

Jeremy R H Tame

List of Publications by Year in descending order

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86
papers

3,660
citations

109321

35
h-index

144013

57
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91
all docs

91
docs citations

91
times ranked

3593
citing authors

#	ARTICLE	IF	CITATIONS
1	Hemoglobin allostery and pharmacology. <i>Molecular Aspects of Medicine</i> , 2022, 84, 101037.	6.4	10
2	Reverse Engineering Analysis of the High-Temperature Reversible Oligomerization and Amyloidogenicity of PSD95-PDZ3. <i>Molecules</i> , 2022, 27, 2813.	3.8	2
3	Structural insights into the HBV receptor and bile acid transporter NTCP. <i>Nature</i> , 2022, 606, 1027-1031.	27.8	44
4	Structural plasticity of a designer protein sheds light on \hat{I}^2 propeller protein evolution. <i>FEBS Journal</i> , 2021, 288, 530-545.	4.7	13
5	Early-stage dynamics of chloride ion pumping rhodopsin revealed by a femtosecond X-ray laser. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	41
6	The symmetric designer protein Pizza as a scaffold for metal coordination. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 945-951.	2.6	3
7	Biophysical reviews meet the editor series™ Jeremy R. H. Tame. <i>Biophysical Reviews</i> , 2021, 13, 295-301.	3.2	3
8	The Taming of the Screw: the natural and artificial development of $\langle \text{mml:math} \text{xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.svg"} \rangle \langle \text{mml:mi} \rangle^2 \langle \text{mml:mi} \rangle \langle \text{mml:math} \rangle$ -propeller proteins. <i>Current Opinion in Structural Biology</i> , 2021, 68, 48-54.	5.7	6
9	Crystal structures of Scone: pseudosymmetric folding of a symmetric designer protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 933-942.	2.3	2
10	Shape and Size Complementarity-Induced Formation of Supramolecular Protein Assemblies with Metal-Oxo Clusters. <i>Crystal Growth and Design</i> , 2021, 21, 1307-1313.	3.0	15
11	A GM1b/asialo-GM1 oligosaccharide binding R-type lectin from purplish bifurcate mussels <i>Mytilisepta virgata</i> and its effect on MAP kinases. <i>FEBS Journal</i> , 2020, 287, 2612-2630.	4.7	9
12	Influence of circular permutations on the structure and stability of a six-fold circular symmetric designer protein. <i>Protein Science</i> , 2020, 29, 2375-2386.	7.6	12
13	Hybrid assemblies of a symmetric designer protein and polyoxometalates with matching symmetry. <i>Chemical Communications</i> , 2020, 56, 11601-11604.	4.1	20
14	Molecular assemblies built with the artificial protein Pizza. <i>Journal of Structural Biology: X</i> , 2020, 4, 100027.	1.3	10
15	Editorial for the Special Issue of <i>Biophysical Reviews</i> focused on the Biophysical Society of Japan with select scientific content from the 57th BSJ annual meeting, Miyazaki, Japan. <i>Biophysical Reviews</i> , 2020, 12, 183-185.	3.2	11
16	Pumping mechanism of NM-R3, a light-driven bacterial chloride importer in the rhodopsin family. <i>Science Advances</i> , 2020, 6, eaay2042.	10.3	7
17	Development and applications of artificial symmetrical proteins. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3959-3968.	4.1	6
18	The structure of SeviL, a GM1b/asialo-GM1 binding R-type lectin from the mussel <i>Mytilisepta virgata</i> . <i>Scientific Reports</i> , 2020, 10, 22102.	3.3	4

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19	Computational design of symmetrical eight-bladed \hat{I}^2 -propeller proteins. <i>IUCr</i> , 2019, 6, 46-55.	2.2	33
20	Design of tryptophan-containing mutants of the symmetrical Pizza protein for biophysical studies. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 1038-1042.	2.1	5
21	The crystal structure and oligomeric form of <i>Escherichia coli</i> I, d -carboxypeptidase A. <i>Biochemical and Biophysical Research Communications</i> , 2018, 499, 594-599.	2.1	6
22	Molecular basis of hemoglobin adaptation in the high-flying bar-headed goose. <i>PLoS Genetics</i> , 2018, 14, e1007331.	3.5	58
23	Protein-templated synthesis of metal-based nanomaterials. <i>Current Opinion in Biotechnology</i> , 2017, 46, 14-19.	6.6	27
24	Evolution-Inspired Computational Design of Symmetric Proteins. <i>Methods in Molecular Biology</i> , 2017, 1529, 309-322.	0.9	12
25	Seeing the light with BLUF proteins. <i>Biophysical Reviews</i> , 2017, 9, 169-176.	3.2	44
26	Direct observation of conformational population shifts in crystalline human hemoglobin. <i>Journal of Biological Chemistry</i> , 2017, 292, 18258-18269.	3.4	9
27	Computational design of a symmetrical \hat{I}^2 -trefoil lectin with cancer cell binding activity. <i>Scientific Reports</i> , 2017, 7, 5943.	3.3	35
28	Molecular mechanism of photoactivation of a light-regulated adenylate cyclase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8562-8567.	7.1	36
29	Crystal structure of MytiLec, a galactose-binding lectin from the mussel <i>Mytilus galloprovincialis</i> with cytotoxicity against certain cancer cell types. <i>Scientific Reports</i> , 2016, 6, 28344.	3.3	39
30	Structural insight into photoactivation of an adenylate cyclase from a photosynthetic cyanobacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6659-6664.	7.1	69
31	The crystal and solution structure of YdiE from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 919-924.	0.8	1
32	Biom mineralization of a Cadmium Chloride Nanocrystal by a Designed Symmetrical Protein. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 9857-9860.	13.8	36
33	Capturing the Hemoglobin Allosteric Transition in a Single Crystal Form. <i>Journal of the American Chemical Society</i> , 2014, 136, 5097-5105.	13.7	43
34	Computational design of a self-assembling symmetrical \hat{I}^2 -propeller protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15102-15107.	7.1	122
35	Protein nanotubes, channels and cages. <i>Amino Acids, Peptides and Proteins</i> , 2012, , 151-189.	0.7	4
36	Structures of haemoglobin from woolly mammoth in liganded and unliganded states. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1441-1449.	2.5	8

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37	Crystal Structures of Penicillin-Binding Protein 3 (PBP3) from Methicillin-Resistant <i>Staphylococcus aureus</i> in the Apo and Cefotaxime-Bound Forms. <i>Journal of Molecular Biology</i> , 2012, 423, 351-364.	4.2	48
38	Influence of Structural Symmetry on Protein Dynamics. <i>PLoS ONE</i> , 2012, 7, e50011.	2.5	14
39	4000 Holes. <i>Journal of Molecular Biology</i> , 2011, 412, 551-552.	4.2	0
40	Crystal structure of unliganded TRAP: implications for dynamic allostery. <i>Biochemical Journal</i> , 2011, 434, 427-434.	3.7	15
41	Autotransporter protein secretion. <i>Biomolecular Concepts</i> , 2011, 2, 525-536.	2.2	5
42	A Conserved Aromatic Residue in the Autochaperone Domain of the Autotransporter Hbp Is Critical for Initiation of Outer Membrane Translocation. <i>Journal of Biological Chemistry</i> , 2010, 285, 38224-38233.	3.4	56
43	A Novel Intein-Like Autoproteolytic Mechanism in Autotransporter Proteins. <i>Journal of Molecular Biology</i> , 2010, 402, 645-656.	4.2	67
44	The nature of the TRAP-Anti-TRAP complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2176-2181.	7.1	27
45	A Self-Assembled Protein Nanotube with High Aspect Ratio. <i>Small</i> , 2009, 5, 2077-2084.	10.0	73
46	RNA and Protein Complexes of trp RNA-Binding Attenuation Protein Characterized by Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 2218-2226.	6.5	13
47	Intersubunit linker length as a modifier of protein stability: Crystal structures and thermostability of mutant TRAP. <i>Protein Science</i> , 2008, 17, 518-526.	7.6	9
48	Structure and Mechanism of HpcG, a Hydratase in the Homoprotocatechuate Degradation Pathway of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2007, 370, 899-911.	4.2	17
49	Dynamic Allostery in the Ring Protein TRAP. <i>Journal of Molecular Biology</i> , 2007, 371, 154-167.	4.2	24
50	Using the Ring-Shaped Protein TRAP to Capture and Confine Gold Nanodots on a Surface.. <i>Small</i> , 2007, 3, 1950-1956.	10.0	36
51	Limited tolerance towards folded elements during secretion of the autotransporter Hbp. <i>Molecular Microbiology</i> , 2007, 63, 1524-1536.	2.5	105
52	Crystal Structure of Penicillin Binding Protein 4 (dacB) from <i>Escherichia coli</i> , both in the Native Form and Covalently Linked to Various Antibiotics. <i>Biochemistry</i> , 2006, 45, 783-792.	2.5	84
53	R-state Haemoglobin with Low Oxygen Affinity: Crystal Structures of Deoxy Human and Carbonmonoxy Horse Haemoglobin Bound to the Effector Molecule L35. <i>Journal of Molecular Biology</i> , 2006, 356, 790-801.	4.2	40
54	1.25Å Resolution Crystal Structures of Human Haemoglobin in the Oxy, Deoxy and Carbonmonoxy Forms. <i>Journal of Molecular Biology</i> , 2006, 360, 690-701.	4.2	261

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55	Expression, purification and crystallization of 2-oxo-hept-4-ene-1,7-dioate hydratase (HpcG) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1010-1012.	0.7	2
56	Rounding up: Engineering 12-Membered Rings from the Cyclic 11-Mer TRAP. <i>Structure</i> , 2006, 14, 925-933.	3.3	37
57	Scoring Functions – the First 100 Years. <i>Journal of Computer-Aided Molecular Design</i> , 2005, 19, 445-451.	2.9	28
58	Crystal Structure of Hemoglobin Protease, a Heme Binding Autotransporter Protein from Pathogenic <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 17339-17345.	3.4	156
59	Novel Mechanisms of pH Sensitivity in Tuna Hemoglobin. <i>Journal of Biological Chemistry</i> , 2004, 279, 28632-28640.	3.4	65
60	Crystal Structures of Unliganded and Half-Liganded Human Hemoglobin Derivatives Cross-Linked between Lys 82 ²¹ and Lys 82 ²² . <i>Biochemistry</i> , 2004, 43, 8711-8717.	2.5	8
61	Crystal Structures of the Liganded and Unliganded Nickel-binding Protein NikA from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 50322-50329.	3.4	77
62	Crystal Structures of Deoxy- and Carbonmonoxyhemoglobin F1 from the Hagfish <i>Eptatretus burgeri</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 21898-21905.	3.4	9
63	Crystal Structure of Horse Carbonmonoxyhemoglobin-Bezafibrate Complex at 1.55-Å... Resolution. <i>Journal of Biological Chemistry</i> , 2002, 277, 38791-38796.	3.4	48
64	The Crystal Structure of HpcE, a Bifunctional Decarboxylase/Isomerase with a Multifunctional Fold. <i>Biochemistry</i> , 2002, 41, 2982-2989.	2.5	26
65	The functional similarity and structural diversity of human and cartilaginous fish hemoglobins. <i>Journal of Molecular Biology</i> , 2001, 307, 259-270.	4.2	46
66	The structures of deoxy human haemoglobin and the mutant Hb Tyr ⁴² His at 120 Å...K. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 805-811.	2.5	75
67	Title is missing!. <i>Journal of Computer - Aided Molecular Design</i> , 2000, 20, 29-42.	1.0	3
68	Generating consistent sets of thermodynamic and structural data for analysis of protein-ligand interactions. , 2000, , 29-42.		3
69	Scoring functions: a view from the bench. , 1999, 13, 99-108.		98
70	Relating structure to thermodynamics: The crystal structures and binding affinity of eight OppA-peptide complexes. <i>Protein Science</i> , 1999, 8, 1432-1444.	7.6	70
71	What is the true structure of liganded haemoglobin?. <i>Trends in Biochemical Sciences</i> , 1999, 24, 372-377.	7.5	41
72	Peptide Binding in OppA, the Crystal Structures of the Periplasmic Oligopeptide Binding Protein in the Unliganded Form and in Complex with Lysyllysine. <i>Biochemistry</i> , 1997, 36, 9747-9758.	2.5	99

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73	The Crystal Structure of a High Oxygen Affinity Species of Haemoglobin (Bar-headed Goose) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	4.2	107
74	Crystal Structure of T State Haemoglobin with Oxygen Bound At All Four Haems. Journal of Molecular Biology, 1996, 256, 775-792.	4.2	168
75	The Crystal Structures of Trout Hb I in the Deoxy and Carbonmonoxy Forms. Journal of Molecular Biology, 1996, 259, 749-760.	4.2	55
76	The role of water in sequence-independent ligand binding by an oligopeptide transporter protein. Nature Structural Biology, 1996, 3, 998-1001.	9.7	119
77	A Hemoglobin-Based Blood Substitute: Transplanting a Novel Allosteric Effect of Crocodile Hb. Biological Chemistry Hoppe-Seyler, 1996, 377, 543-554.	1.4	8
78	The crystal structures of the oligopeptide-binding protein OppA complexed with tripeptide and tetrapeptide ligands. Structure, 1995, 3, 1395-1406.	3.3	91
79	Transplanting a unique allosteric effect from crocodile into human haemoglobin. Nature, 1995, 373, 244-246.	27.8	87
80	[22] Production of human hemoglobin in Escherichia coli using cleavable fusion protein expression vector. Methods in Enzymology, 1994, 231, 347-364.	1.0	18
81	Protein engineering in haemoglobin. Nature, 1992, 355, 777-778.	27.8	0
82	Functional role of the distal valine (E11) residue of $\hat{1}\pm$ subunits in human haemoglobin. Journal of Molecular Biology, 1991, 218, 761-767.	4.2	52
83	Site-directed mutagenesis in haemoglobin. Journal of Molecular Biology, 1991, 218, 769-778.	4.2	52
84	Was the loss of the D helix in $\hat{1}\pm$ globin a functionally neutral mutation?. Nature, 1991, 352, 349-351.	27.8	50
85	Effect of the distal residues on the vibrational modes of the iron-carbon monoxide bond in hemoglobin studied by protein engineering. Biochemistry, 1990, 29, 5562-5566.	2.5	28
86	The role of the distal histidine in myoglobin and haemoglobin. Nature, 1988, 336, 265-266.	27.8	264