Herwig Schler

List of Publications by Year in Descending Order

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	PARP10 Multi-Site Auto- and Histone MARylation Visualized by Acid-Urea Gel Electrophoresis. *Cells*, **2021**, 10,	7.9	3
80	System-wide identification and prioritization of enzyme substrates by thermal analysis. *Nature Communications*, **2021**, 12, 1296	17.4	16
79	MacroGreen, a simple tool for detection of ADP-ribosylated proteins. *Communications Biology*, **2021**, 4, 919	6.7	3
78	Engineering Af1521 improves ADP-ribose binding and identification of ADP-ribosylated proteins. *Nature Communications*, **2020**, 11, 5199	17.4	26
77	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	16.4	51
76	Identification of Poly(ADP-Ribose) Polymerase Macrodomain Inhibitors Using an AlphaScreen Protocol. *SLAS Discovery*, **2018**, 23, 353-362	3.4	14
75	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	2.9	24
74	Structure-activity relationships for inhibitors of Pseudomonas aeruginosa exoenzyme S ADP-ribosyltransferase activity. *European Journal of Medicinal Chemistry*, **2018**, 143, 568-576	6.8	8
73	A Potent and Selective PARP11 Inhibitor Suggests Coupling between Cellular Localization and Catalytic Activity. *Cell Chemical Biology*, **2018**, 25, 1547-1553.e12	8.2	35
72	14-3-3 proteins activate Pseudomonas exotoxins-S and -T by chaperoning a hydrophobic surface. *Nature Communications*, **2018**, 9, 3785	17.4	22
71	A DNA-Encoded Library of Chemical Compounds Based on Common Scaffolding Structures Reveals the Impact of Ligand Geometry on Protein Recognition. *ChemMedChem*, **2018**, 13, 1303-1307	3.7	32
70	Design and synthesis of potent inhibitors of the mono(ADP-ribosyl)transferase, PARP14. *Bioorganic and Medicinal Chemistry Letters*, **2017**, 27, 2907-2911	2.9	19
69	Structural Basis for Potency and Promiscuity in Poly(ADP-ribose) Polymerase (PARP) and Tankyrase Inhibitors. *Journal of Medicinal Chemistry*, **2017**, 60, 1262-1271	8.3	174
68	Small Molecule Microarray Based Discovery of PARP14 Inhibitors. *Angewandte Chemie - International Edition*, **2017**, 56, 248-253	16.4	31
67	Small Molecule Microarray Based Discovery of PARP14 Inhibitors. *Angewandte Chemie*, **2017**, 129, 254-259	3.6	3
66	Identification of Inhibitors of Pseudomonas aeruginosa Exotoxin-S ADP-Ribosyltransferase Activity. *Journal of Biomolecular Screening*, **2016**, 21, 590-5		8
65	Sirtuins are Unaffected by PARP Inhibitors Containing Planar Nicotinamide Bioisosteres. *Chemical Biology and Drug Design*, **2016**, 87, 478-82	2.9	14

64	DNA binding to SMC ATPases-trapped for release. *EMBO Journal*, **2016**, 35, 703-5	13	5
63	Sister Chromatid Cohesion Establishment Factor ESCO1 Operates by Substrate-Assisted Catalysis. *Structure*, **2016**, 24, 789-796	5.2	7
62	Comparative structural analysis of the putative mono-ADP-ribosyltransferases of the ARTD/PARP family. *Current Topics in Microbiology and Immunology*, **2015**, 384, 153-66	3.3	12
61	Identification of structure-activity relationships from screening a structurally compact DNA-encoded chemical library. *Angewandte Chemie - International Edition*, **2015**, 54, 3927-31	16.4	73
60	Towards small molecule inhibitors of mono-ADP-ribosyltransferases. *European Journal of Medicinal Chemistry*, **2015**, 95, 546-51	6.8	37
59	Structural basis for lack of ADP-ribosyltransferase activity in poly(ADP-ribose) polymerase-13/zinc finger antiviral protein. *Journal of Biological Chemistry*, **2015**, 290, 7336-44	5.4	46
58	Tankyrase 1 Inhibitors with Drug-like Properties Identified by Screening a DNA-Encoded Chemical Library. *Journal of Medicinal Chemistry*, **2015**, 58, 5143-9	8.3	54
57	Identification of Structure‐Activity Relationships from Screening a Structurally Compact DNA-Encoded Chemical Library. *Angewandte Chemie*, **2015**, 127, 3999-4003	3.6	12
56	Pivotal and distinct role for Plasmodium actin capping protein alpha during blood infection of the malaria parasite. *Molecular Microbiology*, **2015**, 96, 84-94	4.1	12
55	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, 2807-12	8.3	27
54	PARP inhibitors: polypharmacology versus selective inhibition. *FEBS Journal*, **2013**, 280, 3563-75	5.7	61
53	Pharmacology of ADP-ribosylation. *FEBS Journal*, **2013**, 280, 3542	5.7	1
52	Recognition of mono-ADP-ribosylated ARTD10 substrates by ARTD8 macrodomains. *Structure*, **2013**, 21, 462-75	5.2	80
51	Structural biology of the writers, readers, and erasers in mono- and poly(ADP-ribose) mediated signaling. *Molecular Aspects of Medicine*, **2013**, 34, 1088-108	16.7	50
50	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, 9556-68	8.3	9
49	PARP inhibitor with selectivity toward ADP-ribosyltransferase ARTD3/PARP3. *ACS Chemical Biology*, **2013**, 8, 1698-703	4.9	43
48	The corky root rot pathogen Pyrenochaeta lycopersici secretes a proteinaceous inducer of cell death affecting host plants differentially. *Phytopathology*, **2012**, 102, 878-91	3.8	4
47	Family-wide chemical profiling and structural analysis of PARP and tankyrase inhibitors. *Nature Biotechnology*, **2012**, 30, 283-8	44.5	363

46	Crystal structure of human ADP-ribose transferase ARTD15/PARP16 reveals a novel putative regulatory domain. *Journal of Biological Chemistry*, **2012**, 287, 24077-81	5.4	20
45	Biochemical discrimination between selenium and sulfur 1: a single residue provides selenium specificity to human selenocysteine lyase. *PLoS ONE*, **2012**, 7, e30581	3.7	22
44	Discovery of ligands for ADP-ribosyltransferases via docking-based virtual screening. *Journal of Medicinal Chemistry*, **2012**, 55, 7706-18	8.3	35
43	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, 7705-10	11.5	136
42	Crystal Structures Explain Functional Differences in the Two Actin Depolymerization Factors of the Malaria Parasite. *Journal of Biological Chemistry*, **2011**, 286, 28256-28264	5.4	19
41	Critical role for a stage-specific actin in male exflagellation of the malaria parasite. *Cellular Microbiology*, **2011**, 13, 1714-30	3.9	63
40	Actin regulation in the malaria parasite. *European Journal of Cell Biology*, **2011**, 90, 966-71	6.1	39
39	Cofactor mobility determines reaction outcome in the IMPDH and GMPR (β8 barrel enzymes. *Nature Chemical Biology*, **2011**, 7, 950-8	11.7	27
38	Crystal structures explain functional differences in the two actin depolymerization factors of the malaria parasite. *Journal of Biological Chemistry*, **2011**, 286, 28256-64	5.4	29
37	Comparative structural analysis of lipid binding START domains. *PLoS ONE*, **2011**, 6, e19521	3.7	94
36	Comparative structural analysis of human DEAD-box RNA helicases. *PLoS ONE*, **2010**, 5, e12791	3.7	72
35	Crystal structures of the ATPase domains of four human Hsp70 isoforms: HSPA1L/Hsp70-hom, HSPA2/Hsp70-2, HSPA6/Hsp70BU and HSPA5/BiP/GRP78. *PLoS ONE*, **2010**, 5, e8625	3.7	106
34	PARP-3 is a mono-ADP-ribosylase that activates PARP-1 in the absence of DNA. *Journal of Biological Chemistry*, **2010**, 285, 8054-60	5.4	109
33	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, 11572-83	5.4	32
32	Structural basis for the interaction between tankyrase-2 and a potent Wnt-signaling inhibitor. *Journal of Medicinal Chemistry*, **2010**, 53, 5352-5	8.3	98
31	Crystal structure of the catalytic domain of human PARP2 in complex with PARP inhibitor ABT-888. *Biochemistry*, **2010**, 49, 1056-8	3.2	60
30	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, 768-82	6.5	31
29	Arp1, an actin-related protein, in Plasmodium berghei. *Molecular and Biochemical Parasitology*, **2010** , 173, 88-96	1.9	8

28	Toward a unified nomenclature for mammalian ADP-ribosyltransferases. *Trends in Biochemical Sciences*, **2010**, 35, 208-19	10.3	620
27	Crystallization and preliminary structural characterization of the two actin-depolymerization factors of the malaria parasite. *Acta Crystallographica Section F: Structural Biology Communications*, **2010**, 66, 583-7		3
26	The DEXD/H-box RNA helicase DDX19 is regulated by an {alpha}-helical switch. *Journal of Biological Chemistry*, **2009**, 284, 10296-300	5.4	99
25	Vital role for the Plasmodium actin capping protein (CP) beta-subunit in motility of malaria sporozoites. *Molecular Microbiology*, **2009**, 74, 1356-67	4.1	36
24	Structural basis for inhibitor specificity in human poly(ADP-ribose) polymerase-3. *Journal of Medicinal Chemistry*, **2009**, 52, 3108-11	8.3	79
23	Crystal structure of the ATPase domain of the human AAA+ protein paraplegin/SPG7. *PLoS ONE*, **2009**, 4, e6975	3.7	26
22	Structural basis for parasite-specific functions of the divergent profilin of Plasmodium falciparum. *Structure*, **2008**, 16, 1638-48	5.2	52
21	Actin/myosin-based gliding motility in apicomplexan parasites. *Sub-Cellular Biochemistry*, **2008**, 47, 110-20	3.5	16
20	The crystal structure of human cleavage and polyadenylation specific factor-5 reveals a dimeric Nudix protein with a conserved catalytic site. *Proteins: Structure, Function and Bioinformatics*, **2008**, 73, 1047-52	4.2	10
19	Structure-function analysis of the filamentous actin binding domain of the neuronal scaffolding protein spinophilin. *FEBS Journal*, **2008**, 275, 59-68	5.7	8
18	Structural and functional characterization of human Iba proteins. *FEBS Journal*, **2008**, 275, 4627-40	5.7	14
17	Crystal structure of human inosine triphosphatase. Substrate binding and implication of the inosine triphosphatase deficiency mutation P32T. *Journal of Biological Chemistry*, **2007**, 282, 3182-7	5.4	39
16	Plasmodium motility: actin not actinUike actin. *Trends in Parasitology*, **2006**, 22, 146-7	6.4	24
15	The Connection Between Actin ATPase and Polymerization. *Advances in Molecular and Cell Biology*, **2006**, 37, 49-66		6
14	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, 1294-9		10
13	Structure of the synthetase domain of human CTP synthetase, a target for anticancer therapy. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 613-7		27
12	Regulation of apicomplexan microfilament dynamics by a minimal set of actin-binding proteins. *Traffic*, **2006**, 7, 1433-9	5.7	65
11	Unusual properties of Plasmodium falciparum actin: new insights into microfilament dynamics of apicomplexan parasites. *FEBS Letters*, **2005**, 579, 655-60	3.8	79

10	A Plasmodium actin-depolymerizing factor that binds exclusively to actin monomers. *Molecular Biology of the Cell*, **2005**, 16, 4013-23	3.5	64
9	The role of MeH73 in actin polymerization and ATP hydrolysis. *Journal of Molecular Biology*, **2002**, 317, 577-89	6.5	69
8	Sound attenuation of polymerizing actin reflects supramolecular structures: viscoelastic properties of actin gels modified by cytochalasin D, profilin and alpha-actinin. *Biochemical Journal*, **2001**, 355, 771-8	3.8	20
7	ATPase activity and conformational changes in the regulation of actin. *BBA - Proteins and Proteomics*, **2001**, 1549, 137-47		49
6	Mutational analysis of arginine 177 in the nucleotide binding site of □actin. *FEBS Journal*, **2000**, 267, 4054-4062		20
5	Thermal unfolding of G-actin monitored with the DNase I-inhibition assay stabilities of actin isoforms. *FEBS Journal*, **2000**, 267, 476-86		47
4	Covalent binding of ATPgammaS to the nucleotide-binding site in S14C-actin. *FEBS Letters*, **2000**, 476, 155-9	3.8	13
3	Mutational analysis of Ser14 and Asp157 in the nucleotide-binding site of beta-actin. *FEBS Journal*, **1999**, 265, 210-20		26
2	Studies on the ATP-binding Site of Actin Using Site-directed Mutagenesis **1997**, 261-264		
1	Selectivity profile of the poly(ADP-ribose) polymerase (PARP) inhibitor, A-966492		1