

Rieko Ishima

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

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1684188

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docs citations

13
times ranked

125
citing authors

#	ARTICLE	IF	CITATIONS
1	19F NMR relaxation studies of fluorosubstituted tryptophans. <i>Journal of Biomolecular NMR</i> , 2019, 73, 401-409.	2.8	25
2	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
3	Determinants of Active-Site Inhibitor Interaction with HIV-1 RNase H. <i>ACS Infectious Diseases</i> , 2019, 5, 1963-1974.	3.8	10
4	NMR and MD studies combined to elucidate inhibitor and water interactions of HIV-1 protease and their modulations with resistance mutations. <i>Journal of Biomolecular NMR</i> , 2019, 73, 365-374.	2.8	9
5	Binding thermodynamics of metal ions to HIV-1 ribonuclease H domain. <i>Journal of Thermal Analysis and Calorimetry</i> , 2019, 135, 2647-2653.	3.6	8
6	Entire-Dataset Analysis of NMR Fast-Exchange Titration Spectra: A Mg ²⁺ Titration Analysis for HIV-1 Ribonuclease H Domain. <i>Journal of Physical Chemistry B</i> , 2016, 120, 12420-12431.	2.6	5
7	Retroviral RNase H: Structure, mechanism, and inhibition. <i>The Enzymes</i> , 2021, 50, 227-247.	1.7	4
8	An NMR strategy to detect conformational differences in a protein complexed with highly analogous inhibitors in solution. <i>Methods</i> , 2018, 148, 9-18.	3.8	3
9	Effect of Lysyl-tRNA Synthetase on the Maturation of HIV-1 Reverse Transcriptase. <i>ACS Omega</i> , 2020, 5, 16619-16627.	3.5	2
10	Large Multidomain Protein NMR: HIV-1 Reverse Transcriptase Precursor in Solution. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9545.	4.1	1
11	A synergy of activity, stability, and inhibitor interaction of HIV-1 protease mutants evolved under drug pressure. <i>Protein Science</i> , 2021, 30, 571-582.	7.6	1
12	The reduced form of the antibody CH2 domain. <i>Protein Science</i> , 2021, 30, 1895-1903.	7.6	1
13	Relative domain orientation of the L289K HIV-1 reverse transcriptase monomer. <i>Protein Science</i> , 2022, 31, e4307.	7.6	1