Stephen Muench

List of Publications by Year
in descending order

107 papers	5,007 citations	126907 33 h-index	106344 65 g-index
122 all docs	122 docs citations	122 times ranked	7026 citing authors

#	Article	IF	Citations
1	Moving in the mesoscale: Understanding the mechanics of cytoskeletal molecular motors by combining mesoscale simulations with imaging. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, e1570.	14.6	1
2	Tyrosine 288 in the extracellular domain of the human <scp>P2X7</scp> receptor is critical for receptor function revealed by structural modeling and siteâ€directed mutagenesis. Proteins: Structure, Function and Bioinformatics, 2022, 90, 619-624.	2.6	0
3	Recent developments in the structural characterisation of the IR and IGF1R: implications for the design of IRâ€“IGF1R hybrid receptor modulators. RSC Medicinal Chemistry, 2022, 13, 360-374.	3.9	12
4	Detergent-Free Functionalization of Hybrid Vesicles with Membrane Proteins Using SMALPs. Macromolecules, 2022, 55, 3415-3422.	4.8	4
5	Cryo-EM structure of human mitochondrial HSPD1. IScience, 2021, 24, 102022.	4.1	16
6	Structure of the endocytic adaptor complex reveals the basis for efficient membrane anchoring during clathrin-mediated endocytosis. Nature Communications, 2021, 12, 2889.	12.8	13
7	Targeting KNa1.1 channels in KCNT1-associated epilepsy. Trends in Pharmacological Sciences, 2021, 42, 700-713.	8.7	18
8	On-grid and in-flow mixing for time-resolved cryo-EM. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1233-1240.	2.3	14
9	Fast Grid Preparation for Time-Resolved Cryo-Electron Microscopy. Journal of Visualized Experiments, 2021, , .	0.3	0
10	Cycloalkane-modified amphiphilic polymers provide direct extraction of membrane proteins for CryoEM analysis. Communications Biology, 2021, 4, 1337.	4.4	13
11	Styrene maleic-acid lipid particles (SMALPs) into detergent or amphipols: An exchange protocol for membrane protein characterisation. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183192.	2.6	27
12	Unprecedented Properties of Phenothiazines Unraveled by a NDH-2 Bioelectrochemical Assay Platform. Journal of the American Chemical Society, 2020, 142, 1311-1320.	13.7	18
13	Need for Speed: Examining Protein Behavior during CryoEM Grid Preparation at Different Timescales. Structure, 2020, 28, 1238-1248.e4.	3.3	61
14	Contribution of Val/Ile87 residue in the extracellular domain in agonist-induced current responses of the human and rat P2X7 receptors. Purinergic Signalling, 2020, 16, 485-490.	2.2	4
15	Human TRPC5 structures reveal interaction of a xanthine-based TRPC1/4/5 inhibitor with a conserved lipid binding site. Communications Biology, 2020, 3, 704.	4.4	36
16	Xanthine-based photoaffinity probes allow assessment of ligand engagement by TRPC5 channels. RSC Chemical Biology, 2020, 1, 436-448.	4.1	9
17	Structural Basis for Vascular Endothelial Growth Factor Receptor Activation and Implications for Disease Therapy. Biomolecules, 2020, 10, 1673.	4.0	43
18	Structure-Based Identification and Characterization of Inhibitors of the Epilepsy-Associated KNa1.1 (KCNT1) Potassium Channel. IScience, 2020, 23, 101100.	4.1	29

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19	Potent Tetrahydroquinolone Eliminates Apicomplexan Parasites. Frontiers in Cellular and Infection Microbiology, 2020, 10, 203.	3.9	21
20	Cryo-EM Structure and Molecular Dynamics Analysis of the Fluoroquinolone Resistant Mutant of the AcrB Transporter from Salmonella. Microorganisms, 2020, 8, 943.	3.6	25
21	Structure of the protective nematode protease complex H-gal-GP and its conservation across roundworm parasites. PLoS Pathogens, 2020, 16, e1008465.	4.7	15
22	The active form of quinol-dependent nitric oxide reductase from Neisseria meningitidis is a dimer. IUCrJ, 2020, 7, 404-415.	2.2	10
23	Sample deposition onto cryo-EM grids: from sprays to jets and back. Acta Crystallographica Section D: Structural Biology, 2020, 76, 340-349.	2.3	23
24	Emerging Role of Electron Microscopy in Drug Discovery. Trends in Biochemical Sciences, 2019, 44, 897-898.	7.5	3
25	Structural Insight into Eukaryotic Sterol Transport through Niemann-Pick Type C Proteins. Cell, 2019, 179, 485-497.e18.	28.9	110
26	SMA-PAGE: A new method to examine complexes of membrane proteins using SMALP nano-encapsulation and native gel electrophoresis. Biochimica Et Biophysica Acta - Biomembranes, 2019, 1861, 1437-1445.	2.6	22
27	Dimeric structures of quinol-dependent nitric oxide reductases (qNORs) revealed by cryoâ€“electron microscopy. Science Advances, 2019, 5, eaax1803.	10.3	14
28	Styrene maleic acid recovers proteins from mammalian cells and tissues while avoiding significant cell death. Scientific Reports, 2019, 9, 16408.	3.3	3
29	The expanding toolkit for structural biology: synchrotrons, X-ray lasers and cryoEM. IUCrJ, 2019, 6, 167-177.	2.2	36
30	A cryo-EM grid preparation device for time-resolved structural studies. IUCrJ, 2019, 6, 1024-1031.	2.2	77
31	LAT1 (SLC7A5) and CD98hc (SLC3A2) complex dynamics revealed by single-particle cryo-EM. Acta Crystallographica Section D: Structural Biology, 2019, 75, 660-669.	2.3	16
32	The Growing Role of Electron Microscopy in Anti-parasitic Drug Discovery. Current Medicinal Chemistry, 2019, 25, 5279-5290.	2.4	2
33	The Vacuolar ATPase â€“ A Nano-scale Motor That Drives Cell Biology. Sub-Cellular Biochemistry, 2018, 87, 409-459.	2.4	21
34	A reconstitution method for integral membrane proteins in hybrid lipid-polymer vesicles for enhanced functional durability. Methods, 2018, 147, 142-149.	3.8	30
35	Elucidating the structural basis for differing enzyme inhibitor potency by cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1795-1800.	7.1	24
36	No Longer Hidden Secrets of Proton Pumping: The Resolution Revolution Enlightens V-ATPases. Molecular Cell, 2018, 69, 921-922.	9.7	1

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37	Using a SMALP platform to determine a sub-nm single particle cryo-EM membrane protein structure. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 378-383.	2.6	88
38	Substrate polyspecificity and conformational relevance in ABC transporters: new insights from structural studies. Biochemical Society Transactions, 2018, 46, 1475-1484.	3.4	16
39	CSGID Solves Structures and Identifies Phenotypes for Five Enzymes in Toxoplasma gondii. Frontiers in Cellular and Infection Microbiology, 2018, 8, 352.	3.9	14
40	Approaches to altering particle distributions in cryo-electron microscopy sample preparation. Acta Crystallographica Section D: Structural Biology, 2018, 74, 560-571.	2.3	108
41	X-ray and cryo-EM structures of inhibitor-bound cytochromebc₁complexes for structure-based drug discovery. IUCrJ, 2018, 5, 200-210.	2.2	23
42	Spherical-supported membranes as platforms for screening against membrane protein targets. Analytical Biochemistry, 2018, 549, 58-65.	2.4	6
43	Cryo-EM structures of complex I from mouse heart mitochondria in two biochemically defined states. Nature Structural and Molecular Biology, 2018, 25, 548-556.	8.2	202
44	EM studies of cytochrome bc 1 to elucidate inhibitor binding. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a121-a121.	0.1	0
45	Durable vesicles for reconstitution of membrane proteins in biotechnology. Biochemical Society Transactions, 2017, 45, 15-26.	3.4	53
46	The potential use of single-particle electron microscopy as a tool for structure-based inhibitor design. Acta Crystallographica Section D: Structural Biology, 2017, 73, 534-540.	2.3	8
47	TRPA1â€“FGFR2 binding event is a regulatory oncogenic driver modulated by miRNA-142-3p. Nature Communications, 2017, 8, 947.	12.8	56
48	AtSPX1 affects the AtPHR1â€“DNA-binding equilibrium by binding monomeric AtPHR1 in solution. Biochemical Journal, 2017, 474, 3675-3687.	3.7	36
49	Conformational changes during human P2X7 receptor activation examined by structural modelling and cysteine-based cross-linking studies. Purinergic Signalling, 2017, 13, 135-141.	2.2	7
50	Everyone needs good neighbours â€“ the intricate relationship between the acetylcholine-receptor channel and its membrane environment. IUCrJ, 2017, 4, 306-307.	2.2	0
51	Characterization of the flexibility of the peripheral stalk of prokaryotic rotary A-ATPases by atomistic simulations. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1203-1212.	2.6	2
52	New paradigms for understanding and step changes in treating active and chronic, persistent apicomplexan infections. Scientific Reports, 2016, 6, 29179.	3.3	40
53	The conservation of phosphate-binding residues among PHT1 transporters suggests that distinct transport affinities are unlikely to result from differences in the phosphate-binding site. Biochemical Society Transactions, 2016, 44, 1541-1548.	3.4	18
54	Extracellular and Luminal pH Regulation by Vacuolar H+-ATPase Isoform Expression and Targeting to the Plasma Membrane and Endosomes. Journal of Biological Chemistry, 2016, 291, 8500-8515.	3.4	37

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55	Methods to account for movement and flexibility in cryo-EM data processing. Methods, 2016, 100, 35-41.	3.8	25
56	Editorial. Methods, 2016, 100, 1-2.	3.8	0
57	An introduction to sample preparation and imaging by cryo-electron microscopy for structural biology. Methods, 2016, 100, 3-15.	3.8	178
58	Pi sensing and signalling: from prokaryotic to eukaryotic cells. Biochemical Society Transactions, 2016, 44, 766-773.	3.4	20
59	The varied functions of aluminium-activated malate transportersâ€“much more than aluminium resistance. Biochemical Society Transactions, 2016, 44, 856-862.	3.4	39
60	Rotating with the brakes on and other unresolved features of the vacuolar ATPase. Biochemical Society Transactions, 2016, 44, 851-855.	3.4	8
61	Artificial membranes for membrane protein purification, functionality and structure studies. Biochemical Society Transactions, 2016, 44, 877-882.	3.4	26
62	Polymer-Based Organic Batteries. Chemical Reviews, 2016, 116, 9438-9484.	47.7	919
63	Structure-based identification and characterisation of structurally novel human P2X7 receptor antagonists. Biochemical Pharmacology, 2016, 116, 130-139.	4.4	24
64	Durable proteo-hybrid vesicles for the extended functional lifetime of membrane proteins in bionanotechnology. Chemical Communications, 2016, 52, 11020-11023.	4.1	67
65	The changing landscape of membrane protein structural biology through developments in electron microscopy. Molecular Membrane Biology, 2016, 33, 12-22.	2.0	40
66	A method for detergent-free isolation of membrane proteins in their local lipid environment. Nature Protocols, 2016, 11, 1149-1162.	12.0	305
67	Mechanism of inhibition of mouse <scp>S</scp>lo3 (<scp>K</scp>_{Ca}5.1) potassium channels by quinine, quinidine and barium. British Journal of Pharmacology, 2015, 172, 4355-4363.	5.4	20
68	In situ formation of magnetopolymersomes via electroporation for MRI. Scientific Reports, 2015, 5, 14311.	3.3	18
69	The Acanthamoeba Shikimate Pathway has a Unique Molecular Arrangement and is Essential for Aromatic Amino Acid Biosynthesis. Protist, 2015, 166, 93-105.	1.5	19
70	Structure of the Vacuolar H + -ATPase Rotary Motor Reveals New Mechanistic Insights. Structure, 2015, 23, 461-471.	3.3	34
71	Docking of competitive inhibitors to the P2X7 receptor family reveals key differences responsible for changes in response between rat and human. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 3164-3167.	2.2	24
72	The use of SMALPs as a novel membrane protein scaffold for structure study by negative stain electron microscopy. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 496-501.	2.6	139

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73	Replace, reuse, recycle: improving the sustainable use of phosphorus by plants. Journal of Experimental Botany, 2015, 66, 3523-3540.	4.8	135
74	A Tribute to Stephen Allan Baldwin. Molecular Membrane Biology, 2015, 32, 33-34.	2.0	0
75	Non-Synonymous Single Nucleotide Polymorphisms in the P2X Receptor Genes: Association with Diseases, Impact on Receptor Functions and Potential Use as Diagnosis Biomarkers. International Journal of Molecular Sciences, 2014, 15, 13344-13371.	4.1	45
76	PA1b Inhibitor Binding to Subunits c and e of the Vacuolar ATPase Reveals Its Insecticidal Mechanism. Journal of Biological Chemistry, 2014, 289, 16399-16408.	3.4	28
77	Spiroindolone That Inhibits PfATPase4 Is a Potent, Cidal Inhibitor of Toxoplasma gondii Tachyzoites In Vitro and In Vivo. Antimicrobial Agents and Chemotherapy, 2014, 58, 1789-1792.	3.2	25
78	ALOX12 in Human Toxoplasmosis. Infection and Immunity, 2014, 82, 2670-2679.	2.2	28
79	Subunit Positioning and Stator Filament Stiffness in Regulation and Power Transmission in the V1 Motor of the Manduca sexta V-ATPase. Journal of Molecular Biology, 2014, 426, 286-300.	4.2	24
80	The benzimidazole based drugs show good activity against T. gondii but poor activity against its proposed enoyl reductase enzyme target. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 911-916.	2.2	4
81	Understanding the apparent statorâ€rotor connections in the rotary <scp>ATP</scp>ase family using coarseâ€grained computer modeling. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3298-3311.	2.6	14
82	Design, synthesis, and biological activity of diaryl ether inhibitors of Toxoplasma gondii enoyl reductase. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 2035-2043.	2.2	21
83	Development of a triclosan scaffold which allows for adaptations on both the A- and B-ring for transport peptides. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 3551-3555.	2.2	12
84	Discrimination of Potent Inhibitors of Toxoplasma gondii Enoyl-Acyl Carrier Protein Reductase by a Thermal Shift Assay. Biochemistry, 2013, 52, 9155-9166.	2.5	8
85	Modification of Triclosan Scaffold in Search of Improved Inhibitors for Enoylâ€Acyl Carrier Protein (ACP) Reductase in Toxoplasma gondii. ChemMedChem, 2013, 8, 1138-1160.	3.2	20
86	Flexibility within the Rotor and Stators of the Vacuolar H+-ATPase. PLoS ONE, 2013, 8, e82207.	2.5	16
87	Novel N -Benzoyl-2-Hydroxybenzamide Disrupts Unique Parasite Secretory Pathway. Antimicrobial Agents and Chemotherapy, 2012, 56, 2666-2682.	3.2	32
88	Structural divergence of the rotary ATPases. Quarterly Reviews of Biophysics, 2011, 44, 311-356.	5.7	119
89	T. gondii RP Promoters & Knockdown Reveal Molecular Pathways Associated with Proliferation and Cell-Cycle Arrest. PLoS ONE, 2010, 5, e14057.	2.5	28
90	Archazolid A Binds to the Equatorial Region of the c-Ring of the Vacuolar H+-ATPase*. Journal of Biological Chemistry, 2010, 285, 38304-38314.	3.4	44

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91	Identification of T. gondii epitopes, adjuvants, and host genetic factors that influence protection of mice and humans. Vaccine, 2010, 28, 3977-3989.	3.8	66
92	Identification and Development of Novel Inhibitors of Toxoplasma gondii Enoyl Reductase. Journal of Medicinal Chemistry, 2010, 53, 6287-6300.	6.4	46
93	Cryo-electron Microscopy of the Vacuolar ATPase Motor Reveals its Mechanical and Regulatory Complexity. Journal of Molecular Biology, 2009, 386, 989-999.	4.2	95
94	Molecular Basis for Resistance of Acanthamoeba Tubulins to All Major Classes of Antitubulin Compounds. Antimicrobial Agents and Chemotherapy, 2008, 52, 1133-1135.	3.2	32
95	Novel Triazine JPC-2067-B Inhibits Toxoplasma gondii In Vitro and In Vivo. PLoS Neglected Tropical Diseases, 2008, 2, e190.	3.0	50
96	Type I and type II fatty acid biosynthesis inEimeria tenella: enoyl reductase activity and structure. Parasitology, 2007, 134, 1949-1962.	1.5	23
97	Studies ofToxoplasma gondiiandPlasmodium falciparumenoyl acyl carrier protein reductase and implications for the development of antiparasitic agents. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 328-338.	2.5	40
98	Enzymes of type II fatty acid synthesis and apicoplast differentiation and division in Eimeria tenella. International Journal for Parasitology, 2007, 37, 33-51.	3.1	39
99	Cloning, purification and preliminary crystallographic analysis of theBacillus subtilisGTPase YphCâ€“GDP complex. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 435-437.	0.7	3
100	Expression, purification and preliminary crystallographic analysis of theToxoplasma gondiienoyl reductase. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 604-606.	0.7	9
101	The essential GTPase YphC displays a major domain rearrangement associated with nucleotide binding. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12359-12364.	7.1	35
102	Maternal Inheritance and Stage-Specific Variation of the Apicoplast in Toxoplasma gondii during Development in the Intermediate and Definitive Host. Eukaryotic Cell, 2005, 4, 814-826.	3.4	90
103	Expression, purification and crystallization of thePlasmodium falciparumenoyl reductase. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1246-1248.	2.5	25
104	Delivery of antimicrobials into parasites. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14281-14286.	7.1	72
105	Crystallization and preliminary X-ray crystallographic studies on the class II cholesterol oxidase fromBurkholderia cepaciacontaining bound flavin. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2182-2183.	2.5	2
106	Triclosan inhibits the growth of Plasmodium falciparum and Toxoplasma gondii by inhibition of Apicomplexan Fab I. International Journal for Parasitology, 2001, 31, 109-113.	3.1	190
107	Need for Speed: Examining Protein Behaviour During CryoEM Grid Preparation at Different Timescales. SSRN Electronic Journal, 0, , .	0.4	1