

Chiaki

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

18
papers

511
citations

11
h-index

19
g-index

19
ext. papers

543
ext. citations

5.3
avg, IF

3.19
L-index

#	Paper	IF	Citations
18	Changes in dynamic and static structures of the HIV-1 p24 capsid protein N-domain caused by amino-acid substitution are associated with its viral viability. <i>Protein Science</i> , 2021 , 30, 2233-2245	6.3	1
17	Distinct residual and disordered structures of alpha-synuclein analyzed by amide-proton exchange and NMR signal intensity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020 , 1868, 140464	4	1
16	Effect of Glu12-His89 Interaction on Dynamic Structures in HIV-1 p17 Matrix Protein Elucidated by NMR. <i>PLoS ONE</i> , 2016 , 11, e0167176	3.7	2
15	Comparison of residual alpha- and beta-structures between two intrinsically disordered proteins by using NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 229-38	4	3
14	Flexible and rigid structures in HIV-1 p17 matrix protein monitored by relaxation and amide proton exchange with NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 520-6	4	5
13	Long-range effects of tag sequence on marginally stabilized structure in HIV-1 p24 capsid protein monitored using NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 1638-47	4	
12	Remaining structures at the N- and C-terminal regions of alpha-synuclein accurately elucidated by amide-proton exchange NMR with fitting. <i>FEBS Letters</i> , 2013 , 587, 3709-14	3.8	11
11	Consequences of stabilizing the natively disordered F helix for the folding pathway of apomyoglobin. <i>Journal of Molecular Biology</i> , 2011 , 411, 248-63	6.5	14
10	Energetic frustration of apomyoglobin folding: role of the B helix. <i>Journal of Molecular Biology</i> , 2010 , 396, 1319-28	6.5	16
9	The kinetic and equilibrium molten globule intermediates of apoleghemoglobin differ in structure. <i>Journal of Molecular Biology</i> , 2008 , 378, 715-25	6.5	23
8	Identification of native and non-native structure in kinetic folding intermediates of apomyoglobin. <i>Journal of Molecular Biology</i> , 2006 , 355, 139-56	6.5	98
7	Sequence determinants of a protein folding pathway. <i>Journal of Molecular Biology</i> , 2005 , 351, 383-92	6.5	46
6	Enhanced picture of protein-folding intermediates using organic solvents in H/D exchange and quench-flow experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 4765-70	11.5	52
5	Role of the B helix in early folding events in apomyoglobin: evidence from site-directed mutagenesis for native-like long range interactions. <i>Journal of Molecular Biology</i> , 2003 , 334, 293-307	6.5	48
4	The apomyoglobin folding pathway revisited: structural heterogeneity in the kinetic burst phase intermediate. <i>Journal of Molecular Biology</i> , 2002 , 322, 483-9	6.5	86
3	Conformational and dynamic characterization of the molten globule state of an apomyoglobin mutant with an altered folding pathway. <i>Biochemistry</i> , 2001 , 40, 14459-67	3.2	43
2	Studies of Protein Folding in Wright/Dyson Laboratory. <i>Seibutsu Butsuri</i> , 2001 , 41, 208-210	0	

- 1 Changes in the apomyoglobin folding pathway caused by mutation of the distal histidine residue. *Biochemistry*, **2000**, 39, 11227-37 3.2 62