.	7.5	240
100	A Simple Method for Modeling Transmembrane Helix Oligomers. Journal of Molecular Biology, 2003, 329, 831-840.	4.2	73
101	Construction of helix-bundle membrane proteins. Advances in Protein Chemistry, 2003, 63, 19-46.	4.4	39
102	Oligomerization-dependent Association of the SAM Domains from Schizosaccharomyces pombe Byr2 and Ste4. Journal of Biological Chemistry, 2002, 277, 39585-39593.	3.4	41
103	Bicelle crystallization: a new method for crystallizing membrane proteins yields a monomeric bacteriorhodopsin structure. Journal of Molecular Biology, 2002, 316, 1-6.	4.2	311
104	Evaluation of Câ€“Hâ‹¯O Hydrogen Bonds in Native and Misfolded Proteins. Journal of Molecular Biology, 2002, 322, 497-503.	4.2	24
105	Native interface of the SAM domain polymer of TEL. BMC Structural Biology, 2002, 2, 5.	2.3	35
106	The SAM domain of polyhomeotic forms a helical polymer. Nature Structural Biology, 2002, 9, 453-7.	9.7	131
107	Inactivation mechanism of the membrane protein diacylglycerol kinase in detergent solution. Protein Science, 2001, 10, 378-383.	7.6	40
108	Stabilizing membrane proteins. Current Opinion in Structural Biology, 2001, 11, 397-402.	5.7	232

#	Article	IF	Citations
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.	5.7	24
111	Building a Thermostable Membrane Protein. Journal of Biological Chemistry, 2000, 275, 6975-6979.	3.4	129
112	p53 Family members p63 and p73 are SAM domainâ€containing proteins. Protein Science, 1999, 8, 1708-1710.	7.6	136
113	Oligomeric Structure of the Human EphB2 Receptor SAM Domain. Science, 1999, 283, 833-836.	12.6	222
114	Active Sites of Diacylglycerol Kinase fromEscherichia coliAre Shared between Subunitsâ€. Biochemistry, 1999, 38, 5521-5527.	2.5	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.	4.2	58
116	Helixâ€bundle membrane protein fold templates. Protein Science, 1999, 8, 2711-2719.	7.6	39
117	A Method for Assessing the Stability of a Membrane Proteinâ€. Biochemistry, 1997, 36, 5884-5892.	2.5	239
118	Helix packing in membrane proteins. Journal of Molecular Biology, 1997, 272, 780-789.	4.2	311
119	Helix packing angle preferences. Nature Structural and Molecular Biology, 1997, 4, 915-917.	8.2	76
120	A passive transmembrane helix. Nature Structural Biology, 1997, 4, 986-990.	9.7	23
121	Assigning amino acid sequences to 3â€dimensional protein folds. FASEB Journal, 1996, 10, 126-136.	0.5	101
122	Inverted protein structure prediction. Current Opinion in Structural Biology, 1993, 3, 437-444.	5.7	73
123	Assessment of protein models with three-dimensional profiles. Nature, 1992, 356, 83-85.	27.8	2,958