Matthew Groves

List of Publications by Year
in descending order

77 papers	1,807 citations	331259 21 h-index	301761 39 g-index
78 all docs	78 docs citations	78 times ranked	2982 citing authors

#	Article	IF	Citations
1	High-resolution X-ray and NMR Structures of the SMN Tudor Domain: Conformational Variation in the Binding Site for Symmetrically Dimethylated Arginine Residues. Journal of Molecular Biology, 2003, 327, 507-520.	2.0	155
2	Theory and applications of differential scanning fluorimetry in early-stage drug discovery. Biophysical Reviews, 2020, 12, 85-104.	1.5	137
3	A unique Oct4 interface is crucial for reprogramming to pluripotency. Nature Cell Biology, 2013, 15, 295-301.	4.6	135
4	Methods for Protein Characterization by Mass Spectrometry, Thermal Shift (ThermoFluor) Assay, and Multiangle or Static Light Scattering. Methods in Molecular Biology, 2008, 426, 299-318.	0.4	118
5	ROS-Mediated Signalling in Bacteria: Zinc-Containing Cys-X-X-Cys Redox Centres and Iron-Based Oxidative Stress. Journal of Signal Transduction, 2012, 2012, 1-9.	2.0	100
6	Functional Characterization of Recombinant Chloroplast Signal Recognition Particle. Journal of Biological Chemistry, 2001, 276, 27778-27786.	1.6	70
7	Structural Analysis of the Human Golgi-associated Plant Pathogenesis Related Protein GAPR-1 Implicates Dimerization as a Regulatory Mechanism. Journal of Molecular Biology, 2004, 339, 173-183.	2.0	66
8	Canonical Signal Recognition Particle Components Can Be Bypassed for Posttranslational Protein Targeting in Chloroplasts. Plant Cell, 2007, 19, 1635-1648.	3.1	63
9	The impact of protein characterization in structural proteomics. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1125-1136.	2.5	58
10	A method for the general identification of protein crystals in crystallization experiments using a noncovalent fluorescent dye. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 526-535.	2.5	43
11	Specific Inhibition of the Aspartate Aminotransferase of Plasmodium falciparum. Journal of Molecular Biology, 2011, 405, 956-971.	2.0	42
12	The three-component signalling system HbpSâ€“SenSâ€“SenR as an example of a redox sensing pathway in bacteria. Amino Acids, 2009, 37, 479-486.	1.2	41
13	Acoustic Droplet Ejection Enabled Automated Reaction Scouting. ACS Central Science, 2019, 5, 451-457.	5.3	40
14	Relevance and Effectiveness of Molecular Tumor Board Recommendations for Patients With Nonâ€“Small-Cell Lung Cancer With Rare or Complex Mutational Profiles. JCO Precision Oncology, 2020, 4, 393-410.	1.5	32
15	Fatty Acid- and Retinoid-binding Proteins Have Distinct Binding Pockets for the Two Types of Cargo. Journal of Biological Chemistry, 2009, 284, 35818-35826.	1.6	31
16	Enzyme kinetics and inhibition of histone acetyltransferase KAT8. European Journal of Medicinal Chemistry, 2015, 105, 289-296.	2.6	31
17	Rapid approach to complex boronic acids. Science Advances, 2019, 5, eaaw4607.	4.7	30
18	The (R)-enantiomer of the 6-chromanol derivate SUL-121 improves renal graft perfusion via antagonism of the Î±1-adrenoceptor. Scientific Reports, 2019, 9, 13.	1.6	28

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19	A Systematic Protein Refolding Screen Method using the DGR Approach Reveals that Time and Secondary TSA are Essential Variables. Scientific Reports, 2017, 7, 9355.	1.6	26
20	Dynamic Substrate Enhancement for the Identification of Specific, Secondâ€Siteâ€Binding Fragments Targeting a Set of Protein Tyrosine Phosphatases. ChemBioChem, 2011, 12, 2640-2646.	1.3	25
21	The Vitamin B1 Metabolism of Staphylococcus aureus Is Controlled at Enzymatic and Transcriptional Levels. PLoS ONE, 2009, 4, e7656.	1.1	24
22	The Oligomeric Assembly of the Novel Haem-Degrading Protein HbpS Is Essential for Interaction with Its Cognate Two-Component Sensor Kinase. Journal of Molecular Biology, 2009, 386, 1108-1122.	2.0	22
23	Synthetic Peptides That Antagonize the Angiotensin-Converting Enzyme-2 (ACE-2) Interaction with SARS-CoV-2 Receptor Binding Spike Protein. Journal of Medicinal Chemistry, 2022, 65, 2836-2847.	2.9	22
24	Artificial macrocycles as IL-17A/IL-17RA antagonists. MedChemComm, 2018, 9, 22-26.	3.5	20
25	Nanoscale, automated, high throughput synthesis and screening for the accelerated discovery of protein modifiers. RSC Medicinal Chemistry, 2021, 12, 809-818.	1.7	20
26	The Assembly of the Plasmodial PLP Synthase Complex Follows a Defined Course. PLoS ONE, 2008, 3, e1815.	1.1	20
27	The Human Milk Oligosaccharides 3â€FL, Lactoâ€Nâ€Neotetraose, and LDFT Attenuate Tumor Necrosis Factorâ€Î± Induced Inflammation in Fetal Intestinal Epithelial Cells In Vitro through Shedding or Interacting with Tumor Necrosis Factor Receptor 1. Molecular Nutrition and Food Research, 2021, 65, e2000425.	1.5	19
28	Combining Highâ€Throughput Synthesis and Highâ€Throughput Protein Crystallography for Accelerated Hit Identification. Angewandte Chemie - International Edition, 2021, 60, 18231-18239.	7.2	19
29	Definition of domain boundaries and crystallization of the SMN Tudor domain. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 366-368.	2.5	17
30	Isolation and molecular characterization of novel glucarpidases: Enzymes to improve the antibody directed enzyme pro-drug therapy for cancer treatment. PLoS ONE, 2018, 13, e0196254.	1.1	16
31	A novel mechanism of inhibition by phenylthiourea on PvdP, a tyrosinase synthesizing pyoverdine of Pseudomonas aeruginosa. International Journal of Biological Macromolecules, 2020, 146, 212-221.	3.6	16
32	Molecular docking, synthesis and biological evaluation of Vascular Endothelial Growth Factor (VEGF) B based peptide as antiangiogenic agent targeting the second domain of the Vascular Endothelial Growth Factor Receptor 1 (VEGFR1D2) for anticancer application. Signal Transduction and Targeted Therapy, 2020, 5, 76.	7.1	16
33	Aspartate Aminotransferase - Bridging Carbohydrate and Energy Metabolism in Plasmodium Falciparum. Current Drug Metabolism, 2012, 13, 332-336.	0.7	15
34	Oligomeric interfaces as a tool in drug discovery: Specific interference with activity of malate dehydrogenase of Plasmodium falciparum in vitro. PLoS ONE, 2018, 13, e0195011.	1.1	15
35	Crystallization and preliminary characterization of a novel haem-binding protein ofStreptomyces reticuli. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 386-390.	0.7	13
36	Quantitive evaluation of macromolecular crystallization experiments using 1,8-ANS fluorescence. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 901-908.	2.5	13

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37	Novel Redox-Sensing Modules: Accessory Protein- and Nucleic Acid-Mediated Signaling. Antioxidants and Redox Signaling, 2012, 16, 668-677.	2.5	13
38	Actionability of on-target ALK Resistance Mutations in Patients With Non-Small Cell Lung Cancer: Local Experience and Review of the Literature. Clinical Lung Cancer, 2022, 23, e104-e115.	1.1	13
39	Crystallization of a Golgi-associated PR-1-related protein (GAPR-1) that localizes to lipid-enriched microdomains. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 730-732.	2.5	12
40	Crystal structure of truncated aspartate transcarbamoylase fromPlasmodium falciparum. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 523-533.	0.4	12
41	DXS as a target for structure-based drug design. Future Medicinal Chemistry, 2017, 9, 1277-1294.	1.1	12
42	Iron Binding at Specific Sites within the Octameric HbpS Protects Streptomycetes from Iron-Mediated Oxidative Stress. PLoS ONE, 2013, 8, e71579.	1.1	12
43	Purification, crystallization and preliminary X-ray analysis of the aspartate aminotransferase ofPlasmodium falciparum. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 409-412.	0.7	10
44	Data collection with a tailored X-ray beam size at 2.69â€…Ã… wavelength (4.6â€…keV): sulfur SAD phasing of Cdc23Nterm. Acta Crystallographica Section D: Structural Biology, 2016, 72, 403-412.	1.1	10
45	Afatinib in Osimertinib-Resistant EGFR ex19del/T790M/P794L Mutated NSCLC. Journal of Thoracic Oncology, 2018, 13, e161-e163.	0.5	9
46	Identification of a 1-deoxy-D-xylulose-5-phosphate synthase (DXS) mutant with improved crystallographic properties. Biochemical and Biophysical Research Communications, 2021, 539, 42-47.	1.0	9
47	Drug Target Validation Methods in Malaria - Protein Interference Assay (PIA) as a Tool for Highly Specific Drug Target Validation. Current Drug Targets, 2017, 18, 1069-1085.	1.0	9
48	Octameric alcohol oxidase dissociates into stable, soluble monomers upon incubation with dimethylsulfoxide. Archives of Biochemistry and Biophysics, 2007, 459, 208-213.	1.4	8
49	Identification and Validation of Novel Drug Targets for the Treatment of Plasmodium falciparum Malaria: New Insights. , 0, , .		8
50	Benchmark of Generic Shapes for Macrocycles. Journal of Chemical Information and Modeling, 2020, 60, 6298-6313.	2.5	8
51	Tyrosine kinase inhibitor sensitive PDGFRÎ± mutations in GIST: Two cases and review of the literature. Oncotarget, 2017, 8, 109836-109847.	0.8	8
52	First crystal structures of 1-deoxy-d-xylulose 5-phosphate synthase (DXPS) from Mycobacterium tuberculosis indicate a distinct mechanism of intermediate stabilization. Scientific Reports, 2022, 12, 7221.	1.6	8
53	Mobility of the conserved glycine 155 is required for formation of the active plasmodial Pdx1 dodecamer. Biochimica Et Biophysica Acta - General Subjects, 2009, 1790, 347-350.	1.1	7
54	Cytometric quantification of singlet oxygen in the human malaria parasite Plasmodium falciparum. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2012, 81A, 698-703.	1.1	7

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55	Molecular Target Validation of Aspartate Transcarbamoylase from Plasmodium falciparum by Torin 2. ACS Infectious Diseases, 2020, 6, 986-999.	1.8	7
56	New directions in antimalarial target validation. Expert Opinion on Drug Discovery, 2020, 15, 189-202.	2.5	7
57	Internal structure of an intact Convallaria majalis pollen grain observed with X-ray Fresnel coherent diffractive imaging. Optics Express, 2012, 20, 26778.	1.7	6
58	Structural insights into K48-linked ubiquitin chain formation by the Pex4p-Pex22p complex. Biochemical and Biophysical Research Communications, 2018, 496, 562-567.	1.0	6
59	Live and Let Dye: Visualizing the Cellular Compartments of the Malaria Parasite Plasmodium falciparum. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 694-705.	1.1	6
60	Crystallization and preliminary X-ray diffraction of malate dehydrogenase fromPlasmodium falciparum. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 659-662.	0.7	4
61	Purification, crystallization and preliminary X-ray diffraction analysis of pyridoxal kinase fromPlasmodium falciparum(PfPdxK). Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1550-1555.	0.4	4
62	Identification of a non-competitive inhibitor of Plasmodium falciparum aspartate transcarbamoylase. Biochemical and Biophysical Research Communications, 2018, 497, 835-842.	1.0	4
63	Oligomeric protein interference validates druggability of aspartate interconversion in Plasmodium falciparum. MicrobiologyOpen, 2019, 8, e779.	1.2	4
64	A synthetic peptide as an allosteric inhibitor of human arginase I and II. Molecular Biology Reports, 2021, 48, 1959-1966.	1.0	4
65	Elucidation of haem-binding sites in the actinobacterial protein HbpS. FEMS Microbiology Letters, 2013, 342, 106-112.	0.7	3
66	Design, synthesis and biological evaluation of 1,5-disubstituted Î±-amino tetrazole derivatives as non-covalent inflammasome-caspase-1 complex inhibitors with potential application against immune and inflammatory disorders. European Journal of Medicinal Chemistry, 2022, 229, 114002.	2.6	3
67	Thiosulfate sulfurtransferase prevents hyperglycemic damage to the zebrafish pronephros in an experimental model for diabetes. Scientific Reports, 2022, 12, .	1.6	3
68	The Pex4pâ€“Pex22p complex fromHansenula polymorpha: biophysical analysis, crystallization and X-ray diffraction characterization. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 76-81.	0.4	2
69	The Crystal Structure of the Plasmodium falciparum PdxK Provides an Experimental Model for Pro-Drug Activation. Crystals, 2019, 9, 534.	1.0	2
70	A fragment-based approach identifies an allosteric pocket that impacts malate dehydrogenase activity. Communications Biology, 2021, 4, 949.	2.0	2
71	Lipoic Acid Metabolism as a Potential Chemotherapeutic Target Against Plasmodium falciparum and Staphylococcus aureus. Frontiers in Chemistry, 2021, 9, 742175.	1.8	2
72	Novel Highlight in Malarial Drug Discovery: Aspartate Transcarbamoylase. Frontiers in Cellular and Infection Microbiology, 2022, 12, 841833.	1.8	2

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73	Feasibility of Follow-Up Studies and Reclassification in Spinocerebellar Ataxia Gene Variants of Unknown Significance. Frontiers in Genetics, 2022, 13, 782685.	1.1	2
74	Combining Highâ€Throughput Synthesis and Highâ€Throughput Protein Crystallography for Accelerated Hit Identification. Angewandte Chemie, 2021, 133, 18379-18387.	1.6	1
75	Crystallization and preliminary X-ray analysis of theThermoplasma acidophilum20S proteasome in complex with protein substrates. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 899-902.	0.7	0
76	Applications of Structural Biology and Bioinformatics in the Investigation of Oxidative Stress-Related Processes. , 2014, , 505-534.		0
77	Crystal structure of truncated human coatomer protein complex subunit Î¶1 (CopÎ¶1). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 1-8.	0.4	0