

Ariel Fernández Stigliano

List of Publications by Year in descending order

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416
papers

5,041
citations

117625

34
h-index

138484

58
g-index

428
all docs

428
docs citations

428
times ranked

3744
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Therapeutic Efficacy of a Novel Focal Adhesion Kinase Inhibitor TAE226 in Ovarian Carcinoma. Cancer Research, 2007, 67, 10976-10983.	0.9	201
3	The numerical solution of linear ordinary differential equations by feedforward neural networks. Mathematical and Computer Modelling, 1994, 19, 1-25.	2.0	164
4	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
5	Non-adaptive origins of interactome complexity. Nature, 2011, 474, 502-505.	27.8	118
6	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, 2016, 4, 52-63.	11.4	117
7	Membrane Thickness Cue for Cold Sensing in a Bacterium. Current Biology, 2010, 20, 1539-1544.	3.9	116
8	Solution of nonlinear ordinary differential equations by feedforward neural networks. Mathematical and Computer Modelling, 1994, 20, 19-44.	2.0	107
9	Dehydron: A Structurally Encoded Signal for Protein Interaction. Biophysical Journal, 2003, 85, 1914-1928.	0.5	105
10	Dielectric Modulation of Biological Water. Physical Review Letters, 2004, 93, 228104.	7.8	99
11	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
12	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
13	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
14	Dynamics of Hydrogen Bond Desolvation in Protein Folding. Journal of Molecular Biology, 2002, 321, 659-675.	4.2	79
15	Keeping dry and crossing membranes. Nature Biotechnology, 2004, 22, 1081-1084.	17.5	70
16	A lipid-mediated conformational switch modulates the thermosensing activity of DesK. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3579-3584.	7.1	69
17	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
18	Adherence of Packing Defects in Soluble Proteins. Physical Review Letters, 2003, 91, 018102.	7.8	62

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19	Large-Scale Context in Protein Folding: A Villin Headpiece. <i>Biochemistry</i> , 2003, 42, 664-671.	2.5	56
20	Turning promiscuous kinase inhibitors into safer drugs. <i>Trends in Biotechnology</i> , 2008, 26, 295-301.	9.3	56
21	c-Jun-NH2-kinase-1 Inhibition Leads to Antitumor Activity in Ovarian Cancer. <i>Clinical Cancer Research</i> , 2010, 16, 184-194.	7.0	55
22	Extent of Hydrogen-Bond Protection in Folded Proteins: A Constraint on Packing Architectures. <i>Biophysical Journal</i> , 2002, 83, 2475-2481.	0.5	54
23	Rational Drug Redesign to Overcome Drug Resistance in Cancer Therapy: Imatinib Moving Target. <i>Cancer Research</i> , 2007, 67, 4028-4033.	0.9	53
24	Protein Under-Wrapping Causes Dosage Sensitivity and Decreases Gene Duplicability. <i>PLoS Genetics</i> , 2008, 4, e11.	3.5	53
25	Molecular basis for specificity in the druggable kinome: sequence-based analysis. <i>Bioinformatics</i> , 2007, 23, 563-572.	4.1	52
26	Molecular dimension explored in evolution to promote proteomic complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13460-13465.	7.1	51
27	Conformation-dependent environments in folding proteins. <i>Journal of Chemical Physics</i> , 2001, 114, 2489-2502.	3.0	46
28	Protein folding: could hydrophobic collapse be coupled with hydrogen-bond formation?. <i>FEBS Letters</i> , 2003, 536, 187-192.	2.8	46
29	Reconstruction of perspective shifts and refocusing of a three-dimensional scene from a multi-focus image stack. <i>Applied Optics</i> , 2016, 55, 2380.	2.1	45
30	Dehydration Propensity of Order-Disorder Intermediate Regions in Soluble Proteins. <i>Journal of Proteome Research</i> , 2007, 6, 3519-3526.	3.7	44
31	Correlation of pause sites in MDV-1 RNA replication with kinetic refolding of the growing chain. A Monte Carlo simulation of the Markov process. <i>FEBS Journal</i> , 1989, 182, 161-163.	0.2	41
32	Three-body correlations in protein folding: the origin of cooperativity. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2002, 307, 235-259.	2.6	40
33	The nonconserved wrapping of conserved protein folds reveals a trend toward increasing connectivity in proteomic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2823-2827.	7.1	35
34	All-in-focus image reconstruction under severe defocus. <i>Optics Letters</i> , 2015, 40, 1671.	3.3	35
35	Classy kinetic barriers between conformational substates in RNA. <i>Physical Review Letters</i> , 1990, 64, 2328-2331.	7.8	34
36	Inhibitor design by wrapping packing defects in HIV-1 proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11640-11645.	7.1	34

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37	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
38	Three-dimensional profiling with binary fringes using phase-shifting interferometry algorithms. Applied Optics, 2011, 50, 147.	2.1	32
39	Protein wrapping: a molecular marker for association, aggregation and drug design. Chemical Society Reviews, 2008, 37, 2373.	38.1	31
40	Redesigning Kinase Inhibitors to Enhance Specificity. Journal of Medicinal Chemistry, 2008, 51, 4890-4898.	6.4	31
41	A Priori Inference of Cross Reactivity for Drug-Targeted Kinases. Journal of Medicinal Chemistry, 2006, 49, 3092-3100.	6.4	30
42	Episturctural Tension Promotes Protein Associations. Physical Review Letters, 2012, 108, 188102.	7.8	30
43	Variational Approach to Relaxation in Complex Free Energy Landscapes: The Polymer Folding Problem. Physical Review Letters, 1997, 78, 2668-2671.	7.8	29
44	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
45	Is there a case for selectively promiscuous anticancer drugs?. Drug Discovery Today, 2009, 14, 1-5.	6.4	28
46	Incomplete Protein Packing as a Selectivity Filter in Drug Design. Structure, 2005, 13, 1829-1836.	3.3	26
47	Engineering productive enzyme confinement. Trends in Biotechnology, 2007, 25, 189-190.	9.3	26
48	What factor drives the fibrillogenic association of β^2 -sheets?. FEBS Letters, 2005, 579, 6635-6640.	2.8	25
49	Kinase packing defects as drug targets. Drug Discovery Today, 2007, 12, 917-923.	6.4	25
50	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
51	Transfer of tetracyclines across the H ₂ O 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
52	Protein structure protection commits gene expression patterns. Genome Biology, 2008, 9, R107.	9.6	23
53	Protein Promiscuity: Drug Resistance and Native Functionsâ€™HIV-1 Case. Journal of Biomolecular Structure and Dynamics, 2005, 22, 615-624.	3.5	22
54	Purposely engineered drugâ€™target mismatches for entropy-based drug optimization. Trends in Biotechnology, 2012, 30, 1-7.	9.3	22

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55	Self-organization and mismatch tolerance in protein folding: General theory and an application. <i>Journal of Chemical Physics</i> , 2000, 112, 5212-5222.	3.0	21
56	Color encoding of binary fringes for gamma correction in 3-D profiling. <i>Optics Letters</i> , 2012, 37, 1325.	3.3	21
57	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. <i>Journal of Critical Care</i> , 2015, 30, 1324-1330.	2.2	21
58	Transformative Concepts for Drug Design: Target Wrapping. , 2010, , .		21
59	Denaturation of proteins in methanol/water mixtures. <i>Biophysical Chemistry</i> , 1985, 21, 163-166.	2.8	20
60	Induced Disorder in Protein-Ligand Complexes as a Drug-Design Strategy. <i>Molecular Pharmaceutics</i> , 2008, 5, 430-437.	4.6	20
61	Selective antagonism of anticancer drugs for side-effect removal. <i>Trends in Pharmacological Sciences</i> , 2009, 30, 403-410.	8.7	20
62	Sub-Nanoscale Surface Ruggedness Provides a Water-Tight Seal for Exposed Regions in Soluble Protein Structure. <i>PLoS ONE</i> , 2010, 5, e12844.	2.5	20
63	Center-manifold extension of the adiabatic-elimination method. <i>Physical Review A</i> , 1985, 32, 3070-3072.	2.5	19
64	Activation-energy landscape for metastable RNA folding. <i>Physical Review A</i> , 1990, 42, 3657-3659.	2.5	19
65	Microscopic dynamics from a coarsely defined solution to the protein folding problem. <i>Journal of Mathematical Physics</i> , 1998, 39, 3167-3187.	1.1	19
66	Coarsely resolved topography along protein folding pathways. <i>Journal of Chemical Physics</i> , 2000, 112, 5223-5229.	3.0	19
67	Solvent environment conducive to protein aggregation. <i>FEBS Letters</i> , 2002, 529, 298-302.	2.8	19
68	What caliber pore is like a pipe? Nanotubes as modulators of ionic gradients. <i>Journal of Chemical Physics</i> , 2003, 119, 5315-5319.	3.0	19
69	Continuum equations for dielectric response to macro-molecular assemblies at the nano scale. <i>Journal of Physics A</i> , 2004, 37, 9791-9803.	1.6	18
70	Novel electrochemical approach to the determination of the partition coefficient of neutral weak bases. <i>Journal of Electroanalytical Chemistry</i> , 2006, 594, 80-88.	3.8	18
71	Binding of the Highly Toxic Tetracycline Derivative, Anhydrotetracycline, to Bovine Serum Albumin. <i>Biological and Pharmaceutical Bulletin</i> , 2011, 34, 1301-1306.	1.4	18
72	Single-shot phase recovery using two laterally separated defocused images. <i>Optics Communications</i> , 2013, 293, 1-3.	2.1	18

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73	Folding pathway leading to the most stable conformation of a random RNA chain. <i>Physical Review A</i> , 1992, 45, R8348-R8350.	2.5	17
74	Functionality of Wrapping Defects in Soluble Proteins: What Cannot be Kept Dry Must be Conserved. <i>Journal of Molecular Biology</i> , 2004, 337, 477-483.	4.2	17
75	Electroanalytical procedure to resolve a sample solution containing tetracycline and its toxic degraded product: Anhydrotetracycline. <i>Journal of Electroanalytical Chemistry</i> , 2008, 624, 121-128.	3.8	17
76	The principle of minimal epistemic distortion of the water matrix and its steering role in protein folding. <i>Journal of Chemical Physics</i> , 2013, 139, 085101.	3.0	17
77	Communication: Chemical functionality of interfacial water enveloping nanoscale structural defects in proteins. <i>Journal of Chemical Physics</i> , 2014, 140, 221102.	3.0	17
78	Stochastic dynamical constraints in de novo RNA replication. <i>Journal of Theoretical Biology</i> , 1988, 134, 419-430.	1.7	16
79	Virtual size parameter for the scaling of far-from-equilibrium fluctuations at the onset of a center manifold. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 1986, 119, 168-173.	2.1	15
80	Partial relaxation of enzyme-product binding by refolding of the growing chain in autocatalytic RNA replication. <i>Die Naturwissenschaften</i> , 1989, 76, 69-71.	1.6	15
81	Topologies to geometries in protein folding: Hierarchical and nonhierarchical scenarios. <i>Journal of Chemical Physics</i> , 2001, 114, 5871-5887.	3.0	15
82	Transfer of tylosin across the H ₂ O/1,2-dichloroethane interface. Analysis of degraded product in acid solutions. <i>Journal of Electroanalytical Chemistry</i> , 2010, 650, 47-54.	3.8	15
83	Symmetry-breaking instabilities under nonclassical bifurcation conditions. <i>Physical Review A</i> , 1984, 29, 2029-2032.	2.5	14
84	Transition to a convective roll pattern as obtained from the stochastic center-manifold theory. <i>Physical Review A</i> , 1987, 35, 764-767.	2.5	14
85	H. G. Schuster: <i>Deterministic Chaos</i> , Second Revised Edition, VCH Verlagsgesellschaft, Weinheim. 273 Seiten, Preis: DM 108,-. <i>Zeitschrift Fur Elektrotechnik Und Elektrochemie</i> , 1988, 92, 1059A-1060.	0.9	14
86	Desolvation shell of hydrogen bonds in folded proteins, protein complexes and folding pathways. <i>FEBS Letters</i> , 2002, 527, 166-170.	2.8	14
87	Time-resolved backbone desolvation and mutational hot spots in folding proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 447-457.	2.6	14
88	Taming the induced folding of drug-targeted kinases. <i>Trends in Pharmacological Sciences</i> , 2009, 30, 66-71.	8.7	14
89	Effective propagators for quenched disorder in linear polymers. <i>Biophysical Chemistry</i> , 1987, 28, 89-92.	2.8	13
90	Random energy model for the kinetics of RNA folding. <i>Physical Review Letters</i> , 1990, 65, 2259-2261.	7.8	13

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91	Insufficient hydrogen-bond desolvation and prion-related disease. <i>FEBS Journal</i> , 2002, 269, 4165-4168.	0.2	13
92	Amino Acid Residues at Protein-Protein Interfaces: Why Is Propensity so Different from Relative Abundance?. <i>Journal of Physical Chemistry B</i> , 2003, 107, 9929-9932.	2.6	13
93	Wrapping mimicking in drug-like small molecules disruptive of protein-protein interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1755-1765.	2.6	13
94	Locally attractive normal modes for chemical process. <i>Journal of Mathematical Physics</i> , 1984, 25, 2576-2581.	1.1	12
95	Solvophobic forces and molecular surface area changes in drug-biomolecule associations as with actinomycin-deoxyguanosine in a wide range of methanol/water mixtures. <i>Biophysical Chemistry</i> , 1985, 21, 167-171.	2.8	12
96	Learning to fold RNA with parallel processors. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1993, 201, 557-572.	2.6	12
97	Folding RNA with the minimal loss of entropy. <i>Physical Review E</i> , 1995, 52, R1299-R1302.	2.1	12
98	The Lagrangian Structure of Long-Time Torsional Dynamics Leading to RNA Folding. <i>Journal of Statistical Physics</i> , 1998, 92, 237-267.	1.2	12
99	Nucleation theory for helix unfolding in peptide chains. <i>Physical Review E</i> , 1999, 60, 4645-4651.	2.1	12
100	Intramolecular modulation of electric fields in folding proteins. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2002, 299, 217-220.	2.1	12
101	Distinguishing foldable proteins from nonfolders: When and how do they differ?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 15-23.	2.6	12
102	Solvent-exposed backbone loosens the hydration shell of soluble folded proteins. <i>Journal of Chemical Physics</i> , 2007, 126, 245103.	3.0	12
103	Golden Rule for Buttressing Vulnerable Soluble Proteins. <i>Journal of Proteome Research</i> , 2010, 9, 2643-2648.	3.7	12
104	Optical processing of color images with incoherent illumination: orientation-selective edge enhancement using a modified liquid-crystal display. <i>Optics Express</i> , 2011, 19, 21091.	3.4	12
105	Subfunctionalization reduces the fitness cost of gene duplication in humans by buffering dosage imbalances. <i>BMC Genomics</i> , 2011, 12, 604.	2.8	12
106	Optical implementation of the generalized Hough transform with totally incoherent light. <i>Optics Letters</i> , 2015, 40, 3901.	3.3	12
107	Directed graphs of structurally stable potential energy surfaces representing a-priori reaction pathways. <i>Theoretica Chimica Acta</i> , 1984, 65, 179-190.	0.8	11
108	Autocorrelations in the center manifold of dissipative systems. <i>Physical Review A</i> , 1986, 33, 3314-3319.	2.5	11

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109	Sequence dependence for the melting of globular states in heteropolymers. <i>Chemical Physics Letters</i> , 1989, 154, 396-402.	2.6	11
110	Structural phase transitions and the catalytic role of RNA in proton transfer events. <i>Die Naturwissenschaften</i> , 1989, 76, 469-471.	1.6	11
111	In vitro RNA folding: the principle of sequential minimization of entropy loss at work. <i>Biophysical Chemistry</i> , 1996, 58, 335-339.	2.8	11
112	Semiempirical variational approach to RNA folding. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1998, 248, 336-352.	2.6	11
113	Interbasin motion approach to dynamics of conformationally constrained peptides. <i>Journal of Chemical Physics</i> , 2003, 118, 5673-5682.	3.0	11
114	Molecular Basis for Evolving Modularity in the Yeast Protein Interaction Network. <i>PLoS Computational Biology</i> , 2007, 3, e226.	3.2	11
115	Real-time pattern recognition using an optical generalized Hough transform. <i>Applied Optics</i> , 2015, 54, 10586.	2.1	11
116	Glycosylation of SARS-CoV-2 Steers Evolutionary Outcomes in the Postvaccination Phase. <i>ACS Pharmacology and Translational Science</i> , 2021, 4, 410-412.	4.9	11
117	Conditions for the validity of Ginzburg-Landau equations in far-from-equilibrium kinetics. <i>Physical Review A</i> , 1984, 30, 1522-1524.	2.5	10
118	Assembling of random inhomogeneous polymers: A grand ensemble approach using the replica method. <i>Chemical Physics Letters</i> , 1988, 149, 113-117.	2.6	10
119	The statistical mechanics of kinetically-controlled RNA folding pathways. <i>Annalen Der Physik</i> , 1995, 507, 600-620.	2.4	10
120	What size RNA loop holds bulk solvent?. <i>Chemical Physics Letters</i> , 1995, 242, 460-464.	2.6	10
121	Cooperative walks in a cubic lattice: Protein folding as a many-body problem. <i>Journal of Chemical Physics</i> , 2001, 115, 7293-7297.	3.0	10
122	Comparative electrochemical performance of electrodeposited polypyrrole in protic and aprotic ionic liquids. <i>Journal of Electroanalytical Chemistry</i> , 2015, 737, 23-29.	3.8	10
123	Effect of ligand protonation on the facilitated ion transfer reactions across oil water interfaces. V. Applications of forced hydrodynamic conditions. <i>Journal of Electroanalytical Chemistry</i> , 2016, 765, 100-104.	3.8	10
124	Aceptabilidad de una intervención basada en salud móvil para modificar estilos de vida en prehipertensos de Argentina, Guatemala y Perú: un estudio piloto. <i>Revista Peruana De Medicina De Experimental Y Salud Publica</i> , 2015, 32, 221.	0.4	10
125	Global attractors and global stability for closed chemical systems. <i>Journal of Mathematical Physics</i> , 1984, 25, 406-409.	1.1	9
126	Dramatic Saccharide-Mediated Protection of Chaotropic-Induced Deactivation of Concanavalin A. <i>Archives of Biochemistry and Biophysics</i> , 1997, 340, 154-158.	3.0	9

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127	Pathway heterogeneity in protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 293-310.	2.6	9
128	Human capacitance to dosage imbalance: Coping with inefficient selection. <i>Genome Research</i> , 2009, 19, 2185-2192.	5.5	9
129	A unifying motif of intermolecular cooperativity in protein associations. <i>European Physical Journal E</i> , 2012, 35, 59.	1.6	9
130	Protein packing defects "heat up" interfacial water. <i>European Physical Journal E</i> , 2013, 36, 62.	1.6	9
131	Water promotes the sealing of nanoscale packing defects in folding proteins. <i>Journal of Physics Condensed Matter</i> , 2014, 26, 202101.	1.8	9
132	Ion transfer of weak acids across liquid liquid interfaces. <i>Journal of Electroanalytical Chemistry</i> , 2016, 774, 111-121.	3.8	9
133	Dehydron Analysis: Quantifying the Effect of Hydrophobic Groups on the Strength and Stability of Hydrogen Bonds. <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 473-479.	1.6	9
134	Image segmentation by nonlinear filtering of optical Hough transform. <i>Applied Optics</i> , 2016, 55, 3632.	2.1	9
135	Subordination of fast-relaxing degrees of freedom to order parameters under Ginzburg-Landau regimes. <i>Physical Review A</i> , 1985, 31, 2738-2739.	2.5	8
136	Functional metastable structures in RNA replication. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1991, 176, 499-513.	2.6	8
137	Excluded-volume effects on the stacking of RNA base pairs. <i>Physical Review A</i> , 1991, 44, R7910-R7912.	2.5	8
138	A parallel computation revealing the role of the in vivo environment in shaping the catalytic structure of a mitochondrial RNA transcript. <i>Journal of Theoretical Biology</i> , 1992, 157, 487-503.	1.7	8
139	Feature-similarity protein classifier as a ligand engineering tool. <i>New Biotechnology</i> , 2006, 23, 307-315.	2.7	8
140	Packing defects as selectivity switches for drug-based protein inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 323-328.	7.1	8
141	Hydration Profiles of Amyloidogenic Molecular Structures. <i>Journal of Biological Physics</i> , 2008, 34, 577-590.	1.5	8
142	Analog image contouring using a twisted-nematic liquid-crystal display. <i>Optics Express</i> , 2010, 18, 19163.	3.4	8
143	Incoherent optical processor for nondirectional edge enhancement of color images. <i>Optics Letters</i> , 2011, 36, 4596.	3.3	8
144	Nanoscale thermodynamics of biological interfacial tension. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2011, 467, 559-568.	2.1	8

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145	Edge linking and image segmentation by combining optical and digital methods. <i>Optik</i> , 2013, 124, 3260-3264.	2.9	8
146	Breakdown of the Debye polarization <i>ansatz</i> at protein-water interfaces. <i>Journal of Chemical Physics</i> , 2013, 138, 225103.	3.0	8
147	Synergizing immunotherapy with molecular-targeted anticancer treatment. <i>Drug Discovery Today</i> , 2014, 19, 1427-1432.	6.4	8
148	Packing defects functionalize soluble proteins. <i>FEBS Letters</i> , 2015, 589, 967-973.	2.8	8
149	Reverse Engineering of a Thermosensing Regulator Switch. <i>Journal of Molecular Biology</i> , 2019, 431, 1016-1024.	4.2	8
150	Fully invariant generalized Hough transform by out-of-focus multiview sensing with pupil array. <i>Applied Optics</i> , 2019, 58, 7766.	1.8	8
151	Coherent collective modes in catalytic RNA. <i>European Physical Journal B</i> , 1990, 79, 255-258.	1.5	7
152	A geometric framework for polymer folding. <i>Journal of Mathematical Chemistry</i> , 1996, 19, 331-336.	1.5	7
153	<i>In Silico</i> Drug Profiling of the Human Kinome Based on a Molecular Marker for Cross Reactivity. <i>Molecular Pharmaceutics</i> , 2008, 5, 728-738.	4.6	7
154	Distribution of ionic components between two immiscible solutions. Partition of weak bases. <i>Journal of Electroanalytical Chemistry</i> , 2010, 640, 42-50.	3.8	7
155	Ion transfer across liquid liquid interface under forced hydrodynamic conditions. I: Digital simulations. <i>Journal of Electroanalytical Chemistry</i> , 2012, 666, 42-51.	3.8	7
156	<i>Biomolecular Interfaces</i> . , 2015, , .		7
157	Advanced Modeling Reconciles Counterintuitive Decisions in Lead Optimization. <i>Trends in Biotechnology</i> , 2017, 35, 490-497.	9.3	7
158	Artificial Intelligence Teaches Drugs to Target Proteins by Tackling the Induced Folding Problem. <i>Molecular Pharmaceutics</i> , 2020, 17, 2761-2767.	4.6	7
159	SARS-CoV-2 Glycosylation Suggests That Vaccines Should Have Adopted the S1 Subunit as Antigen. <i>ACS Pharmacology and Translational Science</i> , 2021, 4, 1016-1017.	4.9	7
160	The structural stability restriction rules out certain frontside S N 2 pathways. <i>Theoretica Chimica Acta</i> , 1984, 66, 147-149.	0.8	6
161	Self-organisation in the centre manifold of a dissipative system. <i>Journal of Physics A</i> , 1988, 21, L295-L300.	1.6	6
162	On how hydrolysis at the 3' end is prevented in the splicing of a sequentially folded group I intron. <i>FEBS Letters</i> , 1992, 297, 201-204.	2.8	6

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163	Structure-induced Strain Determining the Internal Cyclization Site in the Yeast <i>cob15</i> Autocatalytic Intron: Theory and Experimental Tests. <i>Journal of Theoretical Biology</i> , 1993, 164, 121-133.	1.7	6
164	Coarse graining the soft-mode dynamics of a folding protein. <i>Physical Chemistry Chemical Physics</i> , 1999, 1, 861-869.	2.8	6
165	Finding the collapse-inducing nucleus in a folding protein. <i>Journal of Chemical Physics</i> , 2001, 114, 8678-8684.	3.0	6
166	Pathway Diversity and Concertedness in Protein Folding: An ab-initio Approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2002, 19, 739-764.	3.5	6
167	Under-wrapped soluble proteins as signals triggering membrane morphology. <i>Journal of Chemical Physics</i> , 2003, 119, 6911-6915.	3.0	6
168	Sequence-space selection of cooperative model proteins. <i>Journal of Physics A</i> , 2004, 37, L197-L202.	1.6	6
169	COVID-19 Evolution in the Post-Vaccination Phase: Endemic or Extinct?. <i>ACS Pharmacology and Translational Science</i> , 2021, 4, 403-405.	4.9	6
170	Pattern of separatrices and intrinsic reaction coordinates for degenerate thermal rearrangements. <i>Theoretica Chimica Acta</i> , 1985, 67, 229-233.	0.8	5
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