Andrzej Kolinski

List of Publications by Citations

211 papers	9,489 citations	52 h-index	90 g-index
223 ext. papers	10,521 ext. citations	5.2 avg, IF	6.53 L-index

#	Paper	IF	Citations
211	AAindex: amino acid index database, progress report 2008. *Nucleic Acids Research*, **2008**, 36, D202-5	20.1	623
210	Coarse-Grained Protein Models and Their Applications. *Chemical Reviews*, **2016**, 116, 7898-936	68.1	489
209	Topology fingerprint approach to the inverse protein folding problem. *Journal of Molecular Biology*, **1992**, 227, 227-38	6.5	317
208	Monte Carlo simulations of protein folding. I. Lattice model and interaction scheme. *Proteins: Structure, Function and Bioinformatics*, **1994**, 18, 338-52	4.2	257
207	CABS-dock web server for the flexible docking of peptides to proteins without prior knowledge of the binding site. *Nucleic Acids Research*, **2015**, 43, W419-24	20.1	237
206	MONSSTER: a method for folding globular proteins with a small number of distance restraints. *Journal of Molecular Biology*, **1997**, 265, 217-41	6.5	234
205	TOUCHSTONE II: a new approach to ab initio protein structure prediction. *Biophysical Journal*, **2003**, 85, 1145-64	2.9	223
204	Protein modeling and structure prediction with a reduced representation.. *Acta Biochimica Polonica* , **2019**, 51, 349-371	2	221
203	Structural genomics and its importance for gene function analysis. *Nature Biotechnology*, **2000**, 18, 283-7	44.5	177
202	A general method for the prediction of the three dimensional structure and folding pathway of globular proteins: Application to designed helical proteins. *Journal of Chemical Physics*, **1993**, 98, 7420-7433	3.9	177
201	Derivation and testing of pair potentials for protein folding. When is the quasichemical approximation correct?. *Protein Science*, **1997**, 6, 676-88	6.3	159
200	Reduced models of proteins and their applications. *Polymer*, **2004**, 45, 511-524	3.9	159
199	Dynamic Monte Carlo simulations of a new lattice model of globular protein folding, structure and dynamics. *Journal of Molecular Biology*, **1991**, 221, 499-531	6.5	155
198	Assessing energy functions for flexible docking. *Journal of Computational Chemistry*, **1998**, 19, 1612-1622	3.5	132
197	Are proteins ideal mixtures of amino acids? Analysis of energy parameter sets. *Protein Science*, **1995** , 4, 2107-17	6.3	131
196	Monte Carlo simulations of protein folding. II. Application to protein A, ROP, and crambin. *Proteins: Structure, Function and Bioinformatics*, **1994**, 18, 353-66	4.2	126
195	Protein-peptide docking: opportunities and challenges. *Drug Discovery Today*, **2018**, 23, 1530-1537	8.8	118

194	CABS-flex 2.0: a web server for fast simulations of flexibility of protein structures. *Nucleic Acids Research*, **2018**, 46, W338-W343	20.1	118
193	Discretized model of proteins. I. Monte Carlo study of cooperativity in homopolypeptides. *Journal of Chemical Physics*, **1992**, 97, 9412-9426	3.9	105
192	Modeling of protein-peptide interactions using the CABS-dock web server for binding site search and flexible docking. *Methods*, **2016**, 93, 72-83	4.6	104
191	Prediction of the folding pathways and structure of the GCN4 leucine zipper. *Journal of Molecular Biology*, **1994**, 237, 361-7	6.5	101
190	CABS-flex: Server for fast simulation of protein structure fluctuations. *Nucleic Acids Research*, **2013**, 41, W427-31	20.1	98
189	Does reptation describe the dynamics of entangled, finite length polymer systems? A model simulation. *Journal of Chemical Physics*, **1987**, 86, 1567-1585	3.9	94
188	Generalized protein structure prediction based on combination of fold-recognition with de novo folding and evaluation of models. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61 Suppl 7, 84-90	4.2	92
187	Backbone building from quadrilaterals: a fast and accurate algorithm for protein backbone reconstruction from alpha carbon coordinates. *Journal of Computational Chemistry*, **2007**, 28, 1593-1597	3.5	90
186	Assembly of protein structure from sparse experimental data: An efficient Monte Carlo model. *Proteins: Structure, Function and Bioinformatics*, **1998**, 32, 475-494	4.2	89
185	Ab initio folding of proteins using restraints derived from evolutionary information. *Proteins: Structure, Function and Bioinformatics*, **1999**, 37, 177-185	4.2	89
184	On the origin of the cooperativity of protein folding: implications from model simulations. *Proteins: Structure, Function and Bioinformatics*, **1996**, 26, 271-87	4.2	89
183	Folding pathway of the b1 domain of protein G explored by multiscale modeling. *Biophysical Journal*, **2008**, 94, 726-36	2.9	85
182	Derivation of protein-specific pair potentials based on weak sequence fragment similarity **2000**, 38, 3-16		84
181	Dynamics and thermodynamics of beta-hairpin assembly: insights from various simulation techniques. *Biophysical Journal*, **1999**, 77, 2942-52	2.9	82
180	The collapse transition of semiflexible polymers. A Monte Carlo simulation of a model system. *Journal of Chemical Physics*, **1986**, 85, 3585-3597	3.9	82
179	Accurate reconstruction of all-atom protein representations from side-chain-based low-resolution models. *Proteins: Structure, Function and Bioinformatics*, **2000**, 41, 86-97	4.2	80
178	Fold assembly of small proteins using monte carlo simulations driven by restraints derived from multiple sequence alignments. *Journal of Molecular Biology*, **1998**, 277, 419-48	6.5	79
177	Characterization of protein-folding pathways by reduced-space modeling. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 12330-5	11.5	78

176	Lattice representations of globular proteins: How good are they?. *Journal of Computational Chemistry*, **1993**, 14, 1194-1202	3.5	77
175	CABS-fold: Server for the de novo and consensus-based prediction of protein structure. *Nucleic Acids Research*, **2013**, 41, W406-11	20.1	75
174	A method for predicting protein structure from sequence. *Current Biology*, **1993**, 3, 414-23	6.3	73
173	Dynamic Monte Carlo simulations of globular protein folding/unfolding pathways. I. Six-member, Greek key beta-barrel proteins. *Journal of Molecular Biology*, **1990**, 212, 787-817	6.5	73
172	Protein fragment reconstruction using various modeling techniques. *Journal of Computer-Aided Molecular Design*, **2003**, 17, 725-38	4.2	72
171	TOUCHSTONE: a unified approach to protein structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53 Suppl 6, 469-79	4.2	69
170	De novo and inverse folding predictions of protein structure and dynamics. *Journal of Computer-Aided Molecular Design*, **1993**, 7, 397-438	4.2	69
169	Monte Carlo studies on the long time dynamic properties of dense cubic lattice multichain systems. I. The homopolymeric melt. *Journal of Chemical Physics*, **1987**, 86, 7164-7173	3.9	64
168	Consistent View of Protein Fluctuations from All-Atom Molecular Dynamics and Coarse-Grained Dynamics with Knowledge-Based Force-Field. *Journal of Chemical Theory and Computation*, **2013**, 9, 119-25	6.4	63
167	2-Ethyl and 2-ethylidene analogues of 1alpha,25-dihydroxy-19-norvitamin D(3): synthesis, conformational analysis, biological activities, and docking to the modeled rVDR ligand binding domain. *Journal of Medicinal Chemistry*, **2002**, 45, 3366-80	8.3	62
166	Comparison of three Monte Carlo conformational search strategies for a proteinlike homopolymer model: Folding thermodynamics and identification of low-energy structures. *Journal of Chemical Physics*, **2000**, 113, 5065	3.9	62
165	Ab initio protein structure prediction via a combination of threading, lattice folding, clustering, and structure refinement. *Proteins: Structure, Function and Bioinformatics*, **2001**, Suppl 5, 149-56	4.2	58
164	Inferring ideal amino acid interaction forms from statistical protein contact potentials. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 49-57	4.2	55
163	Regularities in interaction patterns of globular proteins. *Protein Engineering, Design and Selection*, **1993**, 6, 801-10	1.9	54
162	Static and dynamic properties of a new lattice model of polypeptide chains. *Journal of Chemical Physics*, **1991**, 94, 3978-3985	3.9	54
161	On the short time dynamics of dense polymeric systems and the origin of the glass transition: A model system. *Journal of Chemical Physics*, **1986**, 84, 1922-1931	3.9	54
160	DNA vaccine expressing the mimotope of GD2 ganglioside induces protective GD2 cross-reactive antibody responses. *Cancer Research*, **2005**, 65, 3410-8	10.1	53
159	Does a backwardly read protein sequence have a unique native state?. *Protein Engineering, Design and Selection*, **1996**, 9, 5-14	1.9	50

158	CABS-flex predictions of protein flexibility compared with NMR ensembles. *Bioinformatics*, **2014**, 30, 2150-4	7.2	48
157	Dynamics of Dense Polymer Systems: Computer Simulations and Analytic Theories. *Advances in Chemical Physics*, **2007**, 223-278		48
156	A method for the improvement of threading-based protein models. *Proteins: Structure, Function and Bioinformatics*, **1999**, 37, 592-610	4.2	48
155	Theoretical model of prion propagation: a misfolded protein induces misfolding. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 7835-40	11.5	47
154	A minimal physically realistic protein-like lattice model: designing an energy landscape that ensures all-or-none folding to a unique native state. *Biophysical Journal*, **2003**, 84, 1518-26	2.9	46
153	CABS-flex standalone: a simulation environment for fast modeling of protein flexibility. *Bioinformatics*, **2019**, 35, 694-695	7.2	45
152	Towards the high-resolution protein structure prediction. Fast refinement of reduced models with all-atom force field. *BMC Structural Biology*, **2007**, 7, 43	2.7	44
151	Monte Carlo studies of the thermodynamics and kinetics of reduced protein models: Application to small helical, □and ⁄□proteins. *Journal of Chemical Physics*, **1998**, 108, 2608-2617	3.9	44
150	Prediction of quaternary structure of coiled coils. Application to mutants of the GCN4 leucine zipper. *Journal of Molecular Biology*, **1995**, 251, 448-67	6.5	44
149	BioShell--a package of tools for structural biology computations. *Bioinformatics*, **2006**, 22, 621-2	7.2	42
148	Monte Carlo studies on equilibrium globular protein folding. I. Homopolymeric lattice models of beta-barrel proteins. *Biopolymers*, **1987**, 26, 937-62	2.2	42
147	Human telomerase model shows the role of the TEN domain in advancing the double helix for the next polymerization step. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 9443-8	11.5	41
146	Ab initio protein structure prediction on a genomic scale: application to the Mycoplasma genitalium genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 5993-8	11.5	39
145	Simulation of chaperonin effect on protein folding: a shift from nucleation-condensation to framework mechanism. *Journal of the American Chemical Society*, **2011**, 133, 10283-9	16.4	38
144	Monte Carlo studies on the long time dynamic properties of dense cubic lattice multichain systems. II. Probe polymer in a matrix of different degrees of polymerization. *Journal of Chemical Physics*, **1987**, 86, 7174-7180	3.9	38
143	Modeling of Protein Structural Flexibility and Large-Scale Dynamics: Coarse-Grained Simulations and Elastic Network Models. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	37
142	Multibody coarse-grained potentials for native structure recognition and quality assessment of protein models. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 1923-9	4.2	36
141	Distance matrix-based approach to protein structure prediction. *Journal of Structural and Functional Genomics*, **2009**, 10, 67-81		36

140	Monte Carlo dynamics of a dense system of chain molecules constrained to lie near an interface. A simplified membrane model. *Journal of Chemical Physics*, **1990**, 93, 4440-4446	3.9	36
139	Phenomenological theory of the dynamics of polymer melts. I. Analytic treatment of self-diffusion. *Journal of Chemical Physics*, **1988**, 88, 1407-1417	3.9	36
138	Utility library for structural bioinformatics. *Bioinformatics*, **2008**, 24, 584-5	7.2	35
137	TOUCHSTONEX: protein structure prediction with sparse NMR data. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53, 290-306	4.2	35
136	Combining MONSSTER and LES/PME to Predict Protein Structure from Amino Acid Sequence: Application to the Small Protein CMTI-1. *Journal of the American Chemical Society*, **2000**, 122, 8392-8402	16.4	35
135	Folding simulations and computer redesign of protein A three-helix bundle motifs. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 286-299	4.2	35
134	An Efficient Monte Carlo Model of Protein Chains. Modeling the Short-Range Correlations between Side Group Centers of Mass. *Journal of Physical Chemistry B*, **1998**, 102, 4628-4637	3.4	34
133	A reduced model of short range interactions in polypeptide chains. *Journal of Chemical Physics*, **1995**, 103, 4312-4323	3.9	33
132	Monte Carlo studies on equilibrium globular protein folding. II. Beta-barrel globular protein models. *Biopolymers*, **1989**, 28, 1059-95	2.2	33
131	Protein-peptide molecular docking with large-scale conformational changes: the p53-MDM2 interaction. *Scientific Reports*, **2016**, 6, 37532	4.9	33
130	Modeling of loops in proteins: a multi-method approach. *BMC Structural Biology*, **2010**, 10, 5	2.7	32
129	Effect of double bonds on the dynamics of hydrocarbon chains. *Journal of Chemical Physics*, **1992**, 97, 1240-1249	3.9	32
128	Ab initio folding of proteins using restraints derived from evolutionary information. *Proteins: Structure, Function and Bioinformatics*, **1999**, 37, 177-185	4.2	32
127	Algorithm for rapid reconstruction of protein backbone from alpha carbon coordinates. *Journal of Computational Chemistry*, **1997**, 18, 80-85	3.5	31
126	Computer design of idealized motifs. *Journal of Chemical Physics*, **1995**, 103, 10286-10297	3.9	31
125	Mechanism of Folding and Binding of an Intrinsically Disordered Protein As Revealed by ab Initio Simulations. *Journal of Chemical Theory and Computation*, **2014**, 10, 2224-31	6.4	29
124	HCPM--program for hierarchical clustering of protein models. *Bioinformatics*, **2005**, 21, 3179-80	7.2	29
123	Correlation between knowledge-based and detailed atomic potentials: Application to the unfolding of the GCN4 leucine zipper. *Proteins: Structure, Function and Bioinformatics*, **1999**, 35, 447-452	4.2	29

122	De novo simulations of the folding thermodynamics of the GCN4 leucine zipper. *Biophysical Journal*, **1999**, 77, 54-69	2.9	29
121	Monte Carlo study of local orientational order in a semiflexible polymer melt model. *Macromolecules*, **1986**, 19, 2550-2560	5.5	29
120	From coarse-grained to atomic-level characterization of protein dynamics: transition state for the folding of B domain of protein A. *Journal of Physical Chemistry B*, **2012**, 116, 7026-32	3.4	27
119	Optimization of protein models. *Wiley Interdisciplinary Reviews: Computational Molecular Science*, **2012**, 2, 479-493	7.9	27
118	Type II restriction endonuclease R.Eco29kI is a member of the GIY-YIG nuclease superfamily. *BMC Structural Biology*, **2007**, 7, 48	2.7	27
117	A new combination of replica exchange Monte Carlo and histogram analysis for protein folding and thermodynamics. *Journal of Chemical Physics*, **2001**, 115, 1569-1574	3.9	27
116	A method for the prediction of surface [illegible]turns and transglobular connections in small proteins **1997**, 27, 290-308		26
115	CABS-dock standalone: a toolbox for flexible protein-peptide docking. *Bioinformatics*, **2019**, 35, 4170-4172	7.2	25
114	ClusCo: clustering and comparison of protein models. *BMC Bioinformatics*, **2013**, 14, 62	3.6	25
113	Monte Carlo studies of the long-time dynamics of dense polymer systems. The failure of the reptation model. *Accounts of Chemical Research*, **1987**, 20, 350-356	24.3	25
112	Highly Flexible Protein-Peptide Docking Using CABS-Dock. *Methods in Molecular Biology*, **2017**, 1561, 69-94	1.4	24
111	Modeling of Disordered Protein Structures Using Monte Carlo Simulations and Knowledge-Based Statistical Force Fields. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	24
110	Flexible docking of peptides to proteins using CABS-dock. *Protein Science*, **2020**, 29, 211-222	6.3	24
109	Computational reconstruction of atomistic protein structures from coarse-grained models. *Computational and Structural Biotechnology Journal*, **2020**, 18, 162-176	6.8	24
108	A lattice dynamics study of a Langmuir monolayer of monounsaturated fatty acids. *Journal of Chemical Physics*, **1993**, 98, 7581-7587	3.9	23
107	Order-disorder transitions in tetrahedral lattice polymer systems. *Macromolecules*, **1986**, 19, 2560-2567	5.5	23
106	Denatured proteins and early folding intermediates simulated in a reduced conformational space.. *Acta Biochimica Polonica*, **2019**, 53, 131-143	2	23
105	Collapse transitions in protein-like lattice polymers: The effect of sequence patterns. *Biopolymers*, **1997**, 42, 537-548	2.2	22

104	Protein structure prediction: combining de novo modeling with sparse experimental data. *Journal of Computational Chemistry*, **2007**, 28, 1668-76	3.5	22
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102	Efficient scheme for optimization of parallel tempering Monte Carlo method. *Journal of Physics Condensed Matter*, **2007**, 19, 036225	1.8	21
101	The GOR Method of Protein Secondary Structure Prediction and Its Application as a Protein Aggregation Prediction Tool. *Methods in Molecular Biology*, **2017**, 1484, 7-24	1.4	20
100	Combining coarse-grained protein models with replica-exchange all-atom molecular dynamics. *International Journal of Molecular Sciences*, **2013**, 14, 9893-905	6.3	20
99	Method for predicting the state of association of discretized protein models. Application to leucine zippers. *Biochemistry*, **1996**, 35, 955-67	3.2	20
98	Dynamics of star branched polymers in a matrix of linear chains ⍰ Monte Carlo study. *Macromolecular Theory and Simulations*, **1994**, 3, 715-729	1.5	20
97	Coarse-grained modeling of mucus barrier properties. *Biophysical Journal*, **2012**, 102, 195-200	2.9	19
96	Exploring protein energy landscapes with hierarchical clustering. *International Journal of Quantum Chemistry*, **2005**, 105, 826-830	2.1	19
95	Structural features that predict real-value fluctuations of globular proteins. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1425-35	4.2	18
94	Steps towards flexible docking: modeling of three-dimensional structures of the nuclear receptors bound with peptide ligands mimicking co-activators' sequences. *Journal of Steroid Biochemistry and Molecular Biology*, **2007**, 103, 357-60	5.1	18
93	Monte Carlo study of star-branched polymers on the tetrahedral lattice. I. Conformation of the macromolecule. *Journal of Polymer Science: Polymer Chemistry Edition*, **1982**, 20, 3147-3154		18
92	5-HT2 receptor affinity, docking studies and pharmacological evaluation of a series of 1,3-disubstituted thiourea derivatives. *European Journal of Medicinal Chemistry*, **2016**, 116, 173-186	6.8	18
91	Determinants of secondary structure of polypeptide chains: Interplay between short range and burial interactions. *Journal of Chemical Physics*, **1997**, 107, 953-964	3.9	17
90	Hierarchical modeling of protein interactions. *Journal of Molecular Modeling*, **2007**, 13, 691-8	2	17
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88	Model of three-dimensional structure of vitamin D receptor and its binding mechanism with 1alpha,25-dihydroxyvitamin D(3). *Proteins: Structure, Function and Bioinformatics*, **2001**, 44, 188-99	4.2	17
87	Neural network system for the evaluation of side-chain packing in protein structures. *Protein Engineering, Design and Selection*, **1995**, 8, 225-36	1.9	17

86	Dynamic Monte Carlo study of the conformational properties of long flexible polymers. *Macromolecules*, **1987**, 20, 438-440	5.5	17
85	Protein secondary structure prediction using a small training set (compact model) combined with a Complex-valued neural network approach. *BMC Bioinformatics*, **2016**, 17, 362	3.6	17
84	Protein-peptide docking using CABS-dock and contact information. *Briefings in Bioinformatics*, **2019** , 20, 2299-2305	13.4	17
83	Preformed template fluctuations promote fibril formation: insights from lattice and all-atom models. *Journal of Chemical Physics*, **2015**, 142, 145104	3.9	16
82	Kinetics and mechanical stability of the fibril state control fibril formation time of polypeptide chains: A computational study. *Journal of Chemical Physics*, **2018**, 148, 215106	3.9	16
81	Tertiary structure prediction of the KIX domain of CBP using Monte Carlo simulations driven by restraints derived from multiple sequence alignments. *Proteins: Structure, Function and Bioinformatics*, **1998**, 30, 287-94	4.2	16
80	Use of residual dipolar couplings as restraints in ab initio protein structure prediction. *Biopolymers*, **2003**, 70, 548-62	2.2	16
79	BioShell-Threading: versatile Monte Carlo package for protein 3D threading. *BMC Bioinformatics*, **2014**, 15, 22	3.6	15
78	Reduced protein models and their application to the protein folding problem. *Journal of Biomolecular Structure and Dynamics*, **1998**, 16, 381-96	3.6	15
77	Folding simulations and computer redesign of protein A three-helix bundle motifs. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 286-99	4.2	15
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75	Contact prediction in protein modeling: scoring, folding and refinement of coarse-grained models. *BMC Structural Biology*, **2008**, 8, 36	2.7	13
74	Comparative modeling without implicit sequence alignments. *Bioinformatics*, **2007**, 23, 2522-7	7.2	13
73	Role of Resultant Dipole Moment in Mechanical Dissociation of Biological Complexes. *Molecules*, **2018**, 23,	4.8	13
72	SURPASS Low-Resolution Coarse-Grained Protein Modeling. *Journal of Chemical Theory and Computation*, **2017**, 13, 5766-5779	6.4	12
71	Modeling EphB4-EphrinB2 protein-protein interaction using flexible docking of a short linear motif. *BioMedical Engineering OnLine*, **2017**, 16, 71	4.1	12
70	Coarse-Grained Simulations of Membrane Insertion and Folding of Small Helical Proteins Using the CABS Model. *Journal of Chemical Information and Modeling*, **2016**, 56, 2207-2215	6.1	12
69	A structure-based model fails to probe the mechanical unfolding pathways of the titin I27 domain. *Journal of Chemical Physics*, **2013**, 139, 065103	3.9	12

68	Analysis and optimization of interactions between peptides mimicking the GD2 ganglioside and the monoclonal antibody 14G2a. *International Journal of Molecular Medicine*, **2011**, 28, 47-57	4.4	12
67	Elastic network normal modes provide a basis for protein structure refinement. *Journal of Chemical Physics*, **2012**, 136, 195101	3.9	12
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63	Multiscale Approach to Protein Folding Dynamics **2011**, 281-293		11
62	Predicting the complex structure and functional motions of the outer membrane transporter and signal transducer FecA. *Biophysical Journal*, **2008**, 94, 2482-91	2.9	11
61	Ideal amino acid exchange forms for approximating substitution matrices. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 379-93	4.2	11
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59	Protocols for efficient simulations of long-time protein dynamics using coarse-grained CABS model. *Methods in Molecular Biology*, **2014**, 1137, 235-50	1.4	11
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56	Monte carlo study of star-branched polymers on the tetrahedral lattice. II. Statistical thermodynamics of single macromolecules. *Journal of Polymer Science: Polymer Chemistry Edition*, **1984**, 22, 97-106		10
55	Denatured proteins and early folding intermediates simulated in a reduced conformational space. *Acta Biochimica Polonica*, **2006**, 53, 131-44	2	10
54	Coarse-grained Monte Carlo simulations of mucus: structure, dynamics, and thermodynamics. *Biophysical Journal*, **2010**, 99, 3507-16	2.9	9
53	Theoretical study of molecular mechanism of binding TRAP220 coactivator to Retinoid X Receptor alpha, activated by 9-cis retinoic acid. *Journal of Steroid Biochemistry and Molecular Biology*, **2010**, 121, 124-9	5.1	9
52	A simple technique to estimate partition functions and equilibrium constants from Monte Carlo simulations. *Journal of Chemical Physics*, **1995**, 102, 6189-6193	3.9	9
51	Switch from thermal to force-driven pathways of protein refolding. *Journal of Chemical Physics*, **2017**, 146, 135101	3.9	8

50	Improving thermal stability of thermophilic L-threonine aldolase from Thermotoga maritima. *Journal of Biotechnology*, **2015**, 199, 69-76	3.7	8
49	BioShell Threader: protein homology detection based on sequence profiles and secondary structure profiles. *Nucleic Acids Research*, **2012**, 40, W257-62	20.1	8
48	Improved method for prediction of protein backbone U-turn positions and major secondary structural elements between U-turns. *Proteins: Structure, Function and Bioinformatics*, **1997**, 29, 443-60	4.2	8
47	Unfolding of globular proteins: monte carlo dynamics of a realistic reduced model. *Biophysical Journal*, **2003**, 85, 3271-8	2.9	8
46	Monte carlo calculations of the ? point of star-branched macromolecules on tetrahedral lattice. *Journal of Polymer Science, Polymer Letters Edition*, **1982**, 20, 177-180		8
45	One-Dimensional Structural Properties of Proteins in the Coarse-Grained CABS Model. *Methods in Molecular Biology*, **2017**, 1484, 83-113	1.4	7
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43	A Unified Approach to the Prediction of Protein Structure and Function. *Advances in Chemical Physics*, **2002**, 131-192		7
42	Assembly of protein structure from sparse experimental data: An efficient Monte Carlo model **1998** , 32, 475		7
41	How noise in force fields can affect the structural refinement of protein models?. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 335-41	4.2	6
40	Protein Folding with a Reduced Model and Inaccurate Short-Range Restraints. *Macromolecular Theory and Simulations*, **2005**, 14, 444-451	1.5	6
39	A new approach to prediction of short-range conformational propensities in proteins. *Bioinformatics*, **2005**, 21, 981-7	7.2	6
38	Computer simulations of the properties of the ⍰, ⍰C, and ⍰D de novo designed helical proteins **2000**, 38, 17-28		6
37	A protocol for CABS-dock protein-peptide docking driven by side-chain contact information. *BioMedical Engineering OnLine*, **2017**, 16, 73	4.1	5
36	Coarse-Grained Modeling of the Interplay between Secondary Structure Propensities and Protein Fold Assembly. *Journal of Chemical Theory and Computation*, **2018**, 14, 2277-2287	6.4	5
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