

# Andrzej Kloczkowski

## List of Publications by Year in descending order

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187  
papers

3,102  
citations

185998

28  
h-index

233125

45  
g-index

192  
all docs

192  
docs citations

192  
times ranked

2725  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predictive mathematical models of the growth of the COVID-19 pandemic. <i>Biophysical Journal</i> , 2022, 121, 532a.	0.2	0
2	Final Remarks. <i>Methods in Molecular Biology</i> , 2022, 2340, 469-470.	0.4	0
3	Using Surface Hydrophobicity Together with Empirical Potentials to Identify Protein-Protein Binding Sites: Application to the Interactions of E-cadherins. <i>Methods in Molecular Biology</i> , 2022, 2340, 41-50.	0.4	0
4	Biological and Cheminformatics Studies of Newly Designed Triazole Based Derivatives as Potent Inhibitors against Mushroom Tyrosinase. <i>Molecules</i> , 2022, 27, 1731.	1.7	11
5	Prediction of Site Directed miRNAs as Key Players of Transcriptional Regulators Against Influenza C Virus Infection Through Computational Approaches. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 866072.	1.6	3
6	Innovations in Genomics and Big Data Analytics for Personalized Medicine and Health Care: A Review. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4645.	1.8	45
7	Exploration of Potential Ewing Sarcoma Drugs from FDA-Approved Pharmaceuticals through Computational Drug Repositioning, Pharmacogenomics, Molecular Docking, and MD Simulation Studies. <i>ACS Omega</i> , 2022, 7, 19243-19260.	1.6	7
8	Hematopoietic Stem and Progenitor Cells (HSPCs) and Hematopoietic Microenvironment: Molecular and Bioinformatic Studies of the Zebrafish Models. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7285.	1.8	2
9	DescribePROT: database of amino acid-level protein structure and function predictions. <i>Nucleic Acids Research</i> , 2021, 49, D298-D308.	6.5	46
10	Sulfatase 2 Is Associated with Steroid Resistance in Childhood Nephrotic Syndrome. <i>Journal of Clinical Medicine</i> , 2021, 10, 523.	1.0	1
11	Prediction of Deleterious Protein Mutations. <i>Biophysical Journal</i> , 2021, 120, 269a.	0.2	0
12	Mechanistic insights into TNFR1/MADD death domains in Alzheimer's disease through conformational molecular dynamic analysis. <i>Scientific Reports</i> , 2021, 11, 12256.	1.6	6
13	Modeling SARS-CoV-2 proteins in the CASP-commons experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1987-1996.	1.5	24
14	Predictive Mathematical Models of the Short-Term and Long-Term Growth of the COVID-19 Pandemic. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-14.	0.7	6
15	A Hybrid Levenberg-Marquardt Algorithm on a Recursive Neural Network for Scoring Protein Models. <i>Methods in Molecular Biology</i> , 2021, 2190, 307-316.	0.4	1
16	Robust Prediction of Single and Multiple Point Protein Mutations Stability Changes. <i>Biomolecules</i> , 2020, 10, 67.	1.8	7
17	Entropy, Fluctuations, and Disordered Proteins. Linking between Sequence, Structure, and Disorder Information. <i>Biophysical Journal</i> , 2020, 118, 371a.	0.2	0
18	Robust Sampling of Defective Pathways in Alzheimer's Disease. Implications in Drug Repositioning. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3594.	1.8	9

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19	Prediction of Protein Tertiary Structure via Regularized Template Classification Techniques. <i>Molecules</i> , 2020, 25, 2467.	1.7	3
20	Computer Simulations of Key Peptides Involved in Preeclampsia and Alzheimer's Disease. <i>Biophysical Journal</i> , 2020, 118, 485a.	0.2	0
21	Computational Ways to Enhance Protein Inhibitor Design. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 607323.	1.6	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. <i>ACS Symposium Series</i> , 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. <i>Lecture Notes in Computer Science</i> , 2020, , 589-598.	1.0	1
24	Entropy, Fluctuations, and Disordered Proteins. <i>Entropy</i> , 2019, 21, 764.	1.1	5
25	Robust Sampling of Defective Pathways in Multiple Myeloma. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4681.	1.8	5
26	Deciphering General Characteristics of Residues Constituting Allosteric Communication Paths. <i>Lecture Notes in Computer Science</i> , 2019, , 245-258.	1.0	0
27	Characteristics of Protein Fold Space Exhibits Close Dependence on Domain Usage. <i>Lecture Notes in Computer Science</i> , 2019, , 356-369.	1.0	0
28	On the Relationship between Aggregation Rate and Mechanical Stability in Protein Aggregation. <i>Biophysical Journal</i> , 2019, 116, 196a.	0.2	1
29	Effect of Resultant Dipole Moment on Mechanical Stability of Protein-Peptide Complexes. <i>Biophysical Journal</i> , 2019, 116, 459a.	0.2	0
30	Predicting protein tertiary structure and its uncertainty analysis via particle swarm sampling. <i>Journal of Molecular Modeling</i> , 2019, 25, 79.	0.8	6
31	Explicit-Solvent All-Atom Molecular Dynamics of Peptide Aggregation. <i>Springer Series on Bio- and Neurosystems</i> , 2019, , 541-558.	0.2	0
32	Protein Secondary Structure Assignments and Their Usefulness for Dihedral Angle Prediction. <i>Springer Series on Bio- and Neurosystems</i> , 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. <i>Lecture Notes in Computer Science</i> , 2018, , 211-220.	1.0	2
35	Principal component analysis in protein tertiary structure prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1850005.	0.3	4
36	Classification of Allostery in Proteins: A Deep Learning Approach. <i>Biophysical Journal</i> , 2018, 114, 422a.	0.2	0

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37	Comparing NMR and X-ray protein structure: Lindemann-like parameters and NMR disorder. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2331-2341.	2.0	13
38	Reoptimized UNRES Potential for Protein Model Quality Assessment. <i>Genes</i> , 2018, 9, 601.	1.0	2
39	Modeling of Protein Structural Flexibility and Large-Scale Dynamics: Coarse-Grained Simulations and Elastic Network Models. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3496.	1.8	60
40	A topological order parameter for describing folding free energy landscapes of proteins. <i>Journal of Chemical Physics</i> , 2018, 149, 175101.	1.2	2
41	Combining Prediction of Protein Aggregation Propensities with Prediction of Other One-Dimensional Properties. <i>Biophysical Journal</i> , 2018, 114, 432a.	0.2	0
42	Role of Resultant Dipole Moment in Mechanical Dissociation of Biological Complexes. <i>Molecules</i> , 2018, 23, 1995.	1.7	20
43	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	1.6	19
44	Kinetics and mechanical stability of the fibril state control fibril formation time of polypeptide chains: A computational study. <i>Journal of Chemical Physics</i> , 2018, 148, 215106.	1.2	21
45	On the Use of Principal Component Analysis and Particle Swarm Optimization in Protein Tertiary Structure Prediction. <i>Lecture Notes in Computer Science</i> , 2018, , 107-116.	1.0	0
46	Prediction of Protein Aggregation Propensities using GOR Method. <i>Biophysical Journal</i> , 2017, 112, 198a-199a.	0.2	0
47	Computational Characterization of Oligomerization of FVFLM Peptide and its Ability to Inhibit Beta Amyloid Aggregation. <i>Biophysical Journal</i> , 2017, 112, 200a.	0.2	0
48	Deciphering General Characteristics of Residues Constituting Allosteric Communication Paths. <i>Biophysical Journal</i> , 2017, 112, 499a.	0.2	0
49	Oligomerization of FVFLM peptides and their ability to inhibit beta amyloid peptides aggregation: consideration as a possible model. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 2990-2999.	1.3	33
50	Fast and Accurate Accessible Surface Area Prediction Without a Sequence Profile. <i>Methods in Molecular Biology</i> , 2017, 1484, 127-136.	0.4	7
51	The GOR Method of Protein Secondary Structure Prediction and Its Application as a Protein Aggregation Prediction Tool. <i>Methods in Molecular Biology</i> , 2017, 1484, 7-24.	0.4	33
52	Accurate Prediction of One-Dimensional Protein Structure Features Using SPINE-X. <i>Methods in Molecular Biology</i> , 2017, 1484, 45-53.	0.4	1
53	Predicting Designability of Small Proteins from Graph Features of Contact Maps. <i>Journal of Computational Biology</i> , 2016, 23, 400-411.	0.8	6
54	Protein secondary structure prediction using a small training set (compact model) combined with a Complex-valued neural network approach. <i>BMC Bioinformatics</i> , 2016, 17, 362.	1.2	29

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55	Relationships between Mechanostability, Aggregation Rate and Binding Affinity of Peptides: Insights from All-ATOM Modeling in Explicit Solvent. <i>Biophysical Journal</i> , 2016, 110, 386a.	0.2	1
56	Fold-specific sequence scoring improves protein sequence matching. <i>BMC Bioinformatics</i> , 2016, 17, 328.	1.2	6
57	MQAPsingle: A quasi single-model approach for estimation of the quality of individual protein structure models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1021-1028.	1.5	21
58	Conditional entropy in variation-adjusted windows detects selection signatures associated with expression quantitative trait loci (eQTLs). <i>BMC Genomics</i> , 2015, 16, S8.	1.2	3
59	Multi-class BCGA-ELM based classifier that identifies biomarkers associated with hallmarks of cancer. <i>BMC Bioinformatics</i> , 2015, 16, 166.	1.2	10
60	GENN: A General Neural Network for Learning Tabulated Data with Examples from Protein Structure Prediction. <i>Methods in Molecular Biology</i> , 2015, 1260, 165-178.	0.4	8
61	In Silico Modeling of Human $\beta$ 2C-Adrenoreceptor Interaction with Filamin-2. <i>PLoS ONE</i> , 2014, 9, e103099.	1.1	12
62	BioShell-Threading: versatile Monte Carlo package for protein 3D threading. <i>BMC Bioinformatics</i> , 2014, 15, 22.	1.2	17
63	A Global Machine Learning Based Scoring Function for Protein Structure Prediction. <i>Biophysical Journal</i> , 2014, 106, 656a-657a.	0.2	9
64	A global machine learning based scoring function for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 752-759.	1.5	24
65	Accurate single-sequence prediction of solvent accessible surface area using local and global features. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3170-3176.	1.5	50
66	Protein Model Quality Assessment Prediction by using a Residue Specific Statistical Potential. <i>Biophysical Journal</i> , 2014, 106, 208a.	0.2	0
67	Volumes and Surface Areas: Geometries and Scaling Relationships between Coarse- Grained and Atomic Structures. <i>Current Pharmaceutical Design</i> , 2014, 20, 1208-1222.	0.9	3
68	Distributions of amino acids suggest that certain residue types more effectively determine protein secondary structure. <i>Journal of Molecular Modeling</i> , 2013, 19, 4337-4348.	0.8	4
69	MQAPmulti2 and MQAPsingle2:Toward the Estimation of Model Quality When Not Only Many Models are Available. <i>Biophysical Journal</i> , 2013, 104, 229a.	0.2	0
70	New Methods to Improve Protein Structure Prediction and Refinement. <i>Biophysical Journal</i> , 2013, 104, 229a.	0.2	1
71	De Novo Protein Structure Determination from Incomplete Experimental Data. <i>Biophysical Journal</i> , 2013, 104, 228a.	0.2	0
72	Cyclic AMP $\beta$ 1A signaling mediates cell surface translocation of microvascular smooth muscle $\beta$ 2C adrenoceptors through the actin binding protein filamin $\beta$ 2. <i>FASEB Journal</i> , 2013, 27, 729.15.	0.2	0

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73	Elastic network normal modes provide a basis for protein structure refinement. <i>Journal of Chemical Physics</i> , 2012, 136, 195101.	1.2	17
74	P.R.E.S.S. – AN R-PACKAGE FOR EXPLORING RESIDUAL-LEVEL PROTEIN STRUCTURAL STATISTICS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1242007.	0.3	3
75	The importance of slow motions for protein functional loops. <i>Physical Biology</i> , 2012, 9, 014001.	0.8	27
76	Fast learning optimized prediction methodology (FLOPRED) for protein secondary structure prediction. <i>Journal of Molecular Modeling</i> , 2012, 18, 4275-4289.	0.8	18
77	Combining Statistical Potentials with Dynamics-Based Entropies Improves Selection from Protein Decoys and Docking Poses. <i>Journal of Physical Chemistry B</i> , 2012, 116, 6725-6731.	1.2	24
78	ANM Normal Modes Show the Directions for Protein Structure Refinement. <i>Biophysical Journal</i> , 2012, 102, 25a.	0.2	1
79	How noise in force fields can affect the structural refinement of protein models?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 335-341.	1.5	6
80	Statistical measures on residue-level protein structural properties. <i>Journal of Structural and Functional Genomics</i> , 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. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 137-147.	1.2	16
82	MAVENs: Motion analysis and visualization of elastic networks and structural ensembles. <i>BMC Bioinformatics</i> , 2011, 12, 264.	1.2	37
83	Multibody coarse-grained potentials for native structure recognition and quality assessment of protein models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1923-1929.	1.5	38
84	Exploration of the relationship between topology and designability of conformations. <i>Journal of Chemical Physics</i> , 2011, 134, 235101.	1.2	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9443-9448.	3.3	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. <i>Analysis, Design and Application to Inverse Modelling. Lecture Notes in Computer Science</i> , 2011, , 1-8.	1.0	4
89	Immunoglobulin Structure Exhibits Control over CDR Motion. <i>Immunome Research</i> , 2011, 7, .	0.1	5
90	Potentials 'R'Us web-server for protein energy estimations with coarse-grained knowledge-based potentials. <i>BMC Bioinformatics</i> , 2010, 11, 92.	1.2	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.	0.2	0
94	Models To Approximate the Motions of Protein Loops. Journal of Chemical Theory and Computation, 2010, 6, 3249-3258.	2.3	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.	3.3	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.	1.2	5
97	Small- $\angle$ 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
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.	1.5	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.	1.5	26
103	Oriental distributions of contact clusters in proteins closely resemble those of an icosahedron. Proteins: Structure, Function and Bioinformatics, 2008, 73, 730-741.	1.5	7
104	Use of machine learning algorithms to classify binary protein sequences as highly-designable or poorly-designable. BMC Bioinformatics, 2008, 9, 487.	1.2	4
105	Predicting the Complex Structure and Functional Motions of the Outer Membrane Transporter and Signal Transducer FecA. Biophysical Journal, 2008, 94, 2482-2491.	0.2	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.	2.3	26
107	The ribosome structure controls and directs mRNA entry, translocation and exit dynamics. Physical Biology, 2008, 5, 046005.	0.8	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. <i>Journal of Physics Condensed Matter</i> , 2007, 19, 285220.	0.7	5
110	Generation and enumeration of compact conformations on the two-dimensional triangular and three-dimensional fcc lattices. <i>Journal of Chemical Physics</i> , 2007, 127, 044101.	1.2	9
111	Consensus Data Mining (CDM) Protein Secondary Structure Prediction Server: Combining GOR V and Fragment Database Mining (FDM). <i>Bioinformatics</i> , 2007, 23, 2628-2630.	1.8	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. <i>Macromolecular Symposia</i> , 2007, 256, 40-47.	0.4	8
113	Prediction of Side Chain Orientations in Proteins by Statistical Machine Learning Methods. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 25, 275-287.	2.0	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. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 57-66.	1.5	73
116	Ideal amino acid exchange forms for approximating substitution matrices. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 379-393.	1.5	11
117	The Extent of Cooperativity of Protein Motions Observed with Elastic Network Models Is Similar for Atomic and Coarser-Grained Models. <i>Journal of Chemical Theory and Computation</i> , 2006, 2, 696-704.	2.3	84
118	Filler-induced deformations of amorphous polyethylene chains. The effects of the deformations on elastomeric properties, and some comparisons with experiments. <i>European Polymer Journal</i> , 2006, 42, 796-806.	2.6	21
119	A Consensus Data Mining secondary structure prediction by combining GOR V and Fragment Database Mining. <i>Protein Science</i> , 2006, 15, 2499-2506.	3.1	22
120	Molecular modeling of matrix chain deformation in nanofiber filled composites. <i>Colloid and Polymer Science</i> , 2006, 284, 700-709.	1.0	3
121	Support-vector-machine classification of linear functional motifs in proteins. <i>Journal of Molecular Modeling</i> , 2006, 12, 453-461.	0.8	6
122	A DNA-Centric Look at Protein-DNA Complexes. <i>Structure</i> , 2006, 14, 1341-1342.	1.6	4
123	Functional clustering of yeast proteins from the protein-protein interaction network. <i>BMC Bioinformatics</i> , 2006, 7, 355.	1.2	40
124	The largest eigenvalue method for stereo-regular vinyl chains. <i>Polymer</i> , 2005, 46, 4373-4383.	1.8	7
125	Modeling the elastomeric properties of stereoregular polypropylenes in nanocomposites with spherical fillers. <i>Polymer</i> , 2005, 46, 7301-7308.	1.8	21
126	Some simulations on filler reinforcement in elastomers. <i>Polymer</i> , 2005, 46, 8894-8904.	1.8	65



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127	Prediction of protein secondary structure by mining structural fragment database. <i>Polymer</i> , 2005, 46, 4314-4321.	1.8	28
128	Molecular modeling of phosphorylation sites in proteins using a database of local structure segments. <i>Journal of Molecular Modeling</i> , 2005, 11, 431-438.	0.8	10
129	Inferring ideal amino acid interaction forms from statistical protein contact potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 49-57.	1.5	66
130	GOR V server for protein secondary structure prediction. <i>Bioinformatics</i> , 2005, 21, 2787-2788.	1.8	179
131	Protein Promiscuity: Drug Resistance and Native Functionsâ€™HIV-1 Case. <i>Journal of Biomolecular Structure and Dynamics</i> , 2005, 22, 615-624.	2.0	22
132	Predicting binding sites of hydrolase-inhibitor complexes by combining several methods. <i>BMC Bioinformatics</i> , 2004, 5, 205.	1.2	27
133	The transfer matrix method for lattice proteinsâ€™an application with cooperative interactions. <i>Polymer</i> , 2004, 45, 707-716.	1.8	8
134	The origin and extent of coarse-grained regularities in protein internal packing. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 56-67.	1.5	33
135	Loop Folds in Proteins and Evolutionary Conservation of Folding Nuclei. <i>Journal of Biomolecular Structure and Dynamics</i> , 2002, 20, 323-325.	2.0	6
136	Combining the GOR V algorithm with evolutionary information for protein secondary structure prediction from amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 154-166.	1.5	135
137	Protein secondary structure prediction based on the GOR algorithm incorporating multiple sequence alignment information. <i>Polymer</i> , 2002, 43, 441-449.	1.8	25
138	Application of statistical mechanics to the analysis of various physical properties of elastomeric networks â€™ a review. <i>Polymer</i> , 2002, 43, 1503-1525.	1.8	41
139	Effect of non-Gaussian chains on fluctuations of junctions in bimodal networks. <i>Polymer</i> , 2002, 43, 2569-2574.	1.8	4
140	Monte Carlo simulations on reinforcement of an elastomer by oriented prolate particles. <i>Computational and Theoretical Polymer Science</i> , 2001, 11, 251-262.	1.1	45
141	Contacts between segments in the random-flight model of polymer chains. <i>Computational and Theoretical Polymer Science</i> , 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. <i>Chemistry of Materials</i> , 1998, 10, 784-793.	3.2	6
143	Novel High-Performance Materials from Starch. 3. Influence of Degree of Substitution and Amylose/Amylopectin Ratio on Performance. <i>Chemistry of Materials</i> , 1998, 10, 804-811.	3.2	8
144	Novel High-Performance Materials from Starch. 2. Orientation and Mechanical Properties of Lightly Cross-Linked Starchâ€™Ether Films. <i>Chemistry of Materials</i> , 1998, 10, 794-803.	3.2	12

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145	Transfer matrix method for enumeration and generation of compact self-avoiding walks. I. Square lattices. <i>Journal of Chemical Physics</i> , 1998, 109, 5134-5146.	1.2	28
146	Efficient Method To Count and Generate Compact Protein Lattice Conformations. <i>Macromolecules</i> , 1997, 30, 6691-6694.	2.2	19
147	Mechanical properties and transition temperatures of crosslinked-oriented gelatin. <i>Colloid and Polymer Science</i> , 1997, 275, 307-314.	1.0	49
148	Computer generation and enumeration of compact self-avoiding walks within simple geometries on lattices. <i>Computational and Theoretical Polymer Science</i> , 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. <i>Macromolecules</i> , 1996, 29, 2796-2804.	2.2	23
150	Main-Chain Lyotropic Liquid-Crystalline Elastomers. 2. Orientation and Mechanical Properties of Polyisocyanate Films. <i>Macromolecules</i> , 1996, 29, 2805-2812.	2.2	16
151	Simulations on the reinforcement of poly(dimethylsiloxane) elastomers by randomly distributed filler particles. <i>Journal of Polymer Science, Part B: Polymer Physics</i> , 1996, 34, 1647-1657.	2.4	82
152	Structures and mechanical properties of zone-drawn-zone-annealed blends of cocrystallizing poly(butylene terephthalate) and a poly(ether ester). <i>Journal of Applied Polymer Science</i> , 1996, 59, 1667-1675.	1.3	11
153	Oriented Gelatin—A New Source for High-Performance Materials. <i>Journal of Macromolecular Science - Pure and Applied Chemistry</i> , 1996, 33, 525-540.	1.2	9
154	A simple derivation of the exponent $\hat{\nu}^3$ for Gaussian chains with excluded volume. <i>Macromolecular Theory and Simulations</i> , 1995, 4, 245-252.	0.6	1
155	Dynamic Mechanical Losses in Filled Poly(Dimethylsiloxane) Networks. <i>Rubber Chemistry and Technology</i> , 1995, 68, 601-608.	0.6	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. <i>Macromolecules</i> , 1995, 28, 4927-4931.	2.2	9
157	Theoretical Analysis of the Elastomeric and Optical Properties of Networks of Semirigid Chains in the Swollen State. <i>Macromolecules</i> , 1995, 28, 4920-4926.	2.2	15
158	A Diffused-Constraint Theory for the Elasticity of Amorphous Polymer Networks. 1. Fundamentals and Stress-Strain Isotherms in Elongation. <i>Macromolecules</i> , 1995, 28, 5089-5096.	2.2	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). <i>Polymer</i> , 1994, 35, 5247-5255.	1.8	12
160	Computer simulations on filled elastomeric materials. <i>Chemical Engineering Science</i> , 1994, 49, 2889-2897.	1.9	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. <i>Colloid and Polymer Science</i> , 1994, 272, 284-292.	1.0	16
162	A novel orientation technique for semi-rigid polymers. 2. Mechanical properties of cellulose acetate and hydroxypropylcellulose films. <i>Colloid and Polymer Science</i> , 1994, 272, 393-399.	1.0	13

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163	Correlations among chains along a crosslinked path in a phantom network and their characterization by SANS. <i>Macromolecules</i> , 1992, 25, 2455-2458.	2.2	6
164	Fluctuations, correlations, and small-angle neutron scattering from endlinked Gaussian chains in regular bimodal networks. <i>Macromolecules</i> , 1991, 24, 3266-3275.	2.2	27
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