

Florian Leidner

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

238
citations

1040056

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h-index

1199594

12
g-index

14
all docs

14
docs citations

14
times ranked

251
citing authors

#	ARTICLE	IF	CITATIONS
1	Drug Design Strategies to Avoid Resistance in Direct-Acting Antivirals and Beyond. <i>Chemical Reviews</i> , 2021, 121, 3238-3270.	47.7	40
2	Deciphering Complex Mechanisms of Resistance and Loss of Potency through Coupled Molecular Dynamics and Machine Learning. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 2054-2064.	5.3	11
3	Deciphering Antifungal Drug Resistance in <i>Pneumocystis jirovecii</i> DHFR with Molecular Dynamics and Machine Learning. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2537-2541.	5.4	6
4	Molecular and Structural Mechanism of Pan-Genotypic HCV NS3/4A Protease Inhibition by Glecaprevir. <i>ACS Chemical Biology</i> , 2020, 15, 342-352.	3.4	11
5	Optimizing the refinement of merohedrally twinned P61 HIV-1 proteaseâ€“inhibitor cocrystal structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 302-310.	2.3	1
6	Picomolar to Micromolar: Elucidating the Role of Distal Mutations in HIV-1 Protease in Conferring Drug Resistance. <i>ACS Chemical Biology</i> , 2019, 14, 2441-2452.	3.4	36
7	Target-Specific Prediction of Ligand Affinity with Structure-Based Interaction Fingerprints. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3679-3691.	5.4	16
8	Structural Adaptation of Darunavir Analogues against Primary Mutations in HIV-1 Protease. <i>ACS Infectious Diseases</i> , 2019, 5, 316-325.	3.8	27
9	Structural Analysis of the Active Site and DNA Binding of Human Cytidine Deaminase APOBEC3B. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 637-647.	5.3	16
10	Hydration Structure and Dynamics of Inhibitor-Bound HIV-1 Protease. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 2784-2796.	5.3	28
11	Molecular Mechanism of Resistance in a Clinically Significant Double-Mutant Variant of HCV NS3/4A Protease. <i>Structure</i> , 2018, 26, 1360-1372.e5.	3.3	19
12	Structural analysis of the active site and DNA binding of human cytidine deaminase APOBEC3B. <i>FASEB Journal</i> , 2018, 32, 792.31.	0.5	0
13	Interdependence of Inhibitor Recognition in HIV-1 Protease. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 2300-2309.	5.3	27