

Craig J Morton

List of Publications by Year in descending order

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94
papers

5,387
citations

71102

41
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85541

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99
all docs

99
docs citations

99
times ranked

7787
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanism of Activation of Protein Kinase JAK2 by the Growth Hormone Receptor. <i>Science</i> , 2014, 344, 1249783.	12.6	340
2	Solution Structure of the Link Module: A Hyaluronan-Binding Domain Involved in Extracellular Matrix Stability and Cell Migration. <i>Cell</i> , 1996, 86, 767-775.	28.9	293
3	Structure of the Alzheimer's Disease Amyloid Precursor Protein Copper Binding Domain. <i>Journal of Biological Chemistry</i> , 2003, 278, 17401-17407.	3.4	248
4	Oncogenic protein interfaces: small molecules, big challenges. <i>Nature Reviews Cancer</i> , 2014, 14, 248-262.	28.4	246
5	Anxiety over GABAA receptor structure relieved by AChBP. <i>Trends in Biochemical Sciences</i> , 2002, 27, 280-287.	7.5	169
6	Rational Design of an Organometallic Glutathione Transferase Inhibitor. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 3854-3857.	13.8	169
7	Transitional changes in the CRP structure lead to the exposure of proinflammatory binding sites. <i>Nature Communications</i> , 2017, 8, 14188.	12.8	158
8	The Folding Kinetics and Thermodynamics of the Fyn-SH3 Domain. <i>Biochemistry</i> , 1998, 37, 2529-2537.	2.5	152
9	Intrasteric control of AMPK via the $\hat{A}1$ subunit AMP allosteric regulatory site. <i>Protein Science</i> , 2004, 13, 155-165.	7.6	141
10	Critical Role for the Second Extracellular Loop in the Binding of Both Orthosteric and Allosteric G Protein-coupled Receptor Ligands. <i>Journal of Biological Chemistry</i> , 2007, 282, 25677-25686.	3.4	137
11	Folding kinetics of the SH3 domain of PI3 kinase by real-time NMR combined with optical spectroscopy. <i>Journal of Molecular Biology</i> , 1998, 276, 657-667.	4.2	126
12	Cytoplasmic ATP-sensing Domains Regulate Gating of Skeletal Muscle ClC-1 Chloride Channels. <i>Journal of Biological Chemistry</i> , 2005, 280, 32452-32458.	3.4	106
13	Potent hepatitis C inhibitors bind directly to NS5A and reduce its affinity for RNA. <i>Scientific Reports</i> , 2014, 4, 4765.	3.3	101
14	Solution structure and peptide binding of the SH3 domain from human Fyn. <i>Structure</i> , 1996, 4, 705-714.	3.3	100
15	Water mediated protein-DNA interactions: The relationship of thermodynamics to structural detail. <i>Protein Science</i> , 1996, 5, 2115-2118.	7.6	100
16	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-Kinase. <i>Biochemistry</i> , 1996, 35, 15646-15653.	2.5	99
17	The effects of guanidine hydrochloride on the 'random coil' conformations and NMR chemical shifts of the peptide series GGXGG. <i>Journal of Biomolecular NMR</i> , 1997, 10, 221-230.	2.8	96
18	Identification and characterization of a new cognitive enhancer based on inhibition of insulin-regulated aminopeptidase. <i>FASEB Journal</i> , 2008, 22, 4209-4217.	0.5	95

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19	Molecular Evolution of Glutathione <i>S</i> -Transferases in the Genus <i>Drosophila</i> . <i>Genetics</i> , 2007, 177, 1363-1375.	2.9	92
20	SH3 Domains: Molecular "Velcro". <i>Current Biology</i> , 1994, 4, 615-617.	3.9	91
21	Structures of Perfringolysin O Suggest a Pathway for Activation of Cholesterol-dependent Cytolysins. <i>Journal of Molecular Biology</i> , 2007, 367, 1227-1236.	4.2	87
22	From glutathione transferase to pore in a CLIC. <i>European Biophysics Journal</i> , 2002, 31, 356-364.	2.2	85
23	The biological function of an insect antifreeze protein simulated by molecular dynamics. <i>ELife</i> , 2015, 4, .	6.0	85
24	Solid-State NMR Structure Determination of Melittin in a Lipid Environment. <i>Biophysical Journal</i> , 2001, 81, 2752-2761.	0.5	80
25	A structure-based mechanism of cisplatin resistance mediated by glutathione transferase P1-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13943-13951.	7.1	76
26	Studies of Glutathione Transferase P1-1 Bound to a Platinum(IV)-Based Anticancer Compound Reveal the Molecular Basis of Its Activation. <i>Chemistry - A European Journal</i> , 2011, 17, 7806-7816.	3.3	73
27	An Updated Unified Pharmacophore Model of the Benzodiazepine Binding Site on γ -Aminobutyric Acid Receptors: Correlation with Comparative Models. <i>Current Medicinal Chemistry</i> , 2007, 14, 2755-2775.	2.4	68
28	Structural characterization of respiratory syncytial virus fusion inhibitor escape mutants: homology model of the F protein and a syncytium formation assay. <i>Virology</i> , 2003, 311, 275-288.	2.4	63
29	Copper binding to the Alzheimer's disease amyloid precursor protein. <i>European Biophysics Journal</i> , 2008, 37, 269-279.	2.2	62
30	Recognition and Detoxification of the Insecticide DDT by <i>Drosophila melanogaster</i> Glutathione S-Transferase D1. <i>Journal of Molecular Biology</i> , 2010, 399, 358-366.	4.2	62
31	Crystal structure of <i>Streptococcus pneumoniae</i> pneumolysin provides key insights into early steps of pore formation. <i>Scientific Reports</i> , 2015, 5, 14352.	3.3	62
32	Conversion of a transmembrane to a water-soluble protein complex by a single point mutation. <i>Nature Structural Biology</i> , 2002, 9, 729-733.	9.7	59
33	Complete amino acid sequence of tenebrosin-C, a cardiac stimulatory and haemolytic protein from the sea anemone <i>Actinia tenebrosa</i> . <i>FEBS Journal</i> , 1990, 190, 319-328.	0.2	55
34	Genetic Variants in <i>ERAP1</i> and <i>ERAP2</i> Associated With Immune-Mediated Diseases Influence Protein Expression and the Isoform Profile. <i>Arthritis and Rheumatology</i> , 2018, 70, 255-265.	5.6	52
35	Crystal structure of human insulin-regulated aminopeptidase with specificity for cyclic peptides. <i>Protein Science</i> , 2015, 24, 190-199.	7.6	51
36	Insights into the Structural Basis for Zinc Inhibition of the Glycine Receptor. <i>Journal of Biological Chemistry</i> , 2003, 278, 28985-28992.	3.4	49

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37	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. <i>Journal of Molecular Biology</i> , 2008, 380, 131-144.	4.2	49
38	Hsp90 increases LIM kinase activity by promoting its homoâ€dimerization. <i>FASEB Journal</i> , 2006, 20, 1218-1220.	0.5	46
39	Design of a Conformationally Defined and Proteolytically Stable Circular Mimetic of Brain-derived Neurotrophic Factor. <i>Journal of Biological Chemistry</i> , 2008, 283, 33375-33383.	3.4	45
40	The SH2 domain from the tyrosine kinase Fyn in complex with a phosphotyrosyl peptide reveals insights into domain stability and binding specificity. <i>Structure</i> , 1997, 5, 1313-1323.	3.3	44
41	An intermolecular electrostatic interaction controls the prepore-to-pore transition in a cholesterol-dependent cytolysin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2204-2209.	7.1	44
42	Electrostatic and Hydrophobic Forces Tether the Proximal Region of the Angiotensin II Receptor (AT1A) Carboxyl Terminus to Anionic Lipidsâ€. <i>Biochemistry</i> , 2002, 41, 7830-7840.	2.5	42
43	An Orally Available 3-Ethoxybenzoxazole Capsid Binder with Clinical Activity against Human Rhinovirus. <i>ACS Medicinal Chemistry Letters</i> , 2012, 3, 303-307.	2.8	38
44	Cholesterol-Dependent Cytolysins: Membrane and Protein Structural Requirements for Pore Formation. <i>Chemical Reviews</i> , 2019, 119, 7721-7736.	47.7	35
45	Probing the nature of interactions in SH2 binding interfacesâ€“evidence from electrospray ionization mass spectrometry. <i>Protein Science</i> , 1999, 8, 1962-1970.	7.6	34
46	Structural Basis for Receptor Recognition by the Human CD59-Responsive Cholesterol-Dependent Cytolysins. <i>Structure</i> , 2016, 24, 1488-1498.	3.3	34
47	Design and Evaluation of the Performance of an NMR Screening Fragment Library. <i>Australian Journal of Chemistry</i> , 2013, 66, 1465.	0.9	33
48	The structure of the extracellular domains of human interleukin 11± receptor reveals mechanisms of cytokine engagement. <i>Journal of Biological Chemistry</i> , 2020, 295, 8285-8301.	3.4	33
49	Discovery and Synthesis of C-Nucleosides as Potential New Anti-HCV Agents. <i>ACS Medicinal Chemistry Letters</i> , 2014, 5, 679-684.	2.8	32
50	Cholesterol-dependent cytolysins: from water-soluble state to membrane pore. <i>Biophysical Reviews</i> , 2018, 10, 1337-1348.	3.2	32
51	The structure of the PA28â€20S proteasome complex from <i>Plasmodium falciparum</i> and implications for proteostasis. <i>Nature Microbiology</i> , 2019, 4, 1990-2000.	13.3	31
52	Regulation of Insulin-Regulated Membrane Aminopeptidase Activity by Its C-Terminal Domain. <i>Biochemistry</i> , 2011, 50, 2611-2622.	2.5	30
53	The role of Rdl in resistance to phenylpyrazoles in <i>Drosophila melanogaster</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2014, 54, 11-21.	2.7	30
54	Crystal Structure of a Putative Methyltransferase from <i>Mycobacterium tuberculosis</i> : Misannotation of a Genome Clarified by Protein Structural Analysis. <i>Journal of Bacteriology</i> , 2003, 185, 4057-4065.	2.2	29

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55	Role of the C-terminus in the activity, conformation, and stability of interleukin-6. <i>Protein Science</i> , 1993, 2, 1472-1481.	7.6	28
56	A dual role for the N-terminal domain of the IL-3 receptor in cell signalling. <i>Nature Communications</i> , 2018, 9, 386.	12.8	28
57	Insights into Interactions between the α -Helical Region of the Salmon Calcitonin Antagonists and the Human Calcitonin Receptor using Photoaffinity Labeling. <i>Journal of Biological Chemistry</i> , 2005, 280, 28610-28622.	3.4	27
58	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 16780-16784.	13.8	26
59	Reaction hijacking of tyrosine tRNA synthetase as a new whole-of-life-cycle antimalarial strategy. <i>Science</i> , 2022, 376, 1074-1079.	12.6	25
60	Calorimetric and structural studies of the nitric oxide carrier S-nitrosoglutathione bound to human glutathione transferase P1-1. <i>Protein Science</i> , 2006, 15, 1093-1105.	7.6	24
61	Protein structure and computational drug discovery. <i>Biochemical Society Transactions</i> , 2018, 46, 1367-1379.	3.4	24
62	Preventing serpin aggregation: The molecular mechanism of citrate action upon antitrypsin unfolding. <i>Protein Science</i> , 2008, 17, 2127-2133.	7.6	23
63	Identification of modulating residues defining the catalytic cleft of insulin-regulated aminopeptidase. <i>Biochemistry and Cell Biology</i> , 2008, 86, 251-261.	2.0	22
64	The genetics, structure and function of the M1 aminopeptidase oxytocinase subfamily and their therapeutic potential in immune-mediated disease. <i>Human Immunology</i> , 2019, 80, 281-289.	2.4	22
65	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. <i>Molecular Pharmacology</i> , 2010, 78, 600-607.	2.3	21
66	The speciation of gold and copper cyanide complexes on ion-exchange resins containing different functional groups. <i>Reactive and Functional Polymers</i> , 2000, 44, 121-143.	4.1	20
67	Glutathione transferase P1 as an arsenic drug-sequestering enzyme. <i>Protein Science</i> , 2017, 26, 317-326.	7.6	20
68	Functional and structural analysis of cytokine-selective IL6ST defects that cause recessive hyper-IgE syndrome. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 585-598.	2.9	20
69	Design of proteasome inhibitors with oral efficacy in vivo against <i>Plasmodium falciparum</i> and selectivity over the human proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
70	Thiophene inhibitors of PDE4: Crystal structures show a second binding mode at the catalytic domain of PDE4D2. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 7089-7093.	2.2	18
71	Discovery and in vivo evaluation of alcohol-containing benzothiazoles as potent dual-targeting bacterial DNA supercoiling inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2014, 24, 4215-4222.	2.2	18
72	Fragment library screening identifies hits that bind to the non-catalytic surface of <i>Pseudomonas aeruginosa</i> DsbA1. <i>PLoS ONE</i> , 2017, 12, e0173436.	2.5	17

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73	Influence of the H ₂ O site residue 108 on human glutathione transferase P1 ^h ligand binding: Structure-thermodynamic relationships and thermal stability. <i>Protein Science</i> , 2009, 18, 2454-2470.	7.6	15
74	A Key Motif in the Cholesterol-Dependent Cytolysins Reveals a Large Family of Related Proteins. <i>MBio</i> , 2020, 11, .	4.1	15
75	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. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 976-981.	2.2	14
76	Derivatives of imidazotriazine and pyrrolotriazine C-nucleosides as potential new anti-HCV agents. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2014, 24, 4984-4988.	2.2	13
77	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. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 969-975.	2.2	13
78	Bone marrow transplantation corrects haemolytic anaemia in novel ENU mutagenesis mouse model of TPI deficiency. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	2.4	13
79	Solution structure of synthetic peptides corresponding to the C-terminal helix of interleukin-6. <i>FEBS Journal</i> , 1994, 219, 97-107.	0.2	11
80	Solid-state NMR conformational studies of a melittin-inhibitor complex. <i>European Biophysics Journal</i> , 2002, 31, 383-388.	2.2	10
81	Murine cytomegalovirus resistant to antivirals has genetic correlates with human cytomegalovirus. <i>Journal of General Virology</i> , 2005, 86, 2141-2151.	2.9	10
82	An Intermolecular π -Stacking Interaction Drives Conformational Changes Necessary to β -Barrel Formation in a Pore-Forming Toxin. <i>MBio</i> , 2019, 10, .	4.1	10
83	The Structural Basis for a Transition State That Regulates Pore Formation in a Bacterial Toxin. <i>MBio</i> , 2019, 10, .	4.1	10
84	NMR studies of the solution properties of recombinant murine interleukin-6. <i>BBA - Proteins and Proteomics</i> , 1995, 1249, 189-203.	2.1	8
85	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. <i>Angewandte Chemie</i> , 2019, 131, 16936-16940.	2.0	8
86	X-ray crystallography shines a light on pore-forming toxins. <i>Methods in Enzymology</i> , 2021, 649, 1-46.	1.0	8
87	Cholesterol-dependent cytolysins: The outstanding questions. <i>IUBMB Life</i> , 2022, 74, 1169-1179.	3.4	8
88	Characterization of Tfr ^c -mutant mice with microcytic phenotypes. <i>Blood Advances</i> , 2018, 2, 1914-1922.	5.2	5
89	Sent packing: protein engineering generates a new crystal form of <i>Pseudomonas aeruginosa</i> DsbA1 with increased catalytic surface accessibility. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2386-2395.	2.5	5
90	Structural biology of cell surface receptors implicated in Alzheimer's disease. <i>Biophysical Reviews</i> , 2022, 14, 233-255.	3.2	5

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91	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
92	Discovery of Phosphodiesterase-4 Inhibitors: Serendipity and Rational Drug Design. Australian Journal of Chemistry, 2014, 67, 1780.	0.9	2
93	The Crystal Structure of the Manganese Superoxide Dismutase from <i>Geobacillus stearothermophilus</i> : Parker and Blake (1988) Revisited. Australian Journal of Chemistry, 2020, 73, 145.	0.9	1
94	Structure and Function of the Proteasome Activator PA28 of the Malaria Parasite <i>Plasmodium falciparum</i> . Microscopy and Microanalysis, 2019, 25, 1324-1325.	0.4	0