

Edward Arnold

List of Publications by Year in descending order

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78
papers

4,432
citations

136950

32
h-index

106344

65
g-index

86
all docs

86
docs citations

86
times ranked

4361
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of the SARS-CoV-2 proteome in three dimensions (3D) during the first 6 months of the COVID-19 pandemic. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1054-1080.	2.6	31
2	Structural basis of HIV inhibition by L-nucleosides: Opportunities for drug development and repurposing. <i>Drug Discovery Today</i> , 2022, 27, 1832-1846.	6.4	4
3	Human endogenous retrovirus-K (HERV-K) reverse transcriptase (RT) structure and biochemistry reveals remarkable similarities to HIV-1 RT and opportunities for HERV-K-specific inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	16
4	2,4,5-Trisubstituted Pyrimidines as Potent HIV-1 NNRTIs: Rational Design, Synthesis, Activity Evaluation, and Crystallographic Studies. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 4239-4256.	6.4	33
5	Co-crystallization with diabodies: A case study for the introduction of synthetic symmetry. <i>Structure</i> , 2021, 29, 598-605.e3.	3.3	3
6	Revealing the Structural Plasticity of SARS-CoV-2 nsp7 and nsp8 Using Structural Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1618-1630.	2.8	13
7	Crystal Structure of a Retroviral Polyprotein: Prototype Foamy Virus Protease-Reverse Transcriptase (PR-RT). <i>Viruses</i> , 2021, 13, 1495.	3.3	4
8	HIV-1 gp120 Antagonists Also Inhibit HIV-1 Reverse Transcriptase by Bridging the NNRTI and NRTI Sites. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 16530-16540.	6.4	4
9	Integrative structural biology studies of HIV-1 reverse transcriptase binding to a high-affinity DNA aptamer. <i>Current Research in Structural Biology</i> , 2020, 2, 116-129.	2.2	8
10	Non-Nucleoside Reverse Transcriptase Inhibitors Join Forces with Integrase Inhibitors to Combat HIV. <i>Pharmaceuticals</i> , 2020, 13, 122.	3.8	13
11	Evolving understanding of HIV-1 reverse transcriptase structure, function, inhibition, and resistance. <i>Current Opinion in Structural Biology</i> , 2020, 61, 113-123.	5.7	43
12	Binding interface and impact on protease cleavage for an RNA aptamer to HIV-1 reverse transcriptase. <i>Nucleic Acids Research</i> , 2020, 48, 2709-2722.	14.5	22
13	Discovery and Characterization of Fluorine-Substituted Diarylpyrimidine Derivatives as Novel HIV-1 NNRTIs with Highly Improved Resistance Profiles and Low Activity for the hERG Ion Channel. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 1298-1312.	6.4	37
14	Michael G. Rossmann (1930–2019). <i>Nature Structural and Molecular Biology</i> , 2019, 26, 660-662.	8.2	3
15	Structural Basis of HIV-1 Inhibition by Nucleotide-Competing Reverse Transcriptase Inhibitor INDOPY-1. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9996-10002.	6.4	20
16	Aryl and Arylalkyl Substituted 3-Hydroxypyridin-2(1H)-ones: Synthesis and Evaluation as Inhibitors of Influenza A Endonuclease. <i>ChemMedChem</i> , 2019, 14, 1204-1223.	3.2	4
17	Structure of HIV-1 RT/dsRNA initiation complex prior to nucleotide incorporation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7308-7313.	7.1	26
18	Michael G. Rossmann (1930–2019), pioneer in macromolecular and virus crystallography: scientist, mentor and friend. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 523-527.	2.3	0

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19	Alpha-carboxynucleoside phosphonates: direct-acting inhibitors of viral DNA polymerases. <i>Future Medicinal Chemistry</i> , 2019, 11, 137-154.	2.3	6
20	Structure of HIV-1 reverse transcriptase/d4TTP complex: Novel DNA cross-linking site and pH-dependent conformational changes. <i>Protein Science</i> , 2019, 28, 587-597.	7.6	11
21	Epistasis and entrenchment of drug resistance in HIV-1 subtype B. <i>ELife</i> , 2019, 8, .	6.0	25
22	Developing and Evaluating Inhibitors against the RNase H Active Site of HIV-1 Reverse Transcriptase. <i>Journal of Virology</i> , 2018, 92, .	3.4	30
23	Guanine Î±-carboxy nucleoside phosphonate (G-Î±-CNP) shows a different inhibitory kinetic profile against the DNA polymerases of human immunodeficiency virus (HIV) and herpes viruses. <i>Biochemical Pharmacology</i> , 2017, 136, 51-61.	4.4	9
24	Structural Insights into HIV Reverse Transcriptase Mutations Q151M and Q151M Complex That Confer Multinucleoside Drug Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	16
25	Structural Basis of Mycobacterium tuberculosis Transcription and Transcription Inhibition. <i>Molecular Cell</i> , 2017, 66, 169-179.e8.	9.7	130
26	Rapid experimental SAD phasing and hot-spot identification with halogenated fragments. <i>IUCr</i> , 2016, 3, 51-60.	2.2	27
27	Conformational States of HIV-1 Reverse Transcriptase for Nucleotide Incorporation vs Pyrophosphorolysisâ€”Binding of Foscarnet. <i>ACS Chemical Biology</i> , 2016, 11, 2158-2164.	3.4	38
28	Structure of HIV-1 reverse transcriptase bound to a novel 38-mer hairpin template-primer DNA aptamer. <i>Protein Science</i> , 2016, 25, 46-55.	7.6	33
29	A New Class of Allosteric HIV-1 Integrase Inhibitors Identified by Crystallographic Fragment Screening of the Catalytic Core Domain. <i>Journal of Biological Chemistry</i> , 2016, 291, 23569-23577.	3.4	20
30	Exploring the role of the Î±-carboxyphosphonate moiety in the HIV-RT activity of Î±-carboxy nucleoside phosphonates. <i>Organic and Biomolecular Chemistry</i> , 2016, 14, 2454-2465.	2.8	17
31	Factors influencing the efficacy of rilpivirine in HIV-1 subtype C in low- and middle-income countries. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 367-371.	3.0	6
32	Alpha-carboxy nucleoside phosphonates as universal nucleoside triphosphate mimics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3475-3480.	7.1	29
33	Negative-Strand RNA Virus L Proteins: One Machine, Many Activities. <i>Cell</i> , 2015, 162, 239-241.	28.9	17
34	Differential Isotopic Enrichment To Facilitate Characterization of Asymmetric Multimeric Proteins Using Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 4015-4022.	6.5	4
35	Pronounced Inhibition Shift from HIV Reverse Transcriptase to Herpetic DNA Polymerases by Increasing the Flexibility of Î±-Carboxy Nucleoside Phosphonates. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 8110-8127.	6.4	9
36	Analysis of the Zidovudine Resistance Mutations T215Y, M41L, and L210W in HIV-1 Reverse Transcriptase. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7184-7196.	3.2	8

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37	Transcription inhibition by the depsipeptide antibiotic salinamide A. <i>ELife</i> , 2014, 3, e02451.	6.0	71
38	Drug Resistance in Non-B Subtype HIV-1: Impact of HIV-1 Reverse Transcriptase Inhibitors. <i>Viruses</i> , 2014, 6, 3535-3562.	3.3	27
39	Fragment Screening for Drug Discovery: Efficient Approaches for Exploring Chemical Space. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 116, 81.	2.9	3
40	Advantages of crystallographic fragment screening: Functional and mechanistic insights from a powerful platform for efficient drug discovery. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 116, 92-100.	2.9	73
41	Structures of HIV-1 RT-RNA/DNA ternary complexes with dATP and nevirapine reveal conformational flexibility of RNA/DNA: insights into requirements for RNase H cleavage. <i>Nucleic Acids Research</i> , 2014, 42, 8125-8137.	14.5	60
42	Phenyl Substituted 4-Hydroxypyridazin-3(2 <i>H</i>)-ones and 5-Hydroxypyrimidin-4(3 <i>H</i>)-ones: Inhibitors of Influenza A Endonuclease. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 8086-8098.	6.4	50
43	Mutations in HIV-1 Reverse Transcriptase Affect the Errors Made in a Single Cycle of Viral Replication. <i>Journal of Virology</i> , 2014, 88, 7589-7601.	3.4	46
44	Structure of a Dihydroxycoumarin Active-Site Inhibitor in Complex with the RNase H Domain of HIV-1 Reverse Transcriptase and Structure-Activity Analysis of Inhibitor Analogs. <i>Journal of Molecular Biology</i> , 2014, 426, 2617-2631.	4.2	36
45	Crystallographic Fragment Screening and Structure-Based Optimization Yields a New Class of Influenza Endonuclease Inhibitors. <i>ACS Chemical Biology</i> , 2013, 8, 2501-2508.	3.4	76
46	Phenyl substituted 3-hydroxypyridin-2(1 <i>H</i>)-ones: Inhibitors of influenza A endonuclease. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 6435-6446.	3.0	30
47	Snapshot of the equilibrium dynamics of a drug bound to HIV-1 reverse transcriptase. <i>Nature Chemistry</i> , 2013, 5, 174-181.	13.6	88
48	Detecting Allosteric Sites of HIV-1 Reverse Transcriptase by X-ray Crystallographic Fragment Screening. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 2738-2746.	6.4	78
49	HIV-1 reverse transcriptase and antiviral drug resistance. Part 1. <i>Current Opinion in Virology</i> , 2013, 3, 111-118.	5.4	126
50	HIV-1 reverse transcriptase and antiviral drug resistance. Part 2. <i>Current Opinion in Virology</i> , 2013, 3, 119-128.	5.4	83
51	3-Hydroxyquinolin-2(1 <i>H</i>)-ones As Inhibitors of Influenza A Endonuclease. <i>ACS Medicinal Chemistry Letters</i> , 2013, 4, 547-550.	2.8	44
52	HIV-1 reverse transcriptase complex with DNA and nevirapine reveals non-nucleoside inhibition mechanism. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 253-259.	8.2	176
53	Pingry School SMART Team Project: Modeling Current Strategies in HIV-1 Reverse Transcriptase Inhibitors. <i>FASEB Journal</i> , 2012, 26, lb240.	0.5	0
54	Structures of influenza A proteins and insights into antiviral drug targets. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 530-538.	8.2	292

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55	Structural basis of HIV-1 resistance to AZT by excision. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1202-1209.	8.2	115
56	Structure of HIV-1 Reverse Transcriptase with the Inhibitor Î²-Thujaplicinol Bound at the RNase H Active Site. <i>Structure</i> , 2009, 17, 1625-1635.	3.3	135
57	Structure and Function of HIV-1 Reverse Transcriptase: Molecular Mechanisms of Polymerization and Inhibition. <i>Journal of Molecular Biology</i> , 2009, 385, 693-713.	4.2	426
58	High-resolution structures of HIV-1 reverse transcriptase/TMC278 complexes: Strategic flexibility explains potency against resistance mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1466-1471.	7.1	310
59	Crystal engineering of HIV-1 reverse transcriptase for structure-based drug design. <i>Nucleic Acids Research</i> , 2008, 36, 5083-5092.	14.5	91
60	Linear Interaction Energy (LIE) Models for Ligand Binding in Implicit Solvent: Theory and Application to the Binding of NNRTIs to HIV-1 Reverse Transcriptase. <i>Journal of Chemical Theory and Computation</i> , 2007, 3, 256-277.	5.3	45
61	Structures of Wild-type and AZT-resistant HIV-1 Reverse Transcriptase Complexed with AZTppppA Yield Insights into the Nucleotide Excision Mechanism. <i>FASEB Journal</i> , 2007, 21, A640.	0.5	0
62	Spectroscopic Studies of Rilpivirine (TMC278/R278474) in Complex with HIV-1 Reverse Transcriptase. <i>FASEB Journal</i> , 2007, 21, A630.	0.5	0
63	HIV-1 Reverse Transcriptase Structure with RNase H Inhibitor Dihydroxy Benzoyl Naphthyl Hydrazone Bound at a Novel Site. <i>ACS Chemical Biology</i> , 2006, 1, 702-712.	3.4	132
64	Reply to: Is one solution good enough?. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 185-185.	8.2	3
65	Effects of the Î³67 Complex of Mutations in Human Immunodeficiency Virus Type 1 Reverse Transcriptase on Nucleoside Analog Excision. <i>Journal of Virology</i> , 2004, 78, 9987-9997.	3.4	31
66	Structures of HIV-1 RT-DNA complexes before and after incorporation of the anti-AIDS drug tenofovir. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 469-474.	8.2	157
67	Taking aim at a moving target: designing drugs to inhibit drug-resistant HIV-1 reverse transcriptases. <i>Current Opinion in Structural Biology</i> , 2004, 14, 716-730.	5.7	130
68	Trapping HIV-1 Reverse Transcriptase Before and After Translocation on DNA. <i>Journal of Biological Chemistry</i> , 2003, 278, 16280-16288.	3.4	79
69	HIV-1 Reverse Transcriptase Mutations Found in a Drug-Experienced Patient Confer Reduced Susceptibility to Multiple Nucleoside Reverse Transcriptase Inhibitors. <i>Antiviral Therapy</i> , 2002, 6, 231-238.	1.0	1
70	Molecular dynamics of HIV-1 reverse transcriptase indicates increased flexibility upon DNA binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 176-182.	2.6	30
71	X-ray crystal structure of MTH938 from <i>Methanobacterium thermoautotrophicum</i> at 2.2 Å... resolution reveals a novel tertiary protein fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 486-488.	2.6	5
72	Touching the heart of HIV-1 drug resistance: the fingers close down on the dNTP at the polymerase active site. <i>Chemistry and Biology</i> , 1999, 6, R137-R146.	6.0	107

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73	Pivot residue: an analysis of domain motion in proteins. <i>The Protein Journal</i> , 1999, 18, 807-811.	1.1	6
74	Structure and functional implications of the polymerase active site region in a complex of HIV-1 RT with a double-stranded DNA template-primer and an antibody fab fragment at 2.8 Å... resolution. <i>Journal of Molecular Biology</i> , 1998, 284, 1095-1111.	4.2	317
75	Molecular modeling studies of HIV-1 reverse transcriptase nonnucleoside inhibitors: Total energy of complexation as a predictor of drug placement and activity. <i>Protein Science</i> , 1995, 4, 2203-2222.	7.6	66
76	Buried surface analysis of HIV-1 reverse transcriptase p66/p51 heterodimer and its interaction with dsDNA template/primer. <i>Journal of Molecular Recognition</i> , 1994, 7, 157-161.	2.1	24
77	Identification of a pharmacophore for nucleoside analog inhibitors directed at HIV-1 reverse transcriptase. <i>Journal of Molecular Recognition</i> , 1994, 7, 211-214.	2.1	7
78	Review of HIV-1 reverse transcriptase three-dimensional structure: Implications for drug design. <i>Journal of Computer - Aided Molecular Design</i> , 1993, 1, 129-150.	1.0	127