

Federico Fogolari

List of Publications by Year in descending order

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129
papers

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citations

109321

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all docs

129
docs citations

129
times ranked

6991
citing authors

#	ARTICLE	IF	CITATIONS
1	The corona of protein-gold nanoparticle systems: the role of ionic strength. <i>Physical Chemistry Chemical Physics</i> , 2022, 24, 1630-1637.	2.8	5
2	Biallelic <i>ATOH1</i> Gene Variant in Siblings With Pontocerebellar Hypoplasia, Developmental Delay, and Hearing Loss. <i>Neurology: Genetics</i> , 2022, 8, e677.	1.9	2
3	Case Report: Novel Compound Heterozygous RNASEH2B Mutations Cause Aicardi-Goutières Syndrome. <i>Frontiers in Immunology</i> , 2021, 12, 672952.	4.8	1
4	Entropy of Two-Molecule Correlated Translational-Rotational Motions Using the <i>k</i> th Nearest Neighbor Method. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 3039-3051.	5.3	4
5	Structure of Nanobody Nb23. <i>Molecules</i> , 2021, 26, 3567.	3.8	6
6	Topologically non-trivial metal-organic assemblies inhibit β 2-microglobulin amyloidogenesis. <i>Cell Reports Physical Science</i> , 2021, 2, 100477.	5.6	1
7	Optimal Relabeling of Water Molecules and Single-Molecule Entropy Estimation. <i>Biophysica</i> , 2021, 1, 279-296.	1.4	2
8	A novel de novo <i>HDAC8</i> missense mutation causing Cornelia de Lange syndrome. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1612.	1.2	2
9	NMR-Based Analysis of Nanobodies to SARS-CoV-2 Nsp9 Reveals a Possible Antiviral Strategy Against COVID-19. <i>Advanced Biology</i> , 2021, 5, e2101113.	2.5	9
10	Amplifying the spectrum of SPAST gene mutations.. <i>Acta Biomedica</i> , 2021, 92, e2021220.	0.3	0
11	Insights into a Protein-Nanoparticle System by Paramagnetic Perturbation NMR Spectroscopy. <i>Molecules</i> , 2020, 25, 5187.	3.8	7
12	Generalized Born radii computation using linear models and neural networks. <i>Bioinformatics</i> , 2020, 36, 1757-1764.	4.1	4
13	Missense <i>NR2F1</i> variant in monozygotic twins affected with the Bosch-Boonstra-Schaaf optic atrophy syndrome. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1278.	1.2	7
14	Exploring exchange processes in proteins by paramagnetic perturbation of NMR spectra. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 6247-6259.	2.8	5
15	OSCP subunit of mitochondrial ATP synthase: role in regulation of enzyme function and of its transition to a pore. <i>British Journal of Pharmacology</i> , 2019, 176, 4247-4257.	5.4	32
16	Citrate stabilized gold nanoparticles interfere with amyloid fibril formation: D76N and β 2-microglobulin variants. <i>Nanoscale</i> , 2018, 10, 4793-4806.	5.6	30
17	Interference of citrate-stabilized gold nanoparticles with β 2-microglobulin oligomeric association. <i>Chemical Communications</i> , 2018, 54, 5422-5425.	4.1	11
18	The β 1/EMILIN1 interaction discloses a novel and unique integrin-ligand type of engagement. <i>Matrix Biology</i> , 2018, 66, 50-66.	3.6	11

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19	The unique histidine in OSCP subunit of F ₁ F ₀ -ATP synthase mediates inhibition of the permeability transition pore by acidic pH. <i>EMBO Reports</i> , 2018, 19, 257-268.	4.5	91
20	Effect of anions on Cyclophilin D binding to F-ATP synthase: Implications for the permeability transition pore. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, e111-e112.	1.0	0
21	Dynamics and Thermodynamics of Transthyretin Association from Molecular Dynamics Simulations. <i>BioMed Research International</i> , 2018, 2018, 1-14.	1.9	9
22	Free Energy, Enthalpy and Entropy from Implicit Solvent End-Point Simulations. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 11.	3.5	22
23	The interaction of β_2 -microglobulin with gold nanoparticles: impact of coating, charge and size. <i>Journal of Materials Chemistry B</i> , 2018, 6, 5964-5974.	5.8	7
24	PDB2ENTROPY and PDB2TRENT: Conformational and Translational/Rotational Entropy from Molecular Ensembles. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1319-1324.	5.4	24
25	Citrate-stabilized gold nanoparticles hinder fibrillogenesis of a pathological variant of β_2 -microglobulin. <i>Nanoscale</i> , 2017, 9, 3941-3951.	5.6	26
26	Automation of peak-tracking analysis of stepwise perturbed NMR spectra. <i>Journal of Biomolecular NMR</i> , 2017, 67, 121-134.	2.8	6
27	A specific nanobody prevents amyloidogenesis of D76N β_2 -microglobulin in vitro and modifies its tissue distribution in vivo. <i>Scientific Reports</i> , 2017, 7, 46711.	3.3	18
28	Molecular dynamics simulations of β_2 -microglobulin interaction with hydrophobic surfaces. <i>Molecular BioSystems</i> , 2017, 13, 2625-2637.	2.9	6
29	Short-Chain Alkanethiol Coating for Small-Size Gold Nanoparticles Supporting Protein Stability. <i>Magnetochemistry</i> , 2017, 3, 40.	2.4	4
30	The BR domain of PsrP interacts with extracellular DNA to promote bacterial aggregation; structural insights into pneumococcal biofilm formation. <i>Scientific Reports</i> , 2016, 6, 32371.	3.3	27
31	Similarity Measures Based on the Overlap of Ranked Genes Are Effective for Comparison and Classification of Microarray Data. <i>Journal of Computational Biology</i> , 2016, 23, 603-614.	1.6	3
32	Accurate Estimation of the Entropy of Rotation/Translation Probability Distributions. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 1-8.	5.3	21
33	Chelating effect in short polymers for the design of bidentate binders of increased affinity and selectivity. <i>Scientific Reports</i> , 2015, 5, 15633.	3.3	6
34	Distance-Based Configurational Entropy of Proteins from Molecular Dynamics Simulations. <i>PLoS ONE</i> , 2015, 10, e0132356.	2.5	32
35	From ATP to PTP and Back. <i>Circulation Research</i> , 2015, 116, 1850-1862.	4.5	97
36	Role of Dynamics in the Autoinhibition and Activation of the Hyperpolarization-activated Cyclic Nucleotide-modulated (HCN) Ion Channels. <i>Journal of Biological Chemistry</i> , 2015, 290, 17642-17654.	3.4	23

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37	Accuracy assessment of the linear $P \propto B$ oltzmann equation and reparametrization of the OBC generalized B orn model for nucleic acids and nucleic acid-protein complexes. Journal of Computational Chemistry, 2015, 36, 585-596.	3.3	9
38	Probing the Influence of Citrate-Capped Gold Nanoparticles on an Amyloidogenic Protein. ACS Nano, 2015, 9, 2600-2613.	14.6	80
39	The Accuracy of Generalized Born Forces. , 2015, , 143-155.		1
40	The Oligomycin-Sensitivity Conferring Protein of Mitochondrial ATP Synthase: Emerging New Roles in Mitochondrial Pathophysiology. International Journal of Molecular Sciences, 2014, 15, 7513-7536.	4.1	44
41	SIRT1 gene expression upon genotoxic damage is regulated by APE1 through nCaRE-promoter elements. Molecular Biology of the Cell, 2014, 25, 532-547.	2.1	74
42	Modulation of F-ATP synthase by pH: Role of His112 protonation of OSCP. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, e12-e13.	1.0	0
43	Transcriptomic Analysis Unveils Correlations between Regulative Apoptotic Caspases and Genes of Cholesterol Homeostasis in Human Brain. PLoS ONE, 2014, 9, e110610.	2.5	8
44	Structure, Folding Dynamics, and Amyloidogenesis of D76N β 2-Microglobulin. Journal of Biological Chemistry, 2013, 288, 30917-30930.	3.4	80
45	The TTTT B lymphocyte stimulator promoter haplotype is associated with good response to rituximab therapy in seropositive rheumatoid arthritis resistant to tumor necrosis factor blockers. Arthritis and Rheumatism, 2013, 65, 88-97.	6.7	22
46	A new germline <i>VHL</i> gene mutation in three patients with apparently sporadic pheochromocytoma. Clinical Endocrinology, 2013, 78, 391-397.	2.4	5
47	A differential equation for the Generalized Born radii. Physical Chemistry Chemical Physics, 2013, 15, 9783.	2.8	1
48	Generalized Born forces: Surface integral formulation. Journal of Chemical Physics, 2013, 138, 054112.	3.0	8
49	Reduction of conformational mobility and aggregation in W60G β 2-microglobulin: assessment by ^{15}N NMR relaxation. Magnetic Resonance in Chemistry, 2013, 51, 795-807.	1.9	10
50	Monitoring the Interaction between β 2-Microglobulin and the Molecular Chaperone β -crystallin by NMR and Mass Spectrometry. Journal of Biological Chemistry, 2013, 288, 17844-17858.	3.4	32
51	Dimers of mitochondrial ATP synthase form the permeability transition pore. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5887-5892.	7.1	822
52	Absolute Quantification of Choline-Related Biomarkers in Breast Cancer Biopsies by Liquid Chromatography Electrospray Ionization Mass Spectrometry. Analytical Cellular Pathology, 2013, 36, 71-83.	1.4	23
53	Absolute quantification of choline-related biomarkers in breast cancer biopsies by liquid chromatography electrospray ionization mass spectrometry. Analytical Cellular Pathology, 2013, 36, 71-83.	1.4	15
54	Studying Interactions by Molecular Dynamics Simulations at High Concentration. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-9.	3.0	16

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55	Determining the Energy Landscape of Proteins by a Fast Isotope Exchange NMR Approach. <i>Journal of the American Chemical Society</i> , 2012, 134, 4457-4460.	13.7	9
56	Blues server: electrostatic properties of wild-type and mutated protein structures. <i>Bioinformatics</i> , 2012, 28, 2189-2190.	4.1	72
57	Single-shot NMR measurement of protein unfolding landscapes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 842-849.	2.3	7
58	Blues: a program for the analysis of the electrostatic properties of proteins based on generalized Born radii. <i>BMC Bioinformatics</i> , 2012, 13, S18.	2.6	52
59	The Projection Analysis of NMR Chemical Shifts Reveals Extended EPAC Autoinhibition Determinants. <i>Biophysical Journal</i> , 2012, 102, 630-639.	0.5	83
60	Fast structure similarity searches among protein models: efficient clustering of protein fragments. <i>Algorithms for Molecular Biology</i> , 2012, 7, 16.	1.2	5
61	Rapid oligomer formation of human muscle acylphosphatase induced by heparan sulfate. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 547-554.	8.2	28
62	Nucleotide diversity and linkage disequilibrium in <i>Populus nigra</i> cinnamyl alcohol dehydrogenase (CAD4) gene. <i>Tree Genetics and Genomes</i> , 2011, 7, 1011-1023.	1.6	138
63	Molecular dynamics simulation of β 2-microglobulin in denaturing and stabilizing conditions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 986-1001.	2.6	31
64	Effect of Tetracyclines on the Dynamics of Formation and Deconstruction of β 2-Microglobulin Amyloid Fibrils. <i>Journal of Biological Chemistry</i> , 2011, 286, 2121-2131.	3.4	87
65	Role of Dynamics in the Autoinhibition and Activation of the Exchange Protein Directly Activated by Cyclic AMP (EPAC). <i>Journal of Biological Chemistry</i> , 2011, 286, 42655-42669.	3.4	38
66	CLP-based protein fragment assembly. <i>Theory and Practice of Logic Programming</i> , 2010, 10, 709-724.	1.5	10
67	Structural and Dynamics Characteristics of Acylphosphatase from <i>Sulfolobus solfataricus</i> in the Monomeric State and in the Initial Native-like Aggregates. <i>Journal of Biological Chemistry</i> , 2010, 285, 14689-14700.	3.4	23
68	Native-unlike Long-lived Intermediates along the Folding Pathway of the Amyloidogenic Protein β 2-Microglobulin Revealed by Real-time Two-dimensional NMR. <i>Journal of Biological Chemistry</i> , 2010, 285, 5827-5835.	3.4	55
69	Folding and Fibrillogenesis: Clues from β 2-Microglobulin. <i>Journal of Molecular Biology</i> , 2010, 401, 286-297.	4.2	35
70	Electric dipole reorientation in the interaction of botulinum neurotoxins with neuronal membranes. <i>FEBS Letters</i> , 2009, 583, 2321-2325.	2.8	17
71	Comparison of the structural and functional properties of RNase A and BSâ€RNase: A stepwise mutagenesis approach. <i>Biopolymers</i> , 2009, 91, 1009-1017.	2.4	24
72	Molecular models for intrastrand DNA G-quadruplexes. <i>BMC Structural Biology</i> , 2009, 9, 64.	2.3	18

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73	Conformational stability of neuroglobin helix F – possible effects on the folding pathway within the globin family. FEBS Journal, 2009, 276, 5177-5190.	4.7	8
74	Equilibrium Unfolding Thermodynamics of $\hat{\text{I}}^2$ -Microglobulin Analyzed through Native-State H/D Exchange. Biophysical Journal, 2009, 96, 169-179.	0.5	20
75	NMR-based homology model for the solution structure of the C-terminal globular domain of EMILIN1. Journal of Biomolecular NMR, 2009, 43, 79-96.	2.8	8
76	Helix mobility and recognition function of the rat thyroid transcription factor $\hat{\text{I}}^1$ homeodomain – hints from $\langle \text{sup} \rangle 15 \langle /sup \rangle$ NMR relaxation studies. FEBS Journal, 2008, 275, 435-448.	4.7	7
77	The Controlling Roles of Trp60 and Trp95 in $\hat{\text{I}}^2$ -Microglobulin Function, Folding and Amyloid Aggregation Properties. Journal of Molecular Biology, 2008, 378, 887-897.	4.2	82
78	The Catalytic Site of Glutathione Peroxidases. Antioxidants and Redox Signaling, 2008, 10, 1515-1526.	5.4	151
79	The Solution Structure of DNA-free Pax-8 Paired Box Domain Accounts for Redox Regulation of Transcriptional Activity in the Pax Protein Family. Journal of Biological Chemistry, 2008, 283, 33321-33328.	3.4	21
80	Molecular Dynamics Simulation Suggests Possible Interaction Patterns at Early Steps of $\hat{\text{I}}^2$ -Microglobulin Aggregation. Biophysical Journal, 2007, 92, 1673-1681.	0.5	39
81	Agent-based protein structure prediction. Multiagent and Grid Systems, 2007, 3, 183-197.	0.9	12
82	Scoring predictive models using a reduced representation of proteins: model and energy definition. BMC Structural Biology, 2007, 7, 15.	2.3	25
83	Identification of DNA-binding protein target sequences by physical effective energy functions, free energy analysis of lambda repressor-DNA complexes. BMC Structural Biology, 2007, 7, 61.	2.3	9
84	Estimation of $\text{J}_{\text{HNH}\alpha}$ and $\text{J}_{\text{H}\alpha\text{H}\eta}$ coupling constants from heteronuclear TOCSY spectra. Journal of Biomolecular NMR, 2007, 39, 213-222.	2.8	2
85	Molecular analysis of a human PAX6 homeobox mutant. European Journal of Human Genetics, 2006, 14, 744-751.	2.8	9
86	NMR Dynamic Studies Suggest that Allosteric Activation Regulates Ligand Binding in Chicken Liver Bile Acid-binding Protein. Journal of Biological Chemistry, 2006, 281, 9697-9709.	3.4	50
87	Collagen Plays an Active Role in the Aggregation of $\hat{\text{I}}^2$ -Microglobulin under Physiopathological Conditions of Dialysis-related Amyloidosis. Journal of Biological Chemistry, 2006, 281, 16521-16529.	3.4	128
88	Solution structure of $\hat{\text{I}}^2$ -microglobulin and insights into fibrillogenesis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1753, 76-84.	2.3	25
89	Application of MM/PBSA colony free energy to loop decoy discrimination: Toward correlation between energy and root mean square deviation. Protein Science, 2005, 14, 889-901.	7.6	41
90	A decoy set for the thermostable subdomain from chicken villin headpiece, comparison of different free energy estimators. BMC Bioinformatics, 2005, 6, 301.	2.6	14

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91	Functional analysis of a novel RUNX2 missense mutation found in a family with cleidocranial dysplasia. <i>Journal of Human Genetics</i> , 2005, 50, 679-683.	2.3	12
92	MM/PBSA analysis of molecular dynamics simulations of bovine β -lactoglobulin: Free energy gradients in conformational transitions?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 91-103.	2.6	28
93	Comparative molecular dynamics simulations of HIV-1 integrase and the T66I/M154I mutant: Binding modes and drug resistance to a diketo acid inhibitor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 723-741.	2.6	41
94	Protein Folding Simulation in CCP. <i>Lecture Notes in Computer Science</i> , 2004, , 452-453.	1.3	4
95	Constraint Logic Programming approach to protein structure prediction. <i>BMC Bioinformatics</i> , 2004, 5, 186.	2.6	57
96	Protein Folding in CLP(\mathcal{FD}) with Empirical Contact Energies. <i>Lecture Notes in Computer Science</i> , 2004, , 250-265.	1.3	4
97	Amino acid empirical contact energy definitions for fold recognition in the space of contact maps. <i>BMC Bioinformatics</i> , 2003, 4, 8.	2.6	88
98	Quantitative Correlation of Solvent Polarity with the β -310-Helix Equilibrium: A Heptapeptide Behaves as a Solvent-Driven Molecular Spring. <i>Angewandte Chemie - International Edition</i> , 2003, 42, 3388-3392.	13.8	91
99	NMR Solution Structure of Viscotoxin C1 from <i>Viscum Album Species Coloratum ohwi</i> : A Toward a Structure-Function Analysis of Viscotoxins. <i>Biochemistry</i> , 2003, 42, 12503-12510.	2.5	30
100	Investigations of Sso7d Catalytic Residues by NMR Titration Shifts and Electrostatic Calculations. <i>Biochemistry</i> , 2003, 42, 1421-1429.	2.5	20
101	Protocol for MM/PBSA Molecular Dynamics Simulations of Proteins. <i>Biophysical Journal</i> , 2003, 85, 159-166.	0.5	173
102	EF Loop Conformational Change Triggers Ligand Binding in β -Lactoglobulins. <i>Journal of Biological Chemistry</i> , 2003, 278, 38840-38846.	3.4	67
103	Peptide Models of Folding Initiation Sites of Bovine β -Lactoglobulin: Identification of Nativelike Hydrophobic Interactions Involving G and H Strands. <i>Biochemistry</i> , 2002, 41, 2786-2796.	2.5	20
104	The Poisson-Boltzmann equation for biomolecular electrostatics: a tool for structural biology. <i>Journal of Molecular Recognition</i> , 2002, 15, 377-392.	2.1	469
105	Using Secondary Structure Information for Protein Folding in CLP(\mathcal{FD}) 1 The work is partially supported by MIUR project: Automatic Aggregate "and number" Reasoning for Computing.. <i>Electronic Notes in Theoretical Computer Science</i> , 2002, 76, 83-98.	0.9	8
106	Dimerization, stability and electrostatic properties of porcine β -lactoglobulin. <i>FEBS Journal</i> , 2001, 268, 4477-4488.	0.2	16
107	Monitoring folding/unfolding transitions of proteins by capillary zone electrophoresis: Measurement of α and its variation along the pH scale. <i>Electrophoresis</i> , 2001, 22, 3728-3735.	2.4	13
108	NMR structural determination of viscotxin A3 from <i>Viscum album L.</i> <i>Biochemical Journal</i> , 2000, 350, 569.	3.7	12

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109	NMR structural determination of viscotoxin A3 from <i>Viscum album</i> L.. <i>Biochemical Journal</i> , 2000, 350, 569-577.	3.7	45
110	Electrostatic properties of bovine β -lactoglobulin. , 2000, 39, 317-330.		68
111	Simulation of electrostatic effects in Fab-antigen complex formation. <i>FEBS Journal</i> , 2000, 267, 4861-4869.	0.2	10
112	Bovine β -lactoglobulin: Interaction studies with palmitic acid. <i>Protein Science</i> , 2000, 9, 1347-1356.	7.6	105
113	Comparative stability analysis of the thyroid transcription factor 1 and Antennapedia homeodomains: evidence for residue 54 in controlling the structural stability of the recognition helix. <i>International Journal of Biochemistry and Cell Biology</i> , 1999, 31, 1339-1353.	2.8	5
114	Biomolecular Electrostatics with the Linearized Poisson-Boltzmann Equation. <i>Biophysical Journal</i> , 1999, 76, 1-16.	0.5	122
115	pKaShift Effects on Backbone Amide Base-Catalyzed Hydrogen Exchange Rates in Peptides. <i>Journal of the American Chemical Society</i> , 1998, 120, 3735-3738.	13.7	35
116	Electrostatic and non-electrostatic contributions to the binding free energies of anthracycline antibiotics to DNA. <i>Journal of Molecular Biology</i> , 1997, 274, 253-267.	4.2	104
117	Hydrogen-deuterium exchange studies of the rat thyroid transcription factor 1 homeodomain. <i>Journal of Biomolecular NMR</i> , 1997, 9, 397-407.	2.8	1
118	Structural comparison between retro-inverso and parent peptides: Molecular basis for the biological activity of a retro-inverso analogue of the immunodominant fragment of VP1 coat protein from foot-and-mouth disease virus. , 1997, 41, 569-590.		27
119	On the variational approach to Poisson-Boltzmann free energies. <i>Chemical Physics Letters</i> , 1997, 281, 135-139.	2.6	68
120	Analysis of the Solution Structure of the Homeodomain of Rat Thyroid Transcription Factor 1 by 1H-NMR Spectroscopy and Restrained Molecular Mechanics. <i>FEBS Journal</i> , 1996, 241, 101-113.	0.2	26
121	Improved Processing of Selective NMR Spectra of Biopolymers by Separation of Noise and Signal Subspaces through Singular-Value Decomposition. <i>Journal of Magnetic Resonance Series B</i> , 1996, 113, 160-166.	1.6	5
122	Analysis of the conformation and stability of rat TTF-1 homeodomain by circular dichroism. <i>FEBS Letters</i> , 1994, 354, 293-296.	2.8	19
123	Conformational study of a short Pertussis toxin T cell epitope incorporated in a multiple antigen peptide template by CD and two-dimensional NMR. Analysis of the structural effects on the activity of synthetic immunogens. <i>FEBS Journal</i> , 1993, 217, 171-187.	0.2	9
124	NMR and circular dichroism studies of the lantibiotic nisin in non-aqueous environments. <i>FEBS Letters</i> , 1993, 319, 189-194.	2.8	50
125	Structural study of rat thyroid transcription factor 1 homeodomain (TTF-1 HD) by nuclear magnetic resonance. <i>FEBS Letters</i> , 1993, 336, 397-402.	2.8	13
126	Free Energies Calculated According to Manning's Polyelectrolyte Model Compared with Poisson Boltzmann Predictions. <i>Journal of Biomolecular Structure and Dynamics</i> , 1993, 11, 629-635.	3.5	4

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127	NMR structural characterization of the reaction product between d(GpG) and the octahedral antitumor complex trans-RuCl ₂ (DMSO) ₄ . <i>Biochemistry</i> , 1992, 31, 7094-7103.	2.5	46
128	Limiting-laws of polyelectrolyte solutions. Ionic distribution in mixed-valency counterions systems. I: The model. <i>Biophysical Chemistry</i> , 1991, 41, 73-80.	2.8	38
129	Secondary structure effects on the interaction of different polynucleotides with Ca ²⁺ . <i>Biopolymers</i> , 1990, 30, 325-333.	2.4	11