Herwig SchÃ¼ler

List of Publications by Year
in descending order

80 papers	4,796 citations	101543 36 h-index	98798 67 g-index
88 all docs	88 docs citations	88 times ranked	5561 citing authors

#	Article	IF	Citations
1	System-wide identification and prioritization of enzyme substrates by thermal analysis. Nature Communications, 2021, 12, 1296.	12.8	44
2	PARP10 Multi-Site Auto- and Histone MARylation Visualized by Acid-Urea Gel Electrophoresis. Cells, 2021, 10, 654.	4.1	8
3	MacroGreen, a simple tool for detection of ADP-ribosylated proteins. Communications Biology, 2021, 4, 919.	4.4	13
4	Engineering Af1521 improves ADP-ribose binding and identification of ADP-ribosylated proteins. Nature Communications, 2020, 11, 5199.	12.8	49
5	A Focused DNA-Encoded Chemical Library for the Discovery of Inhibitors of NAD⁺-Dependent Enzymes. Journal of the American Chemical Society, 2019, 141, 5169-5181.	13.7	84
6	Identification of Poly(ADP-Ribose) Polymerase Macrodomain Inhibitors Using an AlphaScreen Protocol. SLAS Discovery, 2018, 23, 353-362.	2.7	23
7	Structureâ€“activity relationships for inhibitors of Pseudomonas aeruginosa exoenzyme S ADP-ribosyltransferase activity. European Journal of Medicinal Chemistry, 2018, 143, 568-576.	5.5	14
8	A Potent and Selective PARP11 Inhibitor Suggests Coupling between Cellular Localization and Catalytic Activity. Cell Chemical Biology, 2018, 25, 1547-1553.e12.	5.2	50
9	14-3-3 proteins activate Pseudomonas exotoxins-S and -T by chaperoning a hydrophobic surface. Nature Communications, 2018, 9, 3785.	12.8	37
10	A DNAâ€Encoded Library of Chemical Compounds Based on Common Scaffolding Structures Reveals the Impact of Ligand Geometry on Protein Recognition. ChemMedChem, 2018, 13, 1303-1307.	3.2	37
11	Design, synthesis and evaluation of potent and selective inhibitors of mono-(ADP-ribosyl)transferases PARP10 and PARP14. Bioorganic and Medicinal Chemistry Letters, 2018, 28, 2050-2054.	2.2	34
12	Design and synthesis of potent inhibitors of the mono(ADP-ribosyl)transferase, PARP14. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 2907-2911.	2.2	23
13	Structural Basis for Potency and Promiscuity in Poly(ADP-ribose) Polymerase (PARP) and Tankyrase Inhibitors. Journal of Medicinal Chemistry, 2017, 60, 1262-1271.	6.4	262
14	Small Molecule Microarray Based Discovery of PARP14 Inhibitors. Angewandte Chemie - International Edition, 2017, 56, 248-253.	13.8	38
15	Small Molecule Microarray Based Discovery of PARP14 Inhibitors. Angewandte Chemie, 2017, 129, 254-259.	2.0	4
16	Sirtuins are Unaffected by PARP Inhibitors Containing Planar Nicotinamide Bioisosteres. Chemical Biology and Drug Design, 2016, 87, 478-482.	3.2	21
17	DNA binding to SMC ATPasesâ€”trapped for release. EMBO Journal, 2016, 35, 703-705.	7.8	5
18	Sister Chromatid Cohesion Establishment Factor ESCO1 Operates by Substrate-Assisted Catalysis. Structure, 2016, 24, 789-796.	3.3	14

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19	Identification of Inhibitors of Pseudomonas aeruginosa Exotoxin-S ADP-Ribosyltransferase Activity. Journal of Biomolecular Screening, 2016, 21, 590-595.	2.6	12
20	Identification of Structureâ€“Activity Relationships from Screening a Structurally Compact DNAâ€Encoded Chemical Library. Angewandte Chemie - International Edition, 2015, 54, 3927-3931.	13.8	86
21	Towards small molecule inhibitors of mono-ADP-ribosyltransferases. European Journal of Medicinal Chemistry, 2015, 95, 546-551.	5.5	46
22	Structural Basis for Lack of ADP-ribosyltransferase Activity in Poly(ADP-ribose) Polymerase-13/Zinc Finger Antiviral Protein. Journal of Biological Chemistry, 2015, 290, 7336-7344.	3.4	70
23	Tankyrase 1 Inhibitors with Drug-like Properties Identified by Screening a DNA-Encoded Chemical Library. Journal of Medicinal Chemistry, 2015, 58, 5143-5149.	6.4	60
24	Pivotal and distinct role for P lasmodium actin capping protein alpha during blood infection of the malaria parasite. Molecular Microbiology, 2015, 96, 84-94.	2.5	16
25	Comparative Structural Analysis of the Putative Mono-ADP-Ribosyltransferases of the ARTD/PARP Family. Current Topics in Microbiology and Immunology, 2014, 384, 153-166.	1.1	12
26	Design, Synthesis, Crystallographic Studies, and Preliminary Biological Appraisal of New Substituted Triazolo[4,3-b]pyridazin-8-amine Derivatives as Tankyrase Inhibitors. Journal of Medicinal Chemistry, 2014, 57, 2807-2812.	6.4	31
27	<scp>PARP</scp> inhibitors: polypharmacology versus selective inhibition. FEBS Journal, 2013, 280, 3563-3575.	4.7	70
28	Pharmacology of ADP-ribosylation. FEBS Journal, 2013, 280, 3542-3542.	4.7	2
29	Recognition of Mono-ADP-Ribosylated ARTD10 Substrates by ARTD8 Macrodomains. Structure, 2013, 21, 462-475.	3.3	107
30	Structural biology of the writers, readers, and erasers in mono- and poly(ADP-ribose) mediated signaling. Molecular Aspects of Medicine, 2013, 34, 1088-1108.	6.4	58
31	Chemical Probes to Study ADP-Ribosylation: Synthesis and Biochemical Evaluation of Inhibitors of the Human ADP-Ribosyltransferase ARTD3/PARP3. Journal of Medicinal Chemistry, 2013, 56, 9556-9568.	6.4	9
32	PARP Inhibitor with Selectivity Toward ADP-Ribosyltransferase ARTD3/PARP3. ACS Chemical Biology, 2013, 8, 1698-1703.	3.4	48
33	Structural basis for the allosteric inhibitory mechanism of human kidney-type glutaminase (KGA) and its regulation by Raf-Mek-Erk signaling in cancer cell metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7705-7710.	7.1	178
34	PARP-3 is a mono-ADP-ribosylase that activates PARP-1 in the absence of DNA.. Journal of Biological Chemistry, 2012, 287, 34494.	3.4	1
35	The Corky Root Rot Pathogen Pyrenochaeta lycopersici Secretes a Proteinaceous Inducer of Cell Death Affecting Host Plants Differentially. Phytopathology, 2012, 102, 878-891.	2.2	4
36	Family-wide chemical profiling and structural analysis of PARP and tankyrase inhibitors. Nature Biotechnology, 2012, 30, 283-288.	17.5	410

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37	Crystal Structure of Human ADP-ribose Transferase ARTD15/PARP16 Reveals a Novel Putative Regulatory Domain. Journal of Biological Chemistry, 2012, 287, 24077-24081.	3.4	23
38	Biochemical Discrimination between Selenium and Sulfur 1: A Single Residue Provides Selenium Specificity to Human Selenocysteine Lyase. PLoS ONE, 2012, 7, e30581.	2.5	28
39	Discovery of Ligands for ADP-Ribosyltransferases via Docking-Based Virtual Screening. Journal of Medicinal Chemistry, 2012, 55, 7706-7718.	6.4	37
40	Cofactor mobility determines reaction outcome in the IMPDH and GMPR (Î²-Î±)8 barrel enzymes. Nature Chemical Biology, 2011, 7, 950-958.	8.0	35
41	Crystal Structures Explain Functional Differences in the Two Actin Depolymerization Factors of the Malaria Parasite. Journal of Biological Chemistry, 2011, 286, 28256-28264.	3.4	19
42	Critical role for a stage-specific actin in male exflagellation of the malaria parasite. Cellular Microbiology, 2011, 13, 1714-1730.	2.1	79
43	Actin regulation in the malaria parasite. European Journal of Cell Biology, 2011, 90, 966-971.	3.6	45
44	Crystal Structures Explain Functional Differences in the Two Actin Depolymerization Factors of the Malaria Parasite. Journal of Biological Chemistry, 2011, 286, 28256-28264.	3.4	34
45	Comparative Structural Analysis of Lipid Binding START Domains. PLoS ONE, 2011, 6, e19521.	2.5	117
46	Arp1, an actin-related protein, in Plasmodium berghei. Molecular and Biochemical Parasitology, 2010, 173, 88-96.	1.1	10
47	Toward a unified nomenclature for mammalian ADP-ribosyltransferases. Trends in Biochemical Sciences, 2010, 35, 208-219.	7.5	724
48	Crystallization and preliminary structural characterization of the two actin-depolymerization factors of the malaria parasite. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 583-587.	0.7	3
49	Comparative Structural Analysis of Human DEAD-Box RNA Helicases. PLoS ONE, 2010, 5, e12791.	2.5	101
50	Crystal Structures of the ATPase Domains of Four Human Hsp70 Isoforms: HSPA1L/Hsp70-hom, HSPA2/Hsp70-2, HSPA6/Hsp70B', and HSPA5/BiP/GRP78. PLoS ONE, 2010, 5, e8625.	2.5	123
51	PARP-3 Is a Mono-ADP-ribosylase That Activates PARP-1 in the Absence of DNA. Journal of Biological Chemistry, 2010, 285, 8054-8060.	3.4	135
52	Structure and Function of a G-actin Sequestering Protein with a Vital Role in Malaria Oocyst Development inside the Mosquito Vector. Journal of Biological Chemistry, 2010, 285, 11572-11583.	3.4	34
53	Structural Basis for the Interaction between Tankyrase-2 and a Potent Wnt-Signaling Inhibitor. Journal of Medicinal Chemistry, 2010, 53, 5352-5355.	6.4	110
54	Crystal Structure of the Catalytic Domain of Human PARP2 in Complex with PARP Inhibitor ABT-888. Biochemistry, 2010, 49, 1056-1058.	2.5	72

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55	Crystal Structure of Human RNA Helicase A (DHX9): Structural Basis for Unselective Nucleotide Base Binding in a DEAD-Box Variant Protein. Journal of Molecular Biology, 2010, 400, 768-782.	4.2	36
56	The DEXD/H-box RNA Helicase DDX19 Is Regulated by an Î±-Helical Switch. Journal of Biological Chemistry, 2009, 284, 10296-10300.	3.4	119
57	Vital role for the Plasmodium actin capping protein (CP) betaâ€subunit in motility of malaria sporozoites. Molecular Microbiology, 2009, 74, 1356-1367.	2.5	42
58	Structural Basis for Inhibitor Specificity in Human Poly(ADP-ribose) Polymerase-3. Journal of Medicinal Chemistry, 2009, 52, 3108-3111.	6.4	88
59	Crystal Structure of the ATPase Domain of the Human AAA+ Protein Paraplegin/SPG7. PLoS ONE, 2009, 4, e6975.	2.5	30
60	The crystal structure of human cleavage and polyadenylation specific factorâ€5 reveals a dimeric Nudix protein with a conserved catalytic site. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1047-1052.	2.6	10
61	Structureâ€“function analysis of the filamentous actin binding domain of the neuronal scaffolding protein spinophilin. FEBS Journal, 2008, 275, 59-68.	4.7	10
62	Structural and functional characterization of human Iba proteins. FEBS Journal, 2008, 275, 4627-4640.	4.7	15
63	Structural Basis for Parasite-Specific Functions of the Divergent Profilin of Plasmodium falciparum. Structure, 2008, 16, 1638-1648.	3.3	60
64	Actin/Myosin-Based Gliding Motility in Apicomplexan Parasites. Sub-Cellular Biochemistry, 2008, 47, 110-120.	2.4	17
65	Crystal Structure of Human Inosine Triphosphatase. Journal of Biological Chemistry, 2007, 282, 3182-3187.	3.4	48
66	Structures of the hydrolase domain of human 10-formyltetrahydrofolate dehydrogenase and its complex with a substrate analogue. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1294-1299.	2.5	10
67	Structure of the synthetase domain of human CTP synthetase, a target for anticancer therapy. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 613-617.	0.7	33
68	Regulation of Apicomplexan Microfilament Dynamics by a Minimal Set of Actin-Binding Proteins. Traffic, 2006, 7, 1433-1439.	2.7	69
69	Plasmodium motility: actin not actin' like actin. Trends in Parasitology, 2006, 22, 146-147.	3.3	25
70	The Connection Between Actin ATPase and Polymerization. Advances in Molecular and Cell Biology, 2006, 37, 49-66.	0.1	8
71	A Plasmodium Actin-depolymerizing Factor That Binds Exclusively to Actin Monomers. Molecular Biology of the Cell, 2005, 16, 4013-4023.	2.1	73
72	Unusual properties ofPlasmodium falciparumactin: new insights into microfilament dynamics of apicomplexan parasites. FEBS Letters, 2005, 579, 655-660.	2.8	83

#	Article	IF	Citations
73	The role of MeH73 in actin polymerization and ATP hydrolysis 1 1Edited by R. Huber. Journal of Molecular Biology, 2002, 317, 577-589.	4.2	95
74	Sound attenuation of polymerizing actin reflects supramolecular structures: viscoelastic properties of actin gels modified by cytochalasin D, profilin and Î±-actinin. Biochemical Journal, 2001, 355, 771-778.	3.7	20
75	ATPase activity and conformational changes in the regulation of actin. BBA - Proteins and Proteomics, 2001, 1549, 137-147.	2.1	53
76	Mutational analysis of arginine 177 in the nucleotide binding site of Î²-actin. FEBS Journal, 2000, 267, 4054-4062.	0.2	21
77	Thermal unfolding of G-actin monitored with the DNaseâ€ƒI-inhibition assay. FEBS Journal, 2000, 267, 476-486.	0.2	59
78	Covalent binding of ATPÎ³S to the nucleotide-binding site in S14C-actin. FEBS Letters, 2000, 476, 155-159.	2.8	13
79	Mutational analysis of Ser14 and Asp157 in the nucleotide-binding site of beta-actin. FEBS Journal, 1999, 265, 210-220.	0.2	32
80	Studies on the ATP-binding Site of Actin Using Site-directed Mutagenesis. , 1997, , 261-264.		0