Karunesh Arora

List of Publications by Year in descending order

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471509 580821 31 982 17 25 citations h-index g-index papers 31 31 31 1132 citing authors docs citations times ranked all docs

#	Article	IF	CITATIONS
1	Frustration and folding of a TIM barrel protein. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16378-16383.	7.1	18
2	Regulation of calreticulin–major histocompatibility complex (MHC) class I interactions by ATP. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5608-17.	7.1	16
3	pH-Induced Stability Switching of the Bacteriophage HK97 Maturation Pathway. Journal of the American Chemical Society, 2014, 136, 3097-3107.	13.7	21
4	Modulation of frustration in folding by sequence permutation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10562-10567.	7.1	24
5	How DNA Polymerase X Preferentially Accommodates Incoming dATP Opposite 8-Oxoguanine on the Template. Biophysical Journal, 2013, 105, 2559-2568.	0.5	9
6	Deconstructing Activation Events in Rhodopsin. Journal of the American Chemical Society, 2013, 135, 10906-10909.	13.7	15
7	Multiple Intermediates, Diverse Conformations, and Cooperative Conformational Changes Underlie the Catalytic Hydride Transfer Reaction of Dihydrofolate Reductase. Topics in Current Chemistry, 2013, 337, 165-187.	4.0	21
8	Models of conformational selection of DNA polymerase X in the presence of oxoG lesions help interpret kinetics data. FASEB Journal, 2013, 27, 758.11.	0.5	0
9	Intrinsic Motions of DNA Polymerases Underlie Their Remarkable Specificity and Selectivity and Suggest a Hybrid Substrate Binding Mechanism. RSC Biomolecular Sciences, 2012, , 81-110.	0.4	2
10	Perspective: pre-chemistry conformational changes in DNA polymerase mechanisms. Theoretical Chemistry Accounts, 2012, 131, 1287.	1.4	34
11	Multiscale Modeling of Virus Structure, Assembly, and Dynamics. Biological and Medical Physics Series, 2012, , 167-189.	0.4	O
12	Molecular dynamics studies of polymerase X/DNA complexes in the presence of OxoG on the templating strand. FASEB Journal, 2012, 26, 539.8.	0.5	0
13	Hexameric Helicase Deconstructed: Interplay of Conformational Changes and Substrate Coupling. Biophysical Journal, 2010, 98, 1449-1457.	0.5	15
14	Structural insights into DNA polymerase X from African swine fever virus in the presence of oxoG lesions. FASEB Journal, 2010, 24, 876.15.	0.5	0
15	Functionally Important Conformations of the Met20 Loop in Dihydrofolate Reductase are Populated by Rapid Thermal Fluctuations. Journal of the American Chemical Society, 2009, 131, 5642-5647.	13.7	56
16	Extracting Kinetic and Stationary Distribution Information from Short MD Trajectories via a Collection of Surrogate Diffusion Models. Journal of Chemical Theory and Computation, 2009, 5, 47-58.	5.3	8
17	Mismatched Base-Pair Simulations for ASFV Pol X/DNA Complexes Help Interpret Frequent G•G Misincorporation. Journal of Molecular Biology, 2008, 384, 1086-1097.	4.2	20
18	Studies of African Swine Fever Virus Polymerase X/DNA complexes in the presence of mismatched base pairs. FASEB Journal, 2008, 22, 990.2.	0.5	0

#	Article	IF	CITATIONS
19	Large-scale allosteric conformational transitions of adenylate kinase appear to involve a population-shift mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18496-18501.	7.1	240
20	Regulation of DNA Repair Fidelity by Molecular Checkpoints: "Gates―in DNA Polymerase β's Substrate Selectionâ€. Biochemistry, 2006, 45, 15142-15156.	2.5	66
21	In Silico Studies of the African Swine Fever Virus DNA Polymerase X Support an Induced-Fit Mechanism. Biophysical Journal, 2006, 90, 42-56.	0.5	32
22	Sequential Side-Chain Residue Motions Transform the Binary into the Ternary State of DNA Polymerase \hat{l} ». Biophysical Journal, 2006, 91, 3182-3195.	0.5	17
23	Subtle but variable conformational rearrangements in the replication cycle of Sulfolobus solfataricus P2 DNA polymerase IV (Dpo4) may accommodate lesion bypass. Protein Science, 2006, 15, 135-151.	7.6	19
24	Harmonic Fourier beads method for studying rare events on rugged energy surfaces. Journal of Chemical Physics, 2006, 125, 174108.	3.0	42
25	Conformational Transition Pathway of Polymerase \hat{l}^2/DNA upon Binding Correct Incoming Substrate. Journal of Physical Chemistry B, 2005, 109, 5358-5367.	2.6	31
26	Mismatch-Induced Conformational Distortions in Polymerase \hat{l}^2 Support an Induced-Fit Mechanism for Fidelity $\hat{a} \in B$. Biochemistry, 2005, 44, 13328-13341.	2.5	57
27	PREFERENTIAL POLYMERIZATION OF 5-(AMINOMETHYL)-2-FURANCARBOXYLIC ACID (AMFC) INTO A CYCLIC TRIPEPTIDE. Journal of Theoretical and Computational Chemistry, 2004, 03, 555-566.	1.8	4
28	Critical Role of Magnesium Ions in DNA Polymerase \hat{l}^2 's Closing and Active Site Assembly. Journal of the American Chemical Society, 2004, 126, 8441-8453.	13.7	127
29	In Silico Evidence for DNA Polymerase-β's Substrate-Induced Conformational Change. Biophysical Journal, 2004, 87, 3088-3099.	0.5	52
30	Deoxyadenosine sugar puckering pathway simulated by the stochastic difference equation algorithm. Chemical Physics Letters, 2003, 378, 1-8.	2.6	33
31	Exploring the Functional Landscape of Biomolecular Machines via Elastic Network Normal Mode Analysis. , 0, , 59-77.		3