

# Alexander Pflug

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4636149/publications.pdf>

Version: 2024-02-01

18  
papers

1,565  
citations

687363

13  
h-index

839539

18  
g-index

20  
all docs

20  
docs citations

20  
times ranked

1747  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of influenza A polymerase bound to the viral RNA promoter. <i>Nature</i> , 2014, 516, 355-360.	27.8	404
2	Structural insight into cap-snatching and RNA synthesis by influenza polymerase. <i>Nature</i> , 2014, 516, 361-366.	27.8	376
3	Capped RNA primer binding to influenza polymerase and implications for the mechanism of cap-binding inhibitors. <i>Nucleic Acids Research</i> , 2018, 46, 956-971.	14.5	154
4	Structural insights into RNA synthesis by the influenza virus transcription-replication machine. <i>Virus Research</i> , 2017, 234, 103-117.	2.2	143
5	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016, 61, 125-137.	9.7	123
6	Structural basis of an essential interaction between influenza polymerase and Pol II CTD. <i>Nature</i> , 2017, 541, 117-121.	27.8	98
7	A Structure-Based Model for the Complete Transcription Cycle of Influenza Polymerase. <i>Cell</i> , 2020, 181, 877-893.e21.	28.9	90
8	<i>Agrobacterium tumefaciens</i> -mediated transformation of <i>Cleome gynandra</i> L., a C4 dicotyledon that is closely related to <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2010, 61, 1311-1319.	4.8	28
9	Diversity of Bisubstrate Binding Modes of Adenosine Analogueâ€œOligoarginine Conjugates in Protein Kinase A and Implications for Protein Substrate Interactions. <i>Journal of Molecular Biology</i> , 2010, 403, 66-77.	4.2	27
10	Structural basis of eukaryotic cell targeting by type III secretion system (T3SS) effectors. <i>Research in Microbiology</i> , 2013, 164, 605-619.	2.1	24
11	Bifunctional Ligands for Inhibition of Tight-Binding Proteinâ€œProtein Interactions. <i>Bioconjugate Chemistry</i> , 2016, 27, 1900-1910.	3.6	19
12	Mutants of protein kinase A that mimic the ATP-binding site of Aurora kinase. <i>Biochemical Journal</i> , 2011, 440, 85-93.	3.7	14
13	Optimization of an Imidazo[1,2- <i>a</i> ]pyridine Series to Afford Highly Selective Type I1/2 Dual Mer/Axl Kinase Inhibitors with <i>In Vivo</i> Efficacy. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 13524-13539.	6.4	13
14	Anomalous dispersion analysis of inhibitor flexibility: a case study of the kinase inhibitor H-89. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 873-877.	0.7	12
15	Generating Selective Leads for Mer Kinase Inhibitorsâ€œExample of a Comprehensive Lead-Generation Strategy. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 3165-3184.	6.4	11
16	Type B and type A influenza polymerases have evolved distinct binding interfaces to recruit the RNA polymerase II CTD. <i>PLoS Pathogens</i> , 2022, 18, e1010328.	4.7	11
17	A-loop interactions in Mer tyrosine kinase give rise to inhibitors with two-step mechanism and long residence time of binding. <i>Biochemical Journal</i> , 2020, 477, 4443-4452.	3.7	10
18	Structural origins of AGC protein kinase inhibitor selectivities: PKA as a drug discovery tool. <i>Biological Chemistry</i> , 2012, 393, 1121-1129.	2.5	7