Andrzej Kolinski

List of Publications by Year in Descending Order

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	Protein-Protein Docking with Large-Scale Backbone Flexibility Using Coarse-Grained Monte-Carlo Simulations. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	2
210	Flexible docking of peptides to proteins using CABS-dock. *Protein Science*, **2020**, 29, 211-222	6.3	24
209	Computational reconstruction of atomistic protein structures from coarse-grained models. *Computational and Structural Biotechnology Journal*, **2020**, 18, 162-176	6.8	24
208	Protocols for All-Atom Reconstruction and High-Resolution Refinement of Protein-Peptide Complex Structures. *Methods in Molecular Biology*, **2020**, 2165, 273-287	1.4	4
207	Protocols for Fast Simulations of Protein Structure Flexibility Using CABS-Flex and SURPASS. *Methods in Molecular Biology*, **2020**, 2165, 337-353	1.4	4
206	CABS-dock standalone: a toolbox for flexible protein-peptide docking. *Bioinformatics*, **2019**, 35, 4170-4172	7.2	25
205	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
204	CABS-flex standalone: a simulation environment for fast modeling of protein flexibility. *Bioinformatics*, **2019**, 35, 694-695	7.2	45
203	Protein modeling and structure prediction with a reduced representation.. *Acta Biochimica Polonica* , **2019**, 51, 349-371	2	221
202	Denatured proteins and early folding intermediates simulated in a reduced conformational space.. *Acta Biochimica Polonica*, **2019**, 53, 131-143	2	23
201	Protein Structure Prediction Using Coarse-Grained Models. *Springer Series on Bio- and Neurosystems* , **2019**, 27-59	0.5	2
200	Explicit-Solvent All-Atom Molecular Dynamics of Peptide Aggregation. *Springer Series on Bio- and Neurosystems*, **2019**, 541-558	0.5	
199	Protein Dynamics Simulations Using Coarse-Grained Models. *Springer Series on Bio- and Neurosystems*, **2019**, 61-87	0.5	1
198	Protein-peptide docking using CABS-dock and contact information. *Briefings in Bioinformatics*, **2019** , 20, 2299-2305	13.4	17
197	Explicit Solvent Molecular Dynamics Simulations of Self-Assembling Amyloidogenic Peptides. *Biophysical Journal*, **2018**, 114, 230a	2.9	
196	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
195	Protein-peptide docking: opportunities and challenges. *Drug Discovery Today*, **2018**, 23, 1530-1537	8.8	118

194	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
193	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
192	Role of Resultant Dipole Moment in Mechanical Dissociation of Biological Complexes. *Molecules*, **2018**, 23,	4.8	13
191	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
190	Highly Flexible Protein-Peptide Docking Using CABS-Dock. *Methods in Molecular Biology*, **2017**, 1561, 69-94	1.4	24
189	Switch from thermal to force-driven pathways of protein refolding. *Journal of Chemical Physics*, **2017**, 146, 135101	3.9	8
188	SURPASS Low-Resolution Coarse-Grained Protein Modeling. *Journal of Chemical Theory and Computation*, **2017**, 13, 5766-5779	6.4	12
187	Modeling EphB4-EphrinB2 protein-protein interaction using flexible docking of a short linear motif. *BioMedical Engineering OnLine*, **2017**, 16, 71	4.1	12
186	A protocol for CABS-dock protein-peptide docking driven by side-chain contact information. *BioMedical Engineering OnLine*, **2017**, 16, 73	4.1	5
185	Toward more efficient simulations of slow processes in large biomolecular systems: Comment on "Ligand diffusion in proteins via enhanced sampling in molecular dynamics" by Jakub Rydzewski and Wieslaw Nowak. *Physics of Life Reviews*, **2017**, 22-23, 75-76	2.1	4
184	One-Dimensional Structural Properties of Proteins in the Coarse-Grained CABS Model. *Methods in Molecular Biology*, **2017**, 1484, 83-113	1.4	7
183	Predicting Real-Valued Protein Residue Fluctuation Using FlexPred. *Methods in Molecular Biology*, **2017**, 1484, 175-186	1.4	3
182	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
181	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
180	Coarse-Grained Protein Models and Their Applications. *Chemical Reviews*, **2016**, 116, 7898-936	68.1	489
179	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
178	Ensemble-based evaluation for protein structure models. *Bioinformatics*, **2016**, 32, i314-i321	7.2	5
177	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

176	Protein-peptide molecular docking with large-scale conformational changes: the p53-MDM2 interaction. *Scientific Reports*, **2016**, 6, 37532	4.9	33
175	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
174	Improving thermal stability of thermophilic L-threonine aldolase from Thermotoga maritima. *Journal of Biotechnology*, **2015**, 199, 69-76	3.7	8
173	Preformed template fluctuations promote fibril formation: insights from lattice and all-atom models. *Journal of Chemical Physics*, **2015**, 142, 145104	3.9	16
172	Coarse-Grained Modeling of Peptide Docking Associated with Large Conformation Transitions of the Binding Protein: Troponin I Fragment-Troponin C System. *Molecules*, **2015**, 20, 10763-80	4.8	10
171	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
170	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
169	CABS-flex predictions of protein flexibility compared with NMR ensembles. *Bioinformatics*, **2014**, 30, 2150-4	7.2	48
168	BioShell-Threading: versatile Monte Carlo package for protein 3D threading. *BMC Bioinformatics*, **2014**, 15, 22	3.6	15
167	Coarse-Grained Protein Models in Structure Prediction. *Springer Series in Bio-/neuroinformatics*, **2014**, 25-53		
166	Coarse-Grained Modeling of Protein Dynamics. *Springer Series in Bio-/neuroinformatics*, **2014**, 55-79		7
165	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
164	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
163	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
162	ClusCo: clustering and comparison of protein models. *BMC Bioinformatics*, **2013**, 14, 62	3.6	25
161	Combining coarse-grained protein models with replica-exchange all-atom molecular dynamics. *International Journal of Molecular Sciences*, **2013**, 14, 9893-905	6.3	20
160	CABS-flex: Server for fast simulation of protein structure fluctuations. *Nucleic Acids Research*, **2013**, 41, W427-31	20.1	98
159	CABS-fold: Server for the de novo and consensus-based prediction of protein structure. *Nucleic Acids Research*, **2013**, 41, W406-11	20.1	75

158	Optimization of profile-to-profile alignment parameters for one-dimensional threading. *Journal of Computational Biology*, **2012**, 19, 879-86	1.7	4
157	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
156	Coarse-grained modeling of mucus barrier properties. *Biophysical Journal*, **2012**, 102, 195-200	2.9	19
155	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
154	Optimization of protein models. *Wiley Interdisciplinary Reviews: Computational Molecular Science*, **2012**, 2, 479-493	7.9	27
153	Structural features that predict real-value fluctuations of globular proteins. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1425-35	4.2	18
152	Elastic network normal modes provide a basis for protein structure refinement. *Journal of Chemical Physics*, **2012**, 136, 195101	3.9	12
151	BioShell Threader: protein homology detection based on sequence profiles and secondary structure profiles. *Nucleic Acids Research*, **2012**, 40, W257-62	20.1	8
150	Lattice Polymers and Protein Models **2011**, 1-20		
149	Multiscale Approach to Protein Folding Dynamics **2011**, 281-293		11
148	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
147	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
146	CABS-NMR--De novo tool for rapid global fold determination from chemical shifts, residual dipolar couplings and sparse methyl-methyl NOEs. *Journal of Computational Chemistry*, **2011**, 32, 536-44	3.5	10
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	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
143	Multiscale Protein and Peptide Docking **2011**, 21-33		
142	Coarse-grained Monte Carlo simulations of mucus: structure, dynamics, and thermodynamics. *Biophysical Journal*, **2010**, 99, 3507-16	2.9	9
141	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

140	Modeling of loops in proteins: a multi-method approach. *BMC Structural Biology*, **2010**, 10, 5	2.7	32
139	TRACER. A new approach to comparative modeling that combines threading with free-space conformational sampling. *Acta Biochimica Polonica*, **2010**, 57, 125-33	2	3
138	Distance matrix-based approach to protein structure prediction. *Journal of Structural and Functional Genomics*, **2009**, 10, 67-81		36
137	Template-Free Predictions of Three-Dimensional Protein Structures: From First Principles to Knowledge-Based Potentials **2008**, 117-141		1
136	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
135	Folding pathway of the b1 domain of protein G explored by multiscale modeling. *Biophysical Journal*, **2008**, 94, 726-36	2.9	85
134	Utility library for structural bioinformatics. *Bioinformatics*, **2008**, 24, 584-5	7.2	35
133	Uncharacterized DUF1574 leptospira proteins are SGNH hydrolases. *Cell Cycle*, **2008**, 7, 542-4	4.7	4
132	Fast and accurate methods for predicting short-range constraints in protein models. *Journal of Computer-Aided Molecular Design*, **2008**, 22, 783-8	4.2	
131	Contact prediction in protein modeling: scoring, folding and refinement of coarse-grained models. *BMC Structural Biology*, **2008**, 8, 36	2.7	13
130	AAindex: amino acid index database, progress report 2008. *Nucleic Acids Research*, **2008**, 36, D202-5	20.1	623
129	Why do proteins divide into domains? Insights from lattice model simulations. *Biomacromolecules*, **2007**, 8, 3519-24	6.9	2
128	Dynamics of Dense Polymer Systems: Computer Simulations and Analytic Theories. *Advances in Chemical Physics*, **2007**, 223-278		48
127	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
126	Protein structure prediction: combining de novo modeling with sparse experimental data. *Journal of Computational Chemistry*, **2007**, 28, 1668-76	3.5	22
125	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
124	Type II restriction endonuclease R.Eco29kI is a member of the GIY-YIG nuclease superfamily. *BMC Structural Biology*, **2007**, 7, 48	2.7	27
123	Ideal amino acid exchange forms for approximating substitution matrices. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 379-93	4.2	11

122	Hierarchical modeling of protein interactions. *Journal of Molecular Modeling*, **2007**, 13, 691-8	2	17
121	Efficient scheme for optimization of parallel tempering Monte Carlo method. *Journal of Physics Condensed Matter*, **2007**, 19, 036225	1.8	21
120	Comparative modeling without implicit sequence alignments. *Bioinformatics*, **2007**, 23, 2522-7	7.2	13
119	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
118	T-Pile--a package for thermodynamic calculations for biomolecules. *Bioinformatics*, **2007**, 23, 1840-2	7.2	2
117	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
116	BioShell--a package of tools for structural biology computations. *Bioinformatics*, **2006**, 22, 621-2	7.2	42
115	Denatured proteins and early folding intermediates simulated in a reduced conformational space. *Acta Biochimica Polonica*, **2006**, 53, 131-44	2	10
114	Ab initio Modeling **2005**, 137-161		
113	Protein Folding with a Reduced Model and Inaccurate Short-Range Restraints. *Macromolecular Theory and Simulations*, **2005**, 14, 444-451	1.5	6
112	Protein structure prediction by tempering spatial constraints. *Journal of Computer-Aided Molecular Design*, **2005**, 19, 603-8	4.2	2
111	Exploring protein energy landscapes with hierarchical clustering. *International Journal of Quantum Chemistry*, **2005**, 105, 826-830	2.1	19
110	Inferring ideal amino acid interaction forms from statistical protein contact potentials. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 49-57	4.2	55
109	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
108	DNA vaccine expressing the mimotope of GD2 ganglioside induces protective GD2 cross-reactive antibody responses. *Cancer Research*, **2005**, 65, 3410-8	10.1	53
107	HCPM--program for hierarchical clustering of protein models. *Bioinformatics*, **2005**, 21, 3179-80	7.2	29
106	A minimal proteinlike lattice model: an alpha-helix motif. *Journal of Chemical Physics*, **2005**, 122, 214915	3.9	12
105	A new approach to prediction of short-range conformational propensities in proteins. *Bioinformatics*, **2005**, 21, 981-7	7.2	6

104	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
103	Protein modeling with reduced representation: statistical potentials and protein folding mechanism.. *Acta Biochimica Polonica*, **2005**, 52, 741-748	2	5
102	Reduced models of proteins and their applications. *Polymer*, **2004**, 45, 511-524	3.9	159
101	Protein fragment reconstruction using various modeling techniques. *Journal of Computer-Aided Molecular Design*, **2003**, 17, 725-38	4.2	72
100	A simple lattice model that exhibits a protein-like cooperative all-or-none folding transition. *Biopolymers*, **2003**, 69, 399-405	2.2	17
99	Use of residual dipolar couplings as restraints in ab initio protein structure prediction. *Biopolymers*, **2003**, 70, 548-62	2.2	16
98	TOUCHSTONEX: protein structure prediction with sparse NMR data. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53, 290-306	4.2	35
97	TOUCHSTONE: a unified approach to protein structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53 Suppl 6, 469-79	4.2	69
96	TOUCHSTONE II: a new approach to ab initio protein structure prediction. *Biophysical Journal*, **2003**, 85, 1145-64	2.9	223
95	Unfolding of globular proteins: monte carlo dynamics of a realistic reduced model. *Biophysical Journal*, **2003**, 85, 3271-8	2.9	8
94	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
93	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
92	Numerical study of the entropy loss of dimerization and the folding thermodynamics of the GCN4 leucine zipper. *Biophysical Journal*, **2002**, 83, 2801-11	2.9	12
91	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
90	A Unified Approach to the Prediction of Protein Structure and Function. *Advances in Chemical Physics*, **2002**, 131-192		7
89	Computer simulations of protein folding with a small number of distance restraints.. *Acta Biochimica Polonica*, **2002**, 49, 683-692	2	2
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	Three-dimensional modeling of the I-TevI homing endonuclease catalytic domain, a GIY-YIG superfamily member, using NMR restraints and Monte Carlo dynamics. *Protein Engineering, Design and Selection*, **2001**, 14, 717-21	1.9	11

86	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
85	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
84	Computer simulations of the properties of the α, αC, and αD de novo designed helical proteins **2000**, 38, 17-28		6
83	Derivation of protein-specific pair potentials based on weak sequence fragment similarity **2000**, 38, 3-16		84
82	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
81	Helix-coil and beta sheet-coil transitions in a simplified, yet realistic protein model. *Macromolecular Theory and Simulations*, **2000**, 9, 523-533	1.5	12
80	Structural genomics and its importance for gene function analysis. *Nature Biotechnology*, **2000**, 18, 283-7	44.5	177
79	Protein Folding: Flexible Lattice Models. *Progress of Theoretical Physics Supplement*, **2000**, 138, 292-300		14
78	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
77	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
76	De novo predictions of the quaternary structure of leucine zippers and other coiled coils. *International Journal of Quantum Chemistry*, **1999**, 75, 165-176	2.1	4
75	Ab initio folding of proteins using restraints derived from evolutionary information. *Proteins: Structure, Function and Bioinformatics*, **1999**, 37, 177-185	4.2	89
74	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
73	A method for the improvement of threading-based protein models. *Proteins: Structure, Function and Bioinformatics*, **1999**, 37, 592-610	4.2	48
72	De novo simulations of the folding thermodynamics of the GCN4 leucine zipper. *Biophysical Journal*, **1999**, 77, 54-69	2.9	29
71	Dynamics and thermodynamics of beta-hairpin assembly: insights from various simulation techniques. *Biophysical Journal*, **1999**, 77, 2942-52	2.9	82
70	Ab initio folding of proteins using restraints derived from evolutionary information. *Proteins: Structure, Function and Bioinformatics*, **1999**, 37, 177-185	4.2	32
69	Assessing energy functions for flexible docking. *Journal of Computational Chemistry*, **1998**, 19, 1612-1622	3.5	132

68	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
67	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
66	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
65	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
64	Computer simulations of de novo designed helical proteins. *Biophysical Journal*, **1998**, 75, 92-105	2.9	22
63	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
62	Reduced protein models and their application to the protein folding problem. *Journal of Biomolecular Structure and Dynamics*, **1998**, 16, 381-96	3.6	15
61	Assembly of protein structure from sparse experimental data: An efficient Monte Carlo model **1998**, 32, 475		7
60	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
59	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
58	Derivation and testing of pair potentials for protein folding. When is the quasichemical approximation correct?. *Protein Science*, **1997**, 6, 676-88	6.3	159
57	Algorithm for rapid reconstruction of protein backbone from alpha carbon coordinates. *Journal of Computational Chemistry*, **1997**, 18, 80-85	3.5	31
56	A method for the prediction of surface □□turns and transglobular connections in small proteins **1997**, 27, 290-308		26
55	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
54	Collapse transitions in protein-like lattice polymers: The effect of sequence patterns. *Biopolymers*, **1997**, 42, 537-548	2.2	22
53	Monte Carlo lattice dynamics and the prediction of protein folds **1997**, 395-429		4
52	High coordination lattice models of protein structure, dynamics and thermodynamics. *Acta Biochimica Polonica*, **1997**, 44, 389-422	2	
51	Method for predicting the state of association of discretized protein models. Application to leucine zippers. *Biochemistry*, **1996**, 35, 955-67	3.2	20

50	Folding simulations and computer redesign of protein A three-helix bundle motifs. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 286-99	4.2	15
49	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
48	Does a backwardly read protein sequence have a unique native state?. *Protein Engineering, Design and Selection*, **1996**, 9, 5-14	1.9	50
47	Folding simulations and computer redesign of protein A three-helix bundle motifs. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 286-299	4.2	35
46	On the origin of the cooperativity of protein folding: Implications from model simulations **1996**, 26, 271		1
45	Are proteins ideal mixtures of amino acids? Analysis of energy parameter sets. *Protein Science*, **1995** , 4, 2107-17	6.3	131
44	Computer design of idealized motifs. *Journal of Chemical Physics*, **1995**, 103, 10286-10297	3.9	31
43	A reduced model of short range interactions in polypeptide chains. *Journal of Chemical Physics*, **1995**, 103, 4312-4323	3.9	33
42	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
41	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
40	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
39	Monte Carlo simulations of protein folding. I. Lattice model and interaction scheme. *Proteins: Structure, Function and Bioinformatics*, **1994**, 18, 338-52	4.2	257
38	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
37	Dynamics of star branched polymers in a matrix of linear chains a Monte Carlo study. *Macromolecular Theory and Simulations*, **1994**, 3, 715-729	1.5	20
36	Prediction of the folding pathways and structure of the GCN4 leucine zipper. *Journal of Molecular Biology*, **1994**, 237, 361-7	6.5	101
35	Regularities in interaction patterns of globular proteins. *Protein Engineering, Design and Selection*, **1993**, 6, 801-10	1.9	54
34	A lattice dynamics study of a Langmuir monolayer of monounsaturated fatty acids. *Journal of Chemical Physics*, **1993**, 98, 7581-7587	3.9	23
33	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

32	Lattice representations of globular proteins: How good are they?. *Journal of Computational Chemistry*, **1993**, 14, 1194-1202	3.5	77
31	A method for predicting protein structure from sequence. *Current Biology*, **1993**, 3, 414-23	6.3	73
30	De novo and inverse folding predictions of protein structure and dynamics. *Journal of Computer-Aided Molecular Design*, **1993**, 7, 397-438	4.2	69
29	Effect of double bonds on the dynamics of hydrocarbon chains. *Journal of Chemical Physics*, **1992**, 97, 1240-1249	3.9	32
28	Discretized model of proteins. I. Monte Carlo study of cooperativity in homopolypeptides. *Journal of Chemical Physics*, **1992**, 97, 9412-9426	3.9	105
27	Topology fingerprint approach to the inverse protein folding problem. *Journal of Molecular Biology*, **1992**, 227, 227-38	6.5	317
26	Static and dynamic properties of a new lattice model of polypeptide chains. *Journal of Chemical Physics*, **1991**, 94, 3978-3985	3.9	54
25	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
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