Celia A Schiffer

List of Publications by Year
in descending order

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138	7,117	50276	74163
papers	citations	46 h-index	75 g-index

153	153	153	6920
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of a permissive secondary mutation that restores the enzymatic activity of oseltamivir resistance mutation H275Y. Journal of Virology, 2022, , jvi0198221.	3.4	0
2	Quantitative structural analysis of influenza virus by cryo-electron tomography and convolutional neural networks. Structure, 2022, 30, 777-786.e3.	3.3	7
3	Call for Papers: Drug Resistance in Infectious Diseases and Beyond. ACS Infectious Diseases, 2022, 8, 665-666.	3.8	0
4	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
5	HIV-1 VIF and human APOBEC3G interaction directly observed through molecular specific labeling using a new dual promotor vector. Journal of Magnetic Resonance, 2022, 339, 107230.	2.1	1
6	Defining the substrate envelope of SARS-CoV-2 main protease to predict and avoid drug resistance. Nature Communications, 2022, 13, .	12.8	63
7	Cryo-EM structure of CtBP2 confirms tetrameric architecture. Structure, 2021, 29, 310-319.e5.	3.3	15
8	Unique structural solution from a VH3-30 antibody targeting the hemagglutinin stem of influenza A viruses. Nature Communications, 2021, 12, 559.	12.8	11
9	NAD(H) phosphates mediate tetramer assembly of human C-terminal binding protein (CtBP). Journal of Biological Chemistry, 2021, 296, 100351.	3.4	4
10	Drug Design Strategies to Avoid Resistance in Direct-Acting Antivirals and Beyond. Chemical Reviews, 2021, 121, 3238-3270.	47.7	40
11	Crystal Structure of SARS-CoV-2 Main Protease in Complex with the Non-Covalent Inhibitor ML188. Viruses, 2021, 13, 174.	3.3	80
12	Inhibiting HTLV-1 Protease: A Viable Antiviral Target. ACS Chemical Biology, 2021, 16, 529-538.	3.4	12
13	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
14	Introduction: Drug Resistance. Chemical Reviews, 2021, 121, 3235-3237.	47.7	53
15	Interactions of APOBEC3s with DNA and RNA. Current Opinion in Structural Biology, 2021, 67, 195-204.	5.7	12
16	Deciphering Antifungal Drug Resistance in Pneumocystis jirovecii DHFR with Molecular Dynamics and Machine Learning. Journal of Chemical Information and Modeling, 2021, 61, 2537-2541.	5.4	6
17	Structural basis of substrate specificity in human cytidine deaminase family APOBEC3s. Journal of Biological Chemistry, 2021, 297, 100909.	3.4	14
18	Affinity maturation of SARS-CoV-2 neutralizing antibodies confers potency, breadth, and resilience to viral escape mutations. Immunity, 2021, 54, 1853-1868.e7.	14.3	230

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19	Discovery of Quinoxaline-Based P1â€“P3 Macrocyclic NS3/4A Protease Inhibitors with Potent Activity against Drug-Resistant Hepatitis C Virus Variants. Journal of Medicinal Chemistry, 2021, 64, 11972-11989.	6.4	15
20	Pan-3C Protease Inhibitor Rupintrivir Binds SARS-CoV-2 Main Protease in a Unique Binding Mode. Biochemistry, 2021, 60, 2925-2931.	2.5	21
21	Viral proteases: Structure, mechanism and inhibition. The Enzymes, 2021, 50, 301-333.	1.7	36
22	Analyses of HIV proteases variants at the threshold of viability reveals relationships between processing efficiency and fitness. Virus Evolution, 2021, 7, veab103.	4.9	6
23	Characterizing Proteinâ€“Ligand Binding Using Atomistic Simulation and Machine Learning: Application to Drug Resistance in HIV-1 Protease. Journal of Chemical Theory and Computation, 2020, 16, 1284-1299.	5.3	19
24	Molecular and Structural Mechanism of Pan-Genotypic HCV NS3/4A Protease Inhibition by Glecaprevir. ACS Chemical Biology, 2020, 15, 342-352.	3.4	11
25	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
26	Genome-scale in vivo CRISPR screen identifies RNLS as a target for beta cell protection in type 1 diabetes. Nature Metabolism, 2020, 2, 934-945.	11.9	53
27	Crystal Structure of a Soluble APOBEC3G Variant Suggests ssDNA to Bind in a Channel that Extends between the Two Domains. Journal of Molecular Biology, 2020, 432, 6042-6060.	4.2	12
28	A cross-reactive human IgA monoclonal antibody blocks SARS-CoV-2 spike-ACE2 interaction. Nature Communications, 2020, 11, 4198.	12.8	132
29	Synthesis and Biological Evaluation of 4/5â€Aroylâ€2â€aminoimidazoles as Microbial Biofilm Inhibitors. ChemistrySelect, 2020, 5, 5965-5969.	1.5	1
30	Optimizing the refinement of merohedrally twinned P61 HIV-1 proteaseâ€“inhibitor cocrystal structures. Acta Crystallographica Section D: Structural Biology, 2020, 76, 302-310.	2.3	1
31	Avoiding Drug Resistance by Substrate Envelope-Guided Design: Toward Potent and Robust HCV NS3/4A Protease Inhibitors. MBio, 2020, 11, .	4.1	15
32	HIV-1 Protease Inhibitors Incorporating Stereochemically Defined P2â€² Ligands To Optimize Hydrogen Bonding in the Substrate Envelope. Journal of Medicinal Chemistry, 2019, 62, 8062-8079.	6.4	21
33	Molecular Determinants of Epistasis in HIV-1 Protease: Elucidating the Interdependence of L89V and L90M Mutations in Resistance. Biochemistry, 2019, 58, 3711-3726.	2.5	15
34	Picomolar to Micromolar: Elucidating the Role of Distal Mutations in HIV-1 Protease in Conferring Drug Resistance. ACS Chemical Biology, 2019, 14, 2441-2452.	3.4	36
35	Target-Specific Prediction of Ligand Affinity with Structure-Based Interaction Fingerprints. Journal of Chemical Information and Modeling, 2019, 59, 3679-3691.	5.4	16
36	Mechanism for APOBEC3G catalytic exclusion of RNA and non-substrate DNA. Nucleic Acids Research, 2019, 47, 7676-7689.	14.5	7

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37	APOBEC3s: DNAâ€editing human cytidine deaminases. Protein Science, 2019, 28, 1552-1566.	7.6	45
38	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
39	Resistance outside the substrate envelope: hepatitis C NS3/4A protease inhibitors. Critical Reviews in Biochemistry and Molecular Biology, 2019, 54, 11-26.	5.2	14
40	Constrained Mutational Sampling of Amino Acids in HIV-1 Protease Evolution. Molecular Biology and Evolution, 2019, 36, 798-810.	8.9	10
41	Structural Adaptation of Darunavir Analogues against Primary Mutations in HIV-1 Protease. ACS Infectious Diseases, 2019, 5, 316-325.	3.8	27
42	Structural Analysis of the Active Site and DNA Binding of Human Cytidine Deaminase APOBEC3B. Journal of Chemical Theory and Computation, 2019, 15, 637-647.	5.3	16
43	Mutations in Influenza A Virus Neuraminidase and Hemagglutinin Confer Resistance against a Broadly Neutralizing Hemagglutinin Stem Antibody. Journal of Virology, 2019, 93, .	3.4	37
44	RNA Exclusion Mechanism of the Cytidine Deaminase APOBEC3G. FASEB Journal, 2019, 33, 493.9.	0.5	0
45	Probing Structural Changes among Analogous Inhibitor-Bound Forms of HIV-1 Protease and a Drug-Resistant Mutant in Solution by Nuclear Magnetic Resonance. Biochemistry, 2018, 57, 1652-1662.	2.5	12
46	Synonymous Mutations at the Beginning of the Influenza A Virus Hemagglutinin Gene Impact Experimental Fitness. Journal of Molecular Biology, 2018, 430, 1098-1115.	4.2	16
47	Assembly of human C-terminal binding protein (CtBP) into tetramers. Journal of Biological Chemistry, 2018, 293, 9101-9112.	3.4	36
48	Hydration Structure and Dynamics of Inhibitor-Bound HIV-1 Protease. Journal of Chemical Theory and Computation, 2018, 14, 2784-2796.	5.3	28
49	Mavyret: A Pan-Genotypic Combination Therapy for the Treatment of Hepatitis C Infection. Biochemistry, 2018, 57, 481-482.	2.5	9
50	HIV-1 Protease Uses Bi-Specific S2/S2â€² Subsites to Optimize Cleavage of Two Classes of Target Sites. Journal of Molecular Biology, 2018, 430, 5182-5195.	4.2	13
51	A call to arms: Unifying the fight against resistance. Science Signaling, 2018, 11, .	3.6	3
52	Molecular Mechanism of Resistance in a Clinically Significant Double-Mutant Variant of HCV NS3/4A Protease. Structure, 2018, 26, 1360-1372.e5.	3.3	19
53	Quinoxaline-Based Linear HCV NS3/4A Protease Inhibitors Exhibit Potent Activity against Drug Resistant Variants. ACS Medicinal Chemistry Letters, 2018, 9, 691-696.	2.8	16
54	Substrate sequence selectivity of APOBEC3A implicates intra-DNA interactions. Scientific Reports, 2018, 8, 7511.	3.3	47

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55	Crystal structure of the catalytic domain of HIV-1 restriction factor APOBEC3G in complex with ssDNA. Nature Communications, 2018, 9, 2460.	12.8	58
56	Structural analysis of the active site and DNA binding of human cytidine deaminase APOBEC3B. FASEB Journal, 2018, 32, 792.31.	0.5	0
57	Crystal structure of APOBEC3A bound to single-stranded DNA reveals structural basis for cytidine deamination and specificity. Nature Communications, 2017, 8, 15024.	12.8	130
58	Citrullination of NF-Î¹B p65 promotes its nuclear localization and TLR-induced expression of IL-1Î² and TNFÎ±. Science Immunology, 2017, 2, .	11.9	80
59	Hepatitis C Virus NS3/4A Protease Inhibitors Incorporating Flexible P2 Quinoxalines Target Drug Resistant Viral Variants. Journal of Medicinal Chemistry, 2017, 60, 5699-5716.	6.4	36
60	Interdependence of Inhibitor Recognition in HIV-1 Protease. Journal of Chemical Theory and Computation, 2017, 13, 2300-2309.	5.3	27
61	Dengue Virus NS2B/NS3 Protease Inhibitors Exploiting the Prime Side. Journal of Virology, 2017, 91, .	3.4	42
62	CRISPR-Cas9â€“mediated saturated mutagenesis screen predicts clinical drug resistance with improved accuracy. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11751-11756.	7.1	50
63	Elucidating the Interdependence of Drug Resistance from Combinations of Mutations. Journal of Chemical Theory and Computation, 2017, 13, 5671-5682.	5.3	27
64	Structural Determination of the Broadly Reactive Anti-IGHV1-69 Anti-idiotypic Antibody G6 and Its Idiotope. Cell Reports, 2017, 21, 3243-3255.	6.4	13
65	Structural and molecular analysis of a protective epitope of <scp>Lyme</scp> disease antigen <scp>OspA</scp> and antibody interactions. Journal of Molecular Recognition, 2017, 30, e2595.	2.1	8
66	Improving Viral Protease Inhibitors to Counter Drug Resistance. Trends in Microbiology, 2016, 24, 547-557.	7.7	81
67	Dengue Protease Substrate Recognition: Binding of the Prime Side. ACS Infectious Diseases, 2016, 2, 734-743.	3.8	19
68	Molecular and Dynamic Mechanism Underlying Drug Resistance in Genotype 3 Hepatitis C NS3/4A Protease. Journal of the American Chemical Society, 2016, 138, 11850-11859.	13.7	55
69	Molecular Basis for Differential Patterns of Drug Resistance in Influenza N1 and N2 Neuraminidase. Journal of Chemical Theory and Computation, 2016, 12, 6098-6108.	5.3	20
70	A Balance between Inhibitor Binding and Substrate Processing Confers Influenza Drug Resistance. Journal of Molecular Biology, 2016, 428, 538-553.	4.2	36
71	Inhibition of <scp>APOBEC</scp>3G activity impedes doubleâ€stranded <scp>DNA</scp> repair. FEBS Journal, 2016, 283, 112-129.	4.7	11
72	Structural and Thermodynamic Effects of Macrocyclization in HCV NS3/4A Inhibitor MK-5172. ACS Chemical Biology, 2016, 11, 900-909.	3.4	39

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73	Structural basis for mutation-induced destabilization of profilin 1 in ALS. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7984-7989.	7.1	71
74	Structure of the Vif-binding domain of the antiviral enzyme APOBEC3G. Nature Structural and Molecular Biology, 2015, 22, 485-491.	8.2	84
75	Structure-Guided Design of a High Affinity Inhibitor to Human CtBP. ACS Chemical Biology, 2015, 10, 1118-1127.	3.4	22
76	Positive Selection Drives Preferred Segment Combinations during Influenza Virus Reassortment. Molecular Biology and Evolution, 2015, 32, 1519-1532.	8.9	16
77	The ssDNA Mutator APOBEC3A Is Regulated by Cooperative Dimerization. Structure, 2015, 23, 903-911.	3.3	79
78	REdiii: a pipeline for automated structure solution. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1059-1067.	2.5	2
79	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
80	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
81	Structural basis and distal effects of Gag substrate coevolution in drug resistance to HIV-1 protease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15993-15998.	7.1	40
82	Substrate-Envelope-Guided Design of Drugs with a High Barrier to the Evolution of Resistance. , 2014, , 1-23.		2
83	Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. PLoS Genetics, 2014, 10, e1004185.	3.5	126
84	HIV-1 Protease-Substrate Coevolution in Nelfinavir Resistance. Journal of Virology, 2014, 88, 7145-7154.	3.4	22
85	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
86	Crystal structures of human CtBP in complex with substrate MTOB reveal active site features useful for inhibitor design. FEBS Letters, 2014, 588, 1743-1748.	2.8	29
87	A computational analysis of the structural determinants of APOBEC3â€™s catalytic activity and vulnerability to HIV-1 Vif. Virology, 2014, 471-473, 105-116.	2.4	23
88	Structural Analysis of Asunaprevir Resistance in HCV NS3/4A Protease. ACS Chemical Biology, 2014, 9, 2485-2490.	3.4	53
89	Drug Resistance Conferred by Mutations Outside the Active Site through Alterations in the Dynamic and Structural Ensemble of HIV-1 Protease. Journal of the American Chemical Society, 2014, 136, 11956-11963.	13.7	83
90	Drug Resistance Mutations Alter Dynamics of Inhibitor-Bound HIV-1 Protease. Journal of Chemical Theory and Computation, 2014, 10, 3438-3448.	5.3	34

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91	Substrate Envelope-Designed Potent HIV-1 Protease Inhibitors to Avoid Drug Resistance. Chemistry and Biology, 2013, 20, 1116-1124.	6.0	52
92	Crystal Structure of the DNA Cytosine Deaminase APOBEC3F: The Catalytically Active and HIV-1 Vif-Binding Domain. Structure, 2013, 21, 1042-1050.	3.3	85
93	Cooperative Effects of Drug-Resistance Mutations in the Flap Region of HIV-1 Protease. ACS Chemical Biology, 2013, 8, 513-518.	3.4	18
94	Evaluating the Role of Macrocycles in the Susceptibility of Hepatitis C Virus NS3/4A Protease Inhibitors to Drug Resistance. ACS Chemical Biology, 2013, 8, 1469-1478.	3.4	58
95	Testing the Substrate-Envelope Hypothesis with Designed Pairs of Compounds. ACS Chemical Biology, 2013, 8, 2433-2441.	3.4	33
96	Improving the Resistance Profile of Hepatitis C NS3/4A Inhibitors: Dynamic Substrate Envelope Guided Design. Journal of Chemical Theory and Computation, 2013, 9, 5693-5705.	5.3	34
97	Prototypical Recombinant Multi-Protease-Inhibitor-Resistant Infectious Molecular Clones of Human Immunodeficiency Virus Type 1. Antimicrobial Agents and Chemotherapy, 2013, 57, 4290-4299.	3.2	23
98	Structural and Thermodynamic Basis of Amprenavir/Darunavir and Atazanavir Resistance in HIV-1 Protease with Mutations at Residue 50. Journal of Virology, 2013, 87, 4176-4184.	3.4	26
99	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. Journal of Biological Chemistry, 2012, 287, 13279-13290.	3.4	43
100	The Molecular Basis of Drug Resistance against Hepatitis C Virus NS3/4A Protease Inhibitors. PLoS Pathogens, 2012, 8, e1002832.	4.7	179
101	Differential Flap Dynamics in Wild-Type and a Drug Resistant Variant of HIV-1 Protease Revealed by Molecular Dynamics and NMR Relaxation. Journal of Chemical Theory and Computation, 2012, 8, 3452-3462.	5.3	55
102	Hydrophobic Core Flexibility Modulates Enzyme Activity in HIV-1 Protease. Journal of the American Chemical Society, 2012, 134, 4163-4168.	13.7	63
103	Methylcytosine and Normal Cytosine Deamination by the Foreign DNA Restriction Enzyme APOBEC3A. Journal of Biological Chemistry, 2012, 287, 34801-34808.	3.4	120
104	Extreme Entropyâ€“Enthalpy Compensation in a Drug-Resistant Variant of HIV-1 Protease. ACS Chemical Biology, 2012, 7, 1536-1546.	3.4	72
105	First-In-Class Small Molecule Inhibitors of the Single-Strand DNA Cytosine Deaminase APOBEC3G. ACS Chemical Biology, 2012, 7, 506-517.	3.4	112
106	HIV-1 Protease and Substrate Coevolution Validates the Substrate Envelope As the Substrate Recognition Pattern. Journal of Chemical Theory and Computation, 2012, 8, 703-714.	5.3	23
107	Dynamics of Preferential Substrate Recognition in HIV-1 Protease: Redefining the Substrate Envelope. Journal of Molecular Biology, 2011, 410, 726-744.	4.2	63
108	Molecular Mechanisms of Viral and Host Cell Substrate Recognition by Hepatitis C Virus NS3/4A Protease. Journal of Virology, 2011, 85, 6106-6116.	3.4	45

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109	Crystal Structure of the APOBEC3G Catalytic Domain Reveals Potential Oligomerization Interfaces. Structure, 2010, 18, 28-38.	3.3	116
110	Drug resistance against HCV NS3/4A inhibitors is defined by the balance of substrate recognition versus inhibitor binding. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20986-20991.	7.1	176
111	Structure-Based Design, Synthesis, and Structureâ˜Activity Relationship Studies of HIV-1 Protease Inhibitors Incorporating Phenyloxazolidinones. Journal of Medicinal Chemistry, 2010, 53, 7699-7708.	6.4	51
112	Decomposing the Energetic Impact of Drug Resistant Mutations in HIV-1 Protease on Binding DRV. Journal of Chemical Theory and Computation, 2010, 6, 1358-1368.	5.3	44
113	Molecular Basis for Drug Resistance in HIV-1 Protease. Viruses, 2010, 2, 2509-2535.	3.3	122
114	Evaluating the Substrate-Envelope Hypothesis: Structural Analysis of Novel HIV-1 Protease Inhibitors Designed To Be Robust against Drug Resistance. Journal of Virology, 2010, 84, 5368-5378.	3.4	104
115	Human Immunodeficiency Virus Type 1 Protease-Correlated Cleavage Site Mutations Enhance Inhibitor Resistance. Journal of Virology, 2009, 83, 11027-11042.	3.4	51
116	Toward the Design of Mutationâ€Resistant Enzyme Inhibitors: Further Evaluation of the Substrate Envelope Hypothesis. Chemical Biology and Drug Design, 2009, 74, 234-245.	3.2	20
117	Lack of synergy for inhibitors targeting a multi-drug-resistant HIV-1 protease. Protein Science, 2009, 11, 418-429.	7.6	96
118	Insights into interferon regulatory factor activation from the crystal structure of dimeric IRF5. Nature Structural and Molecular Biology, 2008, 15, 1213-1220.	8.2	109
119	HIV-1 Protease Inhibitors from Inverse Design in the Substrate Envelope Exhibit Subnanomolar Binding to Drug-Resistant Variants. Journal of the American Chemical Society, 2008, 130, 6099-6113.	13.7	105
120	New approaches to HIV protease inhibitor drug design II: testing the substrate envelope hypothesis to avoid drug resistance and discover robust inhibitors. Current Opinion in HIV and AIDS, 2008, 3, 642-646.	3.8	48
121	Crystal Structure of Lysine Sulfonamide Inhibitor Reveals the Displacement of the Conserved Flap Water Molecule in Human Immunodeficiency Virus Type 1 Protease. Journal of Virology, 2007, 81, 9512-9518.	3.4	36
122	Design of Mutation-resistant HIV Protease Inhibitors with the Substrate Envelope Hypothesis. Chemical Biology and Drug Design, 2007, 69, 298-313.	3.2	51
123	Hydrophobic Sliding: A Possible Mechanism for Drug Resistance in Human Immunodeficiency Virus Type 1 Protease. Structure, 2007, 15, 225-233.	3.3	78
124	Discovery of HIV-1 Protease Inhibitors with Picomolar Affinities IncorporatingN-Aryl-oxazolidinone-5-carboxamides as Novel P2 Ligands. Journal of Medicinal Chemistry, 2006, 49, 7342-7356.	6.4	93
125	Co-evolution of nelfinavir-resistant HIV-1 protease and the p1â€“p6 substrate. Virology, 2006, 347, 405-409.	2.4	49
126	Mechanism of Substrate Recognition by Drug-Resistant Human Immunodeficiency Virus Type 1 Protease Variants Revealed by a Novel Structural Intermediate. Journal of Virology, 2006, 80, 3607-3616.	3.4	52

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127	Role of Invariant Thr80 in Human Immunodeficiency Virus Type 1 Protease Structure, Function, and Viral Infectivity. Journal of Virology, 2006, 80, 6906-6916.	3.4	35
128	Design of HIV-1 Protease Inhibitors Active on Multidrug-Resistant Virus. Journal of Medicinal Chemistry, 2005, 48, 1965-1973.	6.4	74
129	Discovery and Selection of TMC114, a Next Generation HIV-1 Protease InhibitorÂ§. Journal of Medicinal Chemistry, 2005, 48, 1813-1822.	6.4	242
130	Structural and Thermodynamic Basis for the Binding of TMC114, a Next-Generation Human Immunodeficiency Virus Type 1 Protease Inhibitor. Journal of Virology, 2004, 78, 12012-12021.	3.4	240
131	Structural Basis for Coevolution of a Human Immunodeficiency Virus Type 1 Nucleocapsid-p1 Cleavage Site with a V82A Drug-Resistant Mutation in Viral Protease. Journal of Virology, 2004, 78, 12446-12454.	3.4	88
132	Combating Susceptibility to Drug Resistance. Chemistry and Biology, 2004, 11, 1333-1338.	6.0	98
133	Covariation of amino acid positions in HIV-1 protease. Virology, 2003, 314, 536-548.	2.4	75
134	Mutation Patterns and Structural Correlates in Human Immunodeficiency Virus Type 1 Protease following Different Protease Inhibitor Treatments. Journal of Virology, 2003, 77, 4836-4847.	3.4	220
135	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. Journal of Virology, 2002, 76, 10226-10233.	3.4	103
136	Substrate Shape Determines Specificity of Recognition for HIV-1 Protease. Structure, 2002, 10, 369-381.	3.3	292
137	Curling of Flap Tips in HIV-1 Protease as a Mechanism for Substrate Entry and Tolerance of Drug Resistance. Structure, 2000, 8, 1259-1265.	3.3	195
138	Comprehensive fitness landscape of SARS-CoV-2 Mpro reveals insights into viral resistance mechanisms. ELife, 0, 11, .	6.0	52