Water penetration and escape in proteins

DOI: 10.1002/(sici)1097-0134(20000215)38:3<261::aid-prot3>3.0.co;2-q

Citation Report

#	Article	IF	CITATIONS
1	New perspectives on hydrophobic effects. Chemical Physics, 2000, 258, 349-370.	0.9	286
2	High Apparent Dielectric Constants in the Interior of a Protein Reflect Water Penetration. Biophysical Journal, 2000, 79, 1610-1620.	0.2	295
3	The protein–solvent interface: a big splash. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2001, 359, 1515-1527.	1.6	19
4	Dynamics of hydration in hen egg white lysozyme. Journal of Molecular Biology, 2001, 311, 409-419.	2.0	78
5	Functional Dynamics of the Hydrophobic Cleft in the N-Domain of Calmodulin. Biophysical Journal, 2001, 80, 2082-2092.	0.2	78
6	Femtosecond Dynamics of Intracellular Water Probed with Nonlinear Optical Kerr Effect Microspectroscopy. Biophysical Journal, 2001, 80, 3019-3024.	0.2	59
7	Dissecting the Vibrational Entropy Change on Protein/Ligand Binding:Â Burial of a Water Molecule in Bovine Pancreatic Trypsin Inhibitor. Journal of Physical Chemistry B, 2001, 105, 8050-8055.	1.2	79
8	Pressure effect on denaturant-induced unfolding of hen egg white lysozyme. Proteins: Structure, Function and Bioinformatics, 2001, 44, 180-187.	1.5	23
9	Gaussian fluctuations and linear response in an electron transfer protein. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6544-6549.	3.3	92
10	Water as it applies to the function of enzymes. International Review of Cytology, 2002, 215, 49-73.	6.2	19
11	Protein folding mediated by solvation: Water expulsion and formation of the hydrophobic core occur after the structural collapse. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 685-690.	3.3	461
12	Optical Spectra of Fe(II) Cytochrome c Interpreted Using Molecular Dynamics Simulations and Quantum Mechanical Calculations. Journal of Physical Chemistry B, 2002, 106, 5561-5571.	1.2	27
13	Simulations of apo and holo-fatty acid binding protein: structure and dynamics of protein, ligand and internal water 1 1Edited by B. Honig. Journal of Molecular Biology, 2002, 315, 713-736.	2.0	64
14	Understanding protein folding with energy landscape theory Part II: Quantitative aspects. Quarterly Reviews of Biophysics, 2002, 35, 205-286.	2.4	91
15	Water Rotational Relaxation and Diffusion in Hydrated Lysozyme. Journal of the American Chemical Society, 2002, 124, 6787-6791.	6.6	232
16	Mechanisms of cooperativity underlying sequence-independent β-sheet formation. Journal of Chemical Physics, 2002, 116, 4353-4365.	1.2	31
17	Thermodynamic Consequences of Burial of Polar and Non-polar Amino Acid Residues in the Protein Interior. Journal of Molecular Biology, 2002, 320, 343-357.	2.0	110
18	Molecular Dynamics Study of Desulfovibrio africanus Cytochrome c3 in Oxidized and Reduced Forms. Biophysical Journal, 2002, 83, 3049-3065.	0.2	12

λτιών Ρερώ

#	Article	IF	CITATIONS
19	Properties of Water Molecules in the Active Site Gorge of Acetylcholinesterase from Computer Simulation. Biophysical Journal, 2002, 82, 2671-2682.	0.2	48
20	Experimental pKa Values of Buried Residues: Analysis with Continuum Methods and Role of Water Penetration. Biophysical Journal, 2002, 82, 3289-3304.	0.2	193
21	Molecular Dynamics of Water at the Proteinâ^'Solvent Interface. Journal of Physical Chemistry B, 2002, 106, 6617-6633.	1.2	484
22	Extracting hydration sites around proteins from explicit water simulations. Journal of Computational Chemistry, 2002, 23, 861-869.	1.5	76
23	The role of residue 50 and hydration water molecules in homeodomain DNA recognition. European Biophysics Journal, 2002, 31, 306-316.	1.2	21
24	Three-body correlations in protein folding: the origin of cooperativity. Physica A: Statistical Mechanics and Its Applications, 2002, 307, 235-259.	1.2	40
25	Structure of Met-enkephalin in explicit aqueous solution using replica exchange molecular dynamics. Proteins: Structure, Function and Bioinformatics, 2002, 46, 225-234.	1.5	254
26	Water in protein cavities: A procedure to identify internal water and exchange pathways and application to fatty acid-binding protein. Proteins: Structure, Function and Bioinformatics, 2002, 47, 534-545.	1.5	27
27	Static and dynamic water molecules in Cu,Zn superoxide dismutase. Proteins: Structure, Function and Bioinformatics, 2003, 51, 607-615.	1.5	18
28	Protein Side-Chain Motion and Hydration in Proton-Transfer Pathways. Results for Cytochrome P450cam. Journal of the American Chemical Society, 2003, 125, 3931-3940.	6.6	80
29	Posttransition State Desolvation of the Hydrophobic Core of the src-SH3 Protein Domain. Biophysical Journal, 2003, 85, 61-69.	0.2	40
30	A discrete water exit pathway in the membrane protein cytochrome c oxidase. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15539-15542.	3.3	69
31	Molecular structure and hydrophobic solvation thermodynamics at an octane–water interface. Journal of Chemical Physics, 2003, 119, 9199-9206.	1.2	77
32	Water and proteins: A love-hate relationship. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3325-3326.	3.3	168
33	Water clusters in nonpolar cavities. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17002-17005.	3.3	222
34	Native State Hydrogen-Exchange Analysis of Protein Folding and Protein Motional Domains. Methods in Enzymology, 2004, 380, 379-400.	0.4	17
35	Incorporation of the fluorescent amino acid 7-azatryptophan into the core domain 1-47 of hirudin as a probe of hirudin folding and thrombin recognition. Protein Science, 2004, 13, 1489-1502.	3.1	50
36	Analysis of CDK2 active-site hydration: A method to design new inhibitors. Proteins: Structure, Function and Bioinformatics, 2004, 55, 258-274.	1.5	17

#	Article	IF	CITATIONS
37	Temperature dependence of the free energy landscape of the src-SH3 protein domain. Proteins: Structure, Function and Bioinformatics, 2004, 55, 395-406.	1.5	20
38	Zinc-porphyrin Solvation in Folded and Unfolded States of Zn-cytochromec. Inorganic Chemistry, 2004, 43, 7953-7960.	1.9	16
39	Water network dynamics at the critical moment of a peptide's β-turn formation: A molecular dynamics study. Journal of Chemical Physics, 2004, 121, 4925-4935.	1.2	17
40	Two different proteins that compete for binding to thrombin have opposite kinetic and thermodynamic profiles. Protein Science, 2004, 13, 166-176.	3.1	45
41	Hydration of Enzyme in Nonaqueous Media Is Consistent with Solvent Dependence of Its Activity. Biophysical Journal, 2004, 87, 812-821.	0.2	219
42	Molecular Dynamics Simulations of Staphylococcal Nuclease:Â Properties of Water at the Protein Surface. Journal of Physical Chemistry B, 2004, 108, 15928-15937.	1.2	77
43	MHC–Peptide Binding is Assisted by Bound Water Molecules. Journal of Molecular Biology, 2004, 338, 419-435.	2.0	78
44	X-ray and Thermodynamic Studies of Staphylococcal Nuclease Variants 192E and 192K: Insights into Polarity of the Protein Interior. Journal of Molecular Biology, 2004, 341, 565-574.	2.0	35
45	Water as a Conformational Editor in Protein Folding. Journal of Molecular Biology, 2004, 343, 1125-1133.	2.0	29
46	Dynamic Water Networks in Cytochrome c Oxidase from Paracoccus denitrificans Investigated by Molecular Dynamics Simulations. Biophysical Journal, 2004, 86, 1873-1889.	0.2	93
47	Molecular dynamics study of hydration of the protein interior. Computer Physics Communications, 2005, 169, 126-129.	3.0	10
48	Stability of proteins: Temperature, pressure and the role of the solvent. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1749, 187-213.	1.1	154
49	Molecular dynamics study of water penetration in staphylococcal nuclease. Proteins: Structure, Function and Bioinformatics, 2005, 60, 433-449.	1.5	74
50	Statistical and molecular dynamics studies of buried waters in globular proteins. Proteins: Structure, Function and Bioinformatics, 2005, 60, 450-463.	1.5	100
51	Treatment methods for the determination ofl´2H andl´18O of hair keratin by continuous-flow isotope-ratio mass spectrometry. Rapid Communications in Mass Spectrometry, 2005, 19, 2371-2378.	0.7	145
52	Simulations of nanoscale flow: water, proton, and biopolymer transport through carbon nanotube membranes. , 2005, , .		1
53	Deblurred Observation of the Molecular Structure of an Oilâ^'Water Interface. Journal of the American Chemical Society, 2005, 127, 2808-2809.	6.6	56
54	DFT/Electrostatic Calculations of pKaValues in CytochromecOxidase. Journal of Physical Chemistry B, 2005, 109, 3616-3626.	1.2	54

#	Article	IF	CITATIONS
55	Molecular Dynamics Simulations of Alzheimer's β-Amyloid Protofilaments. Journal of Molecular Biology, 2005, 353, 804-821.	2.0	250
56	Water Molecules and Hydrogen-Bonded Networks in Bacteriorhodopsin—Molecular Dynamics Simulations of the Ground State and the M-Intermediate. Biophysical Journal, 2005, 88, 3252-3261.	0.2	51
57	Local Compressibilities of Proteins: Comparison of Optical Experiments and Simulations for Horse Heart Cytochrome-c. Biophysical Journal, 2005, 89, 64-75.	0.2	27
58	Anesthetic Interaction with Ketosteroid Isomerase: Insights from Molecular Dynamics Simulations. Biophysical Journal, 2005, 89, 2350-2356.	0.2	18
59	WATER MEDIATION IN PROTEIN FOLDING AND MOLECULAR RECOGNITION. Annual Review of Biophysics and Biomolecular Structure, 2006, 35, 389-415.	18.3	884
60	Role of Protein Cavities on Unfolding Volume Change and on Internal Dynamics under Pressure. Biophysical Journal, 2006, 91, 3390-3396.	0.2	15
61	The effective correlation timeï,,in jaw cysts determined from 400 MHz NMRT1andT2measurements. Spectroscopy, 2006, 20, 177-183.	0.8	4
62	Amino acid substitutions affecting protein dynamics in eglin C do not affect heat capacity change upon unfolding. Proteins: Structure, Function and Bioinformatics, 2006, 64, 295-300.	1.5	4
63	Locating missing water molecules in protein cavities by the three-dimensional reference interaction site model theory of molecular solvation. Proteins: Structure, Function and Bioinformatics, 2006, 66, 804-813.	1.5	89
64	A molecular dynamics simulation of SNase and its hydration shell at high temperature and high pressure. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 522-534.	1.1	49
65	Hydration structure, thermodynamics, and functions of protein studied by the 3D-RISM theory. Molecular Simulation, 2006, 32, 817-824.	0.9	21
66	Facilitated Hexose Transporters: New Perspectives on Form and Function. Physiology, 2007, 22, 234-240.	1.6	185
67	Water, proton, and ion transport: from nanotubes to proteins. Molecular Physics, 2007, 105, 201-207.	0.8	78
68	Metastable Water Clusters in the Nonpolar Cavities of the Thermostable Protein Tetrabrachion. Journal of the American Chemical Society, 2007, 129, 7369-7377.	6.6	75
69	Significance of Water Molecules in the Inhibition of Cylin-Dependent Kinase 2 and 5 Complexes. Journal of Chemical Information and Modeling, 2007, 47, 1877-1885.	2.5	21
70	How Protein Surfaces Induce Anomalous Dynamics of Hydration Water. Journal of Physical Chemistry B, 2007, 111, 7584-7590.	1.2	221
71	The Dewetting Transition and The Hydrophobic Effect. Journal of the American Chemical Society, 2007, 129, 4847-4852.	6.6	139
72	Role of Flexibility and Polarity as Determinants of the Hydration of Internal Cavities and Pockets in Proteins. Biophysical Journal, 2007, 93, 2791-2804.	0.2	38

		CITATION REPORT		
#	Article		IF	CITATIONS
73	Structural, Energetic, and Dynamic Aspects of Ligand–Receptor Interactions. , 2007,	, 193-213.		8
74	WATGEN: An algorithm for modeling water networks at protein-protein interfaces. Journ Computational Chemistry, 2007, 28, 2241-2251.	nal of	1.5	27
75	Protein Dynamics Tightly Connected to the Dynamics of Surrounding and Internal Wate ChemPhysChem, 2007, 8, 23-33.	er Molecules.	1.0	97
76	Functional role of three water molecules buried within catalytic subunit of cyclic 3â€2,5 monophosphate-dependent protein kinase. Computational and Theoretical Chemistry, 2	′-adenosine 2007, 809, 21-27.	1.5	1
77	Hydration of a hydrophobic cavity and its functional role: A simulation study of human i Proteins: Structure, Function and Bioinformatics, 2007, 67, 868-885.	nterleukin-1î².	1.5	19
78	Water penetration in the low and high pressure native states of ubiquitin. Proteins: Stru Function and Bioinformatics, 2008, 70, 1175-1184.	icture,	1.5	62
79	Exploring the Conserved Water Site and Hydration of a Coiled oil Trimerisation Moti Simulation Study. ChemBioChem, 2008, 9, 1749-1756.	f: A MD	1.3	7
80	Cluster analysis of hydration waters around the active sites of bacterial alanine racemas MD simulation. Biopolymers, 2008, 89, 210-219.	e using a 2â€ns	1.2	9
81	Heat capacity changes upon burial of polar and nonpolar groups in proteins. Protein Sci 1343-1352.	ence, 2008, 10,	3.1	120
82	Mechanism of Auxin Interaction with Auxin Binding Protein (ABP1): A Molecular Dynam Study. Biophysical Journal, 2008, 94, 27-37.	ics Simulation	0.2	46
83	Crystallographic Study of Hydration of an Internal Cavity in Engineered Proteins with Bu or Ionizable Groups. Biophysical Journal, 2008, 94, 3208-3216.	ıried Polar	0.2	28
84	Dynamics at the Protein-Water Interface from 170 Spin Relaxation in Deeply Supercool Biophysical Journal, 2008, 95, 2951-2963.	ed Solutions.	0.2	132
85	Minimizing frustration by folding in an aqueous environment. Archives of Biochemistry Biophysics, 2008, 469, 118-131.	and	1.4	18
86	Water in Nonpolar Confinement: From Nanotubes to Proteins and Beyond. Annual Revi Chemistry, 2008, 59, 713-740.	ew of Physical	4.8	624
87	Open Science Grid Study of the Coupling between Conformation and Water Content in a Protein. Journal of Chemical Information and Modeling, 2008, 48, 2021-2029.	the Interior of	2.5	19
88	Glutamic acid 242 is a valve in the proton pump of cytochrome <i>c</i> oxidase. Procee National Academy of Sciences of the United States of America, 2008, 105, 6255-6259.	edings of the	3.3	125
89	Comment on â€~Diffusion of water and sodium counter-ions in nanopores of a β-lactog molecular dynamics study'. Nanotechnology, 2008, 19, 438001.	lobulin crystal: a	1.3	0
90	Reply to Comment on â€~Diffusion of water and sodium counter-ions in nanopores of β crystal: a molecular simulation study'. Nanotechnology, 2008, 19, 438002. 	-lactoglobulin	1.3	0

#	Article	IF	CITATIONS
91	Role of heavy water in biological sciences with an emphasis on thermostabilization of vaccines. Expert Review of Vaccines, 2009, 8, 1587-1602.	2.0	27
92	Structural coupling between FKBP12 and buried water. Proteins: Structure, Function and Bioinformatics, 2009, 74, 603-611.	1.5	63
93	Computations of Standard Binding Free Energies with Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2009, 113, 2234-2246.	1.2	481
94	Nonlinear Effect of GdnHCl on Hydration Dynamics of Proteins: A 1H Magnetic Relaxation Dispersion Study. Journal of Physical Chemistry B, 2009, 113, 6994-7002.	1.2	10
95	Does the Dynamic Stokes Shift Report on Slow Protein Hydration Dynamics?. Journal of Physical Chemistry B, 2009, 113, 8210-8213.	1.2	113
96	Hydrated and Dehydrated Tertiary Interactions–Opening and Closing–of a Four-Helix Bundle Peptide. Biophysical Journal, 2009, 97, 572-580.	0.2	2
97	Structural and dynamic properties of water around acetylcholinesterase. Protein Science, 2009, 11, 2080-2090.	3.1	95
98	Time scales of water dynamics at biological interfaces: peptides, proteins and cells. Faraday Discussions, 2009, 141, 131-144.	1.6	112
99	Water in the Polar and Nonpolar Cavities of the Protein Interleukin-1β. Journal of Physical Chemistry B, 2010, 114, 16290-16297.	1.2	39
100	Molecular Dynamics Free Energy Calculations to Assess the Possibility of Water Existence in Protein Nonpolar Cavities. Biophysical Journal, 2010, 98, 2974-2983.	0.2	10
101	Computational Study on the Interaction of N1 Substituted Pyrazole Derivatives with B-Raf Kinase: An Unusual Water Wire Hydrogen-Bond Network and Novel Interactions at the Entrance of the Active Site. Journal of Chemical Information and Modeling, 2010, 50, 1101-1112.	2.5	33
102	Water Hydrogen-Bond Dynamics around Amino Acids: The Key Role of Hydrophilic Hydrogen-Bond Acceptor Groups. Journal of Physical Chemistry B, 2010, 114, 2083-2089.	1.2	113
103	Secretory Phospholipase A ₂ Activity toward Diverse Substrates. Journal of Physical Chemistry B, 2011, 115, 6853-6861.	1.2	9
104	Simulations of the confinement of ubiquitin in self-assembled reverse micelles. Journal of Chemical Physics, 2011, 134, 225101.	1.2	54
106	Water in the Active Site of Ketosteroid Isomerase. Biochemistry, 2011, 50, 6689-6700.	1.2	7
107	Role of Packing, Hydration, and Fluctuations on Thermostability. , 2011, , 21-46.		0
108	Comparative void-volume analysis of psychrophilic and mesophilic enzymes: Structural bioinformatics of psychrophilic enzymes reveals sources of core flexibility. BMC Structural Biology, 2011, 11, 42.	2.3	67
109	Protein dynamics and pressure: What can high pressure tell us about protein structural flexibility?. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 934-941.	1.1	24

#	Article	IF	CITATIONS
110	The Role of Conserved Waters in Conformational Transitions of Q61H K-ras. PLoS Computational Biology, 2012, 8, e1002394.	1.5	48
111	Early Turn Formation and Chain Collapse Drive Fast Folding of the Major Cold Shock Protein CspA of <i>Escherichia coli</i> . Biochemistry, 2012, 51, 9104-9111.	1.2	20
112	How does water-nanotube interaction influence water flow through the nanochannel?. Journal of Chemical Physics, 2012, 136, 175101.	1.2	16
113	Hydration Dynamics of a Halophilic Protein in Folded and Unfolded States. Journal of Physical Chemistry B, 2012, 116, 3436-3444.	1.2	52
114	Magnitude and Molecular Origin of Water Slowdown Next to a Protein. Journal of the American Chemical Society, 2012, 134, 4116-4119.	6.6	171
115	Thermodynamic Impact of Embedded Water Molecules in the Unfolding of Human CD2BP2-GYF Domain. Journal of Physical Chemistry B, 2012, 116, 7168-7175.	1.2	5
116	Solvation effect on the structural change of a globular protein: A molecular dynamics study. International Journal of Quantum Chemistry, 2012, 112, 344-350.	1.0	12
117	The effect of protein composition on hydration dynamics. Physical Chemistry Chemical Physics, 2013, 15, 3570.	1.3	25
118	Biomolecular hydration dynamics: a jump model perspective. Chemical Society Reviews, 2013, 42, 5672.	18.7	100
119	Analysis of Protein Dynamics Simulations by a Stochastic Point Process Approach. Journal of Chemical Theory and Computation, 2013, 9, 2838-2848.	2.3	10
120	Thermodynamic framework for identifying free energy inventories of enzyme catalytic cycles. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12271-12276.	3.3	13
121	Power-law trapping of water molecules on the lipid-membrane surface induces water retardation. Physical Review E, 2013, 87, 052715.	0.8	23
122	Interaction of Amyloid Inhibitor Proteins with Amyloid Beta Peptides: Insight from Molecular Dynamics Simulations. PLoS ONE, 2014, 9, e113041.	1.1	40
123	Comparative study of hydration shell dynamics around a hyperactive antifreeze protein and around ubiquitin. Journal of Chemical Physics, 2014, 141, 22D529.	1.2	50
124	Preferential Water Exclusion in Protein Unfolding. Journal of Physical Chemistry B, 2014, 118, 717-723.	1.2	2
125	Water Dynamics in Protein Hydration Shells: The Molecular Origins of the Dynamical Perturbation. Journal of Physical Chemistry B, 2014, 118, 7715-7729.	1.2	207
126	Pressure-Dependent Properties of Elementary Hydrophobic Interactions: Ramifications for Activation Properties of Protein Folding. Journal of Physical Chemistry B, 2014, 118, 7488-7509.	1.2	49
127	The Hole in the Barrel: Water Exchange at the GFP Chromophore. Journal of Physical Chemistry B, 2015, 119, 3464-3478.	1.2	21

#	Article	IF	CITATIONS
128	Manipulating Excited-State Dynamics of Individual Light-Harvesting Chromophores through Restricted Motions in a Hydrated Nanoscale Protein Cavity. Journal of Physical Chemistry B, 2015, 119, 6963-6973.	1.2	11
129	Biological Water or Rather Water in Biology?. Journal of Physical Chemistry Letters, 2015, 6, 2449-2451.	2.1	72
130	Role of Internal Water on Protein Thermal Stability: The Case of Homologous G Domains. Journal of Physical Chemistry B, 2015, 119, 8939-8949.	1.2	21
131	Effect of Glycosylation on an Immunodominant Region in the V1V2 Variable Domain of the HIV-1 Envelope gp120 Protein. PLoS Computational Biology, 2016, 12, e1005094.	1.5	17
132	Water Determines the Structure and Dynamics of Proteins. Chemical Reviews, 2016, 116, 7673-7697.	23.0	645
133	The effect of water dynamics on conformation changes of albumin in pre-denaturation state: photon correlation spectroscopy and simulation. Journal of Molecular Liquids, 2017, 235, 17-23.	2.3	9
134	Water Dynamics in the Hydration Shells of Biomolecules. Chemical Reviews, 2017, 117, 10694-10725.	23.0	574
135	In Silico Studies of Small Molecule Interactions with Enzymes Reveal Aspects of Catalytic Function. Catalysts, 2017, 7, 212.	1.6	21
136	Structural and dynamical heterogeneities at glutamine–water interfaces. Physical Chemistry Chemical Physics, 2019, 21, 16083-16094.	1.3	4
137	Destabilization of Insulin Hexamer in Water–Ethanol Binary Mixture. Journal of Physical Chemistry B, 2019, 123, 10365-10375.	1.2	10
138	Investigating large-amplitude protein loop motions as extreme events using recurrence interval analysis. Physica A: Statistical Mechanics and Its Applications, 2019, 520, 1-10.	1.2	1
139	First-passage fingerprints of water diffusion near glutamine surfaces. Soft Matter, 2020, 16, 9202-9216.	1.2	8
140	Structural and dynamical heterogeneity of water trapped inside Na+-pumping KR2 rhodopsin in the dark state. Journal of Chemical Physics, 2021, 154, 215101.	1.2	2
141	Dynamic Complexity of Chaotic Transitions in High-Dimensional Classical Dynamics: Leu-Enkephalin Folding. Lecture Notes in Computer Science, 2006, , 129-140.	1.0	1
143	Combined DFT and electrostatic calculations of pKas in proteins: study of cytochrome c oxidase. , 2006, , 53-78.		0
144	Energy Landscapes of Protein Self-Assembly: Lessons from Native Topology-Based Models. , 2007, , 37-51.		0
145	Reversible processes in collagen dehydration: A molecular dynamics study. Archives of Biochemistry and Biophysics, 2021, 714, 109079.	1.4	2
147	Protein 3D Hydration: A Case of Bovine Pancreatic Trypsin Inhibitor. International Journal of Molecular Sciences, 2022, 23, 14785.	1.8	2

ARTICLE

IF CITATIONS