

Werner Streicher

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11171420/publications.pdf>

Version: 2024-02-01

20
papers

1,218
citations

840776

11
h-index

794594

19
g-index

20
all docs

20
docs citations

20
times ranked

2390
citing authors

#	ARTICLE	IF	CITATIONS
1	Liquid demixing of intrinsically disordered proteins is seeded by poly(ADP-ribose). <i>Nature Communications</i> , 2015, 6, 8088.	12.8	463
2	Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423.	17.5	237
3	RNF111/Arkadia is a SUMO-targeted ubiquitin ligase that facilitates the DNA damage response. <i>Journal of Cell Biology</i> , 2013, 201, 797-807.	5.2	129
4	DNA damage-induced SUMOylation of HERC2 promotes RNF8 binding via a novel SUMO-binding Zinc finger. <i>Journal of Cell Biology</i> , 2012, 197, 179-187.	5.2	109
5	Investigating the function of Fc-specific binding of IgM to Plasmodium falciparum erythrocyte membrane protein 1 mediating erythrocyte rosetting. <i>Cellular Microbiology</i> , 2015, 17, 819-831.	2.1	52
6	Application of interpretable artificial neural networks to early monoclonal antibodies development. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2019, 141, 81-89.	4.3	48
7	A direct role of M _{ad1} in the spindle assembly checkpoint beyond M _{ad2} kinetochore recruitment. <i>EMBO Reports</i> , 2014, 15, 282-290.	4.5	38
8	Structure of Dimeric and Tetrameric Complexes of the BAR Domain Protein PICK1 Determined by Small-Angle X-Ray Scattering. <i>Structure</i> , 2015, 23, 1258-1270.	3.3	34
9	Structural Analysis of a Complex between Small Ubiquitin-like Modifier 1 (SUMO1) and the ZZ Domain of CREB-binding Protein (CBP/p300) Reveals a New Interaction Surface on SUMO. <i>Journal of Biological Chemistry</i> , 2016, 291, 12658-12672.	3.4	23
10	Characterization of Native Reversible Self-Association of a Monoclonal Antibody Mediated by Fab-Fab Interaction. <i>Journal of Pharmaceutical Sciences</i> , 2020, 109, 443-451.	3.3	17
11	Conformational Stability Study of a Therapeutic Peptide Plectasin Using Molecular Dynamics Simulations in Combination with NMR. <i>Journal of Physical Chemistry B</i> , 2019, 123, 4867-4877.	2.6	14
12	Conformation-specific anti-Mad2 monoclonal antibodies for the dissection of checkpoint signaling. <i>MAbs</i> , 2016, 8, 689-697.	5.2	10
13	Small angle X-ray scattering and molecular dynamic simulations provide molecular insight for stability of recombinant human transferrin. <i>Journal of Structural Biology: X</i> , 2020, 4, 100017.	1.3	9
14	pH- and concentration-dependent supramolecular assembly of a fungal defensin plectasin variant into helical non-amyloid fibrils. <i>Nature Communications</i> , 2022, 13, .	12.8	9
15	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 18175-18188.	3.4	6
16	Development of a fast screening method for selecting excipients in formulations using MD simulations, NMR and microscale thermophoresis. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2021, 158, 11-20.	4.3	5
17	Characterization of the NTPR and BD1 interacting domains of the human PICHA-BEND3 complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 646-651.	0.8	5
18	Combination of high throughput and structural screening to assess protein stability – A screening perspective. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2022, 171, 1-10.	4.3	5

#	ARTICLE	IF	CITATIONS
19	Electrostatics Drive Oligomerization and Aggregation of Human Interferon Alpha-2a. Journal of Physical Chemistry B, 2021, 125, 13657-13669.	2.6	5
20	Structure and Interactions of a Dimeric Variant of sHIP, a Novel Virulence Determinant of Streptococcus pyogenes. Frontiers in Microbiology, 2016, 7, 95.	3.5	0