

Herwig Schler

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

81
papers

3,903
citations

34
h-index

61
g-index

88
ext. papers

4,426
ext. citations

7
avg, IF

5.14
L-index

#	Paper	IF	Citations
81	Toward a unified nomenclature for mammalian ADP-ribosyltransferases. <i>Trends in Biochemical Sciences</i> , 2010 , 35, 208-19	10.3	620
80	Family-wide chemical profiling and structural analysis of PARP and tankyrase inhibitors. <i>Nature Biotechnology</i> , 2012 , 30, 283-8	44.5	363
79	Structural Basis for Potency and Promiscuity in Poly(ADP-ribose) Polymerase (PARP) and Tankyrase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 1262-1271	8.3	174
78	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 7705-10	11.5	136
77	PARP-3 is a mono-ADP-ribosylase that activates PARP-1 in the absence of DNA. <i>Journal of Biological Chemistry</i> , 2010 , 285, 8054-60	5.4	109
76	Crystal structures of the ATPase domains of four human Hsp70 isoforms: HSPA1L/Hsp70-hom, HSPA2/Hsp70-2, HSPA6/Hsp70B ψ and HSPA5/BiP/GRP78. <i>PLoS ONE</i> , 2010 , 5, e8625	3.7	106
75	The DEXD/H-box RNA helicase DDX19 is regulated by an α -helical switch. <i>Journal of Biological Chemistry</i> , 2009 , 284, 10296-300	5.4	99
74	Structural basis for the interaction between tankyrase-2 and a potent Wnt-signaling inhibitor. <i>Journal of Medicinal Chemistry</i> , 2010 , 53, 5352-5	8.3	98
73	Comparative structural analysis of lipid binding START domains. <i>PLoS ONE</i> , 2011 , 6, e19521	3.7	94
72	Recognition of mono-ADP-ribosylated ARTD10 substrates by ARTD8 macrodomains. <i>Structure</i> , 2013 , 21, 462-75	5.2	80
71	Structural basis for inhibitor specificity in human poly(ADP-ribose) polymerase-3. <i>Journal of Medicinal Chemistry</i> , 2009 , 52, 3108-11	8.3	79
70	Unusual properties of Plasmodium falciparum actin: new insights into microfilament dynamics of apicomplexan parasites. <i>FEBS Letters</i> , 2005 , 579, 655-60	3.8	79
69	Identification of structure-activity relationships from screening a structurally compact DNA-encoded chemical library. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 3927-31	16.4	73
68	Comparative structural analysis of human DEAD-box RNA helicases. <i>PLoS ONE</i> , 2010 , 5, e12791	3.7	72
67	The role of MeH73 in actin polymerization and ATP hydrolysis. <i>Journal of Molecular Biology</i> , 2002 , 317, 577-89	6.5	69
66	Regulation of apicomplexan microfilament dynamics by a minimal set of actin-binding proteins. <i>Traffic</i> , 2006 , 7, 1433-9	5.7	65
65	A Plasmodium actin-depolymerizing factor that binds exclusively to actin monomers. <i>Molecular Biology of the Cell</i> , 2005 , 16, 4013-23	3.5	64

64	Critical role for a stage-specific actin in male exflagellation of the malaria parasite. <i>Cellular Microbiology</i> , 2011 , 13, 1714-30	3.9	63
63	PARP inhibitors: polypharmacology versus selective inhibition. <i>FEBS Journal</i> , 2013 , 280, 3563-75	5.7	61
62	Crystal structure of the catalytic domain of human PARP2 in complex with PARP inhibitor ABT-888. <i>Biochemistry</i> , 2010 , 49, 1056-8	3.2	60
61	Tankyrase 1 Inhibitors with Drug-like Properties Identified by Screening a DNA-Encoded Chemical Library. <i>Journal of Medicinal Chemistry</i> , 2015 , 58, 5143-9	8.3	54
60	Structural basis for parasite-specific functions of the divergent profilin of Plasmodium falciparum. <i>Structure</i> , 2008 , 16, 1638-48	5.2	52
59	A Focused DNA-Encoded Chemical Library for the Discovery of Inhibitors of NAD-Dependent Enzymes. <i>Journal of the American Chemical Society</i> , 2019 , 141, 5169-5181	16.4	51
58	Structural biology of the writers, readers, and erasers in mono- and poly(ADP-ribose) mediated signaling. <i>Molecular Aspects of Medicine</i> , 2013 , 34, 1088-108	16.7	50
57	ATPase activity and conformational changes in the regulation of actin. <i>BBA - Proteins and Proteomics</i> , 2001 , 1549, 137-47		49
56	Thermal unfolding of G-actin monitored with the DNase I-inhibition assay stabilities of actin isoforms. <i>FEBS Journal</i> , 2000 , 267, 476-86		47
55	Structural basis for lack of ADP-ribosyltransferase activity in poly(ADP-ribose) polymerase-13/zinc finger antiviral protein. <i>Journal of Biological Chemistry</i> , 2015 , 290, 7336-44	5.4	46
54	PARP inhibitor with selectivity toward ADP-ribosyltransferase ARTD3/PARP3. <i>ACS Chemical Biology</i> , 2013 , 8, 1698-703	4.9	43
53	Actin regulation in the malaria parasite. <i>European Journal of Cell Biology</i> , 2011 , 90, 966-71	6.1	39
52	Crystal structure of human inosine triphosphatase. Substrate binding and implication of the inosine triphosphatase deficiency mutation P32T. <i>Journal of Biological Chemistry</i> , 2007 , 282, 3182-7	5.4	39
51	Towards small molecule inhibitors of mono-ADP-ribosyltransferases. <i>European Journal of Medicinal Chemistry</i> , 2015 , 95, 546-51	6.8	37
50	Vital role for the Plasmodium actin capping protein (CP) beta-subunit in motility of malaria sporozoites. <i>Molecular Microbiology</i> , 2009 , 74, 1356-67	4.1	36
49	Discovery of ligands for ADP-ribosyltransferases via docking-based virtual screening. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 7706-18	8.3	35
48	A Potent and Selective PARP11 Inhibitor Suggests Coupling between Cellular Localization and Catalytic Activity. <i>Cell Chemical Biology</i> , 2018 , 25, 1547-1553.e12	8.2	35
47	Structure and function of a G-actin sequestering protein with a vital role in malaria oocyst development inside the mosquito vector. <i>Journal of Biological Chemistry</i> , 2010 , 285, 11572-83	5.4	32

46	A DNA-Encoded Library of Chemical Compounds Based on Common Scaffolding Structures Reveals the Impact of Ligand Geometry on Protein Recognition. <i>ChemMedChem</i> , 2018 , 13, 1303-1307	3.7	32
45	Small Molecule Microarray Based Discovery of PARP14 Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 248-253	16.4	31
44	Crystal structure of human RNA helicase A (DHX9): structural basis for unselective nucleotide base binding in a DEAD-box variant protein. <i>Journal of Molecular Biology</i> , 2010 , 400, 768-82	6.5	31
43	Crystal structures explain functional differences in the two actin depolymerization factors of the malaria parasite. <i>Journal of Biological Chemistry</i> , 2011 , 286, 28256-64	5.4	29
42	Design, synthesis, crystallographic studies, and preliminary biological appraisal of new substituted triazolo[4,3-b]pyridazin-8-amine derivatives as tankyrase inhibitors. <i>Journal of Medicinal Chemistry</i> , 2014 , 57, 2807-12	8.3	27
41	Cofactor mobility determines reaction outcome in the IMPDH and GMPPase barrel enzymes. <i>Nature Chemical Biology</i> , 2011 , 7, 950-8	11.7	27
40	Structure of the synthetase domain of human CTP synthetase, a target for anticancer therapy. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 613-7		27
39	Mutational analysis of Ser14 and Asp157 in the nucleotide-binding site of beta-actin. <i>FEBS Journal</i> , 1999 , 265, 210-20		26
38	Crystal structure of the ATPase domain of the human AAA+ protein paraplegin/SPG7. <i>PLoS ONE</i> , 2009 , 4, e6975	3.7	26
37	Engineering Af1521 improves ADP-ribose binding and identification of ADP-ribosylated proteins. <i>Nature Communications</i> , 2020 , 11, 5199	17.4	26
36	Design, synthesis and evaluation of potent and selective inhibitors of mono-(ADP-ribosyl)transferases PARP10 and PARP14. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2018 , 28, 2050-2054	2.9	24
35	Plasmodium motility: actin not actin-like actin. <i>Trends in Parasitology</i> , 2006 , 22, 146-7	6.4	24
34	Biochemical discrimination between selenium and sulfur 1: a single residue provides selenium specificity to human selenocysteine lyase. <i>PLoS ONE</i> , 2012 , 7, e30581	3.7	22
33	14-3-3 proteins activate Pseudomonas exotoxins-S and -T by chaperoning a hydrophobic surface. <i>Nature Communications</i> , 2018 , 9, 3785	17.4	22
32	Crystal structure of human ADP-ribose transferase ARTD15/PARP16 reveals a novel putative regulatory domain. <i>Journal of Biological Chemistry</i> , 2012 , 287, 24077-81	5.4	20
31	Sound attenuation of polymerizing actin reflects supramolecular structures: viscoelastic properties of actin gels modified by cytochalasin D, profilin and alpha-actinin. <i>Biochemical Journal</i> , 2001 , 355, 771-83 ^{3.8}		20
30	Mutational analysis of arginine 177 in the nucleotide binding site of beta-actin. <i>FEBS Journal</i> , 2000 , 267, 4054-4062		20
29	Design and synthesis of potent inhibitors of the mono(ADP-ribosyl)transferase, PARP14. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017 , 27, 2907-2911	2.9	19

28	Crystal Structures Explain Functional Differences in the Two Actin Depolymerization Factors of the Malaria Parasite. <i>Journal of Biological Chemistry</i> , 2011 , 286, 28256-28264	5.4	19
27	Actin/myosin-based gliding motility in apicomplexan parasites. <i>Sub-Cellular Biochemistry</i> , 2008 , 47, 110-205	3.5	16
26	System-wide identification and prioritization of enzyme substrates by thermal analysis. <i>Nature Communications</i> , 2021 , 12, 1296	17.4	16
25	Identification of Poly(ADP-Ribose) Polymerase Macrodomain Inhibitors Using an AlphaScreen Protocol. <i>SLAS Discovery</i> , 2018 , 23, 353-362	3.4	14
24	Structural and functional characterization of human Iba proteins. <i>FEBS Journal</i> , 2008 , 275, 4627-40	5.7	14
23	Sirtuins are Unaffected by PARP Inhibitors Containing Planar Nicotinamide Bioisosteres. <i>Chemical Biology and Drug Design</i> , 2016 , 87, 478-82	2.9	14
22	Covalent binding of ATPgammaS to the nucleotide-binding site in S14C-actin. <i>FEBS Letters</i> , 2000 , 476, 155-9	3.8	13
21	Comparative structural analysis of the putative mono-ADP-ribosyltransferases of the ARTD/PARP family. <i>Current Topics in Microbiology and Immunology</i> , 2015 , 384, 153-66	3.3	12
20	Identification of Structure-Activity Relationships from Screening a Structurally Compact DNA-Encoded Chemical Library. <i>Angewandte Chemie</i> , 2015 , 127, 3999-4003	3.6	12
19	Pivotal and distinct role for Plasmodium actin capping protein alpha during blood infection of the malaria parasite. <i>Molecular Microbiology</i> , 2015 , 96, 84-94	4.1	12
18	The crystal structure of human cleavage and polyadenylation specific factor-5 reveals a dimeric Nudix protein with a conserved catalytic site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 73, 1047-52	4.2	10
17	Structures of the hydrolase domain of human 10-formyltetrahydrofolate dehydrogenase and its complex with a substrate analogue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1294-9		10
16	Chemical probes to study ADP-ribosylation: synthesis and biochemical evaluation of inhibitors of the human ADP-ribosyltransferase ARTD3/PARP3. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 9556-68	8.3	9
15	Identification of Inhibitors of Pseudomonas aeruginosa Exotoxin-S ADP-Ribosyltransferase Activity. <i>Journal of Biomolecular Screening</i> , 2016 , 21, 590-5		8
14	Arp1, an actin-related protein, in Plasmodium berghei. <i>Molecular and Biochemical Parasitology</i> , 2010 , 173, 88-96	1.9	8
13	Structure-function analysis of the filamentous actin binding domain of the neuronal scaffolding protein spinophilin. <i>FEBS Journal</i> , 2008 , 275, 59-68	5.7	8
12	Structure-activity relationships for inhibitors of Pseudomonas aeruginosa exoenzyme S ADP-ribosyltransferase activity. <i>European Journal of Medicinal Chemistry</i> , 2018 , 143, 568-576	6.8	8
11	Sister Chromatid Cohesion Establishment Factor ESCO1 Operates by Substrate-Assisted Catalysis. <i>Structure</i> , 2016 , 24, 789-796	5.2	7

10	The Connection Between Actin ATPase and Polymerization. <i>Advances in Molecular and Cell Biology</i> , 2006 , 37, 49-66		6
9	DNA binding to SMC ATPases-trapped for release. <i>EMBO Journal</i> , 2016 , 35, 703-5	13	5
8	The corky root rot pathogen <i>Pyrenochaeta lycopersici</i> secretes a proteinaceous inducer of cell death affecting host plants differentially. <i>Phytopathology</i> , 2012 , 102, 878-91	3.8	4
7	Small Molecule Microarray Based Discovery of PARP14 Inhibitors. <i>Angewandte Chemie</i> , 2017 , 129, 254-259	3.9	3
6	Crystallization and preliminary structural characterization of the two actin-depolymerization factors of the malaria parasite. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 583-7		3
5	PARP10 Multi-Site Auto- and Histone MARYlation Visualized by Acid-Urea Gel Electrophoresis. <i>Cells</i> , 2021 , 10,	7.9	3
4	MacroGreen, a simple tool for detection of ADP-ribosylated proteins. <i>Communications Biology</i> , 2021 , 4, 919	6.7	3
3	Pharmacology of ADP-ribosylation. <i>FEBS Journal</i> , 2013 , 280, 3542	5.7	1
2	Selectivity profile of the poly(ADP-ribose) polymerase (PARP) inhibitor, A-966492		1
1	Studies on the ATP-binding Site of Actin Using Site-directed Mutagenesis 1997 , 261-264		