Johnson Agniswamy

List of Publications by Year
in descending order

30 papers	767 citations	516215 16 h-index	525886 27 g-index
31 all docs	31 docs citations	31 times ranked	736 citing authors

#	Article	IF	Citations
1	Discovery of a new flavin N5-adduct in a tyrosine to phenylalanine variant of d-Arginine dehydrogenase. Archives of Biochemistry and Biophysics, 2022, 715, 109100.	1.4	1
2	A Single-Point Mutation in <scp>d</scp>-Arginine Dehydrogenase Unlocks a Transient Conformational State Resulting in Altered Cofactor Reactivity. Biochemistry, 2021, 60, 711-724.	1.2	7
3	Novel HIV PR inhibitors with C4-substituted bis-THF and bis-fluoro-benzyl target the two active site mutations of highly drug resistant mutant PRS17. Biochemical and Biophysical Research Communications, 2021, 566, 30-35.	1.0	3
4	Highly drugâ€resistant HIVâ€1 protease reveals decreased intraâ€subunit interactions due to clusters of mutations. FEBS Journal, 2020, 287, 3235-3254.	2.2	9
5	Structure-Based Design of Highly Potent HIV-1 Protease Inhibitors Containing New Tricyclic Ring P2-Ligands: Design, Synthesis, Biological, and X-ray Structural Studies. Journal of Medicinal Chemistry, 2020, 63, 4867-4879.	2.9	19
6	Potent antiviral HIV-1 protease inhibitor combats highly drug resistant mutant PR20. Biochemical and Biophysical Research Communications, 2019, 519, 61-66.	1.0	13
7	Highly Drug-Resistant HIV-1 Protease Mutant PRS17 Shows Enhanced Binding to Substrate Analogues. ACS Omega, 2019, 4, 8707-8719.	1.6	16
8	Structural studies of antiviral inhibitor with HIV-1 protease bearing drug resistant substitutions of V32I, I47V and V82I. Biochemical and Biophysical Research Communications, 2019, 514, 974-978.	1.0	18
9	Steric hindrance controls pyridine nucleotide specificity of a flavinâ€dependent NADH:quinone oxidoreductase. Protein Science, 2019, 28, 167-175.	3.1	6
10	Crystal structure of yeast nitronate monooxygenase from Cyberlindnera saturnus. Proteins: Structure, Function and Bioinformatics, 2018, 86, 599-605.	1.5	8
11	Design and Synthesis of Potent HIV-1 Protease Inhibitors Containing Bicyclic Oxazolidinone Scaffold as the P2 Ligands: Structureâ€“Activity Studies and Biological and X-ray Structural Studies. Journal of Medicinal Chemistry, 2018, 61, 9722-9737.	2.9	24
12	Design, synthesis, and X-ray studies of potent HIV-1 protease inhibitors incorporating aminothiochromane and aminotetrahydronaphthalene carboxamide derivatives as the P2 ligands. European Journal of Medicinal Chemistry, 2018, 160, 171-182.	2.6	4
13	Design and Synthesis of Highly Potent HIV-1 Protease Inhibitors Containing Tricyclic Fused Ring Systems as Novel P2 Ligands: Structureâ€“Activity Studies, Biological and X-ray Structural Analysis. Journal of Medicinal Chemistry, 2018, 61, 4561-4577.	2.9	31
14	Design of novel HIV-1 protease inhibitors incorporating isophthalamide-derived P2-P3 ligands: Synthesis, biological evaluation and X-ray structural studies of inhibitor-HIV-1 protease complex. Bioorganic and Medicinal Chemistry, 2017, 25, 5114-5127.	1.4	16
15	Design and Development of Highly Potent HIV-1 Protease Inhibitors with a Crown-Like Oxotricyclic Core as the P2-Ligand To Combat Multidrug-Resistant HIV Variants. Journal of Medicinal Chemistry, 2017, 60, 4267-4278.	2.9	64
16	Probing Lipophilic Adamantyl Group as the P1-Ligand for HIV-1 Protease Inhibitors: Design, Synthesis, Protein X-ray Structural Studies, and Biological Evaluation. Journal of Medicinal Chemistry, 2016, 59, 6826-6837.	2.9	15
17	In vitro heme biotransformation by the HupZ enzyme from Group A streptococcus. BioMetals, 2016, 29, 593-609.	1.8	27
18	Structural Studies of a Rationally Selected Multi-Drug Resistant HIV-1 Protease Reveal Synergistic Effect of Distal Mutations on Flap Dynamics. PLoS ONE, 2016, 11, e0168616.	1.1	39

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19	Substituted Bis-THF Protease Inhibitors with Improved Potency against Highly Resistant Mature HIV-1 Protease PR20. Journal of Medicinal Chemistry, 2015, 58, 5088-5095.	2.9	8
20	Structure-Based Design of Potent HIV-1 Protease Inhibitors with Modified P1-Biphenyl Ligands: Synthesis, Biological Evaluation, and Enzymeâ€“Inhibitor X-ray Structural Studies. Journal of Medicinal Chemistry, 2015, 58, 5334-5343.	2.9	21
21	Design of HIV-1 Protease Inhibitors with Amino-bis-tetrahydrofuran Derivatives as P2-Ligands to Enhance Backbone-Binding Interactions: Synthesis, Biological Evaluation, and Proteinâ€“Ligand X-ray Studies. Journal of Medicinal Chemistry, 2015, 58, 6994-7006.	2.9	13
22	Conformational variation of an extreme drug resistant mutant of HIV protease. Journal of Molecular Graphics and Modelling, 2015, 62, 87-96.	1.3	22
23	Extreme Multidrug Resistant HIV-1 Protease with 20 Mutations Is Resistant to Novel Protease Inhibitors with P1â€²-Pyrrolidinone or P2-Tris-tetrahydrofuran. Journal of Medicinal Chemistry, 2013, 56, 4017-4027.	2.9	34
24	Terminal Interface Conformations Modulate Dimer Stability Prior to Amino Terminal Autoprocessing of HIV-1 Protease. Biochemistry, 2012, 51, 1041-1050.	1.2	29
25	HIV-1 Protease with 20 Mutations Exhibits Extreme Resistance to Clinical Inhibitors through Coordinated Structural Rearrangements. Biochemistry, 2012, 51, 2819-2828.	1.2	78
26	Autocatalytic maturation, physical/chemical properties, and crystal structure of group N HIVâ€1 protease: Relevance to drug resistance. Protein Science, 2010, 19, 2055-2072.	3.1	22
27	HIV-1 Protease: Structural Perspectives on Drug Resistance. Viruses, 2009, 1, 1110-1136.	1.5	128
28	Caspase-3 binds diverse P4 residues in peptides as revealed by crystallography and structural modeling. Apoptosis: an International Journal on Programmed Cell Death, 2009, 14, 741-752.	2.2	22
29	Conformational similarity in the activation of caspase-3 and -7 revealed by the unliganded and inhibited structures of caspase-7. Apoptosis: an International Journal on Programmed Cell Death, 2009, 14, 1135-1144.	2.2	25
30	Plasticity of S2â€“S4 specificity pockets of executioner caspaseâ€7 revealed by structural and kinetic analysis. FEBS Journal, 2007, 274, 4752-4765.	2.2	45