Andrzej Kloczkowski

List of Publications by Year
in descending order

187	3,102	186265	233421
papers	citations	28 h-index	45 g-index

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

#	Article	IF	Citations
1	Predictive mathematical models of the growth of the COVID-19 pandemic. Biophysical Journal, 2022, 121, 532a.	0.5	0
2	Final Remarks. Methods in Molecular Biology, 2022, 2340, 469-470.	0.9	0
3	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.	0.9	0
4	Biological and Cheminformatics Studies of Newly Designed Triazole Based Derivatives as Potent Inhibitors against Mushroom Tyrosinase. Molecules, 2022, 27, 1731.	3.8	11
5	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.	3.5	3
6	Innovations in Genomics and Big Data Analytics for Personalized Medicine and Health Care: A Review. International Journal of Molecular Sciences, 2022, 23, 4645.	4.1	45
7	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.	3.5	7
8	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.	4.1	2
9	DescribePROT: database of amino acid-level protein structure and function predictions. Nucleic Acids Research, 2021, 49, D298-D308.	14.5	46
10	Sulfatase 2 Is Associated with Steroid Resistance in Childhood Nephrotic Syndrome. Journal of Clinical Medicine, 2021, 10, 523.	2.4	1
11	Prediction of Deleterious Protein Mutations. Biophysical Journal, 2021, 120, 269a.	0.5	0
12	Mechanistic insights into TNFR1/MADD death domains in Alzheimerâ€™s disease through conformational molecular dynamic analysis. Scientific Reports, 2021, 11, 12256.	3.3	6
13	Modeling SARSâ€CoVâ€2 proteins in the CASPâ€commons experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1987-1996.	2.6	24
14	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.	1.3	6
15	A Hybrid Levenbergâ€“Marquardt Algorithm on a Recursive Neural Network for Scoring Protein Models. Methods in Molecular Biology, 2021, 2190, 307-316.	0.9	1
16	Robust Prediction of Single and Multiple Point Protein Mutations Stability Changes. Biomolecules, 2020, 10, 67.	4.0	7
17	Entropy, Fluctuations, and Disordered Proteins. Linking between Sequence, Structure, and Disorder Information. Biophysical Journal, 2020, 118, 371a.	0.5	0
18	Robust Sampling of Defective Pathways in Alzheimerâ€™s Disease. Implications in Drug Repositioning. International Journal of Molecular Sciences, 2020, 21, 3594.	4.1	9

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19	Prediction of Protein Tertiary Structure via Regularized Template Classification Techniques. Molecules, 2020, 25, 2467.	3.8	3
20	Computer Simulations of Key Peptides Involved in Preeclampsia and Alzheimer's Disease. Biophysical Journal, 2020, 118, 485a.	0.5	0
21	Computational Ways to Enhance Protein Inhibitor Design. Frontiers in Molecular Biosciences, 2020, 7, 607323.	3.5	2
22	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
23	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.	1.3	1
24	Entropy, Fluctuations, and Disordered Proteins. Entropy, 2019, 21, 764.	2.2	5
25	Robust Sampling of Defective Pathways in Multiple Myeloma. International Journal of Molecular Sciences, 2019, 20, 4681.	4.1	5
26	Deciphering General Characteristics of Residues Constituting Allosteric Communication Paths. Lecture Notes in Computer Science, 2019, , 245-258.	1.3	0
27	Characteristics of Protein Fold Space Exhibits Close Dependence on Domain Usage. Lecture Notes in Computer Science, 2019, , 356-369.	1.3	0
28	On the Relationship between Aggregation Rate and Mechanical Stability in Protein Aggregation. Biophysical Journal, 2019, 116, 196a.	0.5	1
29	Effect of Resultant Dipole Moment on Mechanical Stability of Protein-Peptide Complexes. Biophysical Journal, 2019, 116, 459a.	0.5	0
30	Predicting protein tertiary structure and its uncertainty analysis via particle swarm sampling. Journal of Molecular Modeling, 2019, 25, 79.	1.8	6
31	Explicit-Solvent All-Atom Molecular Dynamics of Peptide Aggregation. Springer Series on Bio- and Neurosystems, 2019, , 541-558.	0.2	0
32	Protein Secondary Structure Assignments and Their Usefulness forÂDihedral Angle Prediction. Springer Series on Bio- and Neurosystems, 2019, , 699-712.	0.2	0
33	Many-to-one binding by intrinsically disordered protein regions. , 2019, , .		4
34	Protein Tertiary Structure Prediction via SVD and PSO Sampling. Lecture Notes in Computer Science, 2018, , 211-220.	1.3	2
35	Principal component analysis in protein tertiary structure prediction. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850005.	0.8	4
36	Classification of Allostery in Proteins: A Deep Learning Approach. Biophysical Journal, 2018, 114, 422a.	0.5	0

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37	Comparing NMR and X-ray protein structure: Lindemann-like parameters and NMR disorder. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2331-2341.	3.5	13
38	Reoptimized UNRES Potential for Protein Model Quality Assessment. Genes, 2018, 9, 601.	2.4	2
39	Modeling of Protein Structural Flexibility and Large-Scale Dynamics: Coarse-Grained Simulations and Elastic Network Models. International Journal of Molecular Sciences, 2018, 19, 3496.	4.1	60
40	A topological order parameter for describing folding free energy landscapes of proteins. Journal of Chemical Physics, 2018, 149, 175101.	3.0	2
41	Combining Prediction of Protein Aggregation Propensities with Prediction of Other One-Dimensional Properties. Biophysical Journal, 2018, 114, 432a.	0.5	0
42	Role of Resultant Dipole Moment in Mechanical Dissociation of Biological Complexes. Molecules, 2018, 23, 1995.	3.8	20
43	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	3.3	19
44	Kinetics and mechanical stability of the fibril state control fibril formation time of polypeptide chains: A computational study. Journal of Chemical Physics, 2018, 148, 215106.	3.0	21
45	On the Use of Principal Component Analysis and Particle Swarm Optimization in Protein Tertiary Structure Prediction. Lecture Notes in Computer Science, 2018, , 107-116.	1.3	0
46	Prediction of Protein Aggregation Propensities using GOR Method. Biophysical Journal, 2017, 112, 198a-199a.	0.5	0
47	Computational Characterization of Oligomerization of FVFLM Peptide and its Ability to Inhibit Beta Amyloid Aggregation. Biophysical Journal, 2017, 112, 200a.	0.5	0
48	Deciphering General Characteristics of Residues Constituting Allosteric Communication Paths. Biophysical Journal, 2017, 112, 499a.	0.5	0
49	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.	2.8	33
50	Fast and Accurate Accessible Surface Area Prediction Without a Sequence Profile. Methods in Molecular Biology, 2017, 1484, 127-136.	0.9	7
51	The GOR Method of Protein Secondary Structure Prediction and Its Application as a Protein Aggregation Prediction Tool. Methods in Molecular Biology, 2017, 1484, 7-24.	0.9	33
52	Accurate Prediction of One-Dimensional Protein Structure Features Using SPINE-X. Methods in Molecular Biology, 2017, 1484, 45-53.	0.9	1
53	Predicting Designability of Small Proteins from Graph Features of Contact Maps. Journal of Computational Biology, 2016, 23, 400-411.	1.6	6
54	Protein secondary structure prediction using a small training set (compact model) combined with a Complex-valued neural network approach. BMC Bioinformatics, 2016, 17, 362.	2.6	29

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55	Relationships between Mechanostability, Aggregation Rate and Binding Affinity of Peptides: Insights from All-ATOM Modeling in Explicit Solvent. Biophysical Journal, 2016, 110, 386a.	0.5	1
56	Fold-specific sequence scoring improves protein sequence matching. BMC Bioinformatics, 2016, 17, 328.	2.6	6
57	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.	2.6	21
58	Conditional entropy in variation-adjusted windows detects selection signatures associated with expression quantitative trait loci (eQTLs). BMC Genomics, 2015, 16, S8.	2.8	3
59	Multi-class BCGA-ELM based classifier that identifies biomarkers associated with hallmarks of cancer. BMC Bioinformatics, 2015, 16, 166.	2.6	10
60	GENN: A GEneral Neural Network for Learning Tabulated Data with Examples from Protein Structure Prediction. Methods in Molecular Biology, 2015, 1260, 165-178.	0.9	8
61	In Silico Modeling of Human Î±2C-Adrenoreceptor Interaction with Filamin-2. PLoS ONE, 2014, 9, e103099.	2.5	12
62	BioShell-Threading: versatile Monte Carlo package for protein 3D threading. BMC Bioinformatics, 2014, 15, 22.	2.6	17
63	A Global Machine Learning Based Scoring Function for Protein Structure Prediction. Biophysical Journal, 2014, 106, 656a-657a.	0.5	9
64	A global machine learning based scoring function for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 752-759.	2.6	24
65	Accurate single-sequence prediction of solvent accessible surface area using local and global features. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3170-3176.	2.6	50
66	Protein Model Quality Assessment Prediction by using a Residue Specific Statistical Potential. Biophysical Journal, 2014, 106, 208a.	0.5	0
67	Volumes and Surface Areas: Geometries and Scaling Relationships between Coarse- Grained and Atomic Structures. Current Pharmaceutical Design, 2014, 20, 1208-1222.	1.9	3
68	Distributions of amino acids suggest that certain residue types more effectively determine protein secondary structure. Journal of Molecular Modeling, 2013, 19, 4337-4348.	1.8	4
69	MQAPmulti2 and MQAPsingle2:Toward the Estimation of Model Quality When Not Only Many Models are Available. Biophysical Journal, 2013, 104, 229a.	0.5	0
70	New Methods to Improve Protein Structure Prediction and Refinement. Biophysical Journal, 2013, 104, 229a.	0.5	1
71	De Novo Protein Structure Determination from Incomplete Experimental Data. Biophysical Journal, 2013, 104, 228a.	0.5	0
72	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.	0.5	0

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73	Elastic network normal modes provide a basis for protein structure refinement. Journal of Chemical Physics, 2012, 136, 195101.	3.0	17
74	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.	0.8	3
75	The importance of slow motions for protein functional loops. Physical Biology, 2012, 9, 014001.	1.8	27
76	Fast learning optimized prediction methodology (FLOPRED) for protein secondary structure prediction. Journal of Molecular Modeling, 2012, 18, 4275-4289.	1.8	18
77	Combining Statistical Potentials with Dynamics-Based Entropies Improves Selection from Protein Decoys and Docking Poses. Journal of Physical Chemistry B, 2012, 116, 6725-6731.	2.6	24
78	ANM Normal Modes Show the Directions for Protein Structure Refinement. Biophysical Journal, 2012, 102, 25a.	0.5	1
79	How noise in force fields can affect the structural refinement of protein models?. Proteins: Structure, Function and Bioinformatics, 2012, 80, 335-341.	2.6	6
80	Statistical measures on residue-level protein structural properties. Journal of Structural and Functional Genomics, 2011, 12, 119-136.	1.2	7
81	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
82	MAVENs: Motion analysis and visualization of elastic networks and structural ensembles. BMC Bioinformatics, 2011, 12, 264.	2.6	37
83	Multibody coarseâ€grained potentials for native structure recognition and quality assessment of protein models. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1923-1929.	2.6	38
84	Exploration of the relationship between topology and designability of conformations. Journal of Chemical Physics, 2011, 134, 235101.	3.0	13
85	P.R.E.S.S. — An R-package for exploring residual-level protein structural statistics. , 2011, , .		0
86	Human telomerase model shows the role of the TEN domain in advancing the double helix for the next polymerization step. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9443-9448.	7.1	47
87	Statistical Contact Potentials in Protein Coarse-Grained Modeling: From Pair to Multi-body Potentials. , 2011, , 127-157.		10
88	Particle Swarm Optimization: A Powerful Family of Stochastic Optimizers. Analysis, Design and Application to Inverse Modelling. Lecture Notes in Computer Science, 2011, , 1-8.	1.3	4
89	Immunoglobulin Structure Exhibits Control over CDR Motion. Immunome Research, 2011, 7, .	0.1	5
90	Potentials 'R'Us web-server for protein energy estimations with coarse-grained knowledge-based potentials. BMC Bioinformatics, 2010, 11, 92.	2.6	31

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91	Structural interpretation of protein-protein interaction network. BMC Structural Biology, 2010, 10, S4.	2.3	10
92	Immunoglobulin functional motions and their effects on the complementarity determining regions. , 2010, , .		0
93	Protein Secondary Structure Prediction Using Knowledge-Based Potentials and An Ensemble of Classifiers. Biophysical Journal, 2010, 98, 52a.	0.5	0
94	Models To Approximate the Motions of Protein Loops. Journal of Chemical Theory and Computation, 2010, 6, 3249-3258.	5.3	1
95	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.	7.1	3
96	Chain dimensions and fluctuations in elastomeric networks in which the junctions alternate regularly in their functionality. Journal of Chemical Physics, 2009, 130, 064905.	3.0	5
97	Smallâ€Angle Neutron Scattering from Elastomeric Networks in which the Junctions Alternate Regularly in their Functionality. Macromolecular Theory and Simulations, 2009, 18, 537-544.	1.4	4
98	Distance matrix-based approach to protein structure prediction. Journal of Structural and Functional Genomics, 2009, 10, 67-81.	1.2	45
99	The energy profiles of atomic conformational transition intermediates of adenylate kinase. Proteins: Structure, Function and Bioinformatics, 2009, 77, 551-558.	2.6	39
100	Computational testing of protein-protein interactions. , 2009, , .		0
101	Data Mining for Protein Secondary Structure Prediction. Structure and Bonding, 2009, , 135-167.	1.0	3
102	Predicting the order in which contacts are broken during single molecule protein stretching experiments. Proteins: Structure, Function and Bioinformatics, 2008, 71, 45-60.	2.6	26
103	Orientational distributions of contact clusters in proteins closely resemble those of an icosahedron. Proteins: Structure, Function and Bioinformatics, 2008, 73, 730-741.	2.6	7
104	Use of machine learning algorithms to classify binary protein sequences as highly-designable or poorly-designable. BMC Bioinformatics, 2008, 9, 487.	2.6	4
105	Predicting the Complex Structure and Functional Motions of the Outer Membrane Transporter and Signal Transducer FecA. Biophysical Journal, 2008, 94, 2482-2491.	0.5	11
106	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.	5.3	26
107	The ribosome structure controls and directs mRNA entry, translocation and exit dynamics. Physical Biology, 2008, 5, 046005.	1.8	61
108	Packing Regularities in Biological Structures Relate to Their Dynamics. , 2007, 350, 251-276.		19

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109	Shape-dependent designability studies of lattice proteins. Journal of Physics Condensed Matter, 2007, 19, 285220.	1.8	5
110	Generation and enumeration of compact conformations on the two-dimensional triangular and three-dimensional fcc lattices. Journal of Chemical Physics, 2007, 127, 044101.	3.0	9
111	Consensus Data Mining (CDM) Protein Secondary Structure Prediction Server: Combining GOR V and Fragment Database Mining (FDM). Bioinformatics, 2007, 23, 2628-2630.	4.1	30
112	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.	0.7	8
113	Prediction of Side Chain Orientations in Proteins by Statistical Machine Learning Methods. Journal of Biomolecular Structure and Dynamics, 2007, 25, 275-287.	3.5	4
114	Theoretical Models and Simulations of Polymer Chains. , 2007, , 67-81.		4
115	Four-body contact potentials derived from two protein datasets to discriminate native structures from decoys. Proteins: Structure, Function and Bioinformatics, 2007, 68, 57-66.	2.6	73
116	Ideal amino acid exchange forms for approximating substitution matrices. Proteins: Structure, Function and Bioinformatics, 2007, 69, 379-393.	2.6	11
117	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.	5.3	84
118	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.	5.4	21
119	A Consensus Data Mining secondary structure prediction by combining GOR V and Fragment Database Mining. Protein Science, 2006, 15, 2499-2506.	7.6	22
120	Molecular modeling of matrix chain deformation in nanofiber filled composites. Colloid and Polymer Science, 2006, 284, 700-709.	2.1	3
121	Support-vector-machine classification of linear functional motifs in proteins. Journal of Molecular Modeling, 2006, 12, 453-461.	1.8	6
122	A DNA-Centric Look at Protein-DNA Complexes. Structure, 2006, 14, 1341-1342.	3.3	4
123	Functional clustering of yeast proteins from the protein-protein interaction network. BMC Bioinformatics, 2006, 7, 355.	2.6	40
124	The largest eigenvalue method for stereo-regular vinyl chains. Polymer, 2005, 46, 4373-4383.	3.8	7
125	Modeling the elastomeric properties of stereoregular polypropylenes in nanocomposites with spherical fillers. Polymer, 2005, 46, 7301-7308.	3.8	21
126	Some simulations on filler reinforcement in elastomers. Polymer, 2005, 46, 8894-8904.	3.8	65

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127	Prediction of protein secondary structure by mining structural fragment database. Polymer, 2005, 46, 4314-4321.	3.8	28
128	Molecular modeling of phosphorylation sites in proteins using a database of local structure segments. Journal of Molecular Modeling, 2005, 11, 431-438.	1.8	10
129	Inferring ideal amino acid interaction forms from statistical protein contact potentials. Proteins: Structure, Function and Bioinformatics, 2005, 59, 49-57.	2.6	66
130	GOR V server for protein secondary structure prediction. Bioinformatics, 2005, 21, 2787-2788.	4.1	179
131	Protein Promiscuity: Drug Resistance and Native Functionsâ€"HIV-1 Case. Journal of Biomolecular Structure and Dynamics, 2005, 22, 615-624.	3.5	22
132	Predicting binding sites of hydrolase-inhibitor complexes by combining several methods. BMC Bioinformatics, 2004, 5, 205.	2.6	27
133	The transfer matrix method for lattice proteinsâ€"an application with cooperative interactions. Polymer, 2004, 45, 707-716.	3.8	8
134	The origin and extent of coarse-grained regularities in protein internal packing. Proteins: Structure, Function and Bioinformatics, 2003, 53, 56-67.	2.6	33
135	Loop Folds in Proteins and Evolutionary Conservation of Folding Nuclei. Journal of Biomolecular Structure and Dynamics, 2002, 20, 323-325.	3.5	6
136	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.	2.6	135
137	Protein secondary structure prediction based on the GOR algorithm incorporating multiple sequence alignment information. Polymer, 2002, 43, 441-449.	3.8	25
138	Application of statistical mechanics to the analysis of various physical properties of elastomeric networks â€" a review. Polymer, 2002, 43, 1503-1525.	3.8	41
139	Effect of non-Gaussian chains on fluctuations of junctions in bimodal networks. Polymer, 2002, 43, 2569-2574.	3.8	4
140	Monte Carlo simulations on reinforcement of an elastomer by oriented prolate particles. Computational and Theoretical Polymer Science, 2001, 11, 251-262.	1.1	45
141	Contacts between segments in the random-flight model of polymer chains. Computational and Theoretical Polymer Science, 1999, 9, 285-294.	1.1	4
142	Novel High-Performance Materials from Starch. 1. Factors Influencing the Lyotropic Liquid Crystallinity of Some Starch Ethers. Chemistry of Materials, 1998, 10, 784-793.	6.7	6
143	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.	6.7	8
144	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.	6.7	12

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145	Transfer matrix method for enumeration and generation of compact self-avoiding walks. I. Square lattices. Journal of Chemical Physics, 1998, 109, 5134-5146.	3.0	28
146	Efficient Method To Count and Generate Compact Protein Lattice Conformations. Macromolecules, 1997, 30, 6691-6694.	4.8	19
147	Mechanical properties and transition temperatures of crosslinked-oriented gelatin. Colloid and Polymer Science, 1997, 275, 307-314.	2.1	49
148	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
149	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.	4.8	23
150	Main-Chain Lyotropic Liquid-Crystalline Elastomers. 2. Orientation and Mechanical Properties of Polyisocyanate Films. Macromolecules, 1996, 29, 2805-2812.	4.8	16
151	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.	2.1	82
152	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.	2.6	11
153	Oriented Gelatinâ€"A New Source for High-Performance Materials. Journal of Macromolecular Science - Pure and Applied Chemistry, 1996, 33, 525-540.	2.2	9
154	A simple derivation of the exponent Î³ for Gaussian chains with excluded volume. Macromolecular Theory and Simulations, 1995, 4, 245-252.	1.4	1
155	Dynamic Mechanical Losses in Filled Poly(Dimethylsiloxane) Networks. Rubber Chemistry and Technology, 1995, 68, 601-608.	1.2	11
156	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.	4.8	9
157	Theoretical Analysis of the Elastomeric and Optical Properties of Networks of Semirigid Chains in the Swollen State. Macromolecules, 1995, 28, 4920-4926.	4.8	15
158	A Diffused-Constraint Theory for the Elasticity of Amorphous Polymer Networks. 1. Fundamentals and Stress-Strain Isotherms in Elongation. Macromolecules, 1995, 28, 5089-5096.	4.8	63
159	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.	3.8	12
160	Computer simulations on filled elastomeric materials. Chemical Engineering Science, 1994, 49, 2889-2897.	3.8	50
161	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.	2.1	16
162	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.	2.1	13

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163	Correlations among chains along a crosslinked path in a phantom network and their characterization by SANS. Macromolecules, 1992, 25, 2455-2458.	4.8	6
164	Fluctuations, correlations, and small-angle neutron scattering from endlinked Gaussian chains in regular bimodal networks. Macromolecules, 1991, 24, 3266-3275.	4.8	27
165	Comment on: Statistical mechanics of rubber elasticity. Journal of Chemical Physics, 1991, 95, 7015-7016.	3.0	3
166	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.	3.0	4
167	A lattice model for segmental orientation in deformed polymeric networks. 2. Effect of chain stiffness and thermotropic interactions. Macromolecules, 1990, 23, 5341-5346.	4.8	28
168	Lattice model for segmental orientation in deformed polymeric networks. 1. Contribution of intermolecular correlations. Macromolecules, 1990, 23, 5335-5340.	4.8	42
169	The relaxation spectrum for Gaussian networks. Macromolecules, 1990, 23, 3481-3490.	4.8	52
170	On the Flory-Ronca theory of systems of rodlike particles. Macromolecules, 1990, 23, 5035-5037.	4.8	2
171	Neutron scattering from elastomeric networks. 2. An alternative phantom network model. Macromolecules, 1990, 23, 1222-1224.	4.8	1
172	On the Paceâ€“Datyner theory of diffusion of small molecules through polymers. Journal of Polymer Science, Part B: Polymer Physics, 1989, 27, 1663-1674.	2.1	9
173	Quadrupoles on the triangular two-dimensional lattice. Influence of the external field of graphite. Langmuir, 1989, 5, 1071-1074.	3.5	0
174	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.	4.8	3
175	Chain dimensions and fluctuations in random elastomeric networks. 2. Dependence of chain dimensions and fluctuations on macroscopic strain. Macromolecules, 1989, 22, 1432-1437.	4.8	14
176	Chain dimensions and fluctuations in random elastomeric networks. 1. Phantom Gaussian networks in the undeformed state. Macromolecules, 1989, 22, 1423-1432.	4.8	68
177	Quadrupoles on the triangular two-dimensional lattice: a simple model of nitrogen on graphite herringbone transition. Langmuir, 1988, 4, 817-821.	3.5	0
178	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
179	A visual representation for the shapes of flexible mesogenic molecules. Liquid Crystals, 1988, 3, 185-194.	2.2	19
180	Freezing of the hard core Yukawa fluid. Journal of Chemical Physics, 1988, 88, 5834-5839.	3.0	13

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181	On the relationship of the nematic-isotropic transition temperature of an oligomer to that of its constituent units. Liquid Crystals, 1988, 3, 95-99.	2.2	9
182	A molecular model for the smecticAphase. Molecular Physics, 1985, 55, 689-700.	1.7	20
183	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.	3.0	19
184	On the tricritical points in the McMillan model of liquid crystals. Molecular Physics, 1985, 55, 1223-1232.	1.7	6
185	A simple model for protection against environmental pollution in reactive coating films. Journal of Colloid and Interface Science, 1984, 99, 404-419.	9.4	2
186	On the mean spherical model for liquid crystals. Molecular Physics, 1982, 46, 13-19.	1.7	8
187	On the stability of the isotropic phase towards nematic and smecticAformation. Molecular Physics, 1981, 42, 51-63.	1.7	32