

JÃ¼rgen Bosch

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

7,606
citations

331670

21
h-index

206112

48
g-index

57
all docs

57
docs citations

57
times ranked

17489
citing authors

#	ARTICLE	IF	CITATIONS
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
2	Guidelines for the use and interpretation of assays for monitoring autophagy (4th) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td (edition) 1,430	9.1	1,430
3	Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. <i>PLoS Pathogens</i> , 2016, 12, e1005763.	4.7	244
4	The apicomplexan glideosome and adhesins â€“ Structures and function. <i>Journal of Structural Biology</i> , 2015, 190, 93-114.	2.8	113
5	Aldolase provides an unusual binding site for thrombospondin-related anonymous protein in the invasion machinery of the malaria parasite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7015-7020.	7.1	76
6	Structure of the MTIP-MyoA complex, a key component of the malaria parasite invasion motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4852-4857.	7.1	67
7	Using Fragment Cocktail Crystallography To Assist Inhibitor Design of <i>Trypanosoma brucei</i> Nucleoside 2-Deoxyribosyltransferaseâ€™. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 5939-5946.	6.4	66
8	Structural characterization and inhibition of the <i>Plasmodium</i> Atg8â€™Atg3 interaction. <i>Journal of Structural Biology</i> , 2012, 180, 551-562.	2.8	58
9	The Closed MTIP-Myosin A-Tail Complex from the Malaria Parasite Invasion Machinery. <i>Journal of Molecular Biology</i> , 2007, 372, 77-88.	4.2	51
10	Identification of Biochemically Distinct Properties of the Small Ubiquitin-related Modifier (SUMO) Conjugation Pathway in <i>Plasmodium falciparum</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 27724-27736.	3.4	51
11	Identification of an Atg8-Atg3 Proteinâ€™Protein Interaction Inhibitor from the Medicines for Malaria Venture Malaria Box Active in Blood and Liver Stage <i>Plasmodium falciparum</i> Parasites. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 4521-4531.	6.4	46
12	Microfluidic assessment of red blood cell mediated microvascular occlusion. <i>Lab on A Chip</i> , 2020, 20, 2086-2099.	6.0	46
13	Characterization of the ATG8-conjugation system in <i>Plasmodium</i> species with special focus on the liver stage. <i>Autophagy</i> , 2014, 10, 269-284.	9.1	42
14	<i>Chromobacterium</i> spp. mediate their anti- <i>Plasmodium</i> activity through secretion of the histone deacetylase inhibitor romidepsin. <i>Scientific Reports</i> , 2018, 8, 6176.	3.3	40
15	Structural Genomics of Pathogenic Protozoa: an Overview. <i>Methods in Molecular Biology</i> , 2008, 426, 497-513.	0.9	38
16	Fragment-Based Cocktail Crystallography by the Medical Structural Genomics of Pathogenic Protozoa Consortium. <i>Current Topics in Medicinal Chemistry</i> , 2009, 9, 1678-1687.	2.1	36
17	Crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>Plasmodium falciparum</i> at 2.25 Å... resolution reveals intriguing extra electron density in the active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 570-577.	2.6	34
18	DXP Synthaseâ€™Catalyzed C-N Bond Formation: Nitroso Substrate Specificity Studies Guide Selective Inhibitor Design. <i>ChemBioChem</i> , 2013, 14, 1309-1315.	2.6	29

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19	Crystal structure of GAP50, the anchor of the invasion machinery in the inner membrane complex of <i>Plasmodium falciparum</i> . <i>Journal of Structural Biology</i> , 2012, 178, 61-73.	2.8	28
20	High-Throughput Activity Assay for Screening Inhibitors of the SARS-CoV-2 Mac1 Macrodomein. <i>ACS Chemical Biology</i> , 2022, 17, 17-23.	3.4	28
21	Structural and mechanistic insights into the function of the unconventional class XIV myosin MyoA from <i>Toxoplasma gondii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10548-E10555.	7.1	27
22	AUTOPHAGY IN PLASMODIUM, A MULTIFUNCTIONAL PATHWAY?. <i>Computational and Structural Biotechnology Journal</i> , 2013, 8, e201308002.	4.1	26
23	PPI inhibitor and stabilizer development in human diseases. <i>Drug Discovery Today: Technologies</i> , 2017, 24, 3-9.	4.0	23
24	The Conserved Macrodomein Is a Potential Therapeutic Target for Coronaviruses and Alphaviruses. <i>Pathogens</i> , 2022, 11, 94.	2.8	21
25	Structure of a ribulose 5-phosphate 3-epimerase from <i>Plasmodium falciparum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 338-342.	2.6	20
26	Inhibition by stabilization: targeting the <i>Plasmodium falciparum</i> aldolase-TRAP complex. <i>Malaria Journal</i> , 2015, 14, 324.	2.3	20
27	Virtual Screening and Experimental Validation Identify Novel Inhibitors of the <i>Plasmodium falciparum</i> Atg8-Atg3 Protein-Protein Interaction. <i>ChemMedChem</i> , 2016, 11, 900-910.	3.2	20
28	Voltage-gated potassium channel proteins and stereoselective S-nitroso-l-cysteine signaling. <i>JCI Insight</i> , 2020, 5, .	5.0	20
29	The Bactofilin Cytoskeleton Protein BacM of <i>Myxococcus xanthus</i> Forms an Extended β^2 -Sheet Structure Likely Mediated by Hydrophobic Interactions. <i>PLoS ONE</i> , 2015, 10, e0121074.	2.5	18
30	Novel Antifungal Compounds Discovered in Medicines for Malaria Venture's Malaria Box. <i>MSphere</i> , 2018, 3, .	2.9	18
31	Identification of Novel Ezrin Inhibitors Targeting Metastatic Osteosarcoma by Screening Open Access Malaria Box. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 2497-2507.	4.1	17
32	Binding of Aldolase and Glyceraldehyde-3-Phosphate Dehydrogenase to the Cytoplasmic Tails of <i>Plasmodium falciparum</i> Merozoite Duffy Binding-Like and Reticulocyte Homology Ligands. <i>MBio</i> , 2012, 3, .	4.1	16
33	Structure of <i>Chlamydomonas reinhardtii</i> THB1, a group 1 truncated hemoglobin with a rare histidine-lysine heme ligation. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 718-725.	0.8	15
34	Characterization and Structural Insights into Selective E1-E2 Interactions in the Human and <i>Plasmodium falciparum</i> SUMO Conjugation Systems. <i>Journal of Biological Chemistry</i> , 2016, 291, 3860-3870.	3.4	15
35	A BAC Transgene Expressing Human CFTR under Control of Its Regulatory Elements Rescues Cftr Knockout Mice. <i>Scientific Reports</i> , 2019, 9, 11828.	3.3	14
36	Development of small molecule inhibitors targeting PBX1 transcription signaling as a novel cancer therapeutic strategy. <i>IScience</i> , 2021, 24, 103297.	4.1	12

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37	Development of a multifunctional tool for drug screening against plasmodial protein-protein interactions via surface plasmon resonance. <i>Journal of Molecular Recognition</i> , 2013, 26, 496-500.	2.1	11
38	Structure of <i>Toxoplasma gondii</i> fructose-1,6-bisphosphate aldolase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1186-1192.	0.8	9
39	Structure-based drug design, synthesis and biological assays of <i>P. falciparum</i> Atg3-Atg8 protein-protein interaction inhibitors. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 473-486.	2.9	9
40	The Î²-propeller domain of the trilobed protease from <i>Pyrococcus furiosus</i> reveals an open Velcro topology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 179-187.	2.5	7
41	The 1.75-Å resolution structure of fission protein Fis1 from <i>Saccharomyces cerevisiae</i> reveals elusive interactions of the autoinhibitory domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1310-1315.	0.7	7
42	Structure-Based Screening of <i>Plasmodium berghei</i> Glutathione S-Transferase Identifies CB-27 as a Novel Antiplasmodial Compound. <i>Frontiers in Pharmacology</i> , 2020, 11, 246.	3.5	7
43	Discovery of <i>Plasmodium</i> (M)TRAP Aldolase Interaction Stabilizers Interfering with Sporozoite Motility and Invasion. <i>ACS Infectious Diseases</i> , 2018, 4, 620-634.	3.8	6
44	Cyclic compression increases F508 Del CFTR expression in ciliated human airway epithelium. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2019, 317, L247-L258.	2.9	6
45	Purification, Crystallization, and Preliminary X-ray Diffraction Analysis of the Tricorn Protease Hexamer from <i>Thermoplasma acidophilum</i> . <i>Journal of Structural Biology</i> , 2001, 134, 83-87.	2.8	5
46	The structure of <i>Plasmodium falciparum</i> 3D7_0606800 reveals a bilobed architecture that supports re-annotation as a Venus Flytrap protein. <i>Protein Science</i> , 2017, 26, 1878-1885.	7.6	2
47	Purification Strategies and Assay Development for an Essential Plasmodial Protease. <i>Biophysical Journal</i> , 2013, 104, 404a.	0.5	1
48	Immunization against a merozoite sheddase promotes multiple invasion of red blood cells and attenuates <i>Plasmodium</i> infection in mice. <i>Malaria Journal</i> , 2014, 13, 313.	2.3	1
49	Differential Fragment SPR (DF-SPR) for Antimalarial Drug Screening. <i>Biophysical Journal</i> , 2013, 104, 380a.	0.5	0
50	Sustained Crystallography Skills through Multimedia-Supported Active Learning. <i>Biophysical Journal</i> , 2014, 106, 218a-219a.	0.5	0
51	Identification of Protein-Protein-Interaction (PPI) Inhibitors and Stabilizers for Antimalarial Drug Development using SPR. <i>Biophysical Journal</i> , 2014, 106, 477a.	0.5	0
52	Targeting the SUMO E1-E2 Enzyme Interaction in <i>Plasmodium falciparum</i> . <i>FASEB Journal</i> , 2015, 29, 717.20.	0.5	0