Craig J Morton

List of Publications by Year
in descending order

94 papers	5,387 citations	71102 41 h-index	85541 71 g-index
99 all docs	99 docs citations	99 times ranked	7787 citing authors

#	Article	IF	Citations
1	Structural biology of cell surface receptors implicated in Alzheimerâ€™s disease. Biophysical Reviews, 2022, 14, 233-255.	3.2	5
2	Reaction hijacking of tyrosine tRNA synthetase as a new whole-of-life-cycle antimalarial strategy. Science, 2022, 376, 1074-1079.	12.6	25
3	Cholesterolâ€dependent cytolysins: The outstanding questions. IUBMB Life, 2022, 74, 1169-1179.	3.4	8
4	Functional and structural analysis of cytokine-selective IL6ST defects that cause recessive hyper-IgE syndrome. Journal of Allergy and Clinical Immunology, 2021, 148, 585-598.	2.9	20
5	Design of proteasome inhibitors with oral efficacy in vivo against Plasmodium falciparum and selectivity over the human proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
6	X-ray crystallography shines a light on pore-forming toxins. Methods in Enzymology, 2021, 649, 1-46.	1.0	8
7	A Key Motif in the Cholesterol-Dependent Cytolysins Reveals a Large Family of Related Proteins. MBio, 2020, 11, .	4.1	15
8	The structure of the extracellular domains of human interleukin 11Î± receptor reveals mechanisms of cytokine engagement. Journal of Biological Chemistry, 2020, 295, 8285-8301.	3.4	33
9	The Crystal Structure of the Manganese Superoxide Dismutase from Geobacillus stearothermophilus: Parker and Blake (1988) Revisited. Australian Journal of Chemistry, 2020, 73, 145.	0.9	1
10	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. Angewandte Chemie, 2019, 131, 16936-16940.	2.0	8
11	The structure of the PA28â€“20S proteasome complex from Plasmodium falciparum and implications for proteostasis. Nature Microbiology, 2019, 4, 1990-2000.	13.3	31
12	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. Angewandte Chemie - International Edition, 2019, 58, 16780-16784.	13.8	26
13	An Intermolecular Ï€-Stacking Interaction Drives Conformational Changes Necessary to Î²-Barrel Formation in a Pore-Forming Toxin. MBio, 2019, 10, .	4.1	10
14	Structure and Function of the Proteasome Activator PA28 of the Malaria Parasite Plasmodium falciparum. Microscopy and Microanalysis, 2019, 25, 1324-1325.	0.4	0
15	Cholesterol-Dependent Cytolysins: Membrane and Protein Structural Requirements for Pore Formation. Chemical Reviews, 2019, 119, 7721-7736.	47.7	35
16	A structure-based mechanism of cisplatin resistance mediated by glutathione transferase P1-1. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13943-13951.	7.1	76
17	The Structural Basis for a Transition State That Regulates Pore Formation in a Bacterial Toxin. MBio, 2019, 10, .	4.1	10
18	The genetics, structure and function of the M1 aminopeptidase oxytocinase subfamily and their therapeutic potential in immune-mediated disease. Human Immunology, 2019, 80, 281-289.	2.4	22

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19	A dual role for the N-terminal domain of the IL-3 receptor in cell signalling. Nature Communications, 2018, 9, 386.	12.8	28
20	Genetic Variants in <scp>ERAP</scp>1 and <scp>ERAP</scp>2 Associated With Immuneâ€Mediated Diseases Influence Protein Expression and the Isoform Profile. Arthritis and Rheumatology, 2018, 70, 255-265.	5.6	52
21	Protein structure and computational drug discovery. Biochemical Society Transactions, 2018, 46, 1367-1379.	3.4	24
22	Characterization of Tfrc-mutant mice with microcytic phenotypes. Blood Advances, 2018, 2, 1914-1922.	5.2	5
23	Bone marrow transplantation corrects haemolytic anaemia in novel ENU mutagenesis mouse model of TPI deficiency. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	13
24	Cholesterol-dependent cytolysins: from water-soluble state to membrane pore. Biophysical Reviews, 2018, 10, 1337-1348.	3.2	32
25	Transitional changes in the CRP structure lead to the exposure of proinflammatory binding sites. Nature Communications, 2017, 8, 14188.	12.8	158
26	Glutathione transferase P1â€1 as an arsenic drugâ€sequestering enzyme. Protein Science, 2017, 26, 317-326.	7.6	20
27	Fragment library screening identifies hits that bind to the non-catalytic surface of Pseudomonas aeruginosa DsbA1. PLoS ONE, 2017, 12, e0173436.	2.5	17
28	Structural Basis for Receptor Recognition by the Human CD59-Responsive Cholesterol-Dependent Cytolysins. Structure, 2016, 24, 1488-1498.	3.3	34
29	Crystal structure of Streptococcus pneumoniae pneumolysin provides key insights into early steps of pore formation. Scientific Reports, 2015, 5, 14352.	3.3	62
30	The biological function of an insect antifreeze protein simulated by molecular dynamics. ELife, 2015, 4, .	6.0	85
31	The discovery of 1,2,3,9b-tetrahydro-5H-imidazo[2,1-a]isoindol-5-ones as a new class of respiratory syncytial virus (RSV) fusion inhibitors. Part 1. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 969-975.	2.2	13
32	1,2,3,9b-Tetrahydro-5H-imidazo[2,1-a]isoindol-5-ones as a new class of respiratory syncytial virus (RSV) fusion inhibitors. Part 2: Identification of BTA9881 as a preclinical candidate. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 976-981.	2.2	14
33	An intermolecular electrostatic interaction controls the prepore-to-pore transition in a cholesterol-dependent cytolysin. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2204-2209.	7.1	44
34	Crystal structure of human insulinâ€regulated aminopeptidase with specificity for cyclic peptides. Protein Science, 2015, 24, 190-199.	7.6	51
35	Sent packing: protein engineering generates a new crystal form ofPseudomonas aeruginosaDsbA1 with increased catalytic surface accessibility. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2386-2395.	2.5	5
36	Discovery of Phosphodiesterase-4 Inhibitors: Serendipity and Rational Drug Design. Australian Journal of Chemistry, 2014, 67, 1780.	0.9	2

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37	Oncogenic protein interfaces: small molecules, big challenges. Nature Reviews Cancer, 2014, 14, 248-262.	28.4	246
38	Mechanism of Activation of Protein Kinase JAK2 by the Growth Hormone Receptor. Science, 2014, 344, 1249783.	12.6	340
39	Discovery and in vivo evaluation of alcohol-containing benzothiazoles as potent dual-targeting bacterial DNA supercoiling inhibitors. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 4215-4222.	2.2	18
40	Derivatives of imidazotriazine and pyrrolotriazine C-nucleosides as potential new anti-HCV agents. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 4984-4988.	2.2	13
41	The role of Rdl in resistance to phenylpyrazoles in Drosophila melanogaster. Insect Biochemistry and Molecular Biology, 2014, 54, 11-21.	2.7	30
42	Discovery and Synthesis of C-Nucleosides as Potential New Anti-HCV Agents. ACS Medicinal Chemistry Letters, 2014, 5, 679-684.	2.8	32
43	Potent hepatitis C inhibitors bind directly to NS5A and reduce its affinity for RNA. Scientific Reports, 2014, 4, 4765.	3.3	101
44	Design and Evaluation of the Performance of an NMR Screening Fragment Library. Australian Journal of Chemistry, 2013, 66, 1465.	0.9	33
45	An Orally Available 3-Ethoxybenzisoxazole Capsid Binder with Clinical Activity against Human Rhinovirus. ACS Medicinal Chemistry Letters, 2012, 3, 303-307.	2.8	38
46	Regulation of Insulin-Regulated Membrane Aminopeptidase Activity by Its C-Terminal Domain. Biochemistry, 2011, 50, 2611-2622.	2.5	30
47	Thiophene inhibitors of PDE4: Crystal structures show a second binding mode at the catalytic domain of PDE4D2. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 7089-7093.	2.2	18
48	Studies of Glutathione Transferase P1â€1 Bound to a Platinum(IV)â€Based Anticancer Compound Reveal the Molecular Basis of Its Activation. Chemistry - A European Journal, 2011, 17, 7806-7816.	3.3	73
49	Recognition and Detoxification of the Insecticide DDT by Drosophila melanogaster Glutathione S-Transferase D1. Journal of Molecular Biology, 2010, 399, 358-366.	4.2	62
50	Phenylalanine-544 Plays a Key Role in Substrate and Inhibitor Binding by Providing a Hydrophobic Packing Point at the Active Site of Insulin-Regulated Aminopeptidase. Molecular Pharmacology, 2010, 78, 600-607.	2.3	21
51	Rational Design of an Organometallic Glutathione Transferase Inhibitor. Angewandte Chemie - International Edition, 2009, 48, 3854-3857.	13.8	169
52	Influence of the Hâ€site residue 108 on human glutathione transferase P1â€1 ligand binding: Structureâ€thermodynamic relationships and thermal stability. Protein Science, 2009, 18, 2454-2470.	7.6	15
53	Copper binding to the Alzheimerâ€™s disease amyloid precursor protein. European Biophysics Journal, 2008, 37, 269-279.	2.2	62
54	The Anti-cancer Drug Chlorambucil as a Substrate for the Human Polymorphic Enzyme Glutathione Transferase P1-1: Kinetic Properties and Crystallographic Characterisation of Allelic Variants. Journal of Molecular Biology, 2008, 380, 131-144.	4.2	49

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55	Preventing serpin aggregation: The molecular mechanism of citrate action upon antitrypsin unfolding. Protein Science, 2008, 17, 2127-2133.	7.6	23
56	Design of a Conformationally Defined and Proteolytically Stable Circular Mimetic of Brain-derived Neurotrophic Factor. Journal of Biological Chemistry, 2008, 283, 33375-33383.	3.4	45
57	Identification and characterization of a new cognitive enhancer based on inhibition of insulinâ€regulated aminopeptidase. FASEB Journal, 2008, 22, 4209-4217.	0.5	95
58	Identification of modulating residues defining the catalytic cleft of insulin-regulated aminopeptidase. Biochemistry and Cell Biology, 2008, 86, 251-261.	2.0	22
59	Critical Role for the Second Extracellular Loop in the Binding of Both Orthosteric and Allosteric G Protein-coupled Receptor Ligands. Journal of Biological Chemistry, 2007, 282, 25677-25686.	3.4	137
60	Molecular Evolution of Glutathione S-Transferases in the Genus Drosophila. Genetics, 2007, 177, 1363-1375.	2.9	92
61	An Updated Unified Pharmacophore Model of the Benzodiazepine Binding Site on γ-Aminobutyric Acida Receptors: Correlation with Comparative Models. Current Medicinal Chemistry, 2007, 14, 2755-2775.	2.4	68
62	Structures of Perfringolysin O Suggest a Pathway for Activation of Cholesterol-dependent Cytolysins. Journal of Molecular Biology, 2007, 367, 1227-1236.	4.2	87
63	Calorimetric and structural studies of the nitric oxide carrier S-nitrosoglutathione bound to human glutathione transferase P1-1. Protein Science, 2006, 15, 1093-1105.	7.6	24
64	Effect of Linker Length on Avidin Binding to Biotinylated Gramicidin A. International Journal of Peptide Research and Therapeutics, 2006, 12, 243-252.	1.9	4
65	Hsp90 increases LIM kinase activity by promoting its homoâ€dimerization. FASEB Journal, 2006, 20, 1218-1220.	0.5	46
66	Murine cytomegalovirus resistant to antivirals has genetic correlates with human cytomegalovirus. Journal of General Virology, 2005, 86, 2141-2151.	2.9	10
67	Cytoplasmic ATP-sensing Domains Regulate Gating of Skeletal Muscle ClC-1 Chloride Channels. Journal of Biological Chemistry, 2005, 280, 32452-32458.	3.4	106
68	Insights into Interactions between the Î±-Helical Region of the Salmon Calcitonin Antagonists and the Human Calcitonin Receptor using Photoaffinity Labeling. Journal of Biological Chemistry, 2005, 280, 28610-28622.	3.4	27
69	Intrasteric control of AMPK via the Â1 subunit AMP allosteric regulatory site. Protein Science, 2004, 13, 155-165.	7.6	141
70	Structural characterization of respiratory syncytial virus fusion inhibitor escape mutants: homology model of the F protein and a syncytium formation assay. Virology, 2003, 311, 275-288.	2.4	63
71	Structure of the Alzheimer's Disease Amyloid Precursor Protein Copper Binding Domain. Journal of Biological Chemistry, 2003, 278, 17401-17407.	3.4	248
72	Insights into the Structural Basis for Zinc Inhibition of the Glycine Receptor. Journal of Biological Chemistry, 2003, 278, 28985-28992.	3.4	49

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73	Crystal Structure of a Putative Methyltransferase from Mycobacterium tuberculosis : Misannotation of a Genome Clarified by Protein Structural Analysis. Journal of Bacteriology, 2003, 185, 4057-4065.	2.2	29
74	Electrostatic and Hydrophobic Forces Tether the Proximal Region of the Angiotensin II Receptor (AT1A) Carboxyl Terminus to Anionic Lipidsâ€. Biochemistry, 2002, 41, 7830-7840.	2.5	42
75	Anxiety over GABAA receptor structure relieved by AChBP. Trends in Biochemical Sciences, 2002, 27, 280-287.	7.5	169
76	From glutathione transferase to pore in a CLIC. European Biophysics Journal, 2002, 31, 356-364.	2.2	85
77	Solid-state NMR conformational studies of a melittin-inhibitor complex. European Biophysics Journal, 2002, 31, 383-388.	2.2	10
78	Conversion of a transmembrane to a water-soluble protein complex by a single point mutation. Nature Structural Biology, 2002, 9, 729-733.	9.7	59
79	Solid-State NMR Structure Determination of Melittin in a Lipid Environment. Biophysical Journal, 2001, 81, 2752-2761.	0.5	80
80	The speciation of gold and copper cyanide complexes on ion-exchange resins containing different functional groups. Reactive and Functional Polymers, 2000, 44, 121-143.	4.1	20
81	Probing the nature of interactions in SH2 binding interfacesâ€“evidence from electrospray ionization mass spectrometry. Protein Science, 1999, 8, 1962-1970.	7.6	34
82	The Folding Kinetics and Thermodynamics of the Fyn-SH3 Domainâ€. Biochemistry, 1998, 37, 2529-2537.	2.5	152
83	Folding kinetics of the SH3 domain of PI3 kinase by real-time NMR combined with optical spectroscopy. Journal of Molecular Biology, 1998, 276, 657-667.	4.2	126
84	The SH2 domain from the tyrosine kinase Fyn in complex with a phosphotyrosyl peptide reveals insights into domain stability and binding specificity. Structure, 1997, 5, 1313-1323.	3.3	44
85	The effects of guanidine hydrochloride on the 'random coil' conformations and NMR chemical shifts of the peptide series GGXGG. Journal of Biomolecular NMR, 1997, 10, 221-230.	2.8	96
86	Structural and Thermodynamic Characterization of the Interaction of the SH3 Domain from Fyn with the Proline-Rich Binding Site on the p85 Subunit of PI3-Kinaseâ€. Biochemistry, 1996, 35, 15646-15653.	2.5	99
87	Solution Structure of the Link Module: A Hyaluronan-Binding Domain Involved in Extracellular Matrix Stability and Cell Migration. Cell, 1996, 86, 767-775.	28.9	293
88	Solution structure and peptide binding of the SH3 domain from human Fyn. Structure, 1996, 4, 705-714.	3.3	100
89	Water mediated proteinâ€ÐNA interactions: The relationship of thermodynamics to structural detail. Protein Science, 1996, 5, 2115-2118.	7.6	100
90	NMR studies of the solution properties of recombinant murine interleukin-6. BBA - Proteins and Proteomics, 1995, 1249, 189-203.	2.1	8

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91	SH3 Domains: Molecular â€˜Velcroâ€™. Current Biology, 1994, 4, 615-617.	3.9	91
92	Solution structure of synthetic peptides corresponding to the C-terminal helix of interleukin-6. FEBS Journal, 1994, 219, 97-107.	0.2	11
93	Role of the Câ€terminus in the activity, conformation, and stability of interleukinâ€6. Protein Science, 1993, 2, 1472-1481.	7.6	28
94	Complete amino acid sequence of tenebrosin-C, a cardiac stimulatory and haemolytic protein from the sea anemone Actinia tenebrosa. FEBS Journal, 1990, 190, 319-328.	0.2	55