

Michael N G James

List of Publications by Year in descending order

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67
papers

5,089
citations

136950

32
h-index

114465

63
g-index

68
all docs

68
docs citations

68
times ranked

5972
citing authors

#	ARTICLE	IF	CITATIONS
1	Treatment and prevention strategies for the COVID 19 pandemic: A review of immunotherapeutic approaches for neutralizing SARS-CoV-2. <i>International Journal of Biological Macromolecules</i> , 2021, 186, 490-500.	7.5	28
2	Transition of the prion protein from a structured cellular form (PrP ^C) to the infectious scrapie agent (PrP ^{Sc}). <i>Protein Science</i> , 2019, 28, 2055-2063.	7.6	30
3	Structural characterization of POM 6 Fab and mouse prion protein complex identifies key regions for prions conformational conversion. <i>FEBS Journal</i> , 2018, 285, 1701-1714.	4.7	6
4	The Ubiquitination of PINK1 Is Restricted to Its Mature 52-kDa Form. <i>Cell Reports</i> , 2017, 20, 30-39.	6.4	40
5	X-ray structural and molecular dynamical studies of the globular domains of cow, deer, elk and Syrian hamster prion proteins. <i>Journal of Structural Biology</i> , 2015, 192, 37-47.	2.8	19
6	Structural Basis of Prion Inhibition by Phenothiazine Compounds. <i>Structure</i> , 2014, 22, 291-303.	3.3	63
7	The Crystal Structure of Shiga Toxin Type 2 with Bound Disaccharide Guides the Design of a Heterobifunctional Toxin Inhibitor. <i>Journal of Biological Chemistry</i> , 2014, 289, 885-894.	3.4	23
8	The toxicity of anti-prion antibodies is mediated by the flexible tail of the prion protein. <i>Nature</i> , 2013, 501, 102-106.	27.8	191
9	The crystal structure of an octapeptide repeat of the Prion protein in complex with a Fab fragment of the POM2 antibody. <i>Protein Science</i> , 2013, 22, 893-903.	7.6	8
10	Insights into mucopolysaccharidosis I from the structure and action of β -L-iduronidase. <i>Nature Chemical Biology</i> , 2013, 9, 739-745.	8.0	48
11	Molecular mechanisms underlying the interaction of protein phosphatase-1c with ASPP proteins. <i>Biochemical Journal</i> , 2013, 449, 649-659.	3.7	27
12	Phosphorylation Status of 72 kDa MMP-2 Determines Its Structure and Activity in Response to Peroxynitrite. <i>PLoS ONE</i> , 2013, 8, e71794.	2.5	35
13	Structure-activity characterization of sulfide:quinone oxidoreductase variants. <i>Journal of Structural Biology</i> , 2012, 178, 319-328.	2.8	32
14	Structural studies on the folded domain of the human prion protein bound to the Fab fragment of the antibody POM1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1501-1512.	2.5	26
15	Expression, purification, crystallization and preliminary crystallographic analysis of the phosphoglycerate kinase from <i>Acinetobacter baumannii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 790-792.	0.7	0
16	Crystal Structure of β -Hexosaminidase B in Complex with Pyrimethamine, a Potential Pharmacological Chaperone. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 1421-1429.	6.4	46
17	Structural insights for the substrate recognition mechanism of LL-diaminopimelate aminotransferase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1528-1533.	2.3	10
18	The Structure of β -Diaminopimelate Aminotransferase from <i>Chlamydia trachomatis</i> : Implications for Its Broad Substrate Specificity. <i>Journal of Molecular Biology</i> , 2011, 411, 649-660.	4.2	14

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19	The Structures of <i>Thermoplasma volcanium</i> Phosphoribosyl Pyrophosphate Synthetase Bound to Ribose-5-Phosphate and ATP Analogs. <i>Journal of Molecular Biology</i> , 2011, 413, 844-856.	4.2	21
20	Expression, purification and preliminary crystallographic analysis of O-acetylhomoserine sulfhydrylase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 959-963.	0.7	4
21	Expression, purification and preliminary crystallographic analysis of Rv3002c, the regulatory subunit of acetolactate synthase (IlvH) from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 933-936.	0.7	2
22	Crystallization and preliminary X-ray diffraction analysis of prion protein bound to the Fab fragment of the POM1 antibody. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1211-1213.	0.7	9
23	Expression, purification and preliminary crystallographic analysis of Rv2247, the \hat{I}^2 subunit of acyl-CoA carboxylase (ACCD6) from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1637-1640.	0.7	2
24	Structure-Activity Analysis of Cathepsin K/Chondroitin 4-Sulfate Interactions. <i>Journal of Biological Chemistry</i> , 2011, 286, 8988-8998.	3.4	33
25	Plant Protein Proteinase Inhibitors: Structure and Mechanism of Inhibition. <i>Current Protein and Peptide Science</i> , 2011, 12, 341-347.	1.4	54
26	Crystal Structure of Sulfide:Quinone Oxidoreductase from <i>Acidithiobacillus ferrooxidans</i> : Insights into Sulfidotrophic Respiration and Detoxification. <i>Journal of Molecular Biology</i> , 2010, 398, 292-305.	4.2	84
27	Preliminary X-ray crystallographic analysis of sulfide:quinone oxidoreductase from <i>Acidithiobacillus ferrooxidans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 839-842.	0.7	6
28	Regulatory RNA elements. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 493-494.	1.9	0
29	Expression, purification and preliminary crystallographic analysis of N-acetylglucosamine-1-phosphate uridylyltransferase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 805-808.	0.7	3
30	The Crystal and Molecular Structures of a Cathepsin K:Chondroitin Sulfate Complex. <i>Journal of Molecular Biology</i> , 2008, 383, 78-91.	4.2	95
31	Mechanism of Substrate Recognition and PLP-induced Conformational Changes in LL-Diaminopimelate Aminotransferase from <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Biology</i> , 2008, 384, 1314-1329.	4.2	20
32	The POM Monoclonals: A Comprehensive Set of Antibodies to Non-Overlapping Prion Protein Epitopes. <i>PLoS ONE</i> , 2008, 3, e3872.	2.5	162
33	Crystal Structure of LL-Diaminopimelate Aminotransferase from <i>Arabidopsis thaliana</i> : A Recently Discovered Enzyme in the Biosynthesis of L-Lysine by Plants and Chlamydia. <i>Journal of Molecular Biology</i> , 2007, 371, 685-702.	4.2	42
34	Crystallographic Structure of Human \hat{I}^2 -Hexosaminidase A: Interpretation of Tay-Sachs Mutations and Loss of GM2 Ganglioside Hydrolysis. <i>Journal of Molecular Biology</i> , 2006, 359, 913-929.	4.2	169
35	The peptidases from fungi and viruses. <i>Biological Chemistry</i> , 2006, 387, 1023-9.	2.5	10
36	Crystal Structure and Mutagenesis of a Protein Phosphatase-1:Calcineurin Hybrid Elucidate the Role of the \hat{I}^2 12- \hat{I}^2 13 Loop in Inhibitor Binding. <i>Journal of Biological Chemistry</i> , 2004, 279, 43198-43206.	3.4	29

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37	Structure of Shiga Toxin Type 2 (Stx2) from Escherichia coli O157:H7. Journal of Biological Chemistry, 2004, 279, 27511-27517.	3.4	252
38	Crystal Structure of Human β -Hexosaminidase B: Understanding the Molecular Basis of Sandhoff and Tay-Sachs Disease. Journal of Molecular Biology, 2003, 327, 1093-1109.	4.2	209
39	Synthesis of pseudoxazolones and their inhibition of the 3C cysteine proteinases from hepatitis A virus and human rhinovirus-14. Journal of the Chemical Society, Perkin Transactions 1, 2002, , 1351-1359.	1.3	9
40	Pseudoxazolones, a new class of inhibitors for cysteine proteinases: inhibition of hepatitis A virus and human rhinovirus 3C proteinases. Chemical Communications, 2001, , 2740-2741.	4.1	3
41	ADP-Binding Site of Escherichia coli Succinyl-CoA Synthetase Revealed by X-ray Crystallography,. Biochemistry, 2000, 39, 17-25.	2.5	43
42	Macrocyclic Inhibitors of Penicillopepsin. 2. X-ray Crystallographic Analyses of Penicillopepsin Complexed with a P3 ⁺ P1 Macrocyclic Peptidyl Inhibitor and with Its Two Acyclic Analogues. Journal of the American Chemical Society, 1998, 120, 4610-4621.	13.7	44
43	Structural characterization of activation β -intermediate 2 ⁺ on the pathway to human gastricsin. Nature Structural Biology, 1997, 4, 1010-1015.	9.7	30
44	Comparative modeling of the three-dimensional structure of the calmodulin-related TCH2 protein from arabidopsis. , 1997, 27, 144-153.		20
45	A critical assessment of comparative molecular modeling of tertiary structures of proteins. Proteins: Structure, Function and Bioinformatics, 1995, 23, 301-317.	2.6	138
46	Crystallization of a soluble, catalytically active form of Escherichia coli leader peptidase. Proteins: Structure, Function and Bioinformatics, 1995, 23, 122-125.	2.6	25
47	Common structural features of the <i>luxI</i> protein and the subunits of bacterial luciferase: Evidence for a (β) ₈ fold in luciferase. Protein Science, 1994, 3, 1914-1926.	7.6	22
48	Structural and kinetic characterization of a β -lactamase-inhibitor protein. Nature, 1994, 368, 657-660.	27.8	128
49	Picornaviral 3C cysteine proteinases have a fold similar to chymotrypsin-like serine proteinases. Nature, 1994, 369, 72-76.	27.8	323
50	Deduction of the 3C proteinases' fold. Nature Structural Biology, 1994, 1, 505-506.	9.7	4
51	Crystallization and preliminary X-ray diffraction studies of two mutants of lactate dehydrogenase from Bacillus stearothermophilus. Proteins: Structure, Function and Bioinformatics, 1992, 13, 158-161.	2.6	2
52	Comparative molecular modeling and crystallization of P-30 protein: A novel antitumor protein of Rana pipiens oocytes and early embryos. Proteins: Structure, Function and Bioinformatics, 1992, 14, 392-400.	2.6	20
53	Molecular structure of the acyl-enzyme intermediate in β -lactam hydrolysis at 1.7 Å... resolution. Nature, 1992, 359, 700-705.	27.8	614
54	Model for the interaction of amphiphilic helices with troponin C and calmodulin. Proteins: Structure, Function and Bioinformatics, 1990, 7, 234-248.	2.6	58

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55	Two trifluoperazine-binding sites on calmodulin predicted from comparative molecular modeling with troponin-C. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 3, 1-17.	2.6	80
56	Comparative molecular model building of two serine proteinases from cytotoxic T lymphocytes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 190-204.	2.6	78
57	Molecular structure of an aspartic proteinase zymogen, porcine pepsinogen, at 1.8 Å... resolution. <i>Nature</i> , 1986, 319, 33-38.	27.8	314
58	The mechanism of activation of porcine pepsinogen (reply). <i>Nature</i> , 1986, 322, 664-664.	27.8	15
59	Calcium Binding to Skeletal Muscle Troponin C and the Regulation of Muscle Contraction. <i>Novartis Foundation Symposium</i> , 1986, 122, 120-144.	1.1	4
60	Structure of the calcium regulatory muscle protein troponin-C at 2.8 Å... resolution. <i>Nature</i> , 1985, 313, 653-659.	27.8	666
61	Carboxylâ€“carboxylate interactions in proteins. <i>Nature</i> , 1982, 295, 79-80.	27.8	106
62	Active Site of alpha-Lytic Protease. <i>Enzyme-Substrate Interactions. FEBS Journal</i> , 1981, 120, 289-294.	0.2	40
63	Comparison of the predicted model of ð±-lytic protease with the X-ray structure. <i>Nature</i> , 1979, 279, 165-168.	27.8	48
64	X-ray crystallography of the binding of the bacterial cell wall trisaccharide NAM-NAG-NAM to lysozyme. <i>Nature</i> , 1979, 282, 875-878.	27.8	125
65	Mechanism of acid protease catalysis based on the crystal structure of penicillopepsin. <i>Nature</i> , 1977, 267, 808-813.	27.8	122
66	Tertiary structural differences between microbial serine proteases and pancreatic serine enzymes. <i>Nature</i> , 1975, 257, 758-763.	27.8	138
67	Structure and Function of Picornavirus Proteinases. , 0, , 199-212.		17