Andrzej Kolinski

List of Publications by Year
in descending order

213	11,589	31976	37204
papers	citations	53 h-index	96 g-index

223	223	223	7316
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Proteinâ€“Protein Docking with Large-Scale Backbone Flexibility Using Coarse-Grained Monte-Carlo Simulations. International Journal of Molecular Sciences, 2021, 22, 7341.	4.1	5
2	Flexible docking of peptides to proteins using CABSâ€dock. Protein Science, 2020, 29, 211-222.	7.6	48
3	Computational reconstruction of atomistic protein structures from coarse-grained models. Computational and Structural Biotechnology Journal, 2020, 18, 162-176.	4.1	43
4	Protocols for All-Atom Reconstruction and High-Resolution Refinement of Proteinâ€“Peptide Complex Structures. Methods in Molecular Biology, 2020, 2165, 273-287.	0.9	7
5	Protocols for Fast Simulations of Protein Structure Flexibility Using CABS-Flex and SURPASS. Methods in Molecular Biology, 2020, 2165, 337-353.	0.9	15
6	CABS-flex standalone: a simulation environment for fast modeling of protein flexibility. Bioinformatics, 2019, 35, 694-695.	4.1	79
7	CABS-dock standalone: a toolbox for flexible proteinâ€“peptide docking. Bioinformatics, 2019, 35, 4170-4172.	4.1	55
8	Modeling of Disordered Protein Structures Using Monte Carlo Simulations and Knowledge-Based Statistical Force Fields. International Journal of Molecular Sciences, 2019, 20, 606.	4.1	45
9	Explicit-Solvent All-Atom Molecular Dynamics of Peptide Aggregation. Springer Series on Bio- and Neurosystems, 2019, , 541-558.	0.2	0
10	Protein Dynamics Simulations Using Coarse-Grained Models. Springer Series on Bio- and Neurosystems, 2019, , 61-87.	0.2	4
11	Proteinâ€“peptide docking using CABS-dock and contact information. Briefings in Bioinformatics, 2019, 20, 2299-2305.	6.5	35
12	Protein Structure Prediction Using Coarse-Grained Models. Springer Series on Bio- and Neurosystems, 2019, , 27-59.	0.2	3
13	Protein modeling and structure prediction with a reduced representation.. Acta Biochimica Polonica, 2019, 51, 349-371.	0.5	284
14	Denatured proteins and early folding intermediates simulated in a reduced conformational space.. Acta Biochimica Polonica, 2019, 53, 131-143.	0.5	25
15	Explicit Solvent Molecular Dynamics Simulations of Self-Assembling Amyloidogenic Peptides. Biophysical Journal, 2018, 114, 230a.	0.5	0
16	Coarse-Grained Modeling of the Interplay between Secondary Structure Propensities and Protein Fold Assembly. Journal of Chemical Theory and Computation, 2018, 14, 2277-2287.	5.3	9
17	Proteinâ€“peptide docking: opportunities and challenges. Drug Discovery Today, 2018, 23, 1530-1537.	6.4	212
18	Modeling of Protein Structural Flexibility and Large-Scale Dynamics: Coarse-Grained Simulations and Elastic Network Models. International Journal of Molecular Sciences, 2018, 19, 3496.	4.1	60

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19	Role of Resultant Dipole Moment in Mechanical Dissociation of Biological Complexes. Molecules, 2018, 23, 1995.	3.8	20
20	CABS-flex 2.0: a web server for fast simulations of flexibility of protein structures. Nucleic Acids Research, 2018, 46, W338-W343.	14.5	249
21	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.	3.0	21
22	Highly Flexible Protein-Peptide Docking Using CABS-Dock. Methods in Molecular Biology, 2017, 1561, 69-94.	0.9	33
23	Switch from thermal to force-driven pathways of protein refolding. Journal of Chemical Physics, 2017, 146, 135101.	3.0	8
24	Prediction of Protein Aggregation Propensities using GOR Method. Biophysical Journal, 2017, 112, 198a-199a.	0.5	0
25	SURPASS Low-Resolution Coarse-Grained Protein Modeling. Journal of Chemical Theory and Computation, 2017, 13, 5766-5779.	5.3	18
26	Toward more efficient simulations of slow processes in large biomolecular systems. Physics of Life Reviews, 2017, 22-23, 75-76.	2.8	4
27	One-Dimensional Structural Properties of Proteins in the Coarse-Grained CABS Model. Methods in Molecular Biology, 2017, 1484, 83-113.	0.9	8
28	Predicting Real-Valued Protein Residue Fluctuation Using FlexPred. Methods in Molecular Biology, 2017, 1484, 175-186.	0.9	4
29	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.	0.9	33
30	Modeling EphB4-EphrinB2 proteinâ€“protein interaction using flexible docking of a short linear motif. BioMedical Engineering OnLine, 2017, 16, 71.	2.7	17
31	A protocol for CABS-dock proteinâ€“peptide docking driven by side-chain contact information. BioMedical Engineering OnLine, 2017, 16, 73.	2.7	9
32	Protein secondary structure prediction using a small training set (compact model) combined with a Complex-valued neural network approach. BMC Bioinformatics, 2016, 17, 362.	2.6	29
33	Protein-peptide molecular docking with large-scale conformational changes: the p53-MDM2 interaction. Scientific Reports, 2016, 6, 37532.	3.3	44
34	5-HT 2 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.	5.5	23
35	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.	5.4	17
36	Coarse-Grained Protein Models and Their Applications. Chemical Reviews, 2016, 116, 7898-7936.	47.7	721

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37	Modeling of proteinâ€“peptide interactions using the CABS-dock web server for binding site search and flexible docking. Methods, 2016, 93, 72-83.	3.8	137
38	Ensemble-based evaluation for protein structure models. Bioinformatics, 2016, 32, i314-i321.	4.1	7
39	Coarse-Grained Modeling of Peptide Docking Associated with Large Conformation Transitions of the Binding Protein: Troponin I Fragmentâ€“Troponin C System. Molecules, 2015, 20, 10763-10780.	3.8	11
40	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-W424.	14.5	331
41	Improving thermal stability of thermophilic l -threonine aldolase from Thermotoga maritima. Journal of Biotechnology, 2015, 199, 69-76.	3.8	8
42	Preformed template fluctuations promote fibril formation: Insights from lattice and all-atom models. Journal of Chemical Physics, 2015, 142, 145104.	3.0	18
43	CABS-flex predictions of protein flexibility compared with NMR ensembles. Bioinformatics, 2014, 30, 2150-2154.	4.1	75
44	BioShell-Threading: versatile Monte Carlo package for protein 3D threading. BMC Bioinformatics, 2014, 15, 22.	2.6	17
45	Coarse-Grained Protein Models in Structure Prediction. Springer Series in Bio-/neuroinformatics, 2014, , 25-53.	0.1	1
46	Coarse-Grained Modeling of Protein Dynamics. Springer Series in Bio-/neuroinformatics, 2014, , 55-79.	0.1	8
47	Mechanism of Folding and Binding of an Intrinsically Disordered Protein As Revealed by ab Initio Simulations. Journal of Chemical Theory and Computation, 2014, 10, 2224-2231.	5.3	41
48	Protocols for Efficient Simulations of Long-Time Protein Dynamics Using Coarse-Grained CABS Model. Methods in Molecular Biology, 2014, 1137, 235-250.	0.9	13
49	A structure-based model fails to probe the mechanical unfolding pathways of the titin I27 domain. Journal of Chemical Physics, 2013, 139, 065103.	3.0	13
50	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, 119-125.	5.3	85
51	ClusCo: clustering and comparison of protein models. BMC Bioinformatics, 2013, 14, 62.	2.6	32
52	Combining Coarse-Grained Protein Models with Replica-Exchange All-Atom Molecular Dynamics. International Journal of Molecular Sciences, 2013, 14, 9893-9905.	4.1	22
53	CABS-flex: server for fast simulation of protein structure fluctuations. Nucleic Acids Research, 2013, 41, W427-W431.	14.5	132
54	CABS-fold: server for the de novo and consensus-based prediction of protein structure. Nucleic Acids Research, 2013, 41, W406-W411.	14.5	86

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55	Elastic network normal modes provide a basis for protein structure refinement. Journal of Chemical Physics, 2012, 136, 195101.	3.0	17
56	BioShell Threader: protein homology detection based on sequence profiles and secondary structure profiles. Nucleic Acids Research, 2012, 40, W257-W262.	14.5	10
57	Optimization of Profile-to-Profile Alignment Parameters for One-Dimensional Threading. Journal of Computational Biology, 2012, 19, 879-886.	1.6	4
58	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, 7026-7032.	2.6	31
59	ANM Normal Modes Show the Directions for Protein Structure Refinement. Biophysical Journal, 2012, 102, 25a.	0.5	1
60	Coarse-Grained Modeling of Mucus Barrier Properties. Biophysical Journal, 2012, 102, 195-200.	0.5	20
61	How noise in force fields can affect the structural refinement of protein models?. Proteins: Structure, Function and Bioinformatics, 2012, 80, 335-341.	2.6	6
62	Optimization of protein models. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2012, 2, 479-493.	14.6	32
63	Structural features that predict realâ€value fluctuations of globular proteins. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1425-1435.	2.6	20
64	Simulation of Chaperonin Effect on Protein Folding: A Shift from Nucleationâ€“Condensation to Framework Mechanism. Journal of the American Chemical Society, 2011, 133, 10283-10289.	13.7	40
65	Lattice Polymers and Protein Models. , 2011, , 1-20.		1
66	Multiscale Approach to Protein Folding Dynamics. , 2011, , 281-293.		11
67	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.	4.0	12
68	Multibody coarseâ€grained potentials for native structure recognition and quality assessment of protein models. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1923-1929.	2.6	38
69	CABSâ€NMRâ€”De novo tool for rapid global fold determination from chemical shifts, residual dipolar couplings and sparse methylâ€methyl noes. Journal of Computational Chemistry, 2011, 32, 536-544.	3.3	14
70	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, 9443-9448.	7.1	47
71	Multiscale Protein and Peptide Docking. , 2011, , 21-33.		0
72	Modeling of loops in proteins: a multi-method approach. BMC Structural Biology, 2010, 10, 5.	2.3	35

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73	Coarse-Grained Monte Carlo Simulations of Mucus: Structure, Dynamics, and Thermodynamics. Biophysical Journal, 2010, 99, 3507-3516.	0.5	13
74	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, 124-129.	2.5	10
75	TRACER. A new approach to comparative modeling that combines threading with free-space conformational sampling. Acta Biochimica Polonica, 2010, 57, 125-33.	0.5	3
76	Distance matrix-based approach to protein structure prediction. Journal of Structural and Functional Genomics, 2009, 10, 67-81.	1.2	45
77	Fast and accurate methods for predicting short-range constraints in protein models. Journal of Computer-Aided Molecular Design, 2008, 22, 783-788.	2.9	0
78	Contact prediction in protein modeling: Scoring, folding and refinement of coarse-grained models. BMC Structural Biology, 2008, 8, 36.	2.3	15
79	Predicting the Complex Structure and Functional Motions of the Outer Membrane Transporter and Signal Transducer FecA. Biophysical Journal, 2008, 94, 2482-2491.	0.5	11
80	Folding Pathway of the B1 Domain of Protein G Explored by Multiscale Modeling. Biophysical Journal, 2008, 94, 726-736.	0.5	96
81	Utility library for structural bioinformatics. Bioinformatics, 2008, 24, 584-585.	4.1	38
82	Uncharacterized DUF1574 leptospira proteins are SGNH hydrolases. Cell Cycle, 2008, 7, 542-544.	2.6	7
83	Efficient scheme for optimization of parallel tempering Monte Carlo method. Journal of Physics Condensed Matter, 2007, 19, 036225.	1.8	25
84	Comparative modeling without implicit sequence alignments. Bioinformatics, 2007, 23, 2522-2527.	4.1	16
85	Characterization of protein-folding pathways by reduced-space modeling. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12330-12335.	7.1	87
86	T-Pile a package for thermodynamic calculations for biomolecules. Bioinformatics, 2007, 23, 1840-1842.	4.1	3
87	Steps towards flexible docking: Modeling of three-dimensional structures of the nuclear receptors bound with peptide ligands mimicking co-activatorsâ€™ sequences. Journal of Steroid Biochemistry and Molecular Biology, 2007, 103, 357-360.	2.5	21
88	AAindex: amino acid index database, progress report 2008. Nucleic Acids Research, 2007, 36, D202-D205.	14.5	871
89	Why Do Proteins Divide into Domains? Insights from Lattice Model Simulations. Biomacromolecules, 2007, 8, 3519-3524.	5.4	2
90	Dynamics of Dense Polymer Systems: Computer Simulations and Analytic Theories. Advances in Chemical Physics, 2007, , 223-278.	0.3	63

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91	Folding pathway of the B1 domain of protein G explored by a multiscale modeling. Nature Precedings, 2007, , .	0.1	0
92	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.	3.3	102
93	Protein structure prediction: Combining de novo modeling with sparse experimental data. Journal of Computational Chemistry, 2007, 28, 1668-1676.	3.3	25
94	Towards the high-resolution protein structure prediction. Fast refinement of reduced models with all-atom force field. BMC Structural Biology, 2007, 7, 43.	2.3	45
95	Type II restriction endonuclease R.Eco29kI is a member of the GIY-YIG nuclease superfamily. BMC Structural Biology, 2007, 7, 48.	2.3	32
96	Ideal amino acid exchange forms for approximating substitution matrices. Proteins: Structure, Function and Bioinformatics, 2007, 69, 379-393.	2.6	11
97	Hierarchical modeling of protein interactions. Journal of Molecular Modeling, 2007, 13, 691-698.	1.8	19
98	BioShell–a package of tools for structural biology computations. Bioinformatics, 2006, 22, 621-622.	4.1	44
99	Denatured proteins and early folding intermediates simulated in a reduced conformational space. Acta Biochimica Polonica, 2006, 53, 131-44.	0.5	10
100	Ab initio Modeling. , 2005, , 137-161.		0
101	Protein Folding with a Reduced Model and Inaccurate Short-Range Restraints. Macromolecular Theory and Simulations, 2005, 14, 444-451.	1.4	8
102	Protein structure prediction by tempering spatial constraints. Journal of Computer-Aided Molecular Design, 2005, 19, 603-608.	2.9	3
103	Exploring protein energy landscapes with hierarchical clustering. International Journal of Quantum Chemistry, 2005, 105, 826-830.	2.0	21
104	Inferring ideal amino acid interaction forms from statistical protein contact potentials. Proteins: Structure, Function and Bioinformatics, 2005, 59, 49-57.	2.6	66
105	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, 84-90.	2.6	99
106	DNA Vaccine Expressing the Mimotope of GD2 Ganglioside Induces Protective GD2 Cross-reactive Antibody Responses. Cancer Research, 2005, 65, 3410-3418.	0.9	64
107	HCPM–program for hierarchical clustering of protein models. Bioinformatics, 2005, 21, 3179-3180.	4.1	30
108	A minimal proteinlike lattice model: An alpha-helix motif. Journal of Chemical Physics, 2005, 122, 214915.	3.0	12

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110	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, 7835-7840.	7.1	51
111	Protein modeling with reduced representation: statistical potentials and protein folding mechanism.. Acta Biochimica Polonica, 2005, 52, 741-748.	0.5	8
112	Reduced models of proteins and their applications. Polymer, 2004, 45, 511-524.	3.8	176
113	Protein fragment reconstruction using various modeling techniques. Journal of Computer-Aided Molecular Design, 2003, 17, 725-738.	2.9	81
114	A simple lattice model that exhibits a protein-like cooperative all-or-none folding transition. Biopolymers, 2003, 69, 399-405.	2.4	21
115	Use of residual dipolar couplings as restraints inab initio protein structure prediction. Biopolymers, 2003, 70, 548-562.	2.4	16
116	TOUCHSTONEX: Protein structure prediction with sparse NMR data. Proteins: Structure, Function and Bioinformatics, 2003, 53, 290-306.	2.6	38
117	TOUCHSTONE: A unified approach to protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2003, 53, 469-479.	2.6	72
118	TOUCHSTONE II: A New Approach to Ab Initio Protein Structure Prediction. Biophysical Journal, 2003, 85, 1145-1164.	0.5	243
119	Unfolding of Globular Proteins: Monte Carlo Dynamics of a Realistic Reduced Model. Biophysical Journal, 2003, 85, 3271-3278.	0.5	13
120	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, 1518-1526.	0.5	51
121	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, 5993-5998.	7.1	41
122	Numerical Study of the Entropy Loss of Dimerization and the Folding Thermodynamics of the GCN4 Leucine Zipper. Biophysical Journal, 2002, 83, 2801-2811.	0.5	12
123	2-Ethyl and 2-Ethylidene Analogues of 1Î±,25-Dihydroxy-19-norvitamin D3:Â Synthesis, Conformational Analysis, Biological Activities, and Docking to the Modeled rVDR Ligand Binding Domain. Journal of Medicinal Chemistry, 2002, 45, 3366-3380.	6.4	70
124	A Unified Approach to the Prediction of Protein Structure and Function. Advances in Chemical Physics, 2002, , 131-192.	0.3	9
125	Computer simulations of protein folding with a small number of distance restraints.. Acta Biochimica Polonica, 2002, 49, 683-692.	0.5	2
126	Ab initio protein structure prediction via a combination of threading, lattice folding, clustering, and structure refinement. Proteins: Structure, Function and Bioinformatics, 2001, 45, 149-156.	2.6	66

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127	Model of three-dimensional structure of vitamin D receptor and its binding mechanism with 1?,25-dihydroxyvitamin D3. Proteins: Structure, Function and Bioinformatics, 2001, 44, 188-199.	2.6	20
128	Three-dimensional modeling of the I-TevI homing endonuclease catalytic domain, a GIYâ€“YIG superfamily member, using NMR restraints and Monte Carlo dynamics. Protein Engineering, Design and Selection, 2001, 14, 717-721.	2.1	16
129	A new combination of replica exchange Monte Carlo and histogram analysis for protein folding and thermodynamics. Journal of Chemical Physics, 2001, 115, 1569-1574.	3.0	29
130	Computer simulations of the properties of the ?2, ?2C, and ?2D de novo designed helical proteins. , 2000, 38, 17-28.		7
131	Derivation of protein-specific pair potentials based on weak sequence fragment similarity. , 2000, 38, 3-16.		104
132	Accurate reconstruction of all-atom protein representations from side-chain-based low-resolution models. Proteins: Structure, Function and Bioinformatics, 2000, 41, 86-97.	2.6	85
133	Helix-coil and beta sheet-coil transitions in a simplified, yet realistic protein model. Macromolecular Theory and Simulations, 2000, 9, 523-533.	1.4	13
134	Structural genomics and its importance for gene function analysis. Nature Biotechnology, 2000, 18, 283-287.	17.5	212
135	Protein Folding: Flexible Lattice Models. Progress of Theoretical Physics Supplement, 2000, 138, 292-300.	0.1	16
136	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.	3.0	66
137	Combining MONSSTER and LES/PME to Predict Protein Structure from Amino Acid Sequence:â€‰ Application to the Small Protein CMTI-1. Journal of the American Chemical Society, 2000, 122, 8392-8402.	13.7	36
138	De novo predictions of the quaternary structure of leucine zippers and other coiled coils. International Journal of Quantum Chemistry, 1999, 75, 165-176.	2.0	5
139	Ab initio folding of proteins using restraints derived from evolutionary information. Proteins: Structure, Function and Bioinformatics, 1999, 37, 177-185.	2.6	119
140	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.	2.6	30
141	A method for the improvement of threading-based protein models. Proteins: Structure, Function and Bioinformatics, 1999, 37, 592-610.	2.6	53
142	De Novo Simulations of the Folding Thermodynamics of the GCN4 Leucine Zipper. Biophysical Journal, 1999, 77, 54-69.	0.5	31
143	Dynamics and Thermodynamics of Î²-Hairpin Assembly: Insights from Various Simulation Techniques. Biophysical Journal, 1999, 77, 2942-2952.	0.5	89
144	Ab initio folding of proteins using restraints derived from evolutionary information. Proteins: Structure, Function and Bioinformatics, 1999, 37, 177-185.	2.6	32

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145	Assessing energy functions for flexible docking. Journal of Computational Chemistry, 1998, 19, 1612-1622.	3.3	144
146	Tertiary structure prediction of the KIX domain of CBP using Monte Carlo simulations driven by restraints derived from multiple sequence alignments. , 1998, 30, 287-294.		17
147	Assembly of protein structure from sparse experimental data: An efficient Monte Carlo model. Proteins: Structure, Function and Bioinformatics, 1998, 32, 475-494.	2.6	101
148	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.	2.6	38
149	Fold assembly of small proteins using Monte Carlo simulations driven by restraints derived from multiple sequence alignments. Journal of Molecular Biology, 1998, 277, 419-448.	4.2	92
150	Computer Simulations of De Novo Designed Helical Proteins. Biophysical Journal, 1998, 75, 92-105.	0.5	24
151	Monte Carlo studies of the thermodynamics and kinetics of reduced protein models: Application to small helical, Î², and Î±/Î² proteins. Journal of Chemical Physics, 1998, 108, 2608-2617.	3.0	45
152	Reduced Protein Models and their Application to the Protein Folding Problem. Journal of Biomolecular Structure and Dynamics, 1998, 16, 381-396.	3.5	19
153	Assembly of protein structure from sparse experimental data: An efficient Monte Carlo model. Proteins: Structure, Function and Bioinformatics, 1998, 32, 475-494.	2.6	7
154	Determinants of secondary structure of polypeptide chains: Interplay between short range and burial interactions. Journal of Chemical Physics, 1997, 107, 953-964.	3.0	17
155	MONSSTER: a method for folding globular proteins with a small number of distance restraints. Journal of Molecular Biology, 1997, 265, 217-241.	4.2	257
156	Derivation and testing of pair potentials for protein folding. When is the quasichemical approximation correct?. Protein Science, 1997, 6, 676-688.	7.6	182
157	Algorithm for rapid reconstruction of protein backbone from alpha carbon coordinates. Journal of Computational Chemistry, 1997, 18, 80-85.	3.3	35
158	A method for the prediction of surface â€œUâ€•turns and transglobular connections in small proteins. , 1997, 27, 290-308.		28
159	Improved method for prediction of protein backbone U-turn positions and major secondary structural elements between U-turns. , 1997, 29, 443-460.		8
160	Collapse transitions in protein-like lattice polymers: The effect of sequence patterns. Biopolymers, 1997, 42, 537-548.	2.4	23
161	Monte Carlo lattice dynamics and the prediction of protein folds. , 1997, , 395-429.		4
162	High coordination lattice models of protein structure, dynamics and thermodynamics. Acta Biochimica Polonica, 1997, 44, 389-422.	0.5	0

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164	Folding simulations and computer redesign of protein A three-helix bundle motifs. Proteins: Structure, Function and Bioinformatics, 1996, 25, 286-299.	2.6	16
165	On the origin of the cooperativity of protein folding: Implications from model simulations. Proteins: Structure, Function and Bioinformatics, 1996, 26, 271-287.	2.6	98
166	Does a backwardly read protein sequence have a unique native state?. Protein Engineering, Design and Selection, 1996, 9, 5-14.	2.1	51
167	Folding simulations and computer redesign of protein A threeâ€helix bundle motifs. Proteins: Structure, Function and Bioinformatics, 1996, 25, 286-299.	2.6	38
168	On the origin of the cooperativity of protein folding: Implications from model simulations. , 1996, 26, 271.		1
169	Are proteins ideal mixtures of amino acids? Analysis of energy parameter sets. Protein Science, 1995, 4, 2107-2117.	7.6	146
170	Computer design of idealized Î²â€motifs. Journal of Chemical Physics, 1995, 103, 10286-10297.	3.0	33
171	A reduced model of short range interactions in polypeptide chains. Journal of Chemical Physics, 1995, 103, 4312-4323.	3.0	39
172	A simple technique to estimate partition functions and equilibrium constants from Monte Carlo simulations. Journal of Chemical Physics, 1995, 102, 6189-6193.	3.0	12
173	Neural network system for the evaluation of side-chain packing in protein structures. Protein Engineering, Design and Selection, 1995, 8, 225-236.	2.1	19
174	Prediction of Quaternary Structure of Coiled Coils. Application to Mutants of the GCN4 Leucine Zipper. Journal of Molecular Biology, 1995, 251, 448-467.	4.2	45
175	Monte carlo simulations of protein folding. I. Lattice model and interaction scheme. Proteins: Structure, Function and Bioinformatics, 1994, 18, 338-352.	2.6	282
176	Monte carlo simulations of protein folding. II. Application to protein A, ROP, and crambin. Proteins: Structure, Function and Bioinformatics, 1994, 18, 353-366.	2.6	148
177	Dynamics of star branched polymers in a matrix of linear chains â€" a Monte Carlo study. Macromolecular Theory and Simulations, 1994, 3, 715-729.	1.4	21
178	Prediction of the Folding Pathways and Structure of the GCN4 Leucine Zipper. Journal of Molecular Biology, 1994, 237, 361-367.	4.2	107
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