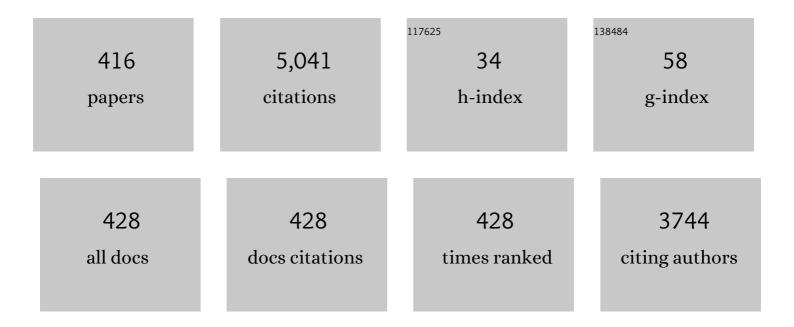
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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Augmented reality three-dimensional visualization with multifocus sensing. , 2022, 1, 355.		5
2	Critical Mutations of the SARS-CoV-2 Virus. WSEAS Transactions on Biology and Biomedicine, 2022, 19, 22-30.	0.5	1
3	Computational multifocus fluorescence microscopy for three-dimensional visualization of multicellular tumor spheroids. Journal of Biomedical Optics, 2022, 27, .	2.6	4
4	Glycosylation of SARS-CoV-2 Steers Evolutionary Outcomes in the Postvaccination Phase. ACS Pharmacology and Translational Science, 2021, 4, 410-412.	4.9	11
5	SARS-CoV-2 Glycosylation Suggests That Vaccines Should Have Adopted the S1 Subunit as Antigen. ACS Pharmacology and Translational Science, 2021, 4, 1016-1017.	4.9	7
6	Toward the Next-Generation COVID-19 Vaccines That Circumvent Antigenic Drift while Defusing Viral Infection. ACS Pharmacology and Translational Science, 2021, 4, 1018-1020.	4.9	4
7	Artificial Intelligence Set to Reverse Engineer Drug Targeting in the Cell. ACS Pharmacology and Translational Science, 2021, 4, 1256-1259.	4.9	0
8	Molecular Biology Clues Portray SARS-CoV-2 as a Gain-of-Function Laboratory Manipulation of Bat CoV RaTG13. ACS Medicinal Chemistry Letters, 2021, 12, 941-942.	2.8	5
9	Artificial Intelligence Deconstructs Drug Targeting <i>In Vivo</i> by Leveraging a Transformer Platform. ACS Medicinal Chemistry Letters, 2021, 12, 1052-1055.	2.8	2
10	COVID-19 Evolution in the Post-Vaccination Phase: Endemic or Extinct?. ACS Pharmacology and Translational Science, 2021, 4, 403-405.	4.9	6
11	Hough Transform Processing in 3D Object Detection and Visualization. , 2021, , .		0
12	Focus stacking and 3D visualization in multispectral microscopy of thick samples. , 2021, , .		0
13	Alternative antigen to defuse SARS-CoV-2 delta variant and its ensuing evolutionary lineage. Expert Opinion on Therapeutic Targets, 2021, , 1-3.	3.4	0
14	Learning Optics with a DIY Polarization-based 3D display. , 2021, , .		0
15	Artificial Intelligence Steering Molecular Therapy in the Absence of Information on Target Structure and Regulation. Journal of Chemical Information and Modeling, 2020, 60, 460-466.	5.4	3
16	Driving the catalytic activity of a transmembrane thermosensor kinase. Cellular and Molecular Life Sciences, 2020, 77, 3905-3912.	5.4	5
17	Defusing SARS-CoV-2: Emergency Brakes in a Vaccine Failure Scenario. ACS Pharmacology and Translational Science, 2020, 3, 1425-1426.	4.9	2
18	Therapeutically Targeted Destabilization of the Quaternary Structure of the Spike Protein in the Dominant G614 Strain of SARS-CoV-2. ACS Pharmacology and Translational Science, 2020, 3, 1027-1029.	4.9	4

#	Article	IF	CITATIONS
19	Structural Impact of Mutation D614G in SARS-CoV-2 Spike Protein: Enhanced Infectivity and Therapeutic Opportunity. ACS Medicinal Chemistry Letters, 2020, 11, 1667-1670.	2.8	64
20	Achilles' Heel of SARS-CoV-2 Structure. ACS Pharmacology and Translational Science, 2020, 3, 1030-1031.	4.9	5
21	Artificial Intelligence Teaches Drugs to Target Proteins by Tackling the Induced Folding Problem. Molecular Pharmaceutics, 2020, 17, 2761-2767.	4.6	7
22	Deep Learning Unravels a Dynamic Hierarchy While Empowering Molecular Dynamics Simulations. Annalen Der Physik, 2020, 532, 1900526.	2.4	1
23	Targeted Disassembling of SARS-CoV-2 as It Gets Ready for Cell Penetration. ACS Medicinal Chemistry Letters, 2020, 11, 2055-2057.	2.8	3
24	Deep Learning to Therapeutically Target Unreported Complexes. Trends in Pharmacological Sciences, 2019, 40, 551-554.	8.7	4
25	Protein structural defects enable pharmaceutical targeting while functionalizing the M2 proton channel. Biochemical and Biophysical Research Communications, 2019, 514, 86-91.	2.1	0
26	Reverse Engineering of a Thermosensing Regulator Switch. Journal of Molecular Biology, 2019, 431, 1016-1024.	4.2	8
27	Drug-based cancer therapy to overcome immune resistance by steering tumor evolution. Expert Opinion on Drug Discovery, 2019, 14, 5-8.	5.0	0
28	Robust object recognition in 3D scene by stereo vision image processing with the generalized Hough transform. , 2019, , .		1
29	Fully invariant generalized Hough transform by out-of-focus multiview sensing with pupil array. Applied Optics, 2019, 58, 7766.	1.8	8
30	Targeted therapy to annihilate the immune-evading phenotype in cancer evolution. Expert Opinion on Therapeutic Targets, 2018, 22, 559-562.	3.4	0
31	Stickiness of the Hydrogen Bond. Annalen Der Physik, 2018, 530, 1800162.	2.4	4
32	All-in-focus image reconstruction robust to ghosting effect. , 2018, , .		2
33	Making Targeted Therapy Compatible with Checkpoint Immunotherapy. Trends in Biotechnology, 2017, 35, 582-584.	9.3	1
34	Incoherent optical generalized Hough transform: pattern recognition and feature extraction applications. Optical Engineering, 2017, 56, 053107.	1.0	5
35	Dielectric response of frustrated water down to a singleâ€molecule contribution. Annalen Der Physik, 2017, 529, 1600373.	2.4	3
36	Advanced Modeling Reconciles Counterintuitive Decisions in Lead Optimization. Trends in Biotechnology, 2017, 35, 490-497.	9.3	7

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37	Engineering Tumor Hypersusceptibility to Checkpoint Immunotherapy. Trends in Cancer, 2017, 3, 675-677.	7.4	2
38	Epistructure-Based Design of Drugs with Controlled Promiscuity. Soft and Biological Matter, 2016, , 351-376.	0.3	1
39	Epistructural Dynamics of Biological Water. Soft and Biological Matter, 2016, , 105-120.	0.3	0
40	Solution to the Protein Folding Problem. Soft and Biological Matter, 2016, , 71-103.	0.3	0
41	Nonâ€Debye frustrated hydration steers biomolecular association: interfacial tension for the drug designer. FEBS Letters, 2016, 590, 3481-3491.	2.8	5
42	Interfacial Physics for Water in Biology. Soft and Biological Matter, 2016, , 1-46.	0.3	0
43	Pattern recognition and feature extraction with an optical Hough transform. , 2016, , .		0
44	Epistructural Drug Design to Treat Cancer Metastasis and the Associated Drug Resistance. Soft and Biological Matter, 2016, , 417-425.	0.3	0
45	Acid–base chemistry of frustrated water at protein interfaces. FEBS Letters, 2016, 590, 215-223.	2.8	1
46	lon transfer of weak acids across liquid liquid interfaces. Journal of Electroanalytical Chemistry, 2016, 774, 111-121.	3.8	9
47	Quantum Mechanical Concepts for Epistructural Drug Design. Soft and Biological Matter, 2016, , 393-401.	0.3	0
48	Reconstruction of perspective shifts and refocusing of a three-dimensional scene from a multi-focus image stack. Applied Optics, 2016, 55, 2380.	2.1	45
49	Effectiveness of an mHealth intervention to improve the cardiometabolic profile of people with prehypertension in low-resource urban settings in Latin America: a randomised controlled trial. Lancet Diabetes and Endocrinology,the, 2016, 4, 52-63.	11.4	117
50	Effect of ligand protonation on the facilitated ion transfer reactions across oil water interfaces. V. Applications of forced hydrodynamic conditions. Journal of Electroanalytical Chemistry, 2016, 765, 100-104.	3.8	10
51	Drug leads for interactive protein targets with unknown structure. Drug Discovery Today, 2016, 21, 531-535.	6.4	1
52	Drug-Target Associations Inducing Protein Folding. Soft and Biological Matter, 2016, , 305-321.	0.3	2
53	Robust Pattern Recognition with Optical Generalized Hough Transform. , 2016, , .		1
54	Image segmentation by nonlinear filtering of optical Hough transform. Applied Optics, 2016, 55, 3632.	2.1	9

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55	Synergizing Engineered Immunotherapy with Molecularly Targeted Cancer Treatment. Soft and Biological Matter, 2016, , 377-391.	0.3	0
56	Dehydron-Rich Proteins in the Order-Disorder Twilight Zone. Soft and Biological Matter, 2016, , 121-150.	0.3	0
57	Catalytic Role of Dehydrons in Soluble Proteins: Biological Chemistry of Frustrated Interfacial Water. Soft and Biological Matter, 2016, , 181-216.	0.3	Ο
58	Structure-Based Drug Discovery Without Structure: Working Around the Paradox to Disrupt Protein Associations. Soft and Biological Matter, 2016, , 403-415.	0.3	0
59	Drug Combinations to Enhance Therapeutic Efficacy and Edit Out Side Effects and Resistance to Inhibition of Drug Resistance. Soft and Biological Matter, 2016, , 323-350.	0.3	0
60	Epistructural Re-engineering of Imatinib to Eliminate Adverse Side Effects. Soft and Biological Matter, 2016, , 239-265.	0.3	0
61	Epistructural Informatics for the Drug Designer. Soft and Biological Matter, 2016, , 267-304.	0.3	0
62	Epistructural Selectivity Filters for Molecular Targeted Therapy. Soft and Biological Matter, 2016, , 217-237.	0.3	0
63	Dehydron as a Marker for Molecular Evolution: Lessons for the Drug Designer. Soft and Biological Matter, 2016, , 151-179.	0.3	0
64	Dielectric Structure of Aqueous Interfaces: From Classical Non-Debye Electrostatics to a Quantum Theory of Interfacial Tension. Soft and Biological Matter, 2016, , 47-70.	0.3	0
65	Discordant identification of pediatric severe sepsis by research and clinical definitions in the SPROUT international point prevalence study. Critical Care, 2015, 19, 325.	5.8	85
66	Drug-Based Disruption of Protein Complexes with Unknown Structure: Towards a Novel Platform for Drug Discovery. Journal of Pharmacogenomics & Pharmacoproteomics, 2015, 06, .	0.2	0
67	Validation of the Pediatric Index of Mortality 2 (PIM2) in Argentina: a prospective, multicenter, observational study. Archivos Argentinos De Pediatria, 2015, 113, .	0.2	0
68	Chemical Functionality of the Aqueous Interface in Soluble Proteins. , 2015, , 151-174.		0
69	Electrostatic Exploration of Biomolecular Interfaces: The Chemical Function of Interfacial Water. , 2015, , 35-51.		0
70	Real-time pattern recognition using an optical generalized Hough transform. Applied Optics, 2015, 54, 10586.	2.1	11
71	Quantum theory of interfacial tension quantitatively predicts spontaneous charging of nonpolar aqueous interfaces. Physics Letters, Section A: General, Atomic and Solid State Physics, 2015, 379, 2405-2408.	2.1	2
72	Pediatric Index of Mortality 2 as a predictor of death risk in children admitted to pediatric intensive care units in Latin America: A prospective, multicenter study. Journal of Critical Care, 2015, 30, 1324-1330.	2.2	21

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73	Biomolecular Interfaces. , 2015, , .		7
74	Semiempirical Solution to the Protein Folding Problem Through a Combination of Structural and Epistructural Approaches. , 2015, , 53-82.		0
75	Packing defects functionalize soluble proteins. FEBS Letters, 2015, 589, 967-973.	2.8	8
76	Challenges of Implementing mHealth Interventions for Lifestyle Modification in Prehypertensive Subjects in Argentina, Guatemala, and Peru. , 2015, , 119-127.		4
77	Optical implementation of the generalized Hough transform with totally incoherent light. Optics Letters, 2015, 40, 3901.	3.3	12
78	All-in-focus image reconstruction under severe defocus. Optics Letters, 2015, 40, 1671.	3.3	35
79	High-Level Quantum Chemistry Empowers the Wrapping Technology for Drug Design. , 2015, , 325-330.		Ο
80	Comparative electrochemical performance of electrodeposited polypyrrole in protic and aprotic ionic liquids. Journal of Electroanalytical Chemistry, 2015, 737, 23-29.	3.8	10
81	Aceptabilidad de una intervención basada en salud móvil para modificar estilos de vida en prehipertensos de Argentina, Guatemala y Perú: un estudio piloto. Revista Peruana De Medicina De Experimental Y Salud Publica, 2015, 32, 221.	0.4	10
82	Proteins in the Order–Disorder Twilight: Unstable Interfaces Promote Protein Aggregation. , 2015, , 97-126.		2
83	Packing Defects and Protein Hydration: Dynamics of the Aqueous Interface. , 2015, , 83-96.		0
84	Engineering Therapeutic Alignments Between Immune Response and Molecularly Targeted Cancer Treatment. , 2015, , 311-323.		0
85	The Aqueous Interface of a Soluble Protein or the Birth of Epistructural Biology. , 2015, , 1-33.		2
86	Evolutionary Roots of Proteomic Complexity and Lessons for the Drug Designer. Journal of Pharmacogenomics & Pharmacoproteomics, 2015, 06, .	0.2	0
87	Evolution of Protein Structure Degradation and Lessons for the Drug Designer. , 2015, , 127-149.		0
88	Multitarget Control of Drug Impact: A Therapeutic Imperative in Cancer Systems Biology. , 2015, , 285-309.		0
89	Biomolecular Interfaces Provide Universal Markers for Drug Specificity and Personalized Medicine. , 2015, , 217-241.		0
90	The Biomolecular Interface as a Selectivity Filter for Drug-Based Targeted Therapy. , 2015, , 175-192.		0

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91	Real-time Optical Realization of Circle Hough Transform with Incoherent Light. , 2015, , .		Ο
92	Evolución de la estructura socioeconómica de la región pampeana argentina. El proceso de concentración de la producción en el perÃodo 1988-2008. Cuadernos De Economia (Colombia), 2015, 34, 143-171.	0.2	1
93	Editorial Expression of Concern: Non-adaptive origins of interactome complexity. Nature, 2014, 516, 440-440.	27.8	Ο
94	Synergizing immunotherapy with molecular-targeted anticancer treatment. Drug Discovery Today, 2014, 19, 1427-1432.	6.4	8
95	Water promotes the sealing of nanoscale packing defects in folding proteins. Journal of Physics Condensed Matter, 2014, 26, 202101.	1.8	9
96	Communication: Chemical functionality of interfacial water enveloping nanoscale structural defects in proteins. Journal of Chemical Physics, 2014, 140, 221102.	3.0	17
97	A lipid-mediated conformational switch modulates the thermosensing activity of DesK. Proceedings of the United States of America, 2014, 111, 3579-3584.	7.1	69
98	Productive induced metastability in allosteric modulation of kinase function. FEBS Journal, 2014, 281, 3079-3091.	4.7	2
99	Protein packing defects "heat up―interfacial water. European Physical Journal E, 2013, 36, 62.	1.6	9
100	Single-shot phase recovery using two laterally separated defocused images. Optics Communications, 2013, 293, 1-3.	2.1	18
101	Edge linking and image segmentation by combining optical and digital methods. Optik, 2013, 124, 3260-3264.	2.9	8
102	Breakdown of the Debye polarization <i>ansatz</i> at protein-water interfaces. Journal of Chemical Physics, 2013, 138, 225103.	3.0	8
103	The principle of minimal episteric distortion of the water matrix and its steering role in protein folding. Journal of Chemical Physics, 2013, 139, 085101.	3.0	17
104	Diseño Electrónico de un Electrocardiógrafo Basado en Arquitectura ARM9. IFMBE Proceedings, 2013, , 786-789.	0.3	0
105	Provisional theory of nanoscale water dielectrics. Journal of Biological Physics and Chemistry, 2013, 13, 9-11.	0.1	Ο
106	Entre la vida y la muerte. Testamentos de don Gabriel y doña Lucrecia Fernández Guarachi (Jesús de) Tj ETQq	0.0 rgBT	/Oyerlock 10
107	Color encoding of binary fringes for gamma correction in 3-D profiling. Optics Letters, 2012, 37, 1325.	3.3	21

108Edge enhancement of color images using a digital micromirror device. Applied Optics, 2012, 51, 3439.1.82

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109	Communication: Nanoscale electrostatic theory of epistructural fields at the protein-water interface. Journal of Chemical Physics, 2012, 137, 231101.	3.0	5
110	Communication: Epistructural thermodynamics of soluble proteins. Journal of Chemical Physics, 2012, 136, 091101.	3.0	0
111	Ion transfer across liquid liquid interface under forced hydrodynamic conditions. I: Digital simulations. Journal of Electroanalytical Chemistry, 2012, 666, 42-51.	3.8	7
112	A unifying motif of intermolecular cooperativity in protein associations. European Physical Journal E, 2012, 35, 59.	1.6	9
113	Likelihood of side effects depends on desired clinical impact: Affinities within a very small set of targets enables inference of promiscuity or specificity of kinase inhibitors. , 2012, , .		Ο
114	Methods for edge enhancement in color images based on derivative operations. , 2012, , .		0
115	Wrapping mimicking in drugâ€like small molecules disruptive of protein–protein interfaces. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1755-1765.	2.6	13
116	Epistructural Tension Promotes Protein Associations. Physical Review Letters, 2012, 108, 188102.	7.8	30
117	Purposely engineered drug–target mismatches for entropy-based drug optimization. Trends in Biotechnology, 2012, 30, 1-7.	9.3	22
118	Supramolecular Evolution of Protein Organization. Annual Review of Genetics, 2012, 47, 130628183942007.	7.6	0
119	Three-dimensional profiling with binary fringes using phase-shifting interferometry algorithms. Applied Optics, 2011, 50, 147.	2.1	32
120	Optical processing of color images with incoherent illumination: orientation-selective edge enhancement using a modified liquid-crystal display. Optics Express, 2011, 19, 21091.	3.4	12
121	Incoherent optical processor for nondirectional edge enhancement of color images. Optics Letters, 2011, 36, 4596.	3.3	8
122	Selectivity Filters to Edit Out Deleterious Side Effects in Kinase Inhibitors. Current Topics in Medicinal Chemistry, 2011, 11, 788-799.	2.1	4
123	Variational mechanics of water at biological interfaces. Journal of Physics A: Mathematical and Theoretical, 2011, 44, 292001.	2.1	2
124	Binding of the Highly Toxic Tetracycline Derivative, Anhydrotetracycline, to Bovine Serum Albumin. Biological and Pharmaceutical Bulletin, 2011, 34, 1301-1306.	1.4	18
125	Subfunctionalization reduces the fitness cost of gene duplication in humans by buffering dosage imbalances. BMC Genomics, 2011, 12, 604.	2.8	12
126	Nanoscale thermodynamics of biological interfacial tension. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2011, 467, 559-568.	2.1	8

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127	Non-adaptive origins of interactome complexity. Nature, 2011, 474, 502-505.	27.8	118
128	Pharmaceutical Industry at the Post-Genomic Junction. Metabolomics: Open Access, 2011, 01, .	0.1	2
129	Distribution of ionic components between two immiscible solutions. Partition of weak bases. Journal of Electroanalytical Chemistry, 2010, 640, 42-50.	3.8	7
130	Membrane Thickness Cue for Cold Sensing in a Bacterium. Current Biology, 2010, 20, 1539-1544.	3.9	116
131	Transfer of tylosin across the H2O/1,2-dichloroethane interface. Analysis of degraded product in acid solutions. Journal of Electroanalytical Chemistry, 2010, 650, 47-54.	3.8	15
132	c-Jun-NH2-kinase-1 Inhibition Leads to Antitumor Activity in Ovarian Cancer. Clinical Cancer Research, 2010, 16, 184-194.	7.0	55
133	Engineering a Thermosensor To Dissect a Transmembrane Signaling System. Biophysical Journal, 2010, 98, 88a.	0.5	0
134	Analog image contouring using a twisted-nematic liquid-crystal display. Optics Express, 2010, 18, 19163.	3.4	8
135	Golden Rule for Buttressing Vulnerable Soluble Proteins. Journal of Proteome Research, 2010, 9, 2643-2648.	3.7	12
136	Induced Disorder in Protein–Ligand Complexes as a Drug-Design Strategy. Molecular Pharmaceutics, 2010, 7, 306-306.	4.6	0
137	Dehydron Analysis: Quantifying the Effect of Hydrophobic Groups on the Strength and Stability of Hydrogen Bonds. Advances in Experimental Medicine and Biology, 2010, 680, 473-479.	1.6	9
138	Transformative Concepts for Drug Design: Target Wrapping. , 2010, , .		21
139	Protein Cooperativity and Wrapping: Two Themes in the Transformative Platform of Molecular Targeted Therapy. , 2010, , 1-15.		5
140	Sub-Nanoscale Surface Ruggedness Provides a Water-Tight Seal for Exposed Regions in Soluble Protein Structure. PLoS ONE, 2010, 5, e12844.	2.5	20
141	Wrapping Deficiencies and De-wetting Patterns in Soluble Proteins: A Blueprint for Drug Design. , 2010, , 49-58.		0
142	Inducing Folding By Crating the Target. , 2010, , 187-196.		0
143	Wrapping as a Selectivity Filter for Molecular Targeted Therapy: Preliminary Evidence. , 2010, , 97-115.		0
144	Last Frontier and Back to the Drawing Board: Protein–Water Interfacial Tension in Drug Design. , 2010, , 217-223.		0

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145	Wrapper Drugs as Therapeutic Editors of Side Effects. , 2010, , 197-210.		Ο
146	Fulfilling a Therapeutic Imperative in Cancer Treatment: Control of Multi-target Drug Impact. , 2010, , 163-186.		0
147	Evolution of Protein Wrapping and Implications for the Drug Designer. , 2010, , 79-96.		0
148	Under-Wrapped Proteins in the Order–Disorder Twilight: Unraveling the Molecular Etiology of Aberrant Aggregation. , 2010, , 59-78.		0
149	Wrapper Drugs for Personalized Medicine. , 2010, , 211-215.		Ο
150	Wrapping Patterns as Universal Markers for Specificity in the Therapeutic Interference with Signaling Pathways. , 2010, , 141-161.		0
151	Re-engineering an Anticancer Drug to Make It Safer: Modifying Imatinib to Curb Its Side Effects. , 2010, , 117-140.		0
152	Wrapping Defects and the Architecture of Soluble Proteins. , 2010, , 17-26.		0
153	Abstract 5468: JNK-1 inhibition leads to antitumor activity in ovarian cancer. , 2010, , .		Ο
154	Human capacitance to dosage imbalance: Coping with inefficient selection. Genome Research, 2009, 19, 2185-2192.	5.5	9
155	Is there a case for selectively promiscuous anticancer drugs?. Drug Discovery Today, 2009, 14, 1-5.	6.4	28
156	Taming the induced folding of drug-targeted kinases. Trends in Pharmacological Sciences, 2009, 30, 66-71.	8.7	14
157	Selective antagonism of anticancer drugs for side-effect removal. Trends in Pharmacological Sciences, 2009, 30, 403-410.	8.7	20
158	Hydration Profiles of Amyloidogenic Molecular Structures. Journal of Biological Physics, 2008, 34, 577-590.	1.5	8
159	Electroanalytical procedure to resolve a sample solution containing tetracycline and its toxic degraded product: Anhydrotetracycline. Journal of Electroanalytical Chemistry, 2008, 624, 121-128.	3.8	17
160	Turning promiscuous kinase inhibitors into safer drugs. Trends in Biotechnology, 2008, 26, 295-301.	9.3	56
161	<i>In Silico</i> Drug Profiling of the Human Kinome Based on a Molecular Marker for Cross Reactivity. Molecular Pharmaceutics, 2008, 5, 728-738.	4.6	7
162	Protein structure protection commits gene expression patterns. Genome Biology, 2008, 9, R107.	9.6	23

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163	Protein wrapping: a molecular marker for association, aggregation and drug design. Chemical Society Reviews, 2008, 37, 2373.	38.1	31
164	Bottom-Up Engineering of Peptide Cell Translocators Based on Environmentally Modulated Quadrupole Switches. ACS Nano, 2008, 2, 61-68.	14.6	3
165	Induced Disorder in Protein–Ligand Complexes as a Drug-Design Strategy. Molecular Pharmaceutics, 2008, 5, 430-437.	4.6	20
166	Redesigning Kinase Inhibitors to Enhance Specificity. Journal of Medicinal Chemistry, 2008, 51, 4890-4898.	6.4	31
167	Protein Under-Wrapping Causes Dosage Sensitivity and Decreases Gene Duplicability. PLoS Genetics, 2008, 4, e11.	3.5	53
168	Folding and Wrapping Soluble Proteins: Exploring the Molecular Basis of Cooperativity and Aggregation. Progress in Molecular Biology and Translational Science, 2008, 83, 53-87.	1.7	5
169	Evolutionary constraints imposed by gene dosage balance. Frontiers in Bioscience - Landmark, 2008, Volume, 4373.	3.0	5
170	Peptide translocators with engineered dehydration-prone hydrogen bonds. Journal of Chemical Physics, 2007, 126, 061102.	3.0	0
171	Solvent-exposed backbone loosens the hydration shell of soluble folded proteins. Journal of Chemical Physics, 2007, 126, 245103.	3.0	12
172	Molecular Basis for Evolving Modularity in the Yeast Protein Interaction Network. PLoS Computational Biology, 2007, 3, e226.	3.2	11
173	Molecular basis for specificity in the druggable kinome: sequence-based analysis. Bioinformatics, 2007, 23, 563-572.	4.1	52
174	Modulating drug impact by wrapping target proteins. Expert Opinion on Drug Discovery, 2007, 2, 249-259.	5.0	1
175	Rational Drug Redesign to Overcome Drug Resistance in Cancer Therapy: Imatinib Moving Target. Cancer Research, 2007, 67, 4028-4033.	0.9	53
176	Therapeutic Efficacy of a Novel Focal Adhesion Kinase Inhibitor TAE226 in Ovarian Carcinoma. Cancer Research, 2007, 67, 10976-10983.	0.9	201
177	Passive Waterâ^'Lipid Peptide Translocators with Conformational Switches:  From Single-Molecule Probe to Cellular Assay. Journal of Physical Chemistry B, 2007, 111, 13987-13992.	2.6	0
178	Dehydration Propensity of Orderâ^'Disorder Intermediate Regions in Soluble Proteins. Journal of Proteome Research, 2007, 6, 3519-3526.	3.7	44
179	Kinase packing defects as drug targets. Drug Discovery Today, 2007, 12, 917-923.	6.4	25
180	Engineering productive enzyme confinement. Trends in Biotechnology, 2007, 25, 189-190.	9.3	26

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181	An anticancer C-Kit kinase inhibitor is reengineered to make it more active and less cardiotoxic. Journal of Clinical Investigation, 2007, 117, 4044-4054.	8.2	148
182	Wrapping technology and the enhancement of specificity in cancer drug treatment. Frontiers in Bioscience - Landmark, 2007, 12, 3617.	3.0	4
183	Electrocardiógrafo de 12 canales con atractivas opciones de conectividad. IFMBE Proceedings, 2007, , 452-455.	0.3	0
184	Dise $ ilde{A}$ ±o de un Electrocardi $ ilde{A}$ 3grafo Digital. IFMBE Proceedings, 2007, , 537-541.	0.3	0
185	Structural and Conformational Prerequisites of Amyloidogenesis. , 2006, , 1-20.		4
186	A Priori Inference of Cross Reactivity for Drug-Targeted Kinases. Journal of Medicinal Chemistry, 2006, 49, 3092-3100.	6.4	30
187	Feature-similarity protein classifier as a ligand engineering tool. New Biotechnology, 2006, 23, 307-315.	2.7	8
188	Novel electrochemical approach to the determination of the partition coefficient of neutral weak bases. Journal of Electroanalytical Chemistry, 2006, 594, 80-88.	3.8	18
189	Incomplete Protein Packing as a Selectivity Filter in Drug Design. Structure, 2006, 14, 947.	3.3	0
190	Packing defects as selectivity switches for drug-based protein inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 323-328.	7.1	8
191	Prediction of the Sugar Mill Shaft Failure Using a Fracture Mechanics Method. , 2005, , 749.		0
192	Transfer of tetracyclines across the H2O 1,2-dichloroethane interface: Analysis of degraded products in strong acid and alkaline solutions. Journal of Electroanalytical Chemistry, 2005, 585, 240-249.	3.8	23
193	Incomplete Protein Packing as a Selectivity Filter in Drug Design. Structure, 2005, 13, 1829-1836.	3.3	26
194	Efficiency Increase in the Extraction of Sugar Cane Juice in the Sugar Cane Mills by Means of the Regulation of Hydraulic Pressures. , 2005, , 637.		1
195	Direct nanoscale dehydration of hydrogen bonds. Journal Physics D: Applied Physics, 2005, 38, 2928-2932.	2.8	4
196	Protein Promiscuity: Drug Resistance and Native Functions—HIV-1 Case. Journal of Biomolecular Structure and Dynamics, 2005, 22, 615-624.	3.5	22
197	The integrated development of network complexity modulates the diverse evolutionary mutation rates of individual proteins. FEBS Letters, 2005, 579, 5718-5722.	2.8	0
198	What factor drives the fibrillogenic association of \hat{I}^2 -sheets?. FEBS Letters, 2005, 579, 6635-6640.	2.8	25

#	Article	IF	CITATIONS
199	Determination of an Optimal Assembly Misalignment in Sugar Cane Mills. , 2005, , .		0
200	Protein Under-wrapping Causes Dosage Sensitivity and Decreases Gene Duplicability. PLoS Genetics, 2005, preprint, e11.	3.5	0
201	Continuum equations for dielectric response to macro-molecular assemblies at the nano scale. Journal of Physics A, 2004, 37, 9791-9803.	1.6	18
202	Sequence-space selection of cooperative model proteins. Journal of Physics A, 2004, 37, L197-L202.	1.6	6
203	Dielectric Modulation of Biological Water. Physical Review Letters, 2004, 93, 228104.	7.8	99
204	Publisher's Note: Dielectric Modulation of Biological Water [Phys. Rev. Lett.93, 228104 (2004)]. Physical Review Letters, 2004, 93, .	7.8	3
205	Buffering the entropic cost of hydrophobic collapse in protein chains. Journal of Chemical Physics, 2004, 121, 11501.	3.0	1
206	Molecular dimension explored in evolution to promote proteomic complexity. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13460-13465.	7.1	51
207	The nonconserved wrapping of conserved protein folds reveals a trend toward increasing connectivity in proteomic networks. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2823-2827.	7.1	35
208	Inhibitor design by wrapping packing defects in HIV-1 proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11640-11645.	7.1	34
209	Keeping dry and crossing membranes. Nature Biotechnology, 2004, 22, 1081-1084.	17.5	70
210	Protein folding: a good structure protector is also a good structure seeker. Physics Letters, Section A: General, Atomic and Solid State Physics, 2004, 321, 263-266.	2.1	1
211	Functionality of Wrapping Defects in Soluble Proteins: What Cannot be Kept Dry Must be Conserved. Journal of Molecular Biology, 2004, 337, 477-483.	4.2	17
212	Lower Limit to the Size of the Primeval Amino Acid Alphabet. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2004, 59, 151-152.	1.4	4
213	Amino Acid Residues at Proteinâ^'Protein Interfaces:Â Why Is Propensity so Different from Relative Abundance?. Journal of Physical Chemistry B, 2003, 107, 9929-9932.	2.6	13
214	Large-Scale Context in Protein Folding: Villin Headpieceâ€. Biochemistry, 2003, 42, 664-671.	2.5	56
215	Protein folding: could hydrophobic collapse be coupled with hydrogen-bond formation?. FEBS Letters, 2003, 536, 187-192.	2.8	46
216	Dehydron: A Structurally Encoded Signal for Protein Interaction. Biophysical Journal, 2003, 85, 1914-1928.	0.5	105

#	Article	IF	CITATIONS
217	Proteins with H-bond packing defects are highly interactive with lipid bilayers: Implications for amyloidogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2391-2396.	7.1	91
218	Insufficiently dehydrated hydrogen bonds as determinants of protein interactions. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 113-118.	7.1	247
219	Adherence of Packing Defects in Soluble Proteins. Physical Review Letters, 2003, 91, 018102.	7.8	62
220	Interbasin motion approach to dynamics of conformationally constrained peptides. Journal of Chemical Physics, 2003, 118, 5673-5682.	3.0	11
221	Under-wrapped soluble proteins as signals triggering membrane morphology. Journal of Chemical Physics, 2003, 119, 6911-6915.	3.0	6
222	What caliber pore is like a pipe? Nanotubes as modulators of ionic gradients. Journal of Chemical Physics, 2003, 119, 5315-5319.	3.0	19
223	Oncogenic Mutations and Packing Defects in Protein Structure. Journal of Biomolecular Structure and Dynamics, 2003, 21, 9-14.	3.5	0
224	Structural defects and the diagnosis of amyloidogenic propensity. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6446-6451.	7.1	86
225	Protein Folding: Is Hierarchical versus Nonhierarchical a Productive Issue?. Journal of Biomolecular Structure and Dynamics, 2002, 19, 735-737.	3.5	4
226	Protein design from in silico dynamic information: the emergence of the `turn–dock–lock' motif. Protein Engineering, Design and Selection, 2002, 15, 1-6.	2.1	3
227	Protein Folding: Where is the Paradox?. Journal of Biomolecular Structure and Dynamics, 2002, 20, 331-332.	3.5	4
228	Pathway Diversity and Concertedness in Protein Folding: An ab-initio Approach. Journal of Biomolecular Structure and Dynamics, 2002, 19, 739-764.	3.5	6
229	How do we probe <i>Ubiquitin's</i> Pathway Heterogeneity?. Journal of Biomolecular Structure and Dynamics, 2002, 19, 949-960.	3.5	0
230	Desolvation shell of hydrogen bonds in folded proteins, protein complexes and folding pathways. FEBS Letters, 2002, 527, 166-170.	2.8	14
231	Solvent environment conducive to protein aggregation. FEBS Letters, 2002, 529, 298-302.	2.8	19
232	Dynamics of Hydrogen Bond Desolvation in Protein Folding. Journal of Molecular Biology, 2002, 321, 659-675.	4.2	79
233	Extent of Hydrogen-Bond Protection in Folded Proteins: A Constraint on Packing Architectures. Biophysical Journal, 2002, 83, 2475-2481.	0.5	54
234	Insufficient hydrogen-bond desolvation and prion-related disease. FEBS Journal, 2002, 269, 4165-4168.	0.2	13

#	Article	IF	CITATIONS
235	Intramolecular modulation of electric fields in folding proteins. Physics Letters, Section A: General, Atomic and Solid State Physics, 2002, 299, 217-220.	2.1	12
236	The protective shell of a hydrogen bond: a motif in protein folding pathways. Physics Letters, Section A: General, Atomic and Solid State Physics, 2002, 302, 144-148.	2.1	1
237	Three-body correlations in protein folding: the origin of cooperativity. Physica A: Statistical Mechanics and Its Applications, 2002, 307, 235-259.	2.6	40
238	Local solvent dielectrics and destabilization of solvent-exposed states in folding proteins. Physica A: Statistical Mechanics and Its Applications, 2002, 316, 77-86.	2.6	0
239	Time-resolved backbone desolvation and mutational hot spots in folding proteins. Proteins: Structure, Function and Bioinformatics, 2002, 47, 447-457.	2.6	14
240	Pathway heterogeneity in protein folding. Proteins: Structure, Function and Bioinformatics, 2002, 48, 293-310.	2.6	9
241	Distinguishing foldable proteins from nonfolders: When and how do they differ?. Proteins: Structure, Function and Bioinformatics, 2002, 49, 15-23.	2.6	12
242	Evolving solvent contexts in protein folding: modeling the self-protecting chain. Physica A: Statistical Mechanics and Its Applications, 2002, 308, 80-88.	2.6	0
243	Protein folding cooperativity in the correlated lattice. Physics Letters, Section A: General, Atomic and Solid State Physics, 2001, 290, 101-105.	2.1	1
244	Coarse semiempirical solution to the protein folding problem. Physica A: Statistical Mechanics and Its Applications, 2001, 293, 358-384.	2.6	5
245	Conformation-dependent environments in folding proteins. Journal of Chemical Physics, 2001, 114, 2489-2502.	3.0	46
246	Topologies to geometries in protein folding: Hierarchical and nonhierarchical scenarios. Journal of Chemical Physics, 2001, 114, 5871-5887.	3.0	15
247	Finding the collapse-inducing nucleus in a folding protein. Journal of Chemical Physics, 2001, 114, 8678-8684.	3.0	6
248	Ribonucleic acid folder: The earliest moves of a good structure seeker. Journal of Chemical Physics, 2001, 114, 9184-9191.	3.0	0
249	Cooperative walks in a cubic lattice: Protein folding as a many-body problem. Journal of Chemical Physics, 2001, 115, 7293-7297.	3.0	10
250	Semiempirical prediction of protein folds. Physical Review E, 2001, 64, 021901.	2.1	0
251	Protein folding: coming to terms with cooperativity. Journal of Biological Physics and Chemistry, 2001, 01, 10-11.	0.1	2
252	Coarsely resolved topography along protein folding pathways. Journal of Chemical Physics, 2000, 112, 5223-5229.	3.0	19

#	Article	IF	CITATIONS
253	Renormalized Hamiltonian for a peptide chain: Digitalizing the protein folding problem. Journal of Mathematical Physics, 2000, 41, 2593-2603.	1.1	2
254	Self-organization and mismatch tolerance in protein folding: General theory and an application. Journal of Chemical Physics, 2000, 112, 5212-5222.	3.0	21
255	Topology to geometry in protein folding: beta -Lactoglobulin. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 14062-14066.	7.1	33
256	Digitalizing the backbone torsional dynamics of a folding protein. Physical Chemistry Chemical Physics, 2000, 2, 1375-1384.	2.8	4
257	Discretized torsional dynamics and the folding of an RNA chain. Physical Review E, 1999, 60, 2105-2119.	2.1	2
258	Nucleation theory for helix unfolding in peptide chains. Physical Review E, 1999, 60, 4645-4651.	2.1	12
259	Energy-level statistics in the fine conformational resolution of RNA folding dynamics. Physical Review E, 1999, 60, 5888-5893.	2.1	1
260	Folding a protein by discretizing its backbone torsional dynamics. Physical Review E, 1999, 59, 5928-5939.	2.1	4
261	From residue matching patterns to protein folding topographies: General model and bovine pancreatic trypsin inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 12991-12996.	7.1	28
262	A variational approach to relaxation in rugged free energy landscapes. Physica A: Statistical Mechanics and Its Applications, 1999, 262, 349-358.	2.6	4
263	Coarse graining the soft-mode dynamics of a folding protein. Physical Chemistry Chemical Physics, 1999, 1, 861-869.	2.8	6
264	How large should proteins be? The minimal size of a good structure seeker. Physical Chemistry Chemical Physics, 1999, 1, 4347-4354.	2.8	3
265	Glassy Relaxation Dynamics and Ruggedness beyond the Ultrametric Limit. Journal of Statistical Physics, 1998, 91, 669-677.	1.2	1
266	The Lagrangian Structure of Long-Time Torsional Dynamics Leading to RNA Folding. Journal of Statistical Physics, 1998, 92, 237-267.	1.2	12
267	Semiempirical variational approach to RNA folding. Physica A: Statistical Mechanics and Its Applications, 1998, 248, 336-352.	2.6	11
268	The RNA folding problem: a variational problem within an adiabatic approximation. Biophysical Chemistry, 1998, 74, 89-98.	2.8	0
269	A variational approach to relaxation in ultrametric spaces. Physica A: Statistical Mechanics and Its Applications, 1998, 256, 359-368.	2.6	5
270	Microscopic dynamics from a coarsely defined solution to the protein folding problem. Journal of Mathematical Physics, 1998, 39, 3167-3187.	1.1	19

#	Article	IF	CITATIONS
271	Adiabatic ansatz in RNA folding dynamics. Physical Review E, 1997, 56, 927-930.	2.1	3
272	Variational Approach to Relaxation in Complex Free Energy Landscapes: The Polymer Folding Problem. Physical Review Letters, 1997, 78, 2668-2671.	7.8	29
273	Dramatic Saccharide-Mediated Protection of Chaotropic-Induced Deactivation of Concanavalin A. Archives of Biochemistry and Biophysics, 1997, 340, 154-158.	3.0	9
274	An Integrated Flow Analysis System for the Recalculation of Hydraulic Machinery Bladings. International Journal of Rotating Machinery, 1996, 2, 139-148.	0.8	1
275	Magnesium-aided folding of group I ribozymes with a minimal loss of entropy. Biophysical Chemistry, 1996, 61, 51-58.	2.8	0
276	In vitro RNA folding: the principle of sequential minimization of entropy loss at work. Biophysical Chemistry, 1996, 58, 335-339.	2.8	11
277	Sequentially folded SV-11 RNA: metastability is relevant to biological function. Biophysical Chemistry, 1996, 61, 101-105.	2.8	1
278	The expediency of RNA folding as revealed by the maximization in information content. Physica A: Statistical Mechanics and Its Applications, 1996, 233, 226-234.	2.6	3
279	An action principle for biopolymer foldingin vitro: A new perspective on the design of expeditiously-folded RNA molecules. Journal of Mathematical Chemistry, 1996, 20, 95-116.	1.5	0
280	A geometric framework for polymer folding. Journal of Mathematical Chemistry, 1996, 19, 331-336.	1.5	7
281	Cooperativity along kinetic pathways in RNA folding. Journal of Physics A, 1996, 29, 6265-6280.	1.6	5
282	Information generation and the loss of conformational entropy during RNA folding. Journal of Physics A, 1996, 29, L433-L438.	1.6	3
283	Statistical folding dynamics for random heteropolymers. Journal of Physics A, 1996, 29, L523-L526.	1.6	0
284	The statistical mechanics of kinetically-controlled RNA folding pathways. Annalen Der Physik, 1995, 507, 600-620.	2.4	10
285	What size RNA loop holds bulk solvent?. Chemical Physics Letters, 1995, 242, 460-464.	2.6	10
286	Statistical mechanics on the space of kinetic folding pathways. Nuovo Cimento Della Societa Italiana Di Fisica D - Condensed Matter, Atomic, Molecular and Chemical Physics, Biophysics, 1995, 17, 983-991.	0.4	5
287	Towards an action principle governing biopolymer foldingin vitro. Journal of Mathematical Chemistry, 1995, 17, 401-410.	1.5	2
288	Folding RNA with the minimal loss of entropy. Physical Review E, 1995, 52, R1299-R1302.	2.1	12

#	Article	IF	CITATIONS
289	Ascribing weights to folding histories: explaining the expediency of biopolymer folding. Journal of Physics A, 1994, 27, 6039-6052.	1.6	5
290	Describing RNA sequential folding by dynamic coarse graining of the extended conformation space. Physical Review E, 1994, 50, R2435-R2438.	2.1	0
291	A measure on the space of polymer folding pathways: Preliminaries for a new scheme of statistical inference. Journal of Statistical Physics, 1994, 77, 1079-1085.	1.2	5
292	Stress Localization in the RNA Backbone: A Mechanical Footprint for Predicting Base-Backbone Tertiary Contacts. Journal of Theoretical Biology, 1994, 166, 443-452.	1.7	1
293	Solution of nonlinear ordinary differential equations by feedforward neural networks. Mathematical and Computer Modelling, 1994, 20, 19-44.	2.0	107
294	The numerical solution of linear ordinary differential equations by feedforward neural networks. Mathematical and Computer Modelling, 1994, 19, 1-25.	2.0	164
295	Memorizing all significant foldings of a random RNA chain. Physica A: Statistical Mechanics and Its Applications, 1994, 203, 359-368.	2.6	0
296	A measure on the space of RNA folding pathways: towards a new scheme of statistical inference. Physica A: Statistical Mechanics and Its Applications, 1994, 210, 403-414.	2.6	0
297	A neural network hamiltonian governing the formation of RNA baseâ€pairing patterns. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1994, 98, 125-128.	0.9	0
298	Microscopic derivation of the lowâ€ <i>T</i> myoglobin O recombination rate law by estimating statistical parameters of folding relaxation. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1994, 98, 260-262.	0.9	4
299	Structure-induced Strain Determining the Internal Cyclization Site in the Yeast cobl5 Autocatalytic Intron: Theory and Experimental Tests. Journal of Theoretical Biology, 1993, 164, 121-133.	1.7	6
300	Learning to fold a random RNA chain. Chemical Physics Letters, 1993, 212, 201-204.	2.6	0
301	Coarse-grained dynamics for proton exchange in RNA. Chemical Physics Letters, 1993, 208, 148-152.	2.6	0
302	Learning to fold RNA with parallel processors. Physica A: Statistical Mechanics and Its Applications, 1993, 201, 557-572.	2.6	12
303	Simulating an exploration of RNA conformation space with an appropriate parallel-updating strategy. Physical Review E, 1993, 48, 3107-3111.	2.1	5
304	A Dynamical Model for Ribozyme Function Based on the Sequential Folding of Pre-mRNA Transcripts. Journal of Biochemistry, 1993, 113, 22-28.	1.7	1
305	Folding pathway leading to the most stable conformation of a random RNA chain. Physical Review A, 1992, 45, R8348-R8350.	2.5	17
306	Computation of the fraction of RNA sequences that fold sequentially into a unique free-energy minimum. Physical Review A, 1992, 46, R4524-R4527.	2.5	1

#	Article	IF	CITATIONS
307	Localization of strain in the RNA backbone and its functional implication. Physical Review Letters, 1992, 69, 546-549.	7.8	Ο
308	How Random are Regulatory Signals in RNA Replication? Evolutionary Constraints do not Play a Decisive Role. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1992, 96, 705-708.	0.9	2
309	On how hydrolysis at the 3′ end is prevented in the splicing of a sequentially folded group I intron. FEBS Letters, 1992, 297, 201-204.	2.8	6
310	Evidence of a tertiary interaction functional in group I $3\hat{a}\in^2$ -splicing. FEBS Letters, 1992, 305, 225-227.	2.8	0
311	A parallel computation revealing the role of the in vivo environment in shaping the catalytic structure of a mitochondrial RNA transcript. Journal of Theoretical Biology, 1992, 157, 487-503.	1.7	8
312	Structural organization of an RNA catalyst with the random energy model as a reference frame. International Journal of Theoretical Physics, 1992, 31, 983-993.	1.2	0
313	Preservation of a kinetically originated folding of the cis antirepressor sequence for transport of HIV-1 viral RNA. Biophysical Chemistry, 1992, 42, 1-6.	2.8	1
314	Noncoexisting structural elements in catalytic pre-messenger RNA's. Biophysical Chemistry, 1992, 45, 27-30.	2.8	0
315	Modulation of the stability of a replication complex and its effect on the rate of chain elongation: extending the notion of processivity. Chemical Physics Letters, 1992, 192, 294-298.	2.6	1
316	Relaxation timescales for conformational substates in disordered polymers. Annalen Der Physik, 1992, 504, 61-65.	2.4	0
317	Phenotypic Traits and Regulatory Role of RNA Folding in Molecular Selection. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 1991, 46, 656-662.	1.4	0
318	Multiprocessed Simulation of Competing Folding Pathways in RNA: The Shaping of the Catalytic Site for Splicing. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1991, 95, 1674-1680.	0.9	0
319	The Relevance of Nonlinear Energy Localization in RNA Self-Splicing. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1991, 95, 31-36.	0.9	0
320	Functional metastable structures in RNA replication. Physica A: Statistical Mechanics and Its Applications, 1991, 176, 499-513.	2.6	8
321	Excluded volume effects on the kinetic assembling of a structural motif for RNA catalysis. Chemical Physics Letters, 1991, 183, 499-504.	2.6	5
322	Is the Distribution of Substates in Biopolymer Folding Ultrametric?. Annalen Der Physik, 1991, 503, 238-240.	2.4	0
323	Early base-pair fluctuations and the activation of mRNA splicing. Physica A: Statistical Mechanics and Its Applications, 1991, 173, 522-531.	2.6	0
324	RNA self-splicing and energy localization. International Journal of Theoretical Physics, 1991, 30, 129-136.	1.2	0

#	Article	IF	CITATIONS
325	Growth of ordered domains beyond a dynamic instability in dissipative systems. International Journal of Theoretical Physics, 1991, 30, 77-82.	1.2	0
326	Ultrametricity in the externally-induced conformational substates of disordered polymers. International Journal of Theoretical Physics, 1991, 30, 83-88.	1.2	1
327	Excluded-volume effects on the stacking of RNA base pairs. Physical Review A, 1991, 44, R7910-R7912.	2.5	8
328	Fluctuations and resulting competing pathways in RNA folding: The activation of splicing. Physical Review A, 1991, 43, 1138-1141.	2.5	2
329	Increasing the Replicative Capacity of a Naturallyâ€Occurring RNA Template. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1990, 94, 463-465.	0.9	0
330	Importance of Metastable RNA Folding in Template-Replicase Interactions. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1990, 94, 650-653.	0.9	0
331	Ergodic and Nonergodic Relaxation Timescales for Metastable RNA Folding. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1990, 94, 1512-1514.	0.9	0
332	New Possibility for Metastable RNA Folding of Biological Significance: A Physicoâ€Chemical View at Biological Regulation and Control. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1990, 94, 1515-1520.	0.9	0
333	Implications of the Soliton Model on a Novel Mode for Proton Transfer Catalysis in RNA. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1990, 94, 461-463.	0.9	0
334	The Importance of Metastable RNA Folding in Biological Regulation and Control. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1990, 94, 615-618.	0.9	2
335	Theoretical Prediction of the Primary Sequence for an RNA Species Fitted for Replication by Qßâ€Replicase. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1990, 94, 785-787.	0.9	0
336	Coherent collective modes in catalytic RNA. European Physical Journal B, 1990, 79, 255-258.	1.5	7
337	Proton exchange activity as a probe for solitons in RNA. Physica A: Statistical Mechanics and Its Applications, 1990, 167, 338-346.	2.6	3
338	Spectrum of relaxation time scales for metastable RNA folding. Physica A: Statistical Mechanics and Its Applications, 1990, 165, 352-360.	2.6	0
339	Statistical mechanical model for proton transfer in RNA. Journal of Physics A, 1990, 23, L247-L252.	1.6	3
340	Glassy kinetic barriers between conformational substates in RNA. Physical Review Letters, 1990, 64, 2328-2331.	7.8	34
341	Random energy model for the kinetics of RNA folding. Physical Review Letters, 1990, 65, 2259-2261.	7.8	13
342	Activation-energy landscape for metastable RNA folding. Physical Review A, 1990, 42, 3657-3659.	2.5	19

#	Article	IF	CITATIONS
343	Kinetic assembling of the biologically active secondary structure for CAR, the target sequence for the Rev protein of HIV-1. Archives of Biochemistry and Biophysics, 1990, 280, 421-424.	3.0	4
344	Externally induced phase transition for random inhomogeneous polymers. Journal of Physics A, 1989, 22, 3137-3142.	1.6	1
345	Effective phase space for isomerizations in liquids. Chemical Physics Letters, 1989, 162, 14-18.	2.6	Ο
346	Correlation of pause sites in MDV-1 RNA replication with kinetic refolding of the growing chain. A Monte Carlo simulation of the Markov process. FEBS Journal, 1989, 182, 161-163.	0.2	41
347	Sequence dependence for the melting of globular states in heteropolymers. Chemical Physics Letters, 1989, 154, 396-402.	2.6	11
348	Pause sites and regulatory role of secondary structure in RNA replication. Biophysical Chemistry, 1989, 34, 29-33.	2.8	5
349	Metastable RNA folding and the enhancement of autocatalytic activity. Die Naturwissenschaften, 1989, 76, 525-526.	1.6	5
350	Partial relaxation of enzyme-product binding by refolding of the growing chain in autocatalytic RNA replication. Die Naturwissenschaften, 1989, 76, 69-71.	1.6	15
351	Structural phase transitions and the catalytic role of RNA in proton transfer events. Die Naturwissenschaften, 1989, 76, 469-471.	1.6	11
352	The microscopic origin of cooperativity and its effect on long-lifetime kinetic modes for template-free RNA synthesis. Journal of the Chemical Society, Faraday Transactions 2, 1989, 85, 1377-1390.	1.1	0
353	Amplification of intrinsic fluctuations along the center manifold. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1989, 93, 95-98.	0.9	3
354	A structural phase transition in RNA. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1989, 93, 574-575.	0.9	0
355	Effect of Primary Structure Disorder on Coilâ€Globule Phase Transitions in Heteropolymers. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1989, 93, 879-882.	0.9	Ο
356	Assembling of random inhomogeneous polymers: A grand ensemble approach using the replica method. Chemical Physics Letters, 1988, 149, 113-117.	2.6	10
357	Far-from-equilibrium fluctuations triggering RNA de novo synthesis. Colloid and Polymer Science, 1988, 266, 385-388.	2.1	Ο
358	Irreversibility paradox revised: Onset of a center manifold in dissipative systems. International Journal of Theoretical Physics, 1988, 27, 725-730.	1.2	0
359	Center Manifold and Phase-Ordering Dynamics for the Onset of Nonequilibrium Organizations. Physica Status Solidi (B): Basic Research, 1988, 149, 127-132.	1.5	0
360	Stochastic dynamical constraints in de novo RNA replication. Journal of Theoretical Biology, 1988, 134, 419-430.	1.7	16

#	Article	IF	CITATIONS
361	The onset of macroscopically detectable amplification of template concentration self-replicating RNA. Biophysical Chemistry, 1988, 29, 317-325.	2.8	0
362	Dispersion of tertiary structures for an ensemble of primary sequences at an externally induced transition of correlation regimes. Biophysical Chemistry, 1988, 32, 167-171.	2.8	0
363	Correlation of subsystems at the onset of a centre manifold organization. Journal of the Chemical Society, Faraday Transactions 2, 1988, 84, 1741-1746.	1.1	0
364	Stochastic interpretation of lag times for the onset of template amplification in RNA replication. Journal of the Chemical Society Faraday Transactions I, 1988, 84, 1543.	1.0	2
365	Phase-ordering dynamics for the onset of a center manifold. Physical Review A, 1988, 38, 4256-4260.	2.5	3
366	Correlation of subsystems for the transition to a convective pattern. Journal of Physics A, 1988, 21, L967-L972.	1.6	1
367	Self-organisation in the centre manifold of a dissipative system. Journal of Physics A, 1988, 21, L295-L300.	1.6	6
368	On renormalisation of fluctuations at the onset of a centre manifold. Journal of Physics A, 1988, 21, L607-L610.	1.6	0
369	The Scaling of Nonequilibrium Fluctuations in Gaseous Thermal Explosions. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1988, 92, 754-760.	0.9	1
370	Dissipation of Fluctuations in Reactive Systems at the Onset of a Center Manifold. Zeitschrift Fur Physikalische Chemie, 1988, 158, 147-153.	2.8	0
371	H. G. Schuster:Deterministic Chaos, Second Revised Edition, VCH Verlagsgesellschaft, Weinheim. 273 Seiten, Preis: DM 108, Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1988, 92, 1059A-1060.	0.9	14
372	Intrinsic fluctuations determined by the existence of a centre manifold. Journal of Physics A, 1987, 20, L509-L513.	1.6	0
373	Intrinsic fluctuations associated with the onset of a centre manifold. Journal of Physics A, 1987, 20, L579-L582.	1.6	0
374	Constraints on the time-reversible Liouville equation in order to derive a stochastic order-parameter equations at the onset of a convective roll pattern. Journal of Physics A, 1987, 20, L763-L767.	1.6	3
375	Transition to a convective roll pattern as obtained from the stochastic center-manifold theory. Physical Review A, 1987, 35, 764-767.	2.5	14
376	Center-manifold renormalization in dynamic critical phenomena for dissipative spin systems. Physical Review A, 1987, 35, 5203-5207.	2.5	3
377	Renormalization Group from a Center Manifold Reduction in Dynamic Critical Phenomena. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1987, 91, 570-573.	0.9	0
378	K. F. Freed: Renormalization Group Theory of Macromolecules, John Wiley and Sons, New York, Chichester, Brisbane, Toronto, Singapore 1987. 361 Seiten, Preis: £ 52.75. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1987, 91, 683-683.	0.9	1

#	Article	IF	CITATIONS
379	Statistical Weights for Primary Structures of Inhomogeneous Polymer Chains. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1987, 91, 611-614.	0.9	0
380	Theory of scaling for fluctuations in thermal explosion conditions. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1987, 91, 159-163.	0.9	3
381	Intrinsic Fluctuations in Macromolecular Self-Replicating Systems. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1987, 91, 1002-1007.	0.9	1
382	Statistics of Disordered Polymers: An Effective Hamiltonian and its Associated Gibbs Measure. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1987, 91, 753-755.	0.9	1
383	Statistics of the ensemble of primary structures for inhomogeneous polymer chains. International Journal of Theoretical Physics, 1987, 26, 489-494.	1.2	0
384	Stochastic theory of ignition processes. International Journal of Theoretical Physics, 1987, 26, 1093-1105.	1.2	1
385	Effective propagators for quenched disorder in linear polymers. Biophysical Chemistry, 1987, 28, 89-92.	2.8	13
386	The steady-state approximation as a centre manifold elimination in chemical kinetics. Journal of the Chemical Society, Faraday Transactions 2, 1986, 82, 849-855.	1.1	2
387	Homology of a Structurally Stable Chemical Rearrangement. Zeitschrift Fur Naturforschung - Section A Journal of Physical Sciences, 1986, 41, 526-528.	1.5	0
388	Pattern of Intrinsic Reaction Coordinates and Separatrices for a Symmetry-Forbidden Reaction. Zeitschrift Fur Naturforschung - Section A Journal of Physical Sciences, 1986, 41, 529-531.	1.5	1
389	Triangulation of the Lowest Energy Sheet for Jahn-Teller Potential Energy Surfaces. Zeitschrift Fur Naturforschung - Section A Journal of Physical Sciences, 1986, 41, 532-534.	1.5	0
390	Virtual size parameter for the scaling of far-from-equilibrium fluctuations at the onset of a center manifold. Physics Letters, Section A: General, Atomic and Solid State Physics, 1986, 119, 168-173.	2.1	15
391	Predicted power spectra for subordinated variables in periodic instabilities making use of a center manifold reduced floquet theory. Physics Letters, Section A: General, Atomic and Solid State Physics, 1986, 114, 346-348.	2.1	1
392	Fundamental sensitivity propagators in dissipative systems with a statistical enslaving of fast-relaxing variables. Physical Review A, 1986, 33, 1913-1917.	2.5	2
393	Entrainment by periodic perturbations in the center manifold at Ginzburg-Landau critical regimes. Physical Review A, 1986, 34, 2307-2314.	2.5	2
394	Autocorrelations in the center manifold of dissipative systems. Physical Review A, 1986, 33, 3314-3319.	2.5	11
395	Homology of Potential Energy Surfaces. Zeitschrift Fur Naturforschung - Section A Journal of Physical Sciences, 1986, 41, 1118-1122.	1.5	0
396	Jahn-Teller distortion motions as separatrices in PES. Theoretica Chimica Acta, 1985, 68, 285-289.	0.8	1

#	Article	IF	CITATIONS
397	Pattern of separatrices and intrinsic reaction coordinates for degenerate thermal rearrangements. Theoretica Chimica Acta, 1985, 67, 229-233.	0.8	5
398	The denaturation maxima of proteins and of drug-biomolecule complex formation in a wide range of methanol/water mixtures. Biophysical Chemistry, 1985, 21, 157-162.	2.8	24
399	Denaturation of proteins in methanol/water mixtures. Biophysical Chemistry, 1985, 21, 163-166.	2.8	20
400	Solvophobic forces and molecular surface area changes in drug-biomolecule associations as with actinomycin-deoxyguanosine in a wide range of methanol/water mixtures. Biophysical Chemistry, 1985, 21, 167-171.	2.8	12
401	Center-manifold extension of the adiabatic-elimination method. Physical Review A, 1985, 32, 3070-3072.	2.5	19
402	[1,3] Sigmatropic thermal rearrangements as vector fields on the 2 sphere. Journal of Chemical Physics, 1985, 82, 3123-3126.	3.0	3
403	Global instability of a monoparametric family of vector fields representing the unfolding of a dissipative structure. Journal of Mathematical Physics, 1985, 26, 2632-2633.	1.1	4
404	A reduction scheme for explosive chemical kinetics. Journal of Chemical Physics, 1985, 83, 4488-4490.	3.0	5
405	Subordination of fast-relaxing degrees of freedom to order parameters under Ginzburg-Landau regimes. Physical Review A, 1985, 31, 2738-2739.	2.5	8
406	Subordination of the fast-relaxing degree of freedom in the center manifold of the Belousov-Zhabotinsky system. Physical Review A, 1985, 31, 2736-2737.	2.5	5
407	A Reactive System with Diffusive Transport Displaying Two Different Symmetry-Breaking Dissipative Structures. Zeitschrift Fur Naturforschung - Section A Journal of Physical Sciences, 1985, 40, 611-618.	1.5	1
408	Locally attractive normal modes for chemical process. Journal of Mathematical Physics, 1984, 25, 2576-2581.	1.1	12
409	Conditions for the validity of Ginzburg-Landau equations in far-from-equilibrium kinetics. Physical Review A, 1984, 30, 1522-1524.	2.5	10
410	Symmetry-breaking instabilities under nonclassical bifurcation conditions. Physical Review A, 1984, 29, 2029-2032.	2.5	14
411	Global attractors and global stability for closed chemical systems. Journal of Mathematical Physics, 1984, 25, 406-409.	1.1	9
412	Spatial-temporal dissipative structures arising in open reactive systems with a negative feedback loop. BioSystems, 1984, 17, 3-9.	2.0	1
413	The structural stability restriction rules out certain frontside S N 2 pathways. Theoretica Chimica Acta, 1984, 66, 147-149.	0.8	6
414	Directed graphs of structurally stable potential energy surfaces representing a-priori reaction pathways. Theoretica Chimica Acta, 1984, 65, 179-190.	0.8	11

#	Article	IF	CITATIONS
415	The lifting of an İnönü–Wigner contraction at the level of universal coverings. Journal of Mathematical Physics, 1982, 23, 2234-2235.	1.1	0
416	Searching for the inside of the Cob15 Ribozyme. Protein Engineering, Design and Selection, 0, , .	2.1	0