

Celia A Schiffer

List of Publications by Year in descending order

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138
papers

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citations

50276

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153
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153
docs citations

153
times ranked

6920
citing authors

#	ARTICLE	IF	CITATIONS
1	Substrate Shape Determines Specificity of Recognition for HIV-1 Protease. <i>Structure</i> , 2002, 10, 369-381.	3.3	292
2	Discovery and Selection of TMC114, a Next Generation HIV-1 Protease Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 1813-1822.	6.4	242
3	Structural and Thermodynamic Basis for the Binding of TMC114, a Next-Generation Human Immunodeficiency Virus Type 1 Protease Inhibitor. <i>Journal of Virology</i> , 2004, 78, 12012-12021.	3.4	240
4	Affinity maturation of SARS-CoV-2 neutralizing antibodies confers potency, breadth, and resilience to viral escape mutations. <i>Immunity</i> , 2021, 54, 1853-1868.e7.	14.3	230
5	Mutation Patterns and Structural Correlates in Human Immunodeficiency Virus Type 1 Protease following Different Protease Inhibitor Treatments. <i>Journal of Virology</i> , 2003, 77, 4836-4847.	3.4	220
6	Curling of Flap Tips in HIV-1 Protease as a Mechanism for Substrate Entry and Tolerance of Drug Resistance. <i>Structure</i> , 2000, 8, 1259-1265.	3.3	195
7	The Molecular Basis of Drug Resistance against Hepatitis C Virus NS3/4A Protease Inhibitors. <i>PLoS Pathogens</i> , 2012, 8, e1002832.	4.7	179
8	Drug resistance against HCV NS3/4A inhibitors is defined by the balance of substrate recognition versus inhibitor binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20986-20991.	7.1	176
9	A cross-reactive human IgA monoclonal antibody blocks SARS-CoV-2 spike-ACE2 interaction. <i>Nature Communications</i> , 2020, 11, 4198.	12.8	132
10	Crystal structure of APOBEC3A bound to single-stranded DNA reveals structural basis for cytidine deamination and specificity. <i>Nature Communications</i> , 2017, 8, 15024.	12.8	130
11	Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. <i>PLoS Genetics</i> , 2014, 10, e1004185.	3.5	126
12	Molecular Basis for Drug Resistance in HIV-1 Protease. <i>Viruses</i> , 2010, 2, 2509-2535.	3.3	122
13	Methylcytosine and Normal Cytosine Deamination by the Foreign DNA Restriction Enzyme APOBEC3A. <i>Journal of Biological Chemistry</i> , 2012, 287, 34801-34808.	3.4	120
14	Crystal Structure of the APOBEC3G Catalytic Domain Reveals Potential Oligomerization Interfaces. <i>Structure</i> , 2010, 18, 28-38.	3.3	116
15	First-In-Class Small Molecule Inhibitors of the Single-Strand DNA Cytosine Deaminase APOBEC3G. <i>ACS Chemical Biology</i> , 2012, 7, 506-517.	3.4	112
16	Insights into interferon regulatory factor activation from the crystal structure of dimeric IRF5. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1213-1220.	8.2	109
17	HIV-1 Protease Inhibitors from Inverse Design in the Substrate Envelope Exhibit Subnanomolar Binding to Drug-Resistant Variants. <i>Journal of the American Chemical Society</i> , 2008, 130, 6099-6113.	13.7	105
18	Evaluating the Substrate-Envelope Hypothesis: Structural Analysis of Novel HIV-1 Protease Inhibitors Designed To Be Robust against Drug Resistance. <i>Journal of Virology</i> , 2010, 84, 5368-5378.	3.4	104

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19	Replacement of the P1 Amino Acid of Human Immunodeficiency Virus Type 1 Gag Processing Sites Can Inhibit or Enhance the Rate of Cleavage by the Viral Protease. <i>Journal of Virology</i> , 2002, 76, 10226-10233.	3.4	103
20	Combating Susceptibility to Drug Resistance. <i>Chemistry and Biology</i> , 2004, 11, 1333-1338.	6.0	98
21	Lack of synergy for inhibitors targeting a multi-drug-resistant HIV-1 protease. <i>Protein Science</i> , 2009, 11, 418-429.	7.6	96
22	Discovery of HIV-1 Protease Inhibitors with Picomolar Affinities Incorporating N-Aryl-oxazolidinone-5-carboxamides as Novel P2 Ligands. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 7342-7356.	6.4	93
23	Structural Basis for Coevolution of a Human Immunodeficiency Virus Type 1 Nucleocapsid-p1 Cleavage Site with a V82A Drug-Resistant Mutation in Viral Protease. <i>Journal of Virology</i> , 2004, 78, 12446-12454.	3.4	88
24	Crystal Structure of the DNA Cytosine Deaminase APOBEC3F: The Catalytically Active and HIV-1 Vif-Binding Domain. <i>Structure</i> , 2013, 21, 1042-1050.	3.3	85
25	Structure of the Vif-binding domain of the antiviral enzyme APOBEC3G. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 485-491.	8.2	84
26	Drug Resistance Conferred by Mutations Outside the Active Site through Alterations in the Dynamic and Structural Ensemble of HIV-1 Protease. <i>Journal of the American Chemical Society</i> , 2014, 136, 11956-11963.	13.7	83
27	Improving Viral Protease Inhibitors to Counter Drug Resistance. <i>Trends in Microbiology</i> , 2016, 24, 547-557.	7.7	81
28	Citrullination of NF- κ B p65 promotes its nuclear localization and TLR-induced expression of IL-1 β and TNF α . <i>Science Immunology</i> , 2017, 2, .	11.9	80
29	Crystal Structure of SARS-CoV-2 Main Protease in Complex with the Non-Covalent Inhibitor ML188. <i>Viruses</i> , 2021, 13, 174.	3.3	80
30	The ssDNA Mutator APOBEC3A Is Regulated by Cooperative Dimerization. <i>Structure</i> , 2015, 23, 903-911.	3.3	79
31	Hydrophobic Sliding: A Possible Mechanism for Drug Resistance in Human Immunodeficiency Virus Type 1 Protease. <i>Structure</i> , 2007, 15, 225-233.	3.3	78
32	Covariation of amino acid positions in HIV-1 protease. <i>Virology</i> , 2003, 314, 536-548.	2.4	75
33	Design of HIV-1 Protease Inhibitors Active on Multidrug-Resistant Virus. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 1965-1973.	6.4	74
34	Extreme Entropy-Enthalpy Compensation in a Drug-Resistant Variant of HIV-1 Protease. <i>ACS Chemical Biology</i> , 2012, 7, 1536-1546.	3.4	72
35	Structural basis for mutation-induced destabilization of profilin 1 in ALS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7984-7989.	7.1	71
36	Dynamics of Preferential Substrate Recognition in HIV-1 Protease: Redefining the Substrate Envelope. <i>Journal of Molecular Biology</i> , 2011, 410, 726-744.	4.2	63

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37	Hydrophobic Core Flexibility Modulates Enzyme Activity in HIV-1 Protease. <i>Journal of the American Chemical Society</i> , 2012, 134, 4163-4168.	13.7	63
38	Defining the substrate envelope of SARS-CoV-2 main protease to predict and avoid drug resistance. <i>Nature Communications</i> , 2022, 13, .	12.8	63
39	Evaluating the Role of Macrocycles in the Susceptibility of Hepatitis C Virus NS3/4A Protease Inhibitors to Drug Resistance. <i>ACS Chemical Biology</i> , 2013, 8, 1469-1478.	3.4	58
40	Crystal structure of the catalytic domain of HIV-1 restriction factor APOBEC3G in complex with ssDNA. <i>Nature Communications</i> , 2018, 9, 2460.	12.8	58
41	Differential Flap Dynamics in Wild-Type and a Drug Resistant Variant of HIV-1 Protease Revealed by Molecular Dynamics and NMR Relaxation. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3452-3462.	5.3	55
42	Molecular and Dynamic Mechanism Underlying Drug Resistance in Genotype 3 Hepatitis C NS3/4A Protease. <i>Journal of the American Chemical Society</i> , 2016, 138, 11850-11859.	13.7	55
43	Structural Analysis of Asunaprevir Resistance in HCV NS3/4A Protease. <i>ACS Chemical Biology</i> , 2014, 9, 2485-2490.	3.4	53
44	Genome-scale in vivo CRISPR screen identifies RNLS as a target for beta cell protection in type 1 diabetes. <i>Nature Metabolism</i> , 2020, 2, 934-945.	11.9	53
45	Introduction: Drug Resistance. <i>Chemical Reviews</i> , 2021, 121, 3235-3237.	47.7	53
46	Mechanism of Substrate Recognition by Drug-Resistant Human Immunodeficiency Virus Type 1 Protease Variants Revealed by a Novel Structural Intermediate. <i>Journal of Virology</i> , 2006, 80, 3607-3616.	3.4	52
47	Substrate Envelope-Designed Potent HIV-1 Protease Inhibitors to Avoid Drug Resistance. <i>Chemistry and Biology</i> , 2013, 20, 1116-1124.	6.0	52
48	Comprehensive fitness landscape of SARS-CoV-2 Mpro reveals insights into viral resistance mechanisms. <i>ELife</i> , 0, 11, .	6.0	52
49	Design of Mutation-resistant HIV Protease Inhibitors with the Substrate Envelope Hypothesis. <i>Chemical Biology and Drug Design</i> , 2007, 69, 298-313.	3.2	51
50	Human Immunodeficiency Virus Type 1 Protease-Correlated Cleavage Site Mutations Enhance Inhibitor Resistance. <i>Journal of Virology</i> , 2009, 83, 11027-11042.	3.4	51
51	Structure-Based Design, Synthesis, and Structure-Activity Relationship Studies of HIV-1 Protease Inhibitors Incorporating Phenyloxazolidinones. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 7699-7708.	6.4	51
52	CRISPR-Cas9-mediated saturated mutagenesis screen predicts clinical drug resistance with improved accuracy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11751-11756.	7.1	50
53	Co-evolution of nelfinavir-resistant HIV-1 protease and the p1-p6 substrate. <i>Virology</i> , 2006, 347, 405-409.	2.4	49
54	New approaches to HIV protease inhibitor drug design II: testing the substrate envelope hypothesis to avoid drug resistance and discover robust inhibitors. <i>Current Opinion in HIV and AIDS</i> , 2008, 3, 642-646.	3.8	48

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55	Substrate sequence selectivity of APOBEC3A implicates intra-DNA interactions. <i>Scientific Reports</i> , 2018, 8, 7511.	3.3	47
56	Molecular Mechanisms of Viral and Host Cell Substrate Recognition by Hepatitis C Virus NS3/4A Protease. <i>Journal of Virology</i> , 2011, 85, 6106-6116.	3.4	45
57	APOBEC3s: DNA editing human cytidine deaminases. <i>Protein Science</i> , 2019, 28, 1552-1566.	7.6	45
58	Decomposing the Energetic Impact of Drug Resistant Mutations in HIV-1 Protease on Binding DRV. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 1358-1368.	5.3	44
59	Context Surrounding Processing Sites Is Crucial in Determining Cleavage Rate of a Subset of Processing Sites in HIV-1 Gag and Gag-Pro-Pol Polyprotein Precursors by Viral Protease. <i>Journal of Biological Chemistry</i> , 2012, 287, 13279-13290.	3.4	43
60	Dengue Virus NS2B/NS3 Protease Inhibitors Exploiting the Prime Side. <i>Journal of Virology</i> , 2017, 91, .	3.4	42
61	Structural basis and distal effects of Gag substrate coevolution in drug resistance to HIV-1 protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15993-15998.	7.1	40
62	Drug Design Strategies to Avoid Resistance in Direct-Acting Antivirals and Beyond. <i>Chemical Reviews</i> , 2021, 121, 3238-3270.	47.7	40
63	Structural and Thermodynamic Effects of Macrocyclization in HCV NS3/4A Inhibitor MK-5172. <i>ACS Chemical Biology</i> , 2016, 11, 900-909.	3.4	39
64	Mutations in Influenza A Virus Neuraminidase and Hemagglutinin Confer Resistance against a Broadly Neutralizing Hemagglutinin Stem Antibody. <i>Journal of Virology</i> , 2019, 93, .	3.4	37
65	Crystal Structure of Lysine Sulfonamide Inhibitor Reveals the Displacement of the Conserved Flap Water Molecule in Human Immunodeficiency Virus Type 1 Protease. <i>Journal of Virology</i> , 2007, 81, 9512-9518.	3.4	36
66	A Balance between Inhibitor Binding and Substrate Processing Confers Influenza Drug Resistance. <i>Journal of Molecular Biology</i> , 2016, 428, 538-553.	4.2	36
67	Hepatitis C Virus NS3/4A Protease Inhibitors Incorporating Flexible P2 Quinoxalines Target Drug Resistant Viral Variants. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 5699-5716.	6.4	36
68	Assembly of human C-terminal binding protein (CtBP) into tetramers. <i>Journal of Biological Chemistry</i> , 2018, 293, 9101-9112.	3.4	36
69	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
70	Viral proteases: Structure, mechanism and inhibition. <i>The Enzymes</i> , 2021, 50, 301-333.	1.7	36
71	Role of Invariant Thr80 in Human Immunodeficiency Virus Type 1 Protease Structure, Function, and Viral Infectivity. <i>Journal of Virology</i> , 2006, 80, 6906-6916.	3.4	35
72	Improving the Resistance Profile of Hepatitis C NS3/4A Inhibitors: Dynamic Substrate Envelope Guided Design. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 5693-5705.	5.3	34

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73	Drug Resistance Mutations Alter Dynamics of Inhibitor-Bound HIV-1 Protease. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 3438-3448.	5.3	34
74	Testing the Substrate-Envelope Hypothesis with Designed Pairs of Compounds. <i>ACS Chemical Biology</i> , 2013, 8, 2433-2441.	3.4	33
75	Crystal structures of human CtBP in complex with substrate MTOB reveal active site features useful for inhibitor design. <i>FEBS Letters</i> , 2014, 588, 1743-1748.	2.8	29
76	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
77	Interdependence of Inhibitor Recognition in HIV-1 Protease. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 2300-2309.	5.3	27
78	Elucidating the Interdependence of Drug Resistance from Combinations of Mutations. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 5671-5682.	5.3	27
79	Structural Adaptation of Darunavir Analogues against Primary Mutations in HIV-1 Protease. <i>ACS Infectious Diseases</i> , 2019, 5, 316-325.	3.8	27
80	Structural and Thermodynamic Basis of Amprenavir/Darunavir and Atazanavir Resistance in HIV-1 Protease with Mutations at Residue 50. <i>Journal of Virology</i> , 2013, 87, 4176-4184.	3.4	26
81	HIV-1 Protease and Substrate Coevolution Validates the Substrate Envelope As the Substrate Recognition Pattern. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 703-714.	5.3	23
82	Prototypical Recombinant Multi-Protease-Inhibitor-Resistant Infectious Molecular Clones of Human Immunodeficiency Virus Type 1. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 4290-4299.	3.2	23
83	A computational analysis of the structural determinants of APOBEC3's catalytic activity and vulnerability to HIV-1 Vif. <i>Virology</i> , 2014, 471-473, 105-116.	2.4	23
84	HIV-1 Protease-Substrate Coevolution in Nelfinavir Resistance. <i>Journal of Virology</i> , 2014, 88, 7145-7154.	3.4	22
85	Structure-Guided Design of a High Affinity Inhibitor to Human CtBP. <i>ACS Chemical Biology</i> , 2015, 10, 1118-1127.	3.4	22
86	HIV-1 Protease Inhibitors Incorporating Stereochemically Defined P2 Ligands To Optimize Hydrogen Bonding in the Substrate Envelope. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 8062-8079.	6.4	21
87	Pan-3C Protease Inhibitor Rupintrivir Binds SARS-CoV-2 Main Protease in a Unique Binding Mode. <i>Biochemistry</i> , 2021, 60, 2925-2931.	2.5	21
88	Toward the Design of Mutation-Resistant Enzyme Inhibitors: Further Evaluation of the Substrate Envelope Hypothesis. <i>Chemical Biology and Drug Design</i> , 2009, 74, 234-245.	3.2	20
89	Molecular Basis for Differential Patterns of Drug Resistance in Influenza N1 and N2 Neuraminidase. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 6098-6108.	5.3	20
90	Dengue Protease Substrate Recognition: Binding of the Prime Side. <i>ACS Infectious Diseases</i> , 2016, 2, 734-743.	3.8	19

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91	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
92	Characterizing Protein-Ligand Binding Using Atomistic Simulation and Machine Learning: Application to Drug Resistance in HIV-1 Protease. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 1284-1299.	5.3	19
93	Cooperative Effects of Drug-Resistance Mutations in the Flap Region of HIV-1 Protease. <i>ACS Chemical Biology</i> , 2013, 8, 513-518.	3.4	18
94	Positive Selection Drives Preferred Segment Combinations during Influenza Virus Reassortment. <i>Molecular Biology and Evolution</i> , 2015, 32, 1519-1532.	8.9	16
95	Synonymous Mutations at the Beginning of the Influenza A Virus Hemagglutinin Gene Impact Experimental Fitness. <i>Journal of Molecular Biology</i> , 2018, 430, 1098-1115.	4.2	16
96	Quinoxaline-Based Linear HCV NS3/4A Protease Inhibitors Exhibit Potent Activity against Drug Resistant Variants. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 691-696.	2.8	16
97	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
98	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
99	Molecular Determinants of Epistasis in HIV-1 Protease: Elucidating the Interdependence of L89V and L90M Mutations in Resistance. <i>Biochemistry</i> , 2019, 58, 3711-3726.	2.5	15
100	Avoiding Drug Resistance by Substrate Envelope-Guided Design: Toward Potent and Robust HCV NS3/4A Protease Inhibitors. <i>MBio</i> , 2020, 11, .	4.1	15
101	Cryo-EM structure of CtBP2 confirms tetrameric architecture. <i>Structure</i> , 2021, 29, 310-319.e5.	3.3	15
102	Discovery of Quinoxaline-Based P1-P3 Macrocyclic NS3/4A Protease Inhibitors with Potent Activity against Drug-Resistant Hepatitis C Virus Variants. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 11972-11989.	6.4	15
103	Resistance outside the substrate envelope: hepatitis C NS3/4A protease inhibitors. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2019, 54, 11-26.	5.2	14
104	Structural basis of substrate specificity in human cytidine deaminase family APOBEC3s. <i>Journal of Biological Chemistry</i> , 2021, 297, 100909.	3.4	14
105	Structural Determination of the Broadly Reactive Anti-IGHV1-69 Anti-idiotypic Antibody G6 and Its Idiotope. <i>Cell Reports</i> , 2017, 21, 3243-3255.	6.4	13
106	HIV-1 Protease Uses Bi-Specific S2/S2' Subsites to Optimize Cleavage of Two Classes of Target Sites. <i>Journal of Molecular Biology</i> , 2018, 430, 5182-5195.	4.2	13
107	Probing Structural Changes among Analogous Inhibitor-Bound Forms of HIV-1 Protease and a Drug-Resistant Mutant in Solution by Nuclear Magnetic Resonance. <i>Biochemistry</i> , 2018, 57, 1652-1662.	2.5	12
108	Crystal Structure of a Soluble APOBEC3G Variant Suggests ssDNA to Bind in a Channel that Extends between the Two Domains. <i>Journal of Molecular Biology</i> , 2020, 432, 6042-6060.	4.2	12

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109	Inhibiting HTLV-1 Protease: A Viable Antiviral Target. ACS Chemical Biology, 2021, 16, 529-538.	3.4	12
110	Interactions of APOBEC3s with DNA and RNA. Current Opinion in Structural Biology, 2021, 67, 195-204.	5.7	12
111	A Direct Interaction with RNA Dramatically Enhances the Catalytic Activity of the HIV-1 Protease In Vitro. Journal of Molecular Biology, 2015, 427, 2360-2378.	4.2	11
112	Inhibition of APOBEC3G activity impedes double-stranded DNA repair. FEBS Journal, 2016, 283, 112-129.	4.7	11
113	Molecular and Structural Mechanism of Pan-Genotypic HCV NS3/4A Protease Inhibition by Glecaprevir. ACS Chemical Biology, 2020, 15, 342-352.	3.4	11
114	Unique structural solution from a VH3-30 antibody targeting the hemagglutinin stem of influenza A viruses. Nature Communications, 2021, 12, 559.	12.8	11
115	Deciphering Complex Mechanisms of Resistance and Loss of Potency through Coupled Molecular Dynamics and Machine Learning. Journal of Chemical Theory and Computation, 2021, 17, 2054-2064.	5.3	11
116	Simultaneously Targeting the NS3 Protease and Helicase Activities for More Effective Hepatitis C Virus Therapy. ACS Chemical Biology, 2015, 10, 1887-1896.	3.4	10
117	Constrained Mutational Sampling of Amino Acids in HIV-1 Protease Evolution. Molecular Biology and Evolution, 2019, 36, 798-810.	8.9	10
118	Mavyret: A Pan-Genotypic Combination Therapy for the Treatment of Hepatitis C Infection. Biochemistry, 2018, 57, 481-482.	2.5	9
119	NMR and MD studies combined to elucidate inhibitor and water interactions of HIV-1 protease and their modulations with resistance mutations. Journal of Biomolecular NMR, 2019, 73, 365-374.	2.8	9
120	Structural and molecular analysis of a protective epitope of Lyme disease antigen OspA and antibody interactions. Journal of Molecular Recognition, 2017, 30, e2595.	2.1	8
121	Development of a Novel Screening Strategy Designed to Discover a New Class of HIV Drugs. Journal of the Association for Laboratory Automation, 2014, 19, 297-303.	2.8	7
122	Mechanism for APOBEC3G catalytic exclusion of RNA and non-substrate DNA. Nucleic Acids Research, 2019, 47, 7676-7689.	14.5	7
123	Quantitative structural analysis of influenza virus by cryo-electron tomography and convolutional neural networks. Structure, 2022, 30, 777-786.e3.	3.3	7
124	Structural Analysis of Potent Hybrid HIV-1 Protease Inhibitors Containing Bis-tetrahydrofuran in a Pseudosymmetric Dipeptide Isostere. Journal of Medicinal Chemistry, 2020, 63, 8296-8313.	6.4	6
125	Deciphering Antifungal Drug Resistance in <i>Pneumocystis jirovecii</i> DHFR with Molecular Dynamics and Machine Learning. Journal of Chemical Information and Modeling, 2021, 61, 2537-2541.	5.4	6
126	Deciphering the Molecular Mechanism of HCV Protease Inhibitor Fluorination as a General Approach to Avoid Drug Resistance. Journal of Molecular Biology, 2022, 434, 167503.	4.2	6

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127	Analyses of HIV proteases variants at the threshold of viability reveals relationships between processing efficiency and fitness. <i>Virus Evolution</i> , 2021, 7, veab103.	4.9	6
128	NAD(H) phosphates mediate tetramer assembly of human C-terminal binding protein (CtBP). <i>Journal of Biological Chemistry</i> , 2021, 296, 100351.	3.4	4
129	A call to arms: Unifying the fight against resistance. <i>Science Signaling</i> , 2018, 11, .	3.6	3
130	Substrate-Envelope-Guided Design of Drugs with a High Barrier to the Evolution of Resistance. , 2014, , 1-23.		2
131	REdiii: a pipeline for automated structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1059-1067.	2.5	2
132	Synthesis and Biological Evaluation of 4/5- <i>Aroyl</i> - <i>2</i> - <i>C</i> aminoimidazoles as Microbial Biofilm Inhibitors. <i>ChemistrySelect</i> , 2020, 5, 5965-5969.	1.5	1
133	Optimizing the refinement of merohedrally twinned P61 HIV-1 protease inhibitor cocrystal structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 302-310.	2.3	1
134	HIV-1 VIF and human APOBEC3G interaction directly observed through molecular specific labeling using a new dual promoter vector. <i>Journal of Magnetic Resonance</i> , 2022, 339, 107230.	2.1	1
135	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
136	RNA Exclusion Mechanism of the Cytidine Deaminase APOBEC3G. <i>FASEB Journal</i> , 2019, 33, 493.9.	0.5	0
137	Identification of a permissive secondary mutation that restores the enzymatic activity of oseltamivir resistance mutation H275Y. <i>Journal of Virology</i> , 2022, , jvi0198221.	3.4	0
138	Call for Papers: Drug Resistance in Infectious Diseases and Beyond. <i>ACS Infectious Diseases</i> , 2022, 8, 665-666.	3.8	0