

Paweł, Sledź

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4521447/publications.pdf>

Version: 2024-02-01

14
papers

1,205
citations

933447

10
h-index

1058476

14
g-index

17
all docs

17
docs citations

17
times ranked

1917
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein structure-based drug design: from docking to molecular dynamics. <i>Current Opinion in Structural Biology</i> , 2018, 48, 93-102.	5.7	405
2	Structural insights into the molecular mechanism of the m6A writer complex. <i>ELife</i> , 2016, 5, .	6.0	386
3	Small-Molecule Inhibitors of METTL3, the Major Human Epitranscriptomic Writer. <i>ChemMedChem</i> , 2020, 15, 744-748.	3.2	106
4	Using Ligand-Mapping Simulations to Design a Ligand Selectively Targeting a Cryptic Surface Pocket of Polo-Like Kinase 1. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 10078-10081.	13.8	71
5	From Crystal Packing to Molecular Recognition: Prediction and Discovery of a Binding Site on the Surface of Polo-Like Kinase 1. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 4003-4006.	13.8	57
6	Molecular basis for cytoplasmic mRNA surveillance by uridylation-triggered decay in <i>Drosophila</i> . <i>EMBO Journal</i> , 2016, 35, 2417-2434.	7.8	50
7	A Reader-Based Assay for m ⁶ A Writers and Erasers. <i>Analytical Chemistry</i> , 2019, 91, 3078-3084.	6.5	36
8	High-Throughput Interrogation of Ligand Binding Mode Using a Fluorescence-Based Assay. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 7680-7683.	13.8	30
9	Flexible Binding of m ⁶ A Reader Protein YTHDC1 to Its Preferred RNA Motif. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 7004-7014.	5.3	18
10	Selectively Disrupting m ⁶ A-Dependent Protein-RNA Interactions with Fragments. <i>ACS Chemical Biology</i> , 2020, 15, 618-625.	3.4	17
11	Binding Motifs in the CBP Bromodomain: An Analysis of 20 Crystal Structures of Complexes with Small Molecules. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 929-934.	2.8	8
12	Hitting a Moving Target: Simulation and Crystallography Study of ATAD2 Bromodomain Blockers. <i>ACS Medicinal Chemistry Letters</i> , 2020, 11, 1573-1580.	2.8	8
13	Understanding the mechanism of action of pyrrolo[3,2- <i>b</i>]quinoxaline-derivatives as kinase inhibitors. <i>RSC Medicinal Chemistry</i> , 2020, 11, 665-675.	3.9	4
14	Ligand retargeting by binding site analogy. <i>European Journal of Medicinal Chemistry</i> , 2019, 175, 107-113.	5.5	2