JÃ¼rgen Bosch

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3652329/publications.pdf

Version: 2024-02-01

52	7,606	331670	206112
papers	citations	21 h-index	48 g-index

57	57	57	17489
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Conserved Macrodomain Is a Potential Therapeutic Target for Coronaviruses and Alphaviruses. Pathogens, 2022, 11, 94.	2.8	21
2	High-Throughput Activity Assay for Screening Inhibitors of the SARS-CoV-2 Mac1 Macrodomain. ACS Chemical Biology, 2022, 17, 17-23.	3.4	28
3	Guidelines for the use and interpretation of assays for monitoring autophagy (4th) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 662	9.1	1,430
4	Development of small molecule inhibitors targeting PBX1 transcription signaling as a novel cancer therapeutic strategy. IScience, 2021, 24, 103297.	4.1	12
5	Structure-Based Screening of Plasmodium berghei Glutathione S-Transferase Identifies CB-27 as a Novel Antiplasmodial Compound. Frontiers in Pharmacology, 2020, 11, 246.	3.5	7
6	Microfluidic assessment of red blood cell mediated microvascular occlusion. Lab on A Chip, 2020, 20, 2086-2099.	6.0	46
7	Voltage-gated potassium channel proteins and stereoselective S-nitroso-l-cysteine signaling. JCI Insight, 2020, 5, .	5.0	20
8	A BAC Transgene Expressing Human CFTR under Control of Its Regulatory Elements Rescues Cftr Knockout Mice. Scientific Reports, 2019, 9, 11828.	3.3	14
9	Cyclic compression increases F508 Del CFTR expression in ciliated human airway epithelium. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2019, 317, L247-L258.	2.9	6
10	Chromobacterium spp. mediate their anti-Plasmodium activity through secretion of the histone deacetylase inhibitor romidepsin. Scientific Reports, 2018, 8, 6176.	3.3	40
11	Structure-based drug design, synthesis and biological assays of P. falciparum Atg3â€“Atg8 proteinâ€“protein interaction inhibitors. Journal of Computer-Aided Molecular Design, 2018, 32, 473-486.	2.9	9
12	Discovery of Plasmodium (M)TRAPâ€“Aldolase Interaction Stabilizers Interfering with Sporozoite Motility and Invasion. ACS Infectious Diseases, 2018, 4, 620-634.	3.8	6
13	Novel Antifungal Compounds Discovered in Medicines for Malaria Ventureâ€™s Malaria Box. MSphere, 2018, 3, .	2.9	18
14	Structural and mechanistic insights into the function of the unconventional class XIV myosin MyoA from Toxoplasma gondii. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10548-E10555.	7.1	27
15	The structure of Plasmodium falciparum 3D7_0606800 reveals a biâ€lobed architecture that supports reâ€annotation as a Venus Flytrap protein. Protein Science, 2017, 26, 1878-1885.	7.6	2
16	PPI inhibitor and stabilizer development in human diseases. Drug Discovery Today: Technologies, 2017, 24, 3-9.	4.0	23
17	Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. PLoS Pathogens, 2016, 12, e1005763.	4.7	244
18	Virtual Screening and Experimental Validation Identify Novel Inhibitors of the Plasmodium falciparum Atg8â€“Atg3 Proteinâ€“Protein Interaction. ChemMedChem, 2016, 11, 900-910.	3.2	20

#	Article	IF	Citations
19	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
20	Characterization and Structural Insights into Selective E1-E2 Interactions in the Human and Plasmodium falciparum SUMO Conjugation Systems. Journal of Biological Chemistry, 2016, 291, 3860-3870.	3.4	15
21	Inhibition by stabilization: targeting the Plasmodium falciparum aldolaseâ€“TRAP complex. Malaria Journal, 2015, 14, 324.	2.3	20
22	The Bactofilin Cytoskeleton Protein BacM of Myxococcus xanthus Forms an Extended Î²-Sheet Structure Likely Mediated by Hydrophobic Interactions. PLoS ONE, 2015, 10, e0121074.	2.5	18
23	Structure ofChlamydomonas reinhardtiiTHB1, a group 1 truncated hemoglobin with a rare histidineâ€“lysine heme ligation. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 718-725.	0.8	15
24	The apicomplexan glideosome and adhesins â€“ Structures and function. Journal of Structural Biology, 2015, 190, 93-114.	2.8	113
25	Identification of Novel Ezrin Inhibitors Targeting Metastatic Osteosarcoma by Screening Open Access Malaria Box. Molecular Cancer Therapeutics, 2015, 14, 2497-2507.	4.1	17
26	Targeting the SUMO E1â€E2 Enzyme Interaction in Plasmodium falciparum. FASEB Journal, 2015, 29, 717.20.	0.5	0
27	Characterization of the ATG8-conjugation system in 2Plasmodiumspecies with special focus on the liver stage. Autophagy, 2014, 10, 269-284.	9.1	42
28	Structure ofToxoplasma gondiifructose-1,6-bisphosphate aldolase. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1186-1192.	0.8	9
29	Immunization against a merozoite sheddase promotes multiple invasion of red blood cells and attenuates Plasmodium infection in mice. Malaria Journal, 2014, 13, 313.	2.3	1
30	Sustained Crystallography Skills through Multimedia-Supported Active Learning. Biophysical Journal, 2014, 106, 218a-219a.	0.5	0
31	Identification of Protein-Protein-Interaction (PPI) Inhibitors and Stabilizers for Antimalarial Drug Development using SPR. Biophysical Journal, 2014, 106, 477a.	0.5	0
32	Identification of an Atg8-Atg3 Proteinâ€“Protein Interaction Inhibitor from the Medicines for Malaria Venture Malaria Box Active in Blood and Liver Stage Plasmodium falciparum Parasites. Journal of Medicinal Chemistry, 2014, 57, 4521-4531.	6.4	46
33	Development of a multifunctional tool for drug screening against plasmodial proteinâ€“protein interactions via surface plasmon resonance. Journal of Molecular Recognition, 2013, 26, 496-500.	2.1	11
34	DXP Synthaseâ€Catalyzed Cï£¿N Bond Formation: Nitroso Substrate Specificity Studies Guide Selective Inhibitor Design. ChemBioChem, 2013, 14, 1309-1315.	2.6	29
35	Differential Fragment SPR (DF-SPR) for Antimalarial Drug Screening. Biophysical Journal, 2013, 104, 380a.	0.5	0
36	Purification Strategies and Assay Development for an Essential Plasmodial Protease. Biophysical Journal, 2013, 104, 404a.	0.5	1

#	Article	IF	Citations
37	AUTOPHAGY IN PLASMODIUM, A MULTIFUNCTIONAL PATHWAY?. Computational and Structural Biotechnology Journal, 2013, 8, e201308002.	4.1	26
38	Identification of Biochemically Distinct Properties of the Small Ubiquitin-related Modifier (SUMO) Conjugation Pathway in Plasmodium falciparum. Journal of Biological Chemistry, 2013, 288, 27724-27736.	3.4	51
39	Binding of Aldolase and Glyceraldehyde-3-Phosphate Dehydrogenase to the Cytoplasmic Tails of Plasmodium falciparum Merozoite Duffy Binding-Like and Reticulocyte Homology Ligands. MBio, 2012, 3, .	4.1	16
40	Structural characterization and inhibition of the Plasmodium Atg8â€“Atg3 interaction. Journal of Structural Biology, 2012, 180, 551-562.	2.8	58
41	Crystal structure of GAP50, the anchor of the invasion machinery in the inner membrane complex of Plasmodium falciparum. Journal of Structural Biology, 2012, 178, 61-73.	2.8	28
42	The 1.75â€…Ã… resolution structure of fission protein Fis1 fromSaccharomyces cerevisiaereveals elusive interactions of the autoinhibitory domain. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1310-1315.	0.7	7
43	Fragment-Based Cocktail Crystallography by the Medical Structural Genomics of Pathogenic Protozoa Consortium. Current Topics in Medicinal Chemistry, 2009, 9, 1678-1687.	2.1	36
44	Structural Genomics of Pathogenic Protozoa: an Overview. Methods in Molecular Biology, 2008, 426, 497-513.	0.9	38
45	Aldolase provides an unusual binding site for thrombospondin-related anonymous protein in the invasion machinery of the malaria parasite. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7015-7020.	7.1	76
46	The Closed MTIP-Myosin A-Tail Complex from the Malaria Parasite Invasion Machinery. Journal of Molecular Biology, 2007, 372, 77-88.	4.2	51
47	The Î²-propeller domain of the trilobed protease fromPyrococcus furiosusreveals an open Velcro topology. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 179-187.	2.5	7
48	Using Fragment Cocktail Crystallography To Assist Inhibitor Design ofTrypanosoma bruceiNucleoside 2-Deoxyribosyltransferaseâ€. Journal of Medicinal Chemistry, 2006, 49, 5939-5946.	6.4	66
49	Structure of the MTIP-MyoA complex, a key component of the malaria parasite invasion motor. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4852-4857.	7.1	67
50	Structure of a ribulose 5-phosphate 3-epimerase from Plasmodium falciparum. Proteins: Structure, Function and Bioinformatics, 2005, 62, 338-342.	2.6	20
51	Crystal structure of glyceraldehyde-3-phosphate dehydrogenase from Plasmodium falciparum at 2.25 Ã… resolution reveals intriguing extra electron density in the active site. Proteins: Structure, Function and Bioinformatics, 2005, 62, 570-577.	2.6	34
52	Purification, Crystallization, and Preliminary X-ray Diffraction Analysis of the Tricorn Protease Hexamer from Thermoplasma acidophilum. Journal of Structural Biology, 2001, 134, 83-87.	2.8	5