Robert L Jernigan

List of Publications by Year
in descending order

230	11,114	43973	35952
papers	citations	48 h-index	97 g-index

243	243	243	7120
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Using Surface Hydrophobicity Together with Empirical Potentials to Identify Proteinâ€“Protein Binding Sites: Application to the Interactions of E-cadherins. Methods in Molecular Biology, 2022, 2340, 41-50.	0.4	0
2	Protein Fluctuations in Response to Random External Forces. Applied Sciences (Switzerland), 2022, 12, 2344.	1.3	2
3	Coarse-graining protein structures into their dynamic communities with DCI, a dynamic community identifier. Bioinformatics, 2022, 38, 2727-2733.	1.8	2
4	Entropies Derived from the Packing Geometries within a Single Protein Structure. ACS Omega, 2022, 7, 20719-20730.	1.6	4
5	New amino acid substitution matrix brings sequence alignments into agreement with structure matches. Proteins: Structure, Function and Bioinformatics, 2021, 89, 671-682.	1.5	14
6	Large-scale multiple inference of collective dependence with applications to protein function. Annals of Applied Statistics, 2021, 15, .	0.5	2
7	Xyloglucan Xylosyltransferase 1 Displays Promiscuity Toward Donor Substrates During in Vitro Reactions. Plant and Cell Physiology, 2021, 62, 1890-1901.	1.5	7
8	Ligand Binding Introduces Significant Allosteric Shifts in the Locations of Protein Fluctuations. Frontiers in Molecular Biosciences, 2021, 8, 733148.	1.6	9
9	hdANM: a new comprehensive dynamics model for protein hinges. Biophysical Journal, 2021, 120, 4955-4965.	0.2	6
10	A Hybrid Levenbergâ€“Marquardt Algorithm on a Recursive Neural Network for Scoring Protein Models. Methods in Molecular Biology, 2021, 2190, 307-316.	0.4	1
11	Simulated Drug Efflux for the AbgT Family of Membrane Transporters. Journal of Chemical Information and Modeling, 2021, 61, 5673-5681.	2.5	1
12	Characterizing and Predicting Protein Hinges for Mechanistic Insight. Journal of Molecular Biology, 2020, 432, 508-522.	2.0	17
13	Entropy, Fluctuations, and Disordered Proteins. Linking between Sequence, Structure, and Disorder Information. Biophysical Journal, 2020, 118, 371a.	0.2	0
14	Using High Order Coevolution Correlations to Identify Sites for Compensating Mutations to Rescue Function. Biophysical Journal, 2020, 118, 532a-533a.	0.2	0
15	Using Sequence and Structure Information to Annotate Gene and Protein Function. Biophysical Journal, 2020, 118, 44a.	0.2	0
16	Broad Concepts from Polymers Applied to Protein Data. ACS Symposium Series, 2020, , 89-101.	0.5	0
17	Structural compliance: A new metric for protein flexibility. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1482-1492.	1.5	9
18	Structure and function of LCI1: a plasma membrane CO 2 channel in the Chlamydomonas CO 2 concentrating mechanism. Plant Journal, 2020, 102, 1107-1126.	2.8	17

#	Article	IF	Citations
19	Functional Annotation of Coding and Non-Coding RNA in Non-Model Organisms. Biophysical Journal, 2020, 118, 461a.	0.2	0
20	Using Alpha Shapes to Characterize Protein Packing and Capture the Multiscale Aspects of Allostery. Biophysical Journal, 2020, 118, 40a.	0.2	0
21	Computational Ways to Enhance Protein Inhibitor Design. Frontiers in Molecular Biosciences, 2020, 7, 607323.	1.6	2
22	Entropy, Fluctuations, and Disordered Proteins. Entropy, 2019, 21, 764.	1.1	5
23	Combinatorial biosynthesis and the basis for substrate promiscuity in class I diterpene synthases. Metabolic Engineering, 2019, 55, 44-58.	3.6	24
24	Coupling dynamics and evolutionary information with structure to identify protein regulatory and functional binding sites. Proteins: Structure, Function and Bioinformatics, 2019, 87, 850-868.	1.5	22
25	Characteristics of Protein Fold Space Exhibits Close Dependence on Domain Usage. Lecture Notes in Computer Science, 2019, , 356-369.	1.0	0
26	Understanding Membrane Transport Processes using ENM and MD Simulations. Biophysical Journal, 2019, 116, 347a.	0.2	0
27	Transport Pathways in Membrane Transporters. Biophysical Journal, 2018, 114, 207a.	0.2	0
28	Comparisons of Protein Dynamics from Experimental Structure Ensembles, Molecular Dynamics Ensembles, and Coarse-Grained Elastic Network Models. Journal of Physical Chemistry B, 2018, 122, 5409-5417.	1.2	25
29	Compensatory Mutations in Protein Sequences from Big-Data. Biophysical Journal, 2018, 114, 574a-575a.	0.2	0
30	Dynamic Communities in Proteins: Allosteric Hotspots and Functional Modules. Biophysical Journal, 2018, 114, 421a.	0.2	0
31	Protein dynamic communities from elastic network models align closely to the communities defined by molecular dynamics. PLoS ONE, 2018, 13, e0199225.	1.1	33
32	Profiling of the Exosomal Cargo of Bovine Milk Reveals the Presence of Immuneâ€•and Growthâ€•modulatory ncRNAs. FASEB Journal, 2018, 32, 747.25.	0.2	0
33	Knowledge-based entropies improve the identification of native protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2928-2933.	3.3	23
34	Altered dynamics upon oligomerization corresponds to key functional sites. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1422-1434.	1.5	12
35	Directional Force Originating from ATP Hydrolysis Drives the GroEL Conformational Change. Biophysical Journal, 2017, 112, 1561-1570.	0.2	22
36	E-Cadherin Functions as a Desmoglein Transporter that Facilitates Assembly of Nascent Desmosomes. Biophysical Journal, 2017, 112, 166a-167a.	0.2	1

#	Article	IF	Citations
37	Predicting Protein Secondary Structure Using Consensus Data Mining (CDM) Based on Empirical Statistics and Evolutionary Information. Methods in Molecular Biology, 2017, 1484, 35-44.	0.4	7
38	Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. PLoS Computational Biology, 2016, 12, e1004826.	1.5	40
39	Predicting Designability of Small Proteins from Graph Features of Contact Maps. Journal of Computational Biology, 2016, 23, 400-411.	0.8	6
40	Molecular determinants of cadherin ideal bond formation: Conformation-dependent unbinding on a multidimensional landscape. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5711-20.	3.3	32
41	Fold-specific sequence scoring improves protein sequence matching. BMC Bioinformatics, 2016, 17, 328.	1.2	6
42	Clusters of Structurally Similar MHC I HLA-A2 Molecules, Found with a New Method, Suggest Mechanisms of T-Cell Receptor Avidity. Biochemistry, 2016, 55, 167-185.	1.2	3
43	Ribosome Mechanics Informs about Mechanism. Journal of Molecular Biology, 2016, 428, 802-810.	2.0	24
44	REGULATORY RNA. , 2016, , .		0
45	Distributions of experimental protein structures on coarse-grained free energy landscapes. Journal of Chemical Physics, 2015, 143, 243153.	1.2	17
46	The Use of Experimental Structures to Model Protein Dynamics. Methods in Molecular Biology, 2015, 1215, 213-236.	0.4	10
47	Aldolases Utilize Different Oligomeric States To Preserve Their Functional Dynamics. Biochemistry, 2015, 54, 3543-3554.	1.2	12
48	ArcA Controls Metabolism, Chemotaxis, and Motility Contributing to the Pathogenicity of Avian Pathogenic Escherichia coli. Infection and Immunity, 2015, 83, 3545-3554.	1.0	41
49	Bridging between NMA and Elastic Network Models: Preserving All-Atom Accuracy in Coarse-Grained Models. PLoS Computational Biology, 2015, 11, e1004542.	1.5	27
50	An analysis of conformational changes upon RNA-protein binding. , 2014, , .		2
51	A Conserved Isoleucine Maintains the Inactive State of Bruton's Tyrosine Kinase. Journal of Molecular Biology, 2014, 426, 3656-3669.	2.0	10
52	Elastic network models capture the motions apparent within ensembles of RNA structures. Rna, 2014, 20, 792-804.	1.6	33
53	The critical role of the loops of triosephosphate isomerase for its oligomerization, dynamics, and functionality. Protein Science, 2014, 23, 213-228.	3.1	37
54	Computational and experimental characterization of RNA cubic nanoscaffolds. Methods, 2014, 67, 256-265.	1.9	55

#	Article	IF	Citations
55	Factors correlating with significant differences between X-ray structures of myoglobin. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 481-491.	2.5	13
56	Volumes and Surface Areas: Geometries and Scaling Relationships between Coarse- Grained and Atomic Structures. Current Pharmaceutical Design, 2014, 20, 1208-1222.	0.9	3
57	Distributions of amino acids suggest that certain residue types more effectively determine protein secondary structure. Journal of Molecular Modeling, 2013, 19, 4337-4348.	0.8	4
58	Incorporating Protein Topology Information in Similarity Matrices for Improved Sequence Matching (A Fold-Specific Scoring System). Biophysical Journal, 2013, 104, 508a.	0.2	0
59	New Methods to Improve Protein Structure Prediction and Refinement. Biophysical Journal, 2013, 104, 229a.	0.2	1
60	Modeling Complex between FBA and TIM: Functional Motions of FBA and TIM are Preserved in their Complex. Biophysical Journal, 2013, 104, 402a.	0.2	0
61	Coarse-Grained Computational Characterization of RNA Nanocube Flexibility Correlates with Experiments. Biophysical Journal, 2013, 104, 16a.	0.2	0
62	Revealing Rotational Modes of Functionalized Gold Nanorods on Live Cell Membranes. Small, 2013, 9, 785-792.	5.2	33
63	Coarse Grained Normal Mode Analysis vs. Refined Gaussian Network Model for Protein Residue-Level Structural Fluctuations. Bulletin of Mathematical Biology, 2013, 75, 124-160.	0.9	31
64	A Computational Investigation on the Connection between Dynamics Properties of Ribosomal Proteins and Ribosome Assembly. PLoS Computational Biology, 2012, 8, e1002530.	1.5	22
65	Elastic network normal modes provide a basis for protein structure refinement. Journal of Chemical Physics, 2012, 136, 195101.	1.2	17
66	P.R.E.S.S. â€" AN R-PACKAGE FOR EXPLORING RESIDUAL-LEVEL PROTEIN STRUCTURAL STATISTICS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1242007.	0.3	3
67	The importance of slow motions for protein functional loops. Physical Biology, 2012, 9, 014001.	0.8	27
68	Fast learning optimized prediction methodology (FLOPRED) for protein secondary structure prediction. Journal of Molecular Modeling, 2012, 18, 4275-4289.	0.8	18
69	Diversity of Sequences Folding to Highly and Poorly Designable Structures. Biophysical Journal, 2012, 102, 456a.	0.2	1
70	Combining Statistical Potentials with Dynamics-Based Entropies Improves Selection from Protein Decoys and Docking Poses. Journal of Physical Chemistry B, 2012, 116, 6725-6731.	1.2	24
71	Computing Entropies for Binding and Refinement of Protein Structures. Biophysical Journal, 2012, 102, 25a.	0.2	0
72	ANM Normal Modes Show the Directions for Protein Structure Refinement. Biophysical Journal, 2012, 102, 25a.	0.2	1

#	Article	IF	Citations
73	Linkage Between Dynamics and Assembly of Ribosomal Proteins. Biophysical Journal, 2012, 102, 450a.	0.2	0
74	Protein Loop Dynamics Are Complex and Depend on the Motions of the Whole Protein. Entropy, 2012, 14, 687-700.	1.1	10
75	How noise in force fields can affect the structural refinement of protein models?. Proteins: Structure, Function and Bioinformatics, 2012, 80, 335-341.	1.5	6
76	Design and Modeling of RNA Nanostructures with Flexible Building Blocks. Biophysical Journal, 2011, 100, 472a.	0.2	0
77	Analysis of protein dynamics using local-DME calculations. International Journal of Bioinformatics Research and Applications, 2011, 7, 146.	0.1	2
78	Crystal structure of the CusBA heavy-metal efflux complex of Escherichia coli. Nature, 2011, 470, 558-562.	13.7	201
79	Statistical measures on residue-level protein structural properties. Journal of Structural and Functional Genomics, 2011, 12, 119-136.	1.2	7
80	Free energies for coarse-grained proteins by integrating multibody statistical contact potentials with entropies from elastic network models. Journal of Structural and Functional Genomics, 2011, 12, 137-147.	1.2	16
81	MAVENs: Motion analysis and visualization of elastic networks and structural ensembles. BMC Bioinformatics, 2011, 12, 264.	1.2	37
82	Multibody coarseâ€grained potentials for native structure recognition and quality assessment of protein models. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1923-1929.	1.5	38
83	Exploration of the relationship between topology and designability of conformations. Journal of Chemical Physics, 2011, 134, 235101.	1.2	13
84	P.R.E.S.S. — An R-package for exploring residual-level protein structural statistics. , 2011, , .		0
85	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.	3.3	47
86	Statistical Contact Potentials in Protein Coarse-Grained Modeling: From Pair to Multi-body Potentials. , 2011, , 127-157.		10
87	Particle Swarm Optimization: A Powerful Family of Stochastic Optimizers. Analysis, Design and Application to Inverse Modelling. Lecture Notes in Computer Science, 2011, , 1-8.	1.0	4
88	Immunoglobulin Structure Exhibits Control over CDR Motion. Immunome Research, 2011, 7, .	0.1	5
89	Potentials 'R'Us web-server for protein energy estimations with coarse-grained knowledge-based potentials. BMC Bioinformatics, 2010, 11, 92.	1.2	31
90	Structural interpretation of protein-protein interaction network. BMC Structural Biology, 2010, 10, S4.	2.3	10

#	Article	IF	Citations
91	Crystal structures of the CusA efflux pump suggest methionine-mediated metal transport. Nature, 2010, 467, 484-488.	13.7	223
92	Immunological implications of a structural analysis of two different porcine IL1Î² proteins expressed in macrophages and embryos. , 2010, , .		2
93	Immunoglobulin functional motions and their effects on the complementarity determining regions. , 2010, , .		0
94	Protein Secondary Structure Prediction Using Knowledge-Based Potentials and An Ensemble of Classifiers. Biophysical Journal, 2010, 98, 52a.	0.2	0
95	Diversity of Function-Related Conformational Changes in Proteins: Coordinate Uncertainty, Fragment Rigidity, and Stability. Biochemistry, 2010, 49, 5683-5704.	1.2	14
96	Models To Approximate the Motions of Protein Loops. Journal of Chemical Theory and Computation, 2010, 6, 3249-3258.	2.3	1
97	Short paths in protein structure space originate in graph structure. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, E137; author reply E138.	3.3	3
98	Protein elastic network models and the ranges of cooperativity. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12347-12352.	3.3	223
99	Distance matrix-based approach to protein structure prediction. Journal of Structural and Functional Genomics, 2009, 10, 67-81.	1.2	45
100	Iterative clusterâ€NMA: A tool for generating conformational transitions in proteins. Proteins: Structure, Function and Bioinformatics, 2009, 74, 760-776.	1.5	36
101	Collective dynamics of the ribosomal tunnel revealed by elastic network modeling. Proteins: Structure, Function and Bioinformatics, 2009, 75, 837-845.	1.5	42
102	Comparisons of experimental and computed protein anisotropic temperature factors. Proteins: Structure, Function and Bioinformatics, 2009, 76, 164-175.	1.5	38
103	The energy profiles of atomic conformational transition intermediates of adenylate kinase. Proteins: Structure, Function and Bioinformatics, 2009, 77, 551-558.	1.5	39
104	Protein flexibility: coordinate uncertainties and interpretation of structural differences. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1140-1161.	2.5	21
105	Focused Functional Dynamics of Supramolecules by Use of a Mixed-Resolution Elastic Network Model. Biophysical Journal, 2009, 97, 1178-1187.	0.2	46
106	PRTAD: A database for protein residue torsion angle distributions. International Journal of Data Mining and Bioinformatics, 2009, 3, 469.	0.1	6
107	Refinement of under-determined loops of Human Prion Protein by database-derived distance constraints. International Journal of Data Mining and Bioinformatics, 2009, 3, 454.	0.1	4
108	Data Mining for Protein Secondary Structure Prediction. Structure and Bonding, 2009, , 135-167.	1.0	3

#	Article	IF	Citations
109	Characterization of Proteinâ€“Protein Interfaces. Protein Journal, 2008, 27, 59-70.	0.7	139
110	Predicting the order in which contacts are broken during single molecule protein stretching experiments. Proteins: Structure, Function and Bioinformatics, 2008, 71, 45-60.	1.5	26
111	Orientational distributions of contact clusters in proteins closely resemble those of an icosahedron. Proteins: Structure, Function and Bioinformatics, 2008, 73, 730-741.	1.5	7
112	Use of machine learning algorithms to classify binary protein sequences as highly-designable or poorly-designable. BMC Bioinformatics, 2008, 9, 487.	1.2	4
113	Close Correspondence between the Motions from Principal Component Analysis of Multiple HIV-1 ProteaseÂStructures and Elastic Network Modes. Structure, 2008, 16, 321-330.	1.6	157
114	Predicting the Complex Structure and Functional Motions of the Outer Membrane Transporter and Signal Transducer FecA. Biophysical Journal, 2008, 94, 2482-2491.	0.2	11
115	Effects of Protein Subunits Removal on the Computed Motions of Partial 30S Structures of the Ribosome. Journal of Chemical Theory and Computation, 2008, 4, 1757-1767.	2.3	26
116	KNOWLEDGE-BASED VERSUS EXPERIMENTALLY ACQUIRED DISTANCE AND ANGLE CONSTRAINTS FOR NMR STRUCTURE REFINEMENT. Journal of Bioinformatics and Computational Biology, 2008, 06, 283-300.	0.3	3
117	The ribosome structure controls and directs mRNA entry, translocation and exit dynamics. Physical Biology, 2008, 5, 046005.	0.8	61
118	Elastic Network Models of Coarse-Grained Proteins Are Effective for Studying the Structural Control Exerted over Their Dynamics. , 2008, , 237-254.		3
119	Packing Regularities in Biological Structures Relate to Their Dynamics. , 2007, 350, 251-276.		19
120	PIDD: database for Protein Inter-atomic Distance Distributions. Nucleic Acids Research, 2007, 35, D202-D207.	6.5	13
121	Shape-dependent designability studies of lattice proteins. Journal of Physics Condensed Matter, 2007, 19, 285220.	0.7	5
122	Generation and enumeration of compact conformations on the two-dimensional triangular and three-dimensional fcc lattices. Journal of Chemical Physics, 2007, 127, 044101.	1.2	9
123	RNABindR: a server for analyzing and predicting RNA-binding sites in proteins. Nucleic Acids Research, 2007, 35, W578-W584.	6.5	177
124	Consensus Data Mining (CDM) Protein Secondary Structure Prediction Server: Combining GOR V and Fragment Database Mining (FDM). Bioinformatics, 2007, 23, 2628-2630.	1.8	30
125	vGNM: A Better Model for Understanding the Dynamics of Proteins in Crystals. Journal of Molecular Biology, 2007, 369, 880-893.	2.0	70
126	Comparison of experimental and computed protein anisotropic temperature factors. , 2007, , .		3

#	Article	IF	Citations
127	Refinement of under-determined loops of human prion protein by database-derived distance constraints. , 2007, , .		1
128	PRTAD: A database for protein residue torsion angle distributions. , 2007, , .		0
129	Prediction of Side Chain Orientations in Proteins by Statistical Machine Learning Methods. Journal of Biomolecular Structure and Dynamics, 2007, 25, 275-287.	2.0	4
130	How Well Can We Understand Large-Scale Protein Motions Using Normal Modes of Elastic Network Models?. Biophysical Journal, 2007, 93, 920-929.	0.2	189
131	Refinement of NMR-determined protein structures with database derived mean-force potentials. Proteins: Structure, Function and Bioinformatics, 2007, 68, 232-242.	1.5	23
132	Four-body contact potentials derived from two protein datasets to discriminate native structures from decoys. Proteins: Structure, Function and Bioinformatics, 2007, 68, 57-66.	1.5	73
133	Ideal amino acid exchange forms for approximating substitution matrices. Proteins: Structure, Function and Bioinformatics, 2007, 69, 379-393.	1.5	11
134	Configurational distributions for finite chain molecules. Journal of Polymer Science Part C Polymer Symposia, 2007, 25, 69-72.	0.1	0
135	The Extent of Cooperativity of Protein Motions Observed with Elastic Network Models Is Similar for Atomic and Coarser-Grained Models. Journal of Chemical Theory and Computation, 2006, 2, 696-704.	2.3	84
136	Loop Motions of Triosephosphate Isomerase Observed with Elastic Networks. Biochemistry, 2006, 45, 1173-1182.	1.2	52
137	Prediction of RNA binding sites in proteins from amino acid sequence. Rna, 2006, 12, 1450-1462.	1.6	162
138	An enhanced elastic network model to represent the motions of domain-swapped proteins. Proteins: Structure, Function and Bioinformatics, 2006, 63, 197-209.	1.5	66
139	A Consensus Data Mining secondary structure prediction by combining GOR V and Fragment Database Mining. Protein Science, 2006, 15, 2499-2506.	3.1	22
140	A DNA-Centric Look at Protein-DNA Complexes. Structure, 2006, 14, 1341-1342.	1.6	4
141	Predicting DNA-binding sites of proteins from amino acid sequence. BMC Bioinformatics, 2006, 7, 262.	1.2	141
142	Functional clustering of yeast proteins from the protein-protein interaction network. BMC Bioinformatics, 2006, 7, 355.	1.2	40
143	Identifying interaction sites in "recalcitrant" proteins: predicted protein and RNA binding sites in rev proteins of HIV-1 and EIAV agree with experimental data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 415-26.	0.7	8
144	IDENTIFYING INTERACTION SITES IN â€œRECALCITRANTâ€•PROTEINS: PREDICTED PROTEIN AND RNA BINDING SITES IN REV PROTEINS OF HIV-1 AND EIAV AGREE WITH EXPERIMENTAL DATA. , 2005, , .		7

#	Article	IF	Citations
145	Prediction of protein secondary structure by mining structural fragment database. Polymer, 2005, 46, 4314-4321.	1.8	28
146	Inferring ideal amino acid interaction forms from statistical protein contact potentials. Proteins: Structure, Function and Bioinformatics, 2005, 59, 49-57.	1.5	66
147	How do side chains orient globally in protein structures?. Proteins: Structure, Function and Bioinformatics, 2005, 61, 513-522.	1.5	10
148	GOR V server for protein secondary structure prediction. Bioinformatics, 2005, 21, 2787-2788.	1.8	179
149	How effective for fold recognition is a potential of mean force that includes relative orientations between contacting residues in proteins?. Journal of Chemical Physics, 2005, 122, 024901.	1.2	57
150	REFINEMENT OF NMR-DETERMINED PROTEIN STRUCTURES WITH DATABASE DERIVED DISTANCE CONSTRAINTS. Journal of Bioinformatics and Computational Biology, 2005, 03, 1315-1329.	0.3	27
151	Protein Promiscuity: Drug Resistance and Native Functionsâ€"HIV-1 Case. Journal of Biomolecular Structure and Dynamics, 2005, 22, 615-624.	2.0	22
152	Rigid-Cluster Models of Conformational Transitions in Macromolecular Machines and Assemblies. Biophysical Journal, 2005, 89, 43-55.	0.2	79
153	Comparison of tRNA Motions in the Free and Ribosomal Bound Structures. Biophysical Journal, 2005, 89, 3399-3409.	0.2	54
154	Formation of an intramolecular triple-stranded DNA structure monitored by fluorescence of 2-aminopurine or 6-methylisoxanthopterin. Nucleic Acids Research, 2004, 32, 432-440.	6.5	27
155	Predicting binding sites of hydrolase-inhibitor complexes by combining several methods. BMC Bioinformatics, 2004, 5, 205.	1.2	27
156	Mixed levels of coarse-graining of large proteins using elastic network model succeeds in extracting the slowest motions. Polymer, 2004, 45, 649-657.	1.8	55
157	Myosin flexibility: Structural domains and collective vibrations. Proteins: Structure, Function and Bioinformatics, 2004, 54, 384-393.	1.5	50
158	The transfer matrix method for lattice proteinsâ€"an application with cooperative interactions. Polymer, 2004, 45, 707-716.	1.8	8
159	Molecular Mechanism of Domain Swapping in Proteins: An Analysis of Slower Motions. Biophysical Journal, 2004, 86, 3846-3854.	0.2	50
160	Global ribosome motions revealed with elastic network model. Journal of Structural Biology, 2004, 147, 302-314.	1.3	284
161	Proteinâ€"DNA Hydrophobic Recognition in the Minor Groove is Facilitated by Sugar Switching. Journal of Molecular Biology, 2004, 337, 65-76.	2.0	77
162	The origin and extent of coarse-grained regularities in protein internal packing. Proteins: Structure, Function and Bioinformatics, 2003, 53, 56-67.	1.5	33

#	Article	IF	Citations
163	Functional motions can be extracted from on-lattice construction of protein structures. Proteins: Structure, Function and Bioinformatics, 2003, 53, 174-181.	1.5	53
164	An elastic network model of HK97 capsid maturation. Journal of Structural Biology, 2003, 143, 107-117.	1.3	83
165	Residue packing in proteins: Uniform distribution on a coarse-grained scale. Journal of Chemical Physics, 2002, 116, 2269-2276.	1.2	38
166	Loop Folds in Proteins and Evolutionary Conservation of Folding Nuclei. Journal of Biomolecular Structure and Dynamics, 2002, 20, 323-325.	2.0	6
167	A New Class of Molecular Shape Descriptors. 1. Theory and Properties. Journal of Chemical Information and Computer Sciences, 2002, 42, 259-273.	2.8	22
168	Efficient Generation of Feasible Pathways for Protein Conformational Transitions. Biophysical Journal, 2002, 83, 1620-1630.	0.2	163
169	Relating Molecular Flexibility to Function: A Case Study of Tubulin. Biophysical Journal, 2002, 83, 663-680.	0.2	143
170	Dynamics of large proteins through hierarchical levels of coarse-grained structures. Journal of Computational Chemistry, 2002, 23, 119-127.	1.5	224
171	Identifying a Folding Nucleus for the Lysozyme/Î±-Lactalbumin Family from Sequence Conservation Clusters. Journal of Molecular Evolution, 2002, 54, 425-436.	0.8	21
172	Important fluctuation dynamics of large protein structures are preserved upon coarse-grained renormalization. International Journal of Quantum Chemistry, 2002, 90, 822-837.	1.0	23
173	Combining the GOR V algorithm with evolutionary information for protein secondary structure prediction from amino acid sequence. Proteins: Structure, Function and Bioinformatics, 2002, 49, 154-166.	1.5	135
174	Long- and short-range interactions in native protein structures are consistent/minimally frustrated in sequence space. Proteins: Structure, Function and Bioinformatics, 2002, 50, 35-43.	1.5	20
175	Protein secondary structure prediction based on the GOR algorithm incorporating multiple sequence alignment information. Polymer, 2002, 43, 441-449.	1.8	25
176	Residue coordination in proteins conforms to the closest packing of spheres. Polymer, 2002, 43, 451-459.	1.8	34
177	Elastic models of conformational transitions in macromolecules. Journal of Molecular Graphics and Modelling, 2002, 21, 151-160.	1.3	117
178	Identifying sequenceâ€“structure pairs undetected by sequence alignments. Protein Engineering, Design and Selection, 2000, 13, 459-475.	1.0	25
179	Contacts between segments in the random-flight model of polymer chains. Computational and Theoretical Polymer Science, 1999, 9, 285-294.	1.1	4
180	Self-consistent estimation of inter-residue protein contact energies based on an equilibrium mixture approximation of residues. , 1999, 34, 49-68.		159

#	Article	IF	Citations
181	Evaluation of short-range interactions as secondary structure energies for protein fold and sequence recognition. Proteins: Structure, Function and Bioinformatics, 1999, 36, 347-356.	1.5	35
182	An empirical energy potential with a reference state for protein fold and sequence recognition. , 1999, 36, 357-369.		93
183	Cooperative Fluctuations and Subunit Communication in Tryptophan Synthaseâ€. Biochemistry, 1999, 38, 3478-3490.	1.2	94
184	Collective Motions in HIV-1 Reverse Transcriptase: Examination of Flexibility and Enzyme Function. Journal of Molecular Biology, 1999, 285, 1023-1037.	2.0	199
185	Selfâ€consistent estimation of interâ€residue protein contact energies based on an equilibrium mixture approximation of residues. Proteins: Structure, Function and Bioinformatics, 1999, 34, 49-68.	1.5	2
186	Evaluation of short-range interactions as secondary structure energies for protein fold and sequence recognition. , 1999, 36, 347.		2
187	Identification of kinetically hot residues in proteins. Protein Science, 1998, 7, 2522-2532.	3.1	114
188	A role for CHâ€¦O interactions in protein-DNA recognition. Journal of Molecular Biology, 1998, 277, 1129-1140.	2.0	171
189	Vibrational dynamics of transfer RNAs: comparison of the free and synthetase-bound forms 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1998, 281, 871-884.	2.0	126
190	Transfer matrix method for enumeration and generation of compact self-avoiding walks. I. Square lattices. Journal of Chemical Physics, 1998, 109, 5134-5146.	1.2	28
191	RNA base-amino acid interaction strengths derived from structures and sequences. Nucleic Acids Research, 1997, 25, 2562-2565.	6.5	24
192	Efficient Method To Count and Generate Compact Protein Lattice Conformations. Macromolecules, 1997, 30, 6691-6694.	2.2	19
193	Computer generation and enumeration of compact self-avoiding walks within simple geometries on lattices. Computational and Theoretical Polymer Science, 1997, 7, 163-173.	1.1	24
194	Understanding the recognition of protein structural classes by amino acid composition. Proteins: Structure, Function and Bioinformatics, 1997, 29, 172-185.	1.5	120
195	Residue â€“ Residue Potentials with a Favorable Contact Pair Term and an Unfavorable High Packing Density Term, for Simulation and Threading. Journal of Molecular Biology, 1996, 256, 623-644.	2.0	1,140
196	Amino Acid Pair Interchanges at Spatially Conserved Locations. Journal of Molecular Biology, 1996, 256, 924-938.	2.0	35
197	Structure-derived potentials and protein simulations. Current Opinion in Structural Biology, 1996, 6, 195-209.	2.6	271
198	Coordination geometry of nonbonded residues in globular proteins. Folding & Design, 1996, 1, 357-370.	4.5	66

#	Article	IF	Citations
199	A small modified hammerhead ribozyme and its conformational characteristics determined by mutagenesis and lattice calculation. Nucleic Acids Research, 1995, 23, 3531-3538.	6.5	9
200	Consistences of individual DNA baseâ€"amino acid interactions in structures and sequences. Nucleic Acids Research, 1995, 23, 4707-4711.	6.5	45
201	Probing the Structure of a Putative Intermediate in Homologous Recombination: The Third Strand in the Parallel DNA Triplex is in Contact with the Major Groove of the Duplex. Journal of Molecular Biology, 1995, 247, 874-889.	2.0	39
202	Protein stability for single substitution mutants and the extent of local compactness in the denatured state. Protein Engineering, Design and Selection, 1994, 7, 1209-1220.	1.0	60
203	Conformations of t-RNA: Base Pairing and Stacking. Journal of Biomolecular Structure and Dynamics, 1994, 12, 145-161.	2.0	5
204	Characterization of interactions and metal ion binding sites in proteins. Current Opinion in Structural Biology, 1994, 4, 256-263.	2.6	86
205	Influence of Fluctuations on DNA Curvature. Journal of Molecular Biology, 1993, 232, 530-554.	2.0	141
206	A new substitution matrix for protein sequence searches based on contact frequencies in protein structures. Protein Engineering, Design and Selection, 1993, 6, 267-278.	1.0	70
207	Conformational Analysis of Receptor Selective Tachykinin Analogs: Senktide and Septide. Journal of Biomolecular Structure and Dynamics, 1992, 10, 429-439.	2.0	7
208	Protein folds. Current Opinion in Structural Biology, 1992, 2, 248-256.	2.6	31
209	Configurational statistics of methyl vinyl ether-maleic anhydride copolymer: selection of important atomic interactions and conformations. Macromolecules, 1991, 24, 731-739.	2.2	5
210	Compact protein conformations. , 1991, , 346-351.		1
211	Conformational Analysis of the Tachykinins in Solution: Substance P and Physalaemin. Journal of Biomolecular Structure and Dynamics, 1990, 8, 687-707.	2.0	48
212	Conformations of folded proteins in restricted spaces. Biochemistry, 1990, 29, 3287-3294.	1.2	233
213	Experimental and Theoretical Protein Folding. Journal of Biomolecular Structure and Dynamics, 1989, 6, 1039-1043.	2.0	0
214	Strong Patterns in Homooligomer Tracts Occurrences in Non-Coding and in Potential Regulatory Sites in Eukaryotic Genomes. Journal of Biomolecular Structure and Dynamics, 1989, 7, 707-722.	2.0	8
215	Distinct patterns in homooligomer tract sequence context in prokaryotic and eukaryotic DNA. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1989, 1008, 329-338.	2.4	4
216	Helix stability in prokaryotic promoter regions. Biochemistry, 1988, 27, 5179-5188.	1.2	31

#	Article	IF	Citations
217	Sequence Context of Oligomer Tracts in Eukaryotic DNA: Biological and Conformational Implications. Journal of Biomolecular Structure and Dynamics, 1988, 6, 543-562.	2.0	9
218	Relationship Between Curved DNA Conformations and Slow Gel Migration. Journal of Biomolecular Structure and Dynamics, 1987, 4, 561-567.	2.0	18
219	Hydrophobic Interactions in the Major Groove Can Influence DNA Local Structure. Journal of Biomolecular Structure and Dynamics, 1986, 4, 41-48.	2.0	42
220	Estimation of effective interresidue contact energies from protein crystal structures: quasi-chemical approximation. Macromolecules, 1985, 18, 534-552.	2.2	1,489
221	Equilibrium folding pathways for model proteins. Journal of Statistical Physics, 1983, 30, 549-559.	0.5	2
222	Equilibrium folding-unfolding pathways of model proteins: Effect of myoglobin-heme contacts. Biopolymers, 1983, 22, 79-85.	1.2	6
223	Most probable intermediates in protein folding-unfolding with a noninteracting globule-coil model. Biochemistry, 1982, 21, 5203-5213.	1.2	15
224	DNA conformational kinetics. Biopolymers, 1979, 18, 83-100.	1.2	1
225	Composite predictions of secondary structures oflac repressor. Biopolymers, 1979, 18, 2625-2643.	1.2	18
226	Conformational Energy Minimization in the Approximation of Limited Range Interactions. Macromolecules, 1979, 12, 1156-1159.	2.2	9
227	Prediction of ?-sheets in immunoglobulin chains. Comparison of various methods and an expanded 20 ï¿½ 20 table for evaluation of the effects of nearest-neighbors on conformations of middle amino acids in proteins. Biopolymers, 1978, 17, 555-572.	1.2	10
228	Missing Magnitudes. Nature, 1973, 245, 59-60.	13.7	5
229	Protein Actions. , 0, , .		10
230	PACKMAN-Molecule: Python Toolbox for Structural Bioinformatics. Bioinformatics Advances, 0, , .	0.9	2