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List of Publications by Year in descending order

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papers

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23567

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178
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14027
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#	ARTICLE	IF	CITATIONS
1	IKK α -deficient lung adenocarcinomas generate an immunosuppressive microenvironment by overproducing Treg-inducing cytokines. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	7
2	Amyloid Oligomers: A Joint Experimental/Computational Perspective on Alzheimer's Disease, Parkinson's Disease, Type II Diabetes, and Amyotrophic Lateral Sclerosis. Chemical Reviews, 2021, 121, 2545-2647.	47.7	406
3	Trastuzumab Blocks the Receiver Function of HER2 Leading to the Population Shifts of HER2-Containing Homodimers and Heterodimers. Antibodies, 2021, 10, 7.	2.5	10
4	Conformational Ensemble of <i>AdoCbl</i> Riboswitch Provides Stable Structural Elements for Conformation Selection and Population Shift in Cobalamin Recognition. Journal of Physical Chemistry B, 2021, 125, 2589-2596.	2.6	6
5	BioChem: A New International and Interdisciplinary Journal. Biochem, 2021, 1, 49-50.	1.2	0
6	Computational Investigation of Gantenerumab and Crenezumab Recognition of A β Fibrils in Alzheimer's Disease Brain Tissue. ACS Chemical Neuroscience, 2020, 11, 3233-3244.	3.5	12
7	Peptide-MHC Binding Reveals Conserved Allosteric Sites in MHC Class I- and Class II-Restricted T Cell Receptors (TCRs). Journal of Molecular Biology, 2020, 432, 166697.	4.2	12
8	Molecular dynamics based improvement of the solubilizing self-cleavable tag Zbasic-I-CM application in the preparation of recombinant proteins in Escherichia coli. Biochemical and Biophysical Research Communications, 2019, 513, 412-418.	2.1	0
9	Antigen binding allosterically promotes Fc receptor recognition. MAbs, 2019, 11, 58-74.	5.2	48
10	Disruption of the Rbm38-eIF4E Complex with a Synthetic Peptide Pep8 Increases p53 Expression. Cancer Research, 2019, 79, 807-818.	0.9	29
11	Conformational stability and dynamics of the cancer-associated isoform β 133p53 are modulated by p53 peptides and p53-specific DNA. FASEB Journal, 2019, 33, 4225-4235.	0.5	22
12	Atomistic-level study of the interactions between hIAPP protofibrils and membranes: Influence of pH and lipid composition. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1818-1825.	2.6	33
13	IKK α inactivation promotes Kras-initiated lung adenocarcinoma development through disrupting major redox regulatory pathways. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E812-E821.	7.1	44
14	Local and global anatomy of antibody-protein antigen recognition. Journal of Molecular Recognition, 2018, 31, e2693.	2.1	49
15	Structure and energetic basis of overrepresented λ light chain in systemic light chain amyloidosis patients. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2294-2303.	3.8	6
16	Structural disorder in four-repeat Tau fibrils reveals a new mechanism for barriers to cross-seeding of Tau isoforms. Journal of Biological Chemistry, 2018, 293, 17336-17348.	3.4	35
17	Intermolecular disulfide bonds between unpaired cysteines retard the C-terminal trans-cleavage of Npu DnaE. Enzyme and Microbial Technology, 2018, 118, 6-12.	3.2	8
18	The distinct structural preferences of tau protein repeat domains. Chemical Communications, 2018, 54, 5700-5703.	4.1	35

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19	Experimental and Computational Protocols for Studies of Cross-Seeding Amyloid Assemblies. <i>Methods in Molecular Biology</i> , 2018, 1777, 429-447.	0.9	8
20	Replica Exchange Molecular Dynamics: A Practical Application Protocol with Solutions to Common Problems and a Peptide Aggregation and Self-Assembly Example. <i>Methods in Molecular Biology</i> , 2018, 1777, 101-119.	0.9	70
21	Peptide-MHC (pMHC) binding to a human antiviral T cell receptor induces long-range allosteric communication between pMHC- and CD3-binding sites. <i>Journal of Biological Chemistry</i> , 2018, 293, 15991-16005.	3.4	45
22	Familial Mutations May Switch Conformational Preferences in α -Synuclein Fibrils. <i>ACS Chemical Neuroscience</i> , 2017, 8, 837-849.	3.5	27
23	Probing Oligomerized Conformations of Defensin in the Membrane. <i>Methods in Molecular Biology</i> , 2017, 1529, 353-362.	0.9	4
24	Human Neuronal Calcium Sensor-1 Protein Avoids Histidine Residues To Decrease pH Sensitivity. <i>Journal of Physical Chemistry B</i> , 2017, 121, 508-517.	2.6	2
25	Binding of protofibrillar $A\beta$ trimers to lipid bilayer surface enhances $A\beta$ structural stability and causes membrane thinning. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 27556-27569.	2.8	32
26	Mechanisms of recognition of amyloid- $A\beta$ ($A\beta$) monomer, oligomer, and fibril by homologous antibodies. <i>Journal of Biological Chemistry</i> , 2017, 292, 18325-18343.	3.4	53
27	Release of Cytochrome C from Bax Pores at the Mitochondrial Membrane. <i>Scientific Reports</i> , 2017, 7, 2635.	3.3	107
28	Prediction of Host-Pathogen Interactions for <i>Helicobacter pylori</i> by Interface Mimicry and Implications to Gastric Cancer. <i>Journal of Molecular Biology</i> , 2017, 429, 3925-3941.	4.2	28
29	Compilation and Analysis of Enzymes, Engineered Antibodies, and Nanoparticles Designed to Interfere with Amyloid- $A\beta$ Aggregation. <i>Israel Journal of Chemistry</i> , 2017, 57, 622-633.	2.3	2
30	Insights Into the Allosteric Inhibition of the SUMO E2 Enzyme Ubc9. <i>Angewandte Chemie</i> , 2016, 128, 5797-5801.	2.0	1
31	How Does Hyperphosphorylation Promote Tau Aggregation and Modulate Filament Structure and Stability?. <i>ACS Chemical Neuroscience</i> , 2016, 7, 565-575.	3.5	27
32	Conformational dynamics of cancer-associated MyD88-TIR domain mutant L252P (L265P) allosterically tilts the landscape toward homo-dimerization. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 347-354.	2.1	18
33	Oncogenic Mutations Differentially Affect Bax Monomer, Dimer, and Oligomeric Pore Formation in the Membrane. <i>Scientific Reports</i> , 2016, 6, 33340.	3.3	11
34	Conformational footprints. <i>Nature Chemical Biology</i> , 2016, 12, 890-891.	8.0	36
35	Insights Into the Allosteric Inhibition of the SUMO E2 Enzyme Ubc9. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 5703-5707.	13.8	20
36	Conformational selection in amyloid-based immunotherapy: Survey of crystal structures of antibody-amyloid complexes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2672-2681.	2.4	23

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37	Protein Ensembles: How Does Nature Harness Thermodynamic Fluctuations for Life? The Diverse Functional Roles of Conformational Ensembles in the Cell. <i>Chemical Reviews</i> , 2016, 116, 6516-6551.	47.7	302
38	Allosteric stabilization of the amyloid- β^2 peptide hairpin by the fluctuating N-terminal. <i>Chemical Communications</i> , 2016, 52, 1733-1736.	4.1	25
39	Dimerization of the SP1 Region of HIV-1 Gag Induces a Helical Conformation and Association into Helical Bundles: Implications for Particle Assembly. <i>Journal of Virology</i> , 2016, 90, 1773-1787.	3.4	34
40	Temperature-Dependent Conformational Properties of Human Neuronal Calcium Sensor-1 Protein Revealed by All-Atom Simulations. <i>Journal of Physical Chemistry B</i> , 2016, 120, 3551-3559.	2.6	4
41	Self-aggregation and coaggregation of the p53 core fragment with its aggregation gatekeeper variant. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 8098-8107.	2.8	23
42	Critical Nucleus Structure and Aggregation Mechanism of the C-terminal Fragment of Copper-Zinc Superoxide Dismutase Protein. <i>ACS Chemical Neuroscience</i> , 2016, 7, 286-296.	3.5	32
43	Coupling of the non-amyloid-component (NAC) domain and the KTK(E/Q)GV repeats stabilize the β^2 -synuclein fibrils. <i>European Journal of Medicinal Chemistry</i> , 2016, 121, 841-850.	5.5	28
44	Amylin- β^2 oligomers at atomic resolution using molecular dynamics simulations: a link between Type 2 diabetes and Alzheimer's disease. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 2330-2338.	2.8	74
45	Principles and Overview of Sampling Methods for Modeling Macromolecular Structure and Dynamics. <i>PLoS Computational Biology</i> , 2016, 12, e1004619.	3.2	188
46	Mapping the Conformation Space of Wildtype and Mutant H-Ras with a Memetic, Cellular, and Multiscale Evolutionary Algorithm. <i>PLoS Computational Biology</i> , 2015, 11, e1004470.	3.2	47
47	Coupling of Zinc-Binding and Secondary Structure in Nonfibrillar β^2 40 Peptide Oligomerization. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 1218-1230.	5.4	16
48	Polymorphism in Self-Assembly of Peptide-Based β^2 -Hairpin Contributes to Network Morphology and Hydrogel Mechanical Rigidity. <i>Journal of Physical Chemistry B</i> , 2015, 119, 482-490.	2.6	37
49	β^2 "Stretching-and-Packing" Cross-Seeding Mechanism Can Trigger Tau Protein Aggregation. <i>Journal of Physical Chemistry Letters</i> , 2015, 6, 3276-3282.	4.6	42
50	β^2 (1-42) fibril structure illuminates self-recognition and replication of amyloid in Alzheimer's disease. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 499-505.	8.2	701
51	Allosteric Effects of the Oncogenic RasQ61L Mutant on Raf-RBD. <i>Structure</i> , 2015, 23, 505-516.	3.3	201
52	Defining the Domain Arrangement of the Mammalian Target of Rapamycin Complex Component Rictor Protein. <i>Journal of Computational Biology</i> , 2015, 22, 876-886.	1.6	17
53	Effects of the C-Terminal Tail on the Conformational Dynamics of Human Neuronal Calcium Sensor-1 Protein. <i>Journal of Physical Chemistry B</i> , 2015, 119, 14236-14244.	2.6	5
54	Dynamics differentiate between active and inactive inteins. <i>European Journal of Medicinal Chemistry</i> , 2015, 91, 51-62.	5.5	11

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55	Investigation of the interactions between the EphB2 receptor and SNEW peptide variants. <i>Growth Factors</i> , 2014, 32, 236-246.	1.7	10
56	Bioinformatics Study of Cancer-Related Mutations within p53 Phosphorylation Site Motifs. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13275-13298.	4.1	5
57	R102Q Mutation Shifts the Salt-Bridge Network and Reduces the Structural Flexibility of Human Neuronal Calcium Sensor-1 Protein. <i>Journal of Physical Chemistry B</i> , 2014, 118, 13112-13122.	2.6	12
58	Multiple conformational selection and induced fit events take place in allosteric propagation. <i>Biophysical Chemistry</i> , 2014, 186, 22-30.	2.8	105
59	Conformational Distribution and α -Helix to β -Sheet Transition of Human Amylin Fragment Dimer. <i>Biomacromolecules</i> , 2014, 15, 122-131.	5.4	69
60	Carbon monoxide in controlling the surface formation of Group VIII metal nanoparticles. <i>Chemical Communications</i> , 2014, 50, 14013-14016.	4.1	22
61	Structural Insight into Tau Protein's Paradox of Intrinsically Disordered Behavior, Self-Acetylation Activity, and Aggregation. <i>Journal of Physical Chemistry Letters</i> , 2014, 5, 3026-3031.	4.6	81
62	Promiscuous and specific recognition among ephrins and Eph receptors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1729-1740.	2.3	35
63	Dipeptide analysis of p53 mutations and evolution of p53 family proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 198-206.	2.3	10
64	Single Mutations in Tau Modulate the Populations of Fibril Conformers through Seed Selection. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1590-1593.	13.8	38
65	Network Effect of Wt-mutant p53 Interactions and Implications on p53 Gene Therapy. <i>Current Pharmaceutical Design</i> , 2014, 20, 1259-1267.	1.9	4
66	Druggable Orthosteric and Allosteric Hot Spots to Target Protein-protein Interactions. <i>Current Pharmaceutical Design</i> , 2014, 20, 1293-1301.	1.9	41
67	Editorial (Thematic Issue: Protein-protein interaction: from interface to interaction network). <i>Current Pharmaceutical Design</i> , 2014, 20, 1171-1172.	1.9	1
68	Structured Crowding and Its Effects on Enzyme Catalysis. <i>Topics in Current Chemistry</i> , 2013, 337, 123-137.	4.0	29
69	A broad view of scaffolding suggests that scaffolding proteins can actively control regulation and signaling of multienzyme complexes through allostery. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 820-829.	2.3	45
70	Allosteric Conformational Barcodes Direct Signaling in the Cell. <i>Structure</i> , 2013, 21, 1509-1521.	3.3	47
71	Protein charge and mass contribute to the spatio-temporal dynamics of protein-protein interactions in a minimal proteome. <i>Proteomics</i> , 2013, 13, 1339-1351.	2.2	20
72	Molecular insights into the reversible formation of tau protein fibrils. <i>Chemical Communications</i> , 2013, 49, 3582.	4.1	34

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73	The Underappreciated Role of Allostery in the Cellular Network. <i>Annual Review of Biophysics</i> , 2013, 42, 169-189.	10.0	152
74	Conformational Basis for Asymmetric Seeding Barrier in Filaments of Three- and Four-Repeat Tau. <i>Journal of the American Chemical Society</i> , 2012, 134, 10271-10278.	13.7	63
75	The growth mechanism of single-walled carbon nanotubes with a controlled diameter. <i>Physica E: Low-Dimensional Systems and Nanostructures</i> , 2012, 44, 2032-2040.	2.7	17
76	Selective Molecular Recognition in Amyloid Growth and Transmission and Cross-Species Barriers. <i>Journal of Molecular Biology</i> , 2012, 421, 172-184.	4.2	76
77	Metal binding sites in amyloid oligomers: Complexes and mechanisms. <i>Coordination Chemistry Reviews</i> , 2012, 256, 2245-2252.	18.8	95
78	Crystal structure of a plectonemic RNA supercoil. <i>Nature Communications</i> , 2012, 3, 901.	12.8	7
79	Structural and Functional Consequences of Phosphate \leftrightarrow Arsenate Substitutions in Selected Nucleotides: DNA, RNA, and ATP. <i>Journal of Physical Chemistry B</i> , 2012, 116, 4801-4811.	2.6	25
80	Cooperativity among Short Amyloid Stretches in Long Amyloidogenic Sequences. <i>PLoS ONE</i> , 2012, 7, e39369.	2.5	10
81	Protein dynamics and conformational selection in bidirectional signal transduction. <i>BMC Biology</i> , 2012, 10, 2.	3.8	69
82	Cross-seeding and Conformational Selection between Three- and Four-repeat Human Tau Proteins. <i>Journal of Biological Chemistry</i> , 2012, 287, 14950-14959.	3.4	63
83	Synergistic Interactions between Repeats in Tau Protein and A β Amyloids May Be Responsible for Accelerated Aggregation via Polymorphic States. <i>Biochemistry</i> , 2011, 50, 5172-5181.	2.5	95
84	The Unique Alzheimer β -Amyloid Triangular Fibril Has a Cavity along the Fibril Axis under Physiological Conditions. <i>Journal of the American Chemical Society</i> , 2011, 133, 2742-2748.	13.7	62
85	Molecular-Level Examination of Cu ²⁺ Binding Structure for Amyloid Fibrils of 40-Residue Alzheimer β by Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2011, 133, 3390-3400.	13.7	182
86	Multiple β -Targeting and Conformational Selection in the Estrogen Receptor: Computation and Experiment. <i>Chemical Biology and Drug Design</i> , 2011, 78, 137-149.	3.2	13
87	Dynamic Allostery: Linkers Are Not Merely Flexible. <i>Structure</i> , 2011, 19, 907-917.	3.3	196
88	Polymorphic Triple β -Sheet Structures Contribute to Amide Hydrogen/Deuterium (H/D) Exchange Protection in the Alzheimer Amyloid β 42 Peptide. <i>Journal of Biological Chemistry</i> , 2011, 286, 34244-34253.	3.4	38
89	Mechanisms of transcription factor selectivity. <i>Trends in Genetics</i> , 2010, 26, 75-83.	6.7	133
90	Enzyme dynamics point to stepwise conformational selection in catalysis. <i>Current Opinion in Chemical Biology</i> , 2010, 14, 652-659.	6.1	195

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91	Polymorphic C-terminal β -Sheet Interactions Determine the Formation of Fibril or Amyloid β -derived Diffusible Ligand-like Globulomer for the Alzheimer $A\beta_{42}$ Dodecamer. <i>Journal of Biological Chemistry</i> , 2010, 285, 37102-37110.	3.4	35
92	Hollow core of Alzheimer's $A\beta_{42}$ amyloid observed by cryoEM is relevant at physiological pH. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14128-14133.	7.1	81
93	Polymorphism of A-Beta1-42 Peptide Oligomer - Membrane Interactions. <i>Biophysical Journal</i> , 2010, 98, 650a.	0.5	0
94	Polymorphism in Alzheimer $A\beta$ Amyloid Organization Reflects Conformational Selection in a Rugged Energy Landscape. <i>Chemical Reviews</i> , 2010, 110, 4820-4838.	47.7	265
95	Why Does Binding of Proteins to DNA or Proteins to Proteins Not Necessarily Spell Function?. <i>ACS Chemical Biology</i> , 2010, 5, 265-272.	3.4	27
96	Zinc ions promote Alzheimer $A\beta$ aggregation via population shift of polymorphic states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9490-9495.	7.1	283
97	Amplification of signaling via cellular allosteric relay and protein disorder: Fig. 1.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6887-6888.	7.1	36
98	The Origin of Allosteric Functional Modulation: Multiple Pre-existing Pathways. <i>Structure</i> , 2009, 17, 1042-1050.	3.3	347
99	Protein-protein interaction networks: how can a hub protein bind so many different partners?. <i>Trends in Biochemical Sciences</i> , 2009, 34, 594-600.	7.5	125
100	How do transcription factors select specific binding sites in the genome?. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1118-1120.	8.2	42
101	Multiple diverse ligands binding at a single protein site: A matter of pre-existing populations. <i>Protein Science</i> , 2009, 11, 184-197.	7.6	364
102	Molecular dynamics simulations of alanine rich β -sheet oligomers: Insight into amyloid formation. <i>Protein Science</i> , 2009, 11, 2335-2350.	7.6	156
103	Polymorphism of Alzheimer's $A\beta_{17-42}$ (p3) Oligomers: The Importance of the Turn Location and Its Conformation. <i>Biophysical Journal</i> , 2009, 97, 1168-1177.	0.5	91
104	In silico protein design by combinatorial assembly of protein building blocks. <i>Protein Science</i> , 2009, 13, 2753-2765.	7.6	48
105	Intra-molecular chaperone: the role of the N-terminal in conformational selection and kinetic control. <i>Physical Biology</i> , 2009, 6, 013001.	1.8	9
106	Models of Toxic β -Sheet Channels of Protegrin-1 Suggest a Common Subunit Organization Motif Shared with Toxic Alzheimer β -Amyloid Ion Channels. <i>Biophysical Journal</i> , 2008, 95, 4631-4642.	0.5	91
107	Annular Structures as Intermediates in Fibril Formation of Alzheimer $A\beta_{17-42}$. <i>Journal of Physical Chemistry B</i> , 2008, 112, 6856-6865.	2.6	70
108	Principles of Protein-Protein Interactions: What are the Preferred Ways For Proteins To Interact?. <i>Chemical Reviews</i> , 2008, 108, 1225-1244.	47.7	568

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109	Molecular dynamics simulations of Alzheimer Abeta40 elongation and lateral association. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 3919.	3.0	17
110	Trp/Met/Phe Hot Spots in Protein-Protein Interactions: Potential Targets in Drug Design. <i>Current Topics in Medicinal Chemistry</i> , 2007, 7, 999-1005.	2.1	94
111	Ligand Binding and Circular Permutation Modify Residue Interaction Network in DHFR. <i>PLoS Computational Biology</i> , 2007, 3, e117.	3.2	42
112	Towards Drugs Targeting Multiple Proteins in a Systems Biology Approach. <i>Current Topics in Medicinal Chemistry</i> , 2007, 7, 943-951.	2.1	51
113	Probing potential binding modes of the p53 tetramer to DNA based on the symmetries encoded in p53 response elements. <i>Nucleic Acids Research</i> , 2007, 35, 7733-7747.	14.5	30
114	Sequence analysis of p53 response-elements suggests multiple binding modes of the p53 tetramer to DNA targets. <i>Nucleic Acids Research</i> , 2007, 35, 2986-3001.	14.5	47
115	Modeling the Alzheimer A β 17-42 Fibril Architecture: Tight Intermolecular Sheet-Sheet Association and Intramolecular Hydrated Cavities. <i>Biophysical Journal</i> , 2007, 93, 3046-3057.	0.5	167
116	Conformational study of the protegrin-1 (PG-1) dimer interaction with lipid bilayers and its effect. <i>BMC Structural Biology</i> , 2007, 7, 21.	2.3	39
117	Consensus features in amyloid fibrils: sheet-sheet recognition via a (polar or nonpolar) zipper structure. <i>Physical Biology</i> , 2006, 3, P1-P4.	1.8	46
118	The Stability of Monomeric Intermediates Controls Amyloid Formation: A β 25-35 and its N27Q Mutant. <i>Biophysical Journal</i> , 2006, 90, 3365-3374.	0.5	59
119	Structural Stability and Dynamics of an Amyloid-Forming Peptide GNNQQNY from the Yeast Prion Sup-35. <i>Biophysical Journal</i> , 2006, 91, 824-833.	0.5	131
120	Interaction of Protegrin-1 with Lipid Bilayers: Membrane Thinning Effect. <i>Biophysical Journal</i> , 2006, 91, 2848-2859.	0.5	65
121	Comparison of the Human and Worm p53 Structures Suggests a Way for Enhancing Stability. <i>Biochemistry</i> , 2006, 45, 3925-3933.	2.5	21
122	Simulations as analytical tools to understand protein aggregation and predict amyloid conformation. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 445-452.	6.1	214
123	Similarity Trap in Protein-Protein Interactions Could Be Carcinogenic: Simulations of p53 Core Domain Complexed with 53BP1 and BRCA1 BRCT Domains. <i>Structure</i> , 2006, 14, 1811-1821.	3.3	16
124	From Structure to Function: Methods and Applications. <i>Current Protein and Peptide Science</i> , 2005, 6, 171-183.	1.4	32
125	Comparison of the protein-protein interfaces in the p53-DNA crystal structures: Towards elucidation of the biological interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3988-3993.	7.1	29
126	Protein-protein interactions: organization, cooperativity and mapping in a bottom-up Systems Biology approach. <i>Physical Biology</i> , 2005, 2, S24-S35.	1.8	93

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127	The contribution of the Trp/Met/Phe residues to physical interactions of p53 with cellular proteins. <i>Physical Biology</i> , 2005, 2, S56-S66.	1.8	16
128	In the Quest for Stable Rescuing Mutants of p53: Computational Mutagenesis of Flexible Loop L1. <i>Biochemistry</i> , 2005, 44, 1423-1432.	2.5	23
129	Hot Regions in Protein-Protein Interactions: The Organization and Contribution of Structurally Conserved Hot Spot Residues. <i>Journal of Molecular Biology</i> , 2005, 345, 1281-1294.	4.2	465
130	A Comparative Study of Amyloid Fibril Formation by Residues 15-19 of the Human Calcitonin Hormone: A Single β -Sheet Model with a Small Hydrophobic Core. <i>Journal of Molecular Biology</i> , 2005, 345, 1213-1227.	4.2	71
131	CD4 Binding Partially Locks the Bridging Sheet in gp120 but Leaves the β 2/3 Strands Flexible. <i>Journal of Molecular Biology</i> , 2005, 350, 514-527.	4.2	24
132	How Similar Are Protein Folding and Protein Binding Nuclei? Examination of Vibrational Motions of Energy Hot Spots and Conserved Residues. <i>Biophysical Journal</i> , 2005, 88, 1552-1559.	0.5	75
133	Insights into amyloid structural formation and assembly through computational approaches. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2004, 11, 143-161.	3.0	19
134	From computational quantum chemistry to computational biology: experiments and computations are (full) partners. <i>Physical Biology</i> , 2004, 1, P23-P26.	1.8	4
135	Characterization of the Conformational State and Flexibility of HIV-1 Glycoprotein gp120 Core Domain. <i>Journal of Biological Chemistry</i> , 2004, 279, 30523-30530.	3.4	29
136	Side chain interactions determine the amyloid organization: a single layer β -sheet molecular structure of the calcitonin peptide segment 15-19. <i>Physical Biology</i> , 2004, 1, 89-99.	1.8	19
137	Release Factors eRF1 and RF2. <i>Journal of Biological Chemistry</i> , 2004, 279, 53875-53885.	3.4	31
138	Is allostery an intrinsic property of all dynamic proteins?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 433-443.	2.6	779
139	The Stability and Dynamics of the Human Calcitonin Amyloid Peptide DFNKF. <i>Biophysical Journal</i> , 2004, 87, 146-158.	0.5	46
140	Protein-Protein Interactions: Hot Spots and Structurally Conserved Residues often Locate in Complemented Pockets that Pre-organized in the Unbound States: Implications for Docking. <i>Journal of Molecular Biology</i> , 2004, 344, 781-795.	4.2	197
141	Interdependence of Backbone Flexibility, Residue Conservation, and Enzyme Function: A Case Study on β 1,4-Galactosyltransferase-I. <i>Biochemistry</i> , 2003, 42, 3674-3687.	2.5	27
142	Energy landscape and dynamics of the β -hairpin G peptide and its isomers: Topology and sequences. <i>Protein Science</i> , 2003, 12, 1882-1893.	7.6	28
143	Triggering Loops and Enzyme Function: Identification of Loops that Trigger and Modulate Movements. <i>Journal of Molecular Biology</i> , 2003, 332, 143-159.	4.2	41
144	Protein-protein interactions: Structurally conserved residues distinguish between binding sites and exposed protein surfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5772-5777.	7.1	553

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145	Binding interactions between the core central domain of 16S rRNA and the ribosomal protein S15 determined by molecular dynamics simulations. <i>Nucleic Acids Research</i> , 2003, 31, 629-638.	14.5	28
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