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	Estimation of effective interresidue contact energies from protein crystal structures: quasi-chemical approximation. Macromolecules, 1985, 18, 534-552.	2.2	1,489
2	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
3	Global ribosome motions revealed with elastic network model. Journal of Structural Biology, 2004, 147, 302-314.	1.3	284
4	Structure-derived potentials and protein simulations. Current Opinion in Structural Biology, 1996, 6, 195-209.	2.6	271
5	Conformations of folded proteins in restricted spaces. Biochemistry, 1990, 29, 3287-3294.	1.2	233
6	Dynamics of large proteins through hierarchical levels of coarse-grained structures. Journal of Computational Chemistry, 2002, 23, 119-127.	1.5	224
7	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
8	Crystal structures of the CusA efflux pump suggest methionine-mediated metal transport. Nature, 2010, 467, 484-488.	13.7	223
9	Crystal structure of the CusBA heavy-metal efflux complex of Escherichia coli. Nature, 2011, 470, 558-562.	13.7	201
10	Collective Motions in HIV-1 Reverse Transcriptase: Examination of Flexibility and Enzyme Function. Journal of Molecular Biology, 1999, 285, 1023-1037.	2.0	199
11	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
12	GOR V server for protein secondary structure prediction. Bioinformatics, 2005, 21, 2787-2788.	1.8	179
13	RNABindR: a server for analyzing and predicting RNA-binding sites in proteins. Nucleic Acids Research, 2007, 35, W578-W584.	6.5	177
14	A role for CHâ€¦O interactions in protein-DNA recognition. Journal of Molecular Biology, 1998, 277, 1129-1140.	2.0	171
15	Efficient Generation of Feasible Pathways for Protein Conformational Transitions. Biophysical Journal, 2002, 83, 1620-1630.	0.2	163
16	Prediction of RNA binding sites in proteins from amino acid sequence. Rna, 2006, 12, 1450-1462.	1.6	162
17	Self-consistent estimation of inter-residue protein contact energies based on an equilibrium mixture approximation of residues. , 1999, 34, 49-68.		159
18	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

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19	Relating Molecular Flexibility to Function: A Case Study of Tubulin. Biophysical Journal, 2002, 83, 663-680.	0.2	143
20	Influence of Fluctuations on DNA Curvature. Journal of Molecular Biology, 1993, 232, 530-554.	2.0	141
21	Predicting DNA-binding sites of proteins from amino acid sequence. BMC Bioinformatics, 2006, 7, 262.	1.2	141
22	Characterization of Proteinâ€“Protein Interfaces. Protein Journal, 2008, 27, 59-70.	0.7	139
23	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
24	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
25	Understanding the recognition of protein structural classes by amino acid composition. Proteins: Structure, Function and Bioinformatics, 1997, 29, 172-185.	1.5	120
26	Elastic models of conformational transitions in macromolecules. Journal of Molecular Graphics and Modelling, 2002, 21, 151-160.	1.3	117
27	Identification of kinetically hot residues in proteins. Protein Science, 1998, 7, 2522-2532.	3.1	114
28	Cooperative Fluctuations and Subunit Communication in Tryptophan Synthaseâ€. Biochemistry, 1999, 38, 3478-3490.	1.2	94
29	An empirical energy potential with a reference state for protein fold and sequence recognition. , 1999, 36, 357-369.		93
30	Characterization of interactions and metal ion binding sites in proteins. Current Opinion in Structural Biology, 1994, 4, 256-263.	2.6	86
31	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
32	An elastic network model of HK97 capsid maturation. Journal of Structural Biology, 2003, 143, 107-117.	1.3	83
33	Rigid-Cluster Models of Conformational Transitions in Macromolecular Machines and Assemblies. Biophysical Journal, 2005, 89, 43-55.	0.2	79
34	Proteinâ€“DNA Hydrophobic Recognition in the Minor Groove is Facilitated by Sugar Switching. Journal of Molecular Biology, 2004, 337, 65-76.	2.0	77
35	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
36	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

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37	vGNM: A Better Model for Understanding the Dynamics of Proteins in Crystals. Journal of Molecular Biology, 2007, 369, 880-893.	2.0	70
38	Coordination geometry of nonbonded residues in globular proteins. Folding & Design, 1996, 1, 357-370.	4.5	66
39	Inferring ideal amino acid interaction forms from statistical protein contact potentials. Proteins: Structure, Function and Bioinformatics, 2005, 59, 49-57.	1.5	66
40	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
41	The ribosome structure controls and directs mRNA entry, translocation and exit dynamics. Physical Biology, 2008, 5, 046005.	0.8	61
42	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
43	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
44	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
45	Computational and experimental characterization of RNA cubic nanoscaffolds. Methods, 2014, 67, 256-265.	1.9	55
46	Comparison of tRNA Motions in the Free and Ribosomal Bound Structures. Biophysical Journal, 2005, 89, 3399-3409.	0.2	54
47	Functional motions can be extracted from on-lattice construction of protein structures. Proteins: Structure, Function and Bioinformatics, 2003, 53, 174-181.	1.5	53
48	Loop Motions of Triosephosphate Isomerase Observed with Elastic Networks. Biochemistry, 2006, 45, 1173-1182.	1.2	52
49	Myosin flexibility: Structural domains and collective vibrations. Proteins: Structure, Function and Bioinformatics, 2004, 54, 384-393.	1.5	50
50	Molecular Mechanism of Domain Swapping in Proteins: An Analysis of Slower Motions. Biophysical Journal, 2004, 86, 3846-3854.	0.2	50
51	Conformational Analysis of the Tachykinins in Solution: Substance P and Physalaemin. Journal of Biomolecular Structure and Dynamics, 1990, 8, 687-707.	2.0	48
52	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
53	Focused Functional Dynamics of Supramolecules by Use of a Mixed-Resolution Elastic Network Model. Biophysical Journal, 2009, 97, 1178-1187.	0.2	46
54	Consistences of individual DNA baseâ€"amino acid interactions in structures and sequences. Nucleic Acids Research, 1995, 23, 4707-4711.	6.5	45

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55	Distance matrix-based approach to protein structure prediction. Journal of Structural and Functional Genomics, 2009, 10, 67-81.	1.2	45
56	Hydrophobic Interactions in the Major Groove Can Influence DNA Local Structure. Journal of Biomolecular Structure and Dynamics, 1986, 4, 41-48.	2.0	42
57	Collective dynamics of the ribosomal tunnel revealed by elastic network modeling. Proteins: Structure, Function and Bioinformatics, 2009, 75, 837-845.	1.5	42
58	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
59	Functional clustering of yeast proteins from the protein-protein interaction network. BMC Bioinformatics, 2006, 7, 355.	1.2	40
60	Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. PLoS Computational Biology, 2016, 12, e1004826.	1.5	40
61	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
62	The energy profiles of atomic conformational transition intermediates of adenylate kinase. Proteins: Structure, Function and Bioinformatics, 2009, 77, 551-558.	1.5	39
63	Residue packing in proteins: Uniform distribution on a coarse-grained scale. Journal of Chemical Physics, 2002, 116, 2269-2276.	1.2	38
64	Comparisons of experimental and computed protein anisotropic temperature factors. Proteins: Structure, Function and Bioinformatics, 2009, 76, 164-175.	1.5	38
65	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
66	MAVENs: Motion analysis and visualization of elastic networks and structural ensembles. BMC Bioinformatics, 2011, 12, 264.	1.2	37
67	The critical role of the loops of triosephosphate isomerase for its oligomerization, dynamics, and functionality. Protein Science, 2014, 23, 213-228.	3.1	37
68	Iterative clusterâ€NMA: A tool for generating conformational transitions in proteins. Proteins: Structure, Function and Bioinformatics, 2009, 74, 760-776.	1.5	36
69	Amino Acid Pair Interchanges at Spatially Conserved Locations. Journal of Molecular Biology, 1996, 256, 924-938.	2.0	35
70	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
71	Residue coordination in proteins conforms to the closest packing of spheres. Polymer, 2002, 43, 451-459.	1.8	34
72	The origin and extent of coarse-grained regularities in protein internal packing. Proteins: Structure, Function and Bioinformatics, 2003, 53, 56-67.	1.5	33

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73	Revealing Rotational Modes of Functionalized Gold Nanorods on Live Cell Membranes. Small, 2013, 9, 785-792.	5.2	33
74	Elastic network models capture the motions apparent within ensembles of RNA structures. Rna, 2014, 20, 792-804.	1.6	33
75	Protein dynamic communities from elastic network models align closely to the communities defined by molecular dynamics. PLoS ONE, 2018, 13, e0199225.	1.1	33
76	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
77	Helix stability in prokaryotic promoter regions. Biochemistry, 1988, 27, 5179-5188.	1.2	31
78	Protein folds. Current Opinion in Structural Biology, 1992, 2, 248-256.	2.6	31
79	Potentials 'R'Us web-server for protein energy estimations with coarse-grained knowledge-based potentials. BMC Bioinformatics, 2010, 11, 92.	1.2	31
80	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
81	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
82	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
83	Prediction of protein secondary structure by mining structural fragment database. Polymer, 2005, 46, 4314-4321.	1.8	28
84	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
85	Predicting binding sites of hydrolase-inhibitor complexes by combining several methods. BMC Bioinformatics, 2004, 5, 205.	1.2	27
86	REFINEMENT OF NMR-DETERMINED PROTEIN STRUCTURES WITH DATABASE DERIVED DISTANCE CONSTRAINTS. Journal of Bioinformatics and Computational Biology, 2005, 03, 1315-1329.	0.3	27
87	The importance of slow motions for protein functional loops. Physical Biology, 2012, 9, 014001.	0.8	27
88	Bridging between NMA and Elastic Network Models: Preserving All-Atom Accuracy in Coarse-Grained Models. PLoS Computational Biology, 2015, 11, e1004542.	1.5	27
89	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
90	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

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91	Identifying sequenceâ€“structure pairs undetected by sequence alignments. Protein Engineering, Design and Selection, 2000, 13, 459-475.	1.0	25
92	Protein secondary structure prediction based on the GOR algorithm incorporating multiple sequence alignment information. Polymer, 2002, 43, 441-449.	1.8	25
93	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
94	RNA base-amino acid interaction strengths derived from structures and sequences. Nucleic Acids Research, 1997, 25, 2562-2565.	6.5	24
95	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
96	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
97	Ribosome Mechanics Informs about Mechanism. Journal of Molecular Biology, 2016, 428, 802-810.	2.0	24
98	Combinatorial biosynthesis and the basis for substrate promiscuity in class I diterpene synthases. Metabolic Engineering, 2019, 55, 44-58.	3.6	24
99	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
100	Refinement of NMR-determined protein structures with database derived mean-force potentials. Proteins: Structure, Function and Bioinformatics, 2007, 68, 232-242.	1.5	23
101	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
102	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
103	Protein Promiscuity: Drug Resistance and Native Functionsâ€”HIV-1 Case. Journal of Biomolecular Structure and Dynamics, 2005, 22, 615-624.	2.0	22
104	A Consensus Data Mining secondary structure prediction by combining GOR V and Fragment Database Mining. Protein Science, 2006, 15, 2499-2506.	3.1	22
105	A Computational Investigation on the Connection between Dynamics Properties of Ribosomal Proteins and Ribosome Assembly. PLoS Computational Biology, 2012, 8, e1002530.	1.5	22
106	Directional Force Originating from ATP Hydrolysis Drives the GroEL Conformational Change. Biophysical Journal, 2017, 112, 1561-1570.	0.2	22
107	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
108	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

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109	Protein flexibility: coordinate uncertainties and interpretation of structural differences. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1140-1161.	2.5	21
110	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
111	Efficient Method To Count and Generate Compact Protein Lattice Conformations. Macromolecules, 1997, 30, 6691-6694.	2.2	19
112	Packing Regularities in Biological Structures Relate to Their Dynamics. , 2007, 350, 251-276.		19
113	Composite predictions of secondary structures oflac repressor. Biopolymers, 1979, 18, 2625-2643.	1.2	18
114	Relationship Between Curved DNA Conformations and Slow Gel Migration. Journal of Biomolecular Structure and Dynamics, 1987, 4, 561-567.	2.0	18
115	Fast learning optimized prediction methodology (FLOPRED) for protein secondary structure prediction. Journal of Molecular Modeling, 2012, 18, 4275-4289.	0.8	18
116	Elastic network normal modes provide a basis for protein structure refinement. Journal of Chemical Physics, 2012, 136, 195101.	1.2	17
117	Distributions of experimental protein structures on coarse-grained free energy landscapes. Journal of Chemical Physics, 2015, 143, 243153.	1.2	17
118	Characterizing and Predicting Protein Hinges for Mechanistic Insight. Journal of Molecular Biology, 2020, 432, 508-522.	2.0	17
119	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
120	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
121	Most probable intermediates in protein folding-unfolding with a noninteracting globule-coil model. Biochemistry, 1982, 21, 5203-5213.	1.2	15
122	Diversity of Function-Related Conformational Changes in Proteins: Coordinate Uncertainty, Fragment Rigidity, and Stability. Biochemistry, 2010, 49, 5683-5704.	1.2	14
123	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
124	PIDD: database for Protein Inter-atomic Distance Distributions. Nucleic Acids Research, 2007, 35, D202-D207.	6.5	13
125	Exploration of the relationship between topology and designability of conformations. Journal of Chemical Physics, 2011, 134, 235101.	1.2	13
126	Factors correlating with significant differences between X-ray structures of myoglobin. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 481-491.	2.5	13

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127	Aldolases Utilize Different Oligomeric States To Preserve Their Functional Dynamics. Biochemistry, 2015, 54, 3543-3554.	1.2	12
128	Altered dynamics upon oligomerization corresponds to key functional sites. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1422-1434.	1.5	12
129	Ideal amino acid exchange forms for approximating substitution matrices. Proteins: Structure, Function and Bioinformatics, 2007, 69, 379-393.	1.5	11
130	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
131	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
132	How do side chains orient globally in protein structures?. Proteins: Structure, Function and Bioinformatics, 2005, 61, 513-522.	1.5	10
133	Structural interpretation of protein-protein interaction network. BMC Structural Biology, 2010, 10, S4.	2.3	10
134	Statistical Contact Potentials in Protein Coarse-Grained Modeling: From Pair to Multi-body Potentials. , 2011, , 127-157.		10
135	Protein Loop Dynamics Are Complex and Depend on the Motions of the Whole Protein. Entropy, 2012, 14, 687-700.	1.1	10
136	A Conserved Isoleucine Maintains the Inactive State of Bruton's Tyrosine Kinase. Journal of Molecular Biology, 2014, 426, 3656-3669.	2.0	10
137	The Use of Experimental Structures to Model Protein Dynamics. Methods in Molecular Biology, 2015, 1215, 213-236.	0.4	10
138	Protein Actions. , 0, , .		10
139	Conformational Energy Minimization in the Approximation of Limited Range Interactions. Macromolecules, 1979, 12, 1156-1159.	2.2	9
140	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
141	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
142	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
143	Structural compliance: A new metric for protein flexibility. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1482-1492.	1.5	9
144	Ligand Binding Introduces Significant Allosteric Shifts in the Locations of Protein Fluctuations. Frontiers in Molecular Biosciences, 2021, 8, 733148.	1.6	9

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145	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
146	The transfer matrix method for lattice proteinsâ€"an application with cooperative interactions. Polymer, 2004, 45, 707-716.	1.8	8
147	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
148	Conformational Analysis of Receptor Selective Tachykinin Analogs: Senktide and Septide. Journal of Biomolecular Structure and Dynamics, 1992, 10, 429-439.	2.0	7
149	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
150	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
151	Statistical measures on residue-level protein structural properties. Journal of Structural and Functional Genomics, 2011, 12, 119-136.	1.2	7
152	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
153	Xyloglucan Xylosyltransferase 1 Displays Promiscuity Toward Donor Substrates During in Vitro Reactions. Plant and Cell Physiology, 2021, 62, 1890-1901.	1.5	7
154	Equilibrium folding-unfolding pathways of model proteins: Effect of myoglobin-heme contacts. Biopolymers, 1983, 22, 79-85.	1.2	6
155	Loop Folds in Proteins and Evolutionary Conservation of Folding Nuclei. Journal of Biomolecular Structure and Dynamics, 2002, 20, 323-325.	2.0	6
156	PRTAD: A database for protein residue torsion angle distributions. International Journal of Data Mining and Bioinformatics, 2009, 3, 469.	0.1	6
157	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
158	Predicting Designability of Small Proteins from Graph Features of Contact Maps. Journal of Computational Biology, 2016, 23, 400-411.	0.8	6
159	Fold-specific sequence scoring improves protein sequence matching. BMC Bioinformatics, 2016, 17, 328.	1.2	6
160	hdANM: a new comprehensive dynamics model for protein hinges. Biophysical Journal, 2021, 120, 4955-4965.	0.2	6
161	Missing Magnitudes. Nature, 1973, 245, 59-60.	13.7	5
162	Configurational statistics of methyl vinyl ether-maleic anhydride copolymer: selection of important atomic interactions and conformations. Macromolecules, 1991, 24, 731-739.	2.2	5

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163	Conformations of t-RNA: Base Pairing and Stacking. Journal of Biomolecular Structure and Dynamics, 1994, 12, 145-161.	2.0	5
164	Shape-dependent designability studies of lattice proteins. Journal of Physics Condensed Matter, 2007, 19, 285220.	0.7	5
165	Entropy, Fluctuations, and Disordered Proteins. Entropy, 2019, 21, 764.	1.1	5
166	Immunoglobulin Structure Exhibits Control over CDR Motion. Immunome Research, 2011, 7, .	0.1	5
167	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
168	Contacts between segments in the random-flight model of polymer chains. Computational and Theoretical Polymer Science, 1999, 9, 285-294.	1.1	4
169	A DNA-Centric Look at Protein-DNA Complexes. Structure, 2006, 14, 1341-1342.	1.6	4
170	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
171	Use of machine learning algorithms to classify binary protein sequences as highly-designable or poorly-designable. BMC Bioinformatics, 2008, 9, 487.	1.2	4
172	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
173	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
174	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
175	Entropies Derived from the Packing Geometries within a Single Protein Structure. ACS Omega, 2022, 7, 20719-20730.	1.6	4
176	Comparison of experimental and computed protein anisotropic temperature factors. , 2007, , .		3
177	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
178	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
179	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
180	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

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181	Data Mining for Protein Secondary Structure Prediction. Structure and Bonding, 2009, , 135-167.	1.0	3
182	Volumes and Surface Areas: Geometries and Scaling Relationships between Coarse- Grained and Atomic Structures. Current Pharmaceutical Design, 2014, 20, 1208-1222.	0.9	3
183	Elastic Network Models of Coarse-Grained Proteins Are Effective for Studying the Structural Control Exerted over Their Dynamics. , 2008, , 237-254.		3
184	Equilibrium folding pathways for model proteins. Journal of Statistical Physics, 1983, 30, 549-559.	0.5	2
185	Immunological implications of a structural analysis of two different porcine IL1Î² proteins expressed in macrophages and embryos. , 2010, , .		2
186	Analysis of protein dynamics using local-DME calculations. International Journal of Bioinformatics Research and Applications, 2011, 7, 146.	0.1	2
187	An analysis of conformational changes upon RNA-protein binding. , 2014, , .		2
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