

Matthew Groves

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Synthetic Peptides That Antagonize the Angiotensin-Converting Enzyme-2 (ACE-2) Interaction with SARS-CoV-2 Receptor Binding Spike Protein. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 2836-2847. | 2.9 | 22 |
| 2 | Actionability of on-target ALK Resistance Mutations in Patients With Non-Small Cell Lung Cancer: Local Experience and Review of the Literature. <i>Clinical Lung Cancer</i> , 2022, 23, e104-e115. | 1.1 | 13 |
| 3 | Design, synthesis and biological evaluation of 1,5-disubstituted β -amino tetrazole derivatives as non-covalent inflammasome-caspase-1 complex inhibitors with potential application against immune and inflammatory disorders. <i>European Journal of Medicinal Chemistry</i> , 2022, 229, 114002. | 2.6 | 3 |
| 4 | Novel Highlight in Malarial Drug Discovery: Aspartate Transcarbamoylase. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 841833. | 1.8 | 2 |
| 5 | Feasibility of Follow-Up Studies and Reclassification in Spinocerebellar Ataxia Gene Variants of Unknown Significance. <i>Frontiers in Genetics</i> , 2022, 13, 782685. | 1.1 | 2 |
| 6 | First crystal structures of 1-deoxy-d-xylulose 5-phosphate synthase (DXPS) from <i>Mycobacterium tuberculosis</i> indicate a distinct mechanism of intermediate stabilization. <i>Scientific Reports</i> , 2022, 12, 7221. | 1.6 | 8 |
| 7 | Thiosulfate sulfurtransferase prevents hyperglycemic damage to the zebrafish pronephros in an experimental model for diabetes. <i>Scientific Reports</i> , 2022, 12, . | 1.6 | 3 |
| 8 | Nanoscale, automated, high throughput synthesis and screening for the accelerated discovery of protein modifiers. <i>RSC Medicinal Chemistry</i> , 2021, 12, 809-818. | 1.7 | 20 |
| 9 | Identification of a 1-deoxy-D-xylulose-5-phosphate synthase (DXS) mutant with improved crystallographic properties. <i>Biochemical and Biophysical Research Communications</i> , 2021, 539, 42-47. | 1.0 | 9 |
| 10 | A synthetic peptide as an allosteric inhibitor of human arginase I and II. <i>Molecular Biology Reports</i> , 2021, 48, 1959-1966. | 1.0 | 4 |
| 11 | The Human Milk Oligosaccharides 3 α -FL, Lacto-N β -Neotetraose, and LDFT Attenuate Tumor Necrosis Factor α -Induced Inflammation in Fetal Intestinal Epithelial Cells In Vitro through Shedding or Interacting with Tumor Necrosis Factor Receptor 1. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2000425. | 1.5 | 19 |
| 12 | Combining High-Throughput Synthesis and High-Throughput Protein Crystallography for Accelerated Hit Identification. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 18231-18239. | 7.2 | 19 |
| 13 | Combining High-Throughput Synthesis and High-Throughput Protein Crystallography for Accelerated Hit Identification. <i>Angewandte Chemie</i> , 2021, 133, 18379-18387. | 1.6 | 1 |
| 14 | A fragment-based approach identifies an allosteric pocket that impacts malate dehydrogenase activity. <i>Communications Biology</i> , 2021, 4, 949. | 2.0 | 2 |
| 15 | Lipoic Acid Metabolism as a Potential Chemotherapeutic Target Against <i>Plasmodium falciparum</i> and <i>Staphylococcus aureus</i> . <i>Frontiers in Chemistry</i> , 2021, 9, 742175. | 1.8 | 2 |
| 16 | Live and Let Dye: Visualizing the Cellular Compartments of the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 694-705. | 1.1 | 6 |
| 17 | A novel mechanism of inhibition by phenylthiourea on PvdP, a tyrosinase synthesizing pyoverdine of <i>Pseudomonas aeruginosa</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 146, 212-221. | 3.6 | 16 |
| 18 | Benchmark of Generic Shapes for Macrocycles. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 6298-6313. | 2.5 | 8 |

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| 19 | 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. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 76. | 7.1 | 16 |
| 20 | Molecular Target Validation of Aspartate Transcarbamoylase from <i>Plasmodium falciparum</i> by Torin 2. <i>ACS Infectious Diseases</i> , 2020, 6, 986-999. | 1.8 | 7 |
| 21 | Theory and applications of differential scanning fluorimetry in early-stage drug discovery. <i>Biophysical Reviews</i> , 2020, 12, 85-104. | 1.5 | 137 |
| 22 | New directions in antimalarial target validation. <i>Expert Opinion on Drug Discovery</i> , 2020, 15, 189-202. | 2.5 | 7 |
| 23 | Relevance and Effectiveness of Molecular Tumor Board Recommendations for Patients With Non-Small-Cell Lung Cancer With Rare or Complex Mutational Profiles. <i>JCO Precision Oncology</i> , 2020, 4, 393-410. | 1.5 | 32 |
| 24 | Rapid approach to complex boronic acids. <i>Science Advances</i> , 2019, 5, eaaw4607. | 4.7 | 30 |
| 25 | The (R)-enantiomer of the 6-chromanol derivate SUL-121 improves renal graft perfusion via antagonism of the α_1 -adrenoceptor. <i>Scientific Reports</i> , 2019, 9, 13. | 1.6 | 28 |
| 26 | Oligomeric protein interference validates druggability of aspartate interconversion in <i>Plasmodium falciparum</i> . <i>MicrobiologyOpen</i> , 2019, 8, e7779. | 1.2 | 4 |
| 27 | Acoustic Droplet Ejection Enabled Automated Reaction Scouting. <i>ACS Central Science</i> , 2019, 5, 451-457. | 5.3 | 40 |
| 28 | The Crystal Structure of the <i>Plasmodium falciparum</i> PdxK Provides an Experimental Model for Pro-Drug Activation. <i>Crystals</i> , 2019, 9, 534. | 1.0 | 2 |
| 29 | Identification of a non-competitive inhibitor of <i>Plasmodium falciparum</i> aspartate transcarbamoylase. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 835-842. | 1.0 | 4 |
| 30 | The Pex4p-Pex22p complex from <i>Hansenula polymorpha</i> : biophysical analysis, crystallization and X-ray diffraction characterization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 76-81. | 0.4 | 2 |
| 31 | Structural insights into K48-linked ubiquitin chain formation by the Pex4p-Pex22p complex. <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 562-567. | 1.0 | 6 |
| 32 | Afatinib in Osimertinib-Resistant EGFR ex19del/T790M/P794L Mutated NSCLC. <i>Journal of Thoracic Oncology</i> , 2018, 13, e161-e163. | 0.5 | 9 |
| 33 | Artificial macrocycles as IL-17A/IL-17RA antagonists. <i>MedChemComm</i> , 2018, 9, 22-26. | 3.5 | 20 |
| 34 | Oligomeric interfaces as a tool in drug discovery: Specific interference with activity of malate dehydrogenase of <i>Plasmodium falciparum</i> in vitro. <i>PLoS ONE</i> , 2018, 13, e0195011. | 1.1 | 15 |
| 35 | Isolation and molecular characterization of novel glucaripidases: Enzymes to improve the antibody directed enzyme pro-drug therapy for cancer treatment. <i>PLoS ONE</i> , 2018, 13, e0196254. | 1.1 | 16 |
| 36 | Crystal structure of truncated human coatamer protein complex subunit β 1 (Cop β 1). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 1-8. | 0.4 | 0 |

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|----|--|-----|-----------|
| 37 | A Systematic Protein Refolding Screen Method using the DGR Approach Reveals that Time and Secondary TSA are Essential Variables. <i>Scientific Reports</i> , 2017, 7, 9355. | 1.6 | 26 |
| 38 | DXS as a target for structure-based drug design. <i>Future Medicinal Chemistry</i> , 2017, 9, 1277-1294. | 1.1 | 12 |
| 39 | Tyrosine kinase inhibitor sensitive PDGFR ^T mutations in GIST: Two cases and review of the literature. <i>Oncotarget</i> , 2017, 8, 109836-109847. | 0.8 | 8 |
| 40 | Drug Target Validation Methods in Malaria - Protein Interference Assay (PIA) as a Tool for Highly Specific Drug Target Validation. <i>Current Drug Targets</i> , 2017, 18, 1069-1085. | 1.0 | 9 |
| 41 | Data collection with a tailored X-ray beam size at 2.69 Å... wavelength (4.6 keV): sulfur SAD phasing of Cdc23Nterm. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 403-412. | 1.1 | 10 |
| 42 | Crystal structure of truncated aspartate transcarbamoylase from <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 523-533. | 0.4 | 12 |
| 43 | Enzyme kinetics and inhibition of histone acetyltransferase KAT8. <i>European Journal of Medicinal Chemistry</i> , 2015, 105, 289-296. | 2.6 | 31 |
| 44 | Purification, crystallization and preliminary X-ray diffraction analysis of pyridoxal kinase from <i>Plasmodium falciparum</i> (PfPdxK). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1550-1555. | 0.4 | 4 |
| 45 | Applications of Structural Biology and Bioinformatics in the Investigation of Oxidative Stress-Related Processes. , 2014, , 505-534. | | 0 |
| 46 | A unique Oct4 interface is crucial for reprogramming to pluripotency. <i>Nature Cell Biology</i> , 2013, 15, 295-301. | 4.6 | 135 |
| 47 | Elucidation of haem-binding sites in the actinobacterial protein HbpS. <i>FEMS Microbiology Letters</i> , 2013, 342, 106-112. | 0.7 | 3 |
| 48 | Iron Binding at Specific Sites within the Octameric HbpS Protects Streptomycetes from Iron-Mediated Oxidative Stress. <i>PLoS ONE</i> , 2013, 8, e71579. | 1.1 | 12 |
| 49 | Internal structure of an intact <i>Convallaria majalis</i> pollen grain observed with X-ray Fresnel coherent diffractive imaging. <i>Optics Express</i> , 2012, 20, 26778. | 1.7 | 6 |
| 50 | Aspartate Aminotransferase - Bridging Carbohydrate and Energy Metabolism in <i>Plasmodium falciparum</i> . <i>Current Drug Metabolism</i> , 2012, 13, 332-336. | 0.7 | 15 |
| 51 | ROS-Mediated Signalling in Bacteria: Zinc-Containing Cys-X-X-Cys Redox Centres and Iron-Based Oxidative Stress. <i>Journal of Signal Transduction</i> , 2012, 2012, 1-9. | 2.0 | 100 |
| 52 | Novel Redox-Sensing Modules: Accessory Protein- and Nucleic Acid-Mediated Signaling. <i>Antioxidants and Redox Signaling</i> , 2012, 16, 668-677. | 2.5 | 13 |
| 53 | Cytometric quantification of singlet oxygen in the human malaria parasite <i>Plasmodium falciparum</i> . <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012, 81A, 698-703. | 1.1 | 7 |
| 54 | Crystallization and preliminary X-ray diffraction of malate dehydrogenase from <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 659-662. | 0.7 | 4 |

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|----|--|-----|-----------|
| 55 | Specific Inhibition of the Aspartate Aminotransferase of <i>Plasmodium falciparum</i> . <i>Journal of Molecular Biology</i> , 2011, 405, 956-971. | 2.0 | 42 |
| 56 | Dynamic Substrate Enhancement for the Identification of Specific, Second-Site Binding Fragments Targeting a Set of Protein Tyrosine Phosphatases. <i>ChemBioChem</i> , 2011, 12, 2640-2646. | 1.3 | 25 |
| 57 | Quantitative evaluation of macromolecular crystallization experiments using 1,8-ANS fluorescence. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 901-908. | 2.5 | 13 |
| 58 | Purification, crystallization and preliminary X-ray analysis of the aspartate aminotransferase of <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 409-412. | 0.7 | 10 |
| 59 | The Vitamin B1 Metabolism of <i>Staphylococcus aureus</i> Is Controlled at Enzymatic and Transcriptional Levels. <i>PLoS ONE</i> , 2009, 4, e7656. | 1.1 | 24 |
| 60 | Fatty Acid- and Retinoid-binding Proteins Have Distinct Binding Pockets for the Two Types of Cargo. <i>Journal of Biological Chemistry</i> , 2009, 284, 35818-35826. | 1.6 | 31 |
| 61 | The three-component signalling system Hbp-Sen-SenR as an example of a redox sensing pathway in bacteria. <i>Amino Acids</i> , 2009, 37, 479-486. | 1.2 | 41 |
| 62 | Mobility of the conserved glycine 155 is required for formation of the active plasmodial Pdx1 dodecamer. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2009, 1790, 347-350. | 1.1 | 7 |
| 63 | The Oligomeric Assembly of the Novel Haem-Degrading Protein HbpS Is Essential for Interaction with Its Cognate Two-Component Sensor Kinase. <i>Journal of Molecular Biology</i> , 2009, 386, 1108-1122. | 2.0 | 22 |
| 64 | Crystallization and preliminary characterization of a novel haem-binding protein of <i>Streptomyces reticuli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 386-390. | 0.7 | 13 |
| 65 | Crystallization and preliminary X-ray analysis of the <i>Thermoplasma acidophilum</i> 20S proteasome in complex with protein substrates. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 899-902. | 0.7 | 0 |
| 66 | Methods for Protein Characterization by Mass Spectrometry, Thermal Shift (ThermoFluor) Assay, and Multiangle or Static Light Scattering. <i>Methods in Molecular Biology</i> , 2008, 426, 299-318. | 0.4 | 118 |
| 67 | The Assembly of the Plasmodial PLP Synthase Complex Follows a Defined Course. <i>PLoS ONE</i> , 2008, 3, e1815. | 1.1 | 20 |
| 68 | Canonical Signal Recognition Particle Components Can Be Bypassed for Posttranslational Protein Targeting in Chloroplasts. <i>Plant Cell</i> , 2007, 19, 1635-1648. | 3.1 | 63 |
| 69 | Octameric alcohol oxidase dissociates into stable, soluble monomers upon incubation with dimethylsulfoxide. <i>Archives of Biochemistry and Biophysics</i> , 2007, 459, 208-213. | 1.4 | 8 |
| 70 | A method for the general identification of protein crystals in crystallization experiments using a noncovalent fluorescent dye. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 526-535. | 2.5 | 43 |
| 71 | The impact of protein characterization in structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1125-1136. | 2.5 | 58 |
| 72 | Crystallization of a Golgi-associated PR-1-related protein (GAPR-1) that localizes to lipid-enriched microdomains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 730-732. | 2.5 | 12 |

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| 73 | Structural Analysis of the Human Golgi-associated Plant Pathogenesis Related Protein CAPR-1 Implicates Dimerization as a Regulatory Mechanism. <i>Journal of Molecular Biology</i> , 2004, 339, 173-183. | 2.0 | 66 |
| 74 | Definition of domain boundaries and crystallization of the SMN Tudor domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 366-368. | 2.5 | 17 |
| 75 | High-resolution X-ray and NMR Structures of the SMN Tudor Domain: Conformational Variation in the Binding Site for Symmetrically Dimethylated Arginine Residues. <i>Journal of Molecular Biology</i> , 2003, 327, 507-520. | 2.0 | 155 |
| 76 | Functional Characterization of Recombinant Chloroplast Signal Recognition Particle. <i>Journal of Biological Chemistry</i> , 2001, 276, 27778-27786. | 1.6 | 70 |
| 77 | Identification and Validation of Novel Drug Targets for the Treatment of Plasmodium falciparum Malaria: New Insights. , 0, , . | | 8 |