Andrzej Kloczkowski

List of Publications by Year
in descending order

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187	3,102	185998	233125
papers	citations	28 h-index	45 g-index

192	192	192	2725
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	GOR V server for protein secondary structure prediction. Bioinformatics, 2005, 21, 2787-2788.	1.8	179
2	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
3	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
4	Simulations on the reinforcement of poly(dimethylsiloxane) elastomers by randomly distributed filler particles. Journal of Polymer Science, Part B: Polymer Physics, 1996, 34, 1647-1657.	2.4	82
5	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
6	Chain dimensions and fluctuations in random elastomeric networks. 1. Phantom Gaussian networks in the undeformed state. Macromolecules, 1989, 22, 1423-1432.	2.2	68
7	Inferring ideal amino acid interaction forms from statistical protein contact potentials. Proteins: Structure, Function and Bioinformatics, 2005, 59, 49-57.	1.5	66
8	Some simulations on filler reinforcement in elastomers. Polymer, 2005, 46, 8894-8904.	1.8	65
9	A Diffused-Constraint Theory for the Elasticity of Amorphous Polymer Networks. 1. Fundamentals and Stress-Strain Isotherms in Elongation. Macromolecules, 1995, 28, 5089-5096.	2.2	63
10	The ribosome structure controls and directs mRNA entry, translocation and exit dynamics. Physical Biology, 2008, 5, 046005.	0.8	61
11	Modeling of Protein Structural Flexibility and Large-Scale Dynamics: Coarse-Grained Simulations and Elastic Network Models. International Journal of Molecular Sciences, 2018, 19, 3496.	1.8	60
12	The relaxation spectrum for Gaussian networks. Macromolecules, 1990, 23, 3481-3490.	2.2	52
13	Computer simulations on filled elastomeric materials. Chemical Engineering Science, 1994, 49, 2889-2897.	1.9	50
14	Accurate single-sequence prediction of solvent accessible surface area using local and global features. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3170-3176.	1.5	50
15	Mechanical properties and transition temperatures of crosslinked-oriented gelatin. Colloid and Polymer Science, 1997, 275, 307-314.	1.0	49
16	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
17	DescribePROT: database of amino acid-level protein structure and function predictions. Nucleic Acids Research, 2021, 49, D298-D308.	6.5	46
18	Monte Carlo simulations on reinforcement of an elastomer by oriented prolate particles. Computational and Theoretical Polymer Science, 2001, 11, 251-262.	1.1	45

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19	Distance matrix-based approach to protein structure prediction. Journal of Structural and Functional Genomics, 2009, 10, 67-81.	1.2	45
20	Innovations in Genomics and Big Data Analytics for Personalized Medicine and Health Care: A Review. International Journal of Molecular Sciences, 2022, 23, 4645.	1.8	45
21	Lattice model for segmental orientation in deformed polymeric networks. 1. Contribution of intermolecular correlations. Macromolecules, 1990, 23, 5335-5340.	2.2	42
22	Application of statistical mechanics to the analysis of various physical properties of elastomeric networks â€" a review. Polymer, 2002, 43, 1503-1525.	1.8	41
23	Functional clustering of yeast proteins from the protein-protein interaction network. BMC Bioinformatics, 2006, 7, 355.	1.2	40
24	The energy profiles of atomic conformational transition intermediates of adenylate kinase. Proteins: Structure, Function and Bioinformatics, 2009, 77, 551-558.	1.5	39
25	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
26	MAVENs: Motion analysis and visualization of elastic networks and structural ensembles. BMC Bioinformatics, 2011, 12, 264.	1.2	37
27	The origin and extent of coarse-grained regularities in protein internal packing. Proteins: Structure, Function and Bioinformatics, 2003, 53, 56-67.	1.5	33
28	Oligomerization of FVFLM peptides and their ability to inhibit beta amyloid peptides aggregation: consideration as a possible model. Physical Chemistry Chemical Physics, 2017, 19, 2990-2999.	1.3	33
29	The GOR Method of Protein Secondary Structure Prediction and Its Application as a Protein Aggregation Prediction Tool. Methods in Molecular Biology, 2017, 1484, 7-24.	0.4	33
30	On the stability of the isotropic phase towards nematic and smecticAformation. Molecular Physics, 1981, 42, 51-63.	0.8	32
31	Potentials 'R'Us web-server for protein energy estimations with coarse-grained knowledge-based potentials. BMC Bioinformatics, 2010, 11, 92.	1.2	31
32	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
33	Protein secondary structure prediction using a small training set (compact model) combined with a Complex-valued neural network approach. BMC Bioinformatics, 2016, 17, 362.	1.2	29
34	A lattice model for segmental orientation in deformed polymeric networks. 2. Effect of chain stiffness and thermotropic interactions. Macromolecules, 1990, 23, 5341-5346.	2.2	28
35	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
36	Prediction of protein secondary structure by mining structural fragment database. Polymer, 2005, 46, 4314-4321.	1.8	28

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37	Fluctuations, correlations, and small-angle neutron scattering from endlinked Gaussian chains in regular bimodal networks. Macromolecules, 1991, 24, 3266-3275.	2.2	27
38	Predicting binding sites of hydrolase-inhibitor complexes by combining several methods. BMC Bioinformatics, 2004, 5, 205.	1.2	27
39	The importance of slow motions for protein functional loops. Physical Biology, 2012, 9, 014001.	0.8	27
40	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
41	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
42	Protein secondary structure prediction based on the GOR algorithm incorporating multiple sequence alignment information. Polymer, 2002, 43, 441-449.	1.8	25
43	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
44	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
45	A global machine learning based scoring function for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 752-759.	1.5	24
46	Modeling SARSâ€CoVâ€2 proteins in the CASPâ€commons experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1987-1996.	1.5	24
47	Main-Chain Lyotropic Liquid-Crystalline Elastomers. 1. Syntheses of Cross-Linked Polyisocyanate Gels Acquiring Liquid-Crystalline Behavior in the Swollen State. Macromolecules, 1996, 29, 2796-2804.	2.2	23
48	Protein Promiscuity: Drug Resistance and Native Functionsâ€"HIV-1 Case. Journal of Biomolecular Structure and Dynamics, 2005, 22, 615-624.	2.0	22
49	A Consensus Data Mining secondary structure prediction by combining GOR V and Fragment Database Mining. Protein Science, 2006, 15, 2499-2506.	3.1	22
50	Modeling the elastomeric properties of stereoregular polypropylenes in nanocomposites with spherical fillers. Polymer, 2005, 46, 7301-7308.	1.8	21
51	Filler-induced deformations of amorphous polyethylene chains. The effects of the deformations on elastomeric properties, and some comparisons with experiments. European Polymer Journal, 2006, 42, 796-806.	2.6	21
52	MQAPsingle: A quasi single-model approach for estimation of the quality of individual protein structure models. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1021-1028.	1.5	21
53	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.	1.2	21
54	A molecular model for the smecticAphase. Molecular Physics, 1985, 55, 689-700.	0.8	20

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55	Role of Resultant Dipole Moment in Mechanical Dissociation of Biological Complexes. Molecules, 2018, 23, 1995.	1.7	20
56	Increased power output and resonance effects in a thermal engine driven by a first or second order model reaction. Journal of Chemical Physics, 1985, 82, 2457-2465.	1.2	19
57	A visual representation for the shapes of flexible mesogenic molecules. Liquid Crystals, 1988, 3, 185-194.	0.9	19
58	Efficient Method To Count and Generate Compact Protein Lattice Conformations. Macromolecules, 1997, 30, 6691-6694.	2.2	19
59	Packing Regularities in Biological Structures Relate to Their Dynamics. , 2007, 350, 251-276.		19
60	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	1.6	19
61	Fast learning optimized prediction methodology (FLOPRED) for protein secondary structure prediction. Journal of Molecular Modeling, 2012, 18, 4275-4289.	0.8	18
62	Elastic network normal modes provide a basis for protein structure refinement. Journal of Chemical Physics, 2012, 136, 195101.	1.2	17
63	BioShell-Threading: versatile Monte Carlo package for protein 3D threading. BMC Bioinformatics, 2014, 15, 22.	1.2	17
64	A novel orientation technique for semi-rigid polymers. 1. Preparation of cross-linked cellulose acetate and hydroxypropylcellulose films having permanent anisotropy in the swollen state. Colloid and Polymer Science, 1994, 272, 284-292.	1.0	16
65	Main-Chain Lyotropic Liquid-Crystalline Elastomers. 2. Orientation and Mechanical Properties of Polyisocyanate Films. Macromolecules, 1996, 29, 2805-2812.	2.2	16
66	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
67	Theoretical Analysis of the Elastomeric and Optical Properties of Networks of Semirigid Chains in the Swollen State. Macromolecules, 1995, 28, 4920-4926.	2.2	15
68	Chain dimensions and fluctuations in random elastomeric networks. 2. Dependence of chain dimensions and fluctuations on macroscopic strain. Macromolecules, 1989, 22, 1432-1437.	2.2	14
69	Freezing of the hard core Yukawa fluid. Journal of Chemical Physics, 1988, 88, 5834-5839.	1.2	13
70	A novel orientation technique for semi-rigid polymers. 2. Mechanical properties of cellulose acetate and hydroxypropylcellulose films. Colloid and Polymer Science, 1994, 272, 393-399.	1.0	13
71	Exploration of the relationship between topology and designability of conformations. Journal of Chemical Physics, 2011, 134, 235101.	1.2	13
72	Comparing NMR and X-ray protein structure: Lindemann-like parameters and NMR disorder. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2331-2341.	2.0	13

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73	Structural and mechanical studies of a blend of poly(butylene terephthalate) and poly(ether ester) based on poly(butylene terephthalate) and poly(ethylene glycol). Polymer, 1994, 35, 5247-5255.	1.8	12
74	Novel High-Performance Materials from Starch. 2. Orientation and Mechanical Properties of Lightly Cross-Linked Starchâ^'Ether Films. Chemistry of Materials, 1998, 10, 794-803.	3.2	12
75	In Silico Modeling of Human Î±2C-Adrenoreceptor Interaction with Filamin-2. PLoS ONE, 2014, 9, e103099.	1.1	12
76	Dynamic Mechanical Losses in Filled Poly(Dimethylsiloxane) Networks. Rubber Chemistry and Technology, 1995, 68, 601-608.	0.6	11
77	Structures and mechanical properties of zone-drawn-zone-annealed blends of cocrystallizing poly(butylene terephthalate) and a poly(ether ester). Journal of Applied Polymer Science, 1996, 59, 1667-1675.	1.3	11
78	Ideal amino acid exchange forms for approximating substitution matrices. Proteins: Structure, Function and Bioinformatics, 2007, 69, 379-393.	1.5	11
79	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
80	Biological and Cheminformatics Studies of Newly Designed Triazole Based Derivatives as Potent Inhibitors against Mushroom Tyrosinase. Molecules, 2022, 27, 1731.	1.7	11
81	Molecular modeling of phosphorylation sites in proteins using a database of local structure segments. Journal of Molecular Modeling, 2005, 11, 431-438.	0.8	10
82	Structural interpretation of protein-protein interaction network. BMC Structural Biology, 2010, 10, S4.	2.3	10
83	Statistical Contact Potentials in Protein Coarse-Grained Modeling: From Pair to Multi-body Potentials. , 2011, , 127-157.		10
84	Multi-class BCGA-ELM based classifier that identifies biomarkers associated with hallmarks of cancer. BMC Bioinformatics, 2015, 16, 166.	1.2	10
85	On the relationship of the nematic-isotropic transition temperature of an oligomer to that of its constituent units. Liquid Crystals, 1988, 3, 95-99.	0.9	9
86	On the Paceâ€"Datyner theory of diffusion of small molecules through polymers. Journal of Polymer Science, Part B: Polymer Physics, 1989, 27, 1663-1674.	2.4	9
87	Experimental Studies of Elastomeric and Optical Properties, and Strain-Induced Liquid-Crystalline Phase Transitions, in Deformed (Hydroxypropyl)cellulose Networks in the Swollen State. Macromolecules, 1995, 28, 4927-4931.	2.2	9
88	Oriented Gelatinâ€"A New Source for High-Performance Materials. Journal of Macromolecular Science - Pure and Applied Chemistry, 1996, 33, 525-540.	1.2	9
89	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
90	A Global Machine Learning Based Scoring Function for Protein Structure Prediction. Biophysical Journal, 2014, 106, 656a-657a.	0.2	9

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91	Robust Sampling of Defective Pathways in Alzheimerâ€™s Disease. Implications in Drug Repositioning. International Journal of Molecular Sciences, 2020, 21, 3594.	1.8	9
92	On the mean spherical model for liquid crystals. Molecular Physics, 1982, 46, 13-19.	0.8	8
93	Novel High-Performance Materials from Starch. 3. Influence of Degree of Substitution and Amylose/Amylopectin Ratio on Performance. Chemistry of Materials, 1998, 10, 804-811.	3.2	8
94	The transfer matrix method for lattice proteinsâ€”an application with cooperative interactions. Polymer, 2004, 45, 707-716.	1.8	8
95	Monte Carlo Simulations on Nanoparticles in Elastomers. Effects of the Particles on the Dimensions of the Polymer Chains and the Mechanical Properties of the Networks. Macromolecular Symposia, 2007, 256, 40-47.	0.4	8
96	GENN: A GEneral Neural Network for Learning Tabulated Data with Examples from Protein Structure Prediction. Methods in Molecular Biology, 2015, 1260, 165-178.	0.4	8
97	The largest eigenvalue method for stereo-regular vinyl chains. Polymer, 2005, 46, 4373-4383.	1.8	7
98	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
99	Statistical measures on residue-level protein structural properties. Journal of Structural and Functional Genomics, 2011, 12, 119-136.	1.2	7
100	Fast and Accurate Accessible Surface Area Prediction Without a Sequence Profile. Methods in Molecular Biology, 2017, 1484, 127-136.	0.4	7
101	Robust Prediction of Single and Multiple Point Protein Mutations Stability Changes. Biomolecules, 2020, 10, 67.	1.8	7
102	Exploration of Potential Ewing Sarcoma Drugs from FDA-Approved Pharmaceuticals through Computational Drug Repositioning, Pharmacogenomics, Molecular Docking, and MD Simulation Studies. ACS Omega, 2022, 7, 19243-19260.	1.6	7
103	On the tricritical points in the McMillan model of liquid crystals. Molecular Physics, 1985, 55, 1223-1232.	0.8	6
104	Correlations among chains along a crosslinked path in a phantom network and their characterization by SANS. Macromolecules, 1992, 25, 2455-2458.	2.2	6
105	Novel High-Performance Materials from Starch. 1. Factors Influencing the Lyotropic Liquid Crystallinity of Some Starch Ethers. Chemistry of Materials, 1998, 10, 784-793.	3.2	6
106	Loop Folds in Proteins and Evolutionary Conservation of Folding Nuclei. Journal of Biomolecular Structure and Dynamics, 2002, 20, 323-325.	2.0	6
107	Support-vector-machine classification of linear functional motifs in proteins. Journal of Molecular Modeling, 2006, 12, 453-461.	0.8	6
108	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

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109	Predicting Designability of Small Proteins from Graph Features of Contact Maps. Journal of Computational Biology, 2016, 23, 400-411.	0.8	6
110	Fold-specific sequence scoring improves protein sequence matching. BMC Bioinformatics, 2016, 17, 328.	1.2	6
111	Predicting protein tertiary structure and its uncertainty analysis via particle swarm sampling. Journal of Molecular Modeling, 2019, 25, 79.	0.8	6
112	Mechanistic insights into TNFR1/MADD death domains in Alzheimerâ€™s disease through conformational molecular dynamic analysis. Scientific Reports, 2021, 11, 12256.	1.6	6
113	Predictive Mathematical Models of the Short-Term and Long-Term Growth of the COVID-19 Pandemic. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-14.	0.7	6
114	Shape-dependent designability studies of lattice proteins. Journal of Physics Condensed Matter, 2007, 19, 285220.	0.7	5
115	Chain dimensions and fluctuations in elastomeric networks in which the junctions alternate regularly in their functionality. Journal of Chemical Physics, 2009, 130, 064905.	1.2	5
116	Entropy, Fluctuations, and Disordered Proteins. Entropy, 2019, 21, 764.	1.1	5
117	Robust Sampling of Defective Pathways in Multiple Myeloma. International Journal of Molecular Sciences, 2019, 20, 4681.	1.8	5
118	Immunoglobulin Structure Exhibits Control over CDR Motion. Immunome Research, 2011, 7, .	0.1	5
119	A closed form solution for the internal dynamics of polymer chains. I. Bonds with independent rotational potentials. Journal of Chemical Physics, 1990, 92, 4513-4518.	1.2	4
120	Contacts between segments in the random-flight model of polymer chains. Computational and Theoretical Polymer Science, 1999, 9, 285-294.	1.1	4
121	Effect of non-Gaussian chains on fluctuations of junctions in bimodal networks. Polymer, 2002, 43, 2569-2574.	1.8	4
122	A DNA-Centric Look at Protein-DNA Complexes. Structure, 2006, 14, 1341-1342.	1.6	4
123	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
124	Theoretical Models and Simulations of Polymer Chains. , 2007, , 67-81.		4
125	Use of machine learning algorithms to classify binary protein sequences as highly-designable or poorly-designable. BMC Bioinformatics, 2008, 9, 487.	1.2	4
126	Smallâ€Angle Neutron Scattering from Elastomeric Networks in which the Junctions Alternate Regularly in their Functionality. Macromolecular Theory and Simulations, 2009, 18, 537-544.	0.6	4

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127	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
128	Principal component analysis in protein tertiary structure prediction. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850005.	0.3	4
129	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
130	Many-to-one binding by intrinsically disordered protein regions. , 2019, , .		4
131	Small-angle neutron scattering from elastomeric networks. 1. Calculated scattering from a path containing several junctions in the James-Guth model. Macromolecules, 1989, 22, 4502-4506.	2.2	3
132	Comment on: Statistical mechanics of rubber elasticity. Journal of Chemical Physics, 1991, 95, 7015-7016.	1.2	3
133	Molecular modeling of matrix chain deformation in nanofiber filled composites. Colloid and Polymer Science, 2006, 284, 700-709.	1.0	3
134	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
135	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
136	Conditional entropy in variation-adjusted windows detects selection signatures associated with expression quantitative trait loci (eQTLs). BMC Genomics, 2015, 16, S8.	1.2	3
137	Prediction of Protein Tertiary Structure via Regularized Template Classification Techniques. Molecules, 2020, 25, 2467.	1.7	3
138	Data Mining for Protein Secondary Structure Prediction. Structure and Bonding, 2009, , 135-167.	1.0	3
139	Volumes and Surface Areas: Geometries and Scaling Relationships between Coarse- Grained and Atomic Structures. Current Pharmaceutical Design, 2014, 20, 1208-1222.	0.9	3
140	Prediction of Site Directed miRNAs as Key Players of Transcriptional Regulators Against Influenza C Virus Infection Through Computational Approaches. Frontiers in Molecular Biosciences, 2022, 9, 866072.	1.6	3
141	A simple model for protection against environmental pollution in reactive coating films. Journal of Colloid and Interface Science, 1984, 99, 404-419.	5.0	2
142	Transition temperatures of binary nematic mixtures predicted by the Humphries-James-Luckhurst theory. Journal of the Chemical Society, Faraday Transactions 2, 1988, 84, 155.	1.1	2
143	On the Flory-Ronca theory of systems of rodlike particles. Macromolecules, 1990, 23, 5035-5037.	2.2	2
144	Protein Tertiary Structure Prediction via SVD and PSO Sampling. Lecture Notes in Computer Science, 2018, , 211-220.	1.0	2

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145	Reoptimized UNRES Potential for Protein Model Quality Assessment. Genes, 2018, 9, 601.	1.0	2
146	A topological order parameter for describing folding free energy landscapes of proteins. Journal of Chemical Physics, 2018, 149, 175101.	1.2	2
147	Computational Ways to Enhance Protein Inhibitor Design. Frontiers in Molecular Biosciences, 2020, 7, 607323.	1.6	2
148	Hematopoietic Stem and Progenitor Cells (HSPCs) and Hematopoietic Microenvironment: Molecular and Bioinformatic Studies of the Zebrafish Models. International Journal of Molecular Sciences, 2022, 23, 7285.	1.8	2
149	Neutron scattering from elastomeric networks. 2. An alternative phantom network model. Macromolecules, 1990, 23, 1222-1224.	2.2	1
150	A simple derivation of the exponent Î³ for Gaussian chains with excluded volume. Macromolecular Theory and Simulations, 1995, 4, 245-252.	0.6	1
151	Models To Approximate the Motions of Protein Loops. Journal of Chemical Theory and Computation, 2010, 6, 3249-3258.	2.3	1
152	ANM Normal Modes Show the Directions for Protein Structure Refinement. Biophysical Journal, 2012, 102, 25a.	0.2	1
153	New Methods to Improve Protein Structure Prediction and Refinement. Biophysical Journal, 2013, 104, 229a.	0.2	1
154	Relationships between Mechanostability, Aggregation Rate and Binding Affinity of Peptides: Insights from All-ATOM Modeling in Explicit Solvent. Biophysical Journal, 2016, 110, 386a.	0.2	1
155	Accurate Prediction of One-Dimensional Protein Structure Features Using SPINE-X. Methods in Molecular Biology, 2017, 1484, 45-53.	0.4	1
156	On the Relationship between Aggregation Rate and Mechanical Stability in Protein Aggregation. Biophysical Journal, 2019, 116, 196a.	0.2	1
157	Sulfatase 2 Is Associated with Steroid Resistance in Childhood Nephrotic Syndrome. Journal of Clinical Medicine, 2021, 10, 523.	1.0	1
158	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
159	The Utilization of Different Classifiers to Perform Drug Repositioning in Inclusion Body Myositis Supports the Concept of Biological Invariance. Lecture Notes in Computer Science, 2020, , 589-598.	1.0	1
160	Quadrupoles on the triangular two-dimensional lattice: a simple model of nitrogen on graphite herringbone transition. Langmuir, 1988, 4, 817-821.	1.6	0
161	Quadrupoles on the triangular two-dimensional lattice. Influence of the external field of graphite. Langmuir, 1989, 5, 1071-1074.	1.6	0
162	Computational testing of protein-protein interactions. , 2009, , .		0

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163	Immunoglobulin functional motions and their effects on the complementarity determining regions. , 2010, , .		0
164	Protein Secondary Structure Prediction Using Knowledge-Based Potentials and An Ensemble of Classifiers. Biophysical Journal, 2010, 98, 52a.	0.2	0
165	P.R.E.S.S. — An R-package for exploring residual-level protein structural statistics. , 2011, , .		0
166	MQAPmulti2 and MQAPsingle2:Toward the Estimation of Model Quality When Not Only Many Models are Available. Biophysical Journal, 2013, 104, 229a.	0.2	0
167	De Novo Protein Structure Determination from Incomplete Experimental Data. Biophysical Journal, 2013, 104, 228a.	0.2	0
168	Protein Model Quality Assessment Prediction by using a Residue Specific Statistical Potential. Biophysical Journal, 2014, 106, 208a.	0.2	0
169	Prediction of Protein Aggregation Propensities using GOR Method. Biophysical Journal, 2017, 112, 198a-199a.	0.2	0
170	Computational Characterization of Oligomerization of FVFLM Peptide and its Ability to Inhibit Beta Amyloid Aggregation. Biophysical Journal, 2017, 112, 200a.	0.2	0
171	Deciphering General Characteristics of Residues Constituting Allosteric Communication Paths. Biophysical Journal, 2017, 112, 499a.	0.2	0
172	Classification of Allostery in Proteins: A Deep Learning Approach. Biophysical Journal, 2018, 114, 422a.	0.2	0
173	Combining Prediction of Protein Aggregation Propensities with Prediction of Other One-Dimensional Properties. Biophysical Journal, 2018, 114, 432a.	0.2	0
174	Deciphering General Characteristics of Residues Constituting Allosteric Communication Paths. Lecture Notes in Computer Science, 2019, , 245-258.	1.0	0
175	Characteristics of Protein Fold Space Exhibits Close Dependence on Domain Usage. Lecture Notes in Computer Science, 2019, , 356-369.	1.0	0
176	Effect of Resultant Dipole Moment on Mechanical Stability of Protein-Peptide Complexes. Biophysical Journal, 2019, 116, 459a.	0.2	0
177	Explicit-Solvent All-Atom Molecular Dynamics of Peptide Aggregation. Springer Series on Bio- and Neurosystems, 2019, , 541-558.	0.2	0
178	Entropy, Fluctuations, and Disordered Proteins. Linking between Sequence, Structure, and Disorder Information. Biophysical Journal, 2020, 118, 371a.	0.2	0
179	Computer Simulations of Key Peptides Involved in Preeclampsia and Alzheimer's Disease. Biophysical Journal, 2020, 118, 485a.	0.2	0
180	Prediction of Deleterious Protein Mutations. Biophysical Journal, 2021, 120, 269a.	0.2	0

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181	Cyclic AMPâ€Rap1A signaling mediates cell surface translocation of microvascular smooth muscle Î± 2C adrenoceptors through the actin binding protein filaminâ€2. FASEB Journal, 2013, 27, 729.15.	0.2	0
182	On the Use of Principal Component Analysis and Particle Swarm Optimization in Protein Tertiary Structure Prediction. Lecture Notes in Computer Science, 2018, , 107-116.	1.0	0
183	Protein Secondary Structure Assignments and Their Usefulness forÂDihedral Angle Prediction. Springer Series on Bio- and Neurosystems, 2019, , 699-712.	0.2	0
184	Applications of Basic Ideas of Statistical Mechanics of Chain Molecules to Proteins. Exact Counting of Number of Conformations of Compact Chains with Volume Exclusion for Evaluation of Chain Entropies. ACS Symposium Series, 2020, , 103-115.	0.5	0
185	Predictive mathematical models of the growth of the COVID-19 pandemic. Biophysical Journal, 2022, 121, 532a.	0.2	0
186	Final Remarks. Methods in Molecular Biology, 2022, 2340, 469-470.	0.4	0
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