Alexei V Finkelstein

List of Publications by Year
in descending order

147 papers	7,204 citations	66343 42 h-index	58581 82 g-index
150 all docs	150 docs citations	150 times ranked	4922 citing authors

#	Article	IF	Citations
1	Calculation of Crystal-Solution Dissociation Constants. Biomolecules, 2022, 12, 147.	4.0	0
2	The Molten Globule State of a Globular Protein in a Cell Is More or Less Frequent Case Rather than an Exception. Molecules, 2022, 27, 4361.	3.8	5
3	How Can Ice Emerge at 0 Â°C?. Biomolecules, 2022, 12, 981.	4.0	3
4	Solution of Levinthalâ€™s Paradox and a Physical Theory of Protein Folding Times. Biomolecules, 2020, 10, 250.	4.0	21
5	The Reverse Side of a Coin: â€œFactor-Freeâ€•Ribosomal Protein Synthesis In Vitro is a Consequence of the In Vivo Proofreading Mechanism. Biomolecules, 2019, 9, 588.	4.0	0
6	Life in Phases: Intra- and Inter- Molecular Phase Transitions in Protein Solutions. Biomolecules, 2019, 9, 842.	4.0	52
7	What is Responsible for Atypical Dependence of the Rate of Amyloid Formation on Protein Concentration: Fibril-Catalyzed Initiation of New Fibrils or Competition with Oligomers?. Journal of Physical Chemistry Letters, 2018, 9, 1002-1006.	4.6	5
8	50+ Years of Protein Folding. Biochemistry (Moscow), 2018, 83, S3-S18.	1.5	31
9	The Molten Globule Concept: 45 Years Later. Biochemistry (Moscow), 2018, 83, S33-S47.	1.5	26
10	Two Views on the Protein Folding Puzzle. , 2018, , 391-412.		0
11	There and back again: Two views on the protein folding puzzle. Physics of Life Reviews, 2017, 21, 56-71.	2.8	33
12	Intermediate states of apomyoglobin: Are they parts of the same area of conformations diagram?. Biochemistry (Moscow), 2017, 82, 625-631.	1.5	5
13	Sublimation Entropy and Dissociation Constants Prediction by Quantitative Evaluation of Molecular Mobility in Crystals. Journal of Physical Chemistry Letters, 2017, 8, 2758-2763.	4.6	4
14	Some additional remarks to the solution of the protein folding puzzle. Physics of Life Reviews, 2017, 21, 77-79.	2.8	4
15	Lecture 1. , 2016, , 3-13.		0
16	Lecture 2. , 2016, , 17-25.		0
17	Lecture 3. , 2016, , 27-37.		0
18	Lecture 4. , 2016, , 39-50.		0

#	Article	IF	Citations
19	Lecture 5. , 2016, , 51-65.		1
20	Lecture 6. , 2016, , 67-82.		0
21	Lecture 7. , 2016, , 85-99.		0
22	Lecture 8. , 2016, , 101-122.		0
23	Lecture 9. , 2016, , 123-137.		0
24	Lecture 11. , 2016, , 151-163.		1
25	Lecture 13. , 2016, , 181-197.		0
26	Lecture 14. , 2016, , 199-213.		0
27	Lecture 15. , 2016, , 215-231.		1
28	Lecture 16. , 2016, , 233-250.		0
29	Lecture 18. , 2016, , 275-287.		0
30	Lecture 19. , 2016, , 289-306.		1
31	Lecture 20. , 2016, , 307-321.		1
32	Lecture 21. , 2016, , 323-346.		1
33	Lecture 22. , 2016, , 349-366.		0
34	Lecture 23. , 2016, , 367-383.		0
35	Calculation of mobility and entropy of the binding of molecules by crystals. Molecular Biology, 2016, 50, 452-461.	1.3	5
36	Reduction of the Search Space for the Folding of Proteins at the Level of Formation and Assembly of Secondary Structures: A New View on the Solution of Levinthalâ€²s Paradox. ChemPhysChem, 2015, 16, 3375-3378.	2.1	16

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37	Time to Overcome the High, Long, and Bumpy Free Energy Barrier in a Multi-Stage Process: The Generalized Steady-State Approach. Journal of Physical Chemistry B, 2015, 119, 158-163.	2.6	8
38	Strict experimental evidence that apo-chaperonin GroEL does not accelerate protein folding, although it does accelerate one of its steps. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6831-E6832.	7.1	12
39	Determination of the Size of the Primary and Secondary Folding Nuclei of Protofibrils from the Concentration Dependence of the Rate and the Lag-Time of Their Formation. , 2015, , 47-66.		2
40	A structural perspective of compensatory evolution. Current Opinion in Structural Biology, 2014, 26, 104-112.	5.7	42
41	How to Determine the Size of Folding Nuclei of Protofibrils from the Concentration Dependence of the Rate and Lag-Time of Aggregation. I. Modeling the Amyloid Protofibril Formation. Journal of Physical Chemistry B, 2014, 118, 1189-1197.	2.6	48
42	How to Determine the Size of Folding Nuclei of Protofibrils from the Concentration Dependence of the Rate and Lag-Time of Aggregation. II. Experimental Application for Insulin and LysPro Insulin: Aggregation Morphology, Kinetics, and Sizes of Nuclei. Journal of Physical Chemistry B, 2014, 118, 1198-1206.	2.6	27
43	Restrictions to protein folding determined by the protein size. FEBS Letters, 2013, 587, 1884-1890.	2.8	19
44	Levinthalâ€™s question answered â€¦ again?. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1013-1015.	3.5	7
45	Golden triangle for folding rates of globular proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 147-150.	7.1	58
46	Development and Testing of PFFSol1.1, a New Polarizable Atomic Force Field for Calculation of Molecular Interactions in Implicit Water Environment. Journal of Physical Chemistry B, 2012, 116, 4646-4654.	2.6	12
47	Cunning Simplicity of a Stoichiometry Driven Protein Folding Thesis. Journal of Biomolecular Structure and Dynamics, 2011, 28, 595-598.	3.5	4
48	Analogy-based protein structure prediction: III. Optimizing the combination of the substitution matrix and pseudopotentials used to align protein sequences with spatial structures. Molecular Biology, 2010, 44, 109-118.	1.3	3
49	Protein Folding as Flow across a Network of Foldingâ^'Unfolding Pathways. 1. The Mid-Transition Case. Journal of Physical Chemistry B, 2010, 114, 7920-7929.	2.6	6
50	Folding Intermediate and Folding Nucleus for Iâ†'N and Uâ†'Iâ†'N Transitions in Apomyoglobin: Contributions by Conserved and Nonconserved Residues. Biophysical Journal, 2010, 98, 1694-1702.	0.5	23
51	Protein Folding as Flow across a Network of Foldingâ^'Unfolding Pathways. 2. The â€œIn-Waterâ€•Case. Journal of Physical Chemistry B, 2010, 114, 7930-7934.	2.6	6
52	How strong are side chain interactions in the folding intermediate?. Protein Science, 2009, 18, 2152-2159.	7.6	21
53	Analogy-based protein structure prediction: I. A new database of spatially similar and dissimilar structures of protein domains for testing and optimizing prediction methods. Molecular Biology, 2009, 43, 665-676.	1.3	1
54	Analogy-based protein structure prediction: II. Testing of substitution matrices and pseudopotentials used to align protein sequences with spatial structures. Molecular Biology, 2009, 43, 677-684.	1.3	1

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55	MANY-ATOM VAN DER WAALS INTERACTIONS LEAD TO DIRECTION-SENSITIVE INTERACTIONS OF COVALENT BONDS. Journal of Bioinformatics and Computational Biology, 2008, 06, 693-707.	0.8	3
56	Protein Structure and Its Folding Rate. , 2008, , 273-301.		0
57	Understanding the Folding Rates and Folding Nuclei of Globular Proteins. Current Protein and Peptide Science, 2007, 8, 521-536.	1.4	18
58	Average and extreme multi-atom Van der Waals interactions: Strong coupling of multi-atom Van der Waals interactions with covalent bonding. Chemistry Central Journal, 2007, 1, 21.	2.6	12
59	TREND OF AMINO ACID COMPOSITION OF PROTEINS OF DIFFERENT TAXA. Journal of Bioinformatics and Computational Biology, 2006, 04, 597-608.	0.8	82
60	Three-state protein folding: Experimental determination of free-energy profile. Protein Science, 2005, 14, 2658-2667.	7.6	34
61	Comparison of X-ray and NMR structures: Is there a systematic difference in residue contacts between X-ray- and NMR-resolved protein structures?. Proteins: Structure, Function and Bioinformatics, 2005, 60, 139-147.	2.6	78
62	Theoretical study of protein folding: outlining folding nuclei and estimation of protein folding rates. Journal of Physics Condensed Matter, 2005, 17, S1539-S1551.	1.8	10
63	Prediction of protein folding rates from the amino acid sequence-predicted secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8942-8944.	7.1	171
64	Making optimal use of empirical energy functions: Force-field parameterization in crystal space. Proteins: Structure, Function and Bioinformatics, 2004, 57, 678-683.	2.6	772
65	From analysis of protein structural alignments toward a novel approach to align protein sequences. Proteins: Structure, Function and Bioinformatics, 2004, 54, 569-582.	2.6	16
66	Physics of protein folding. Physics of Life Reviews, 2004, 1, 23-56.	2.8	92
67	Outlining Folding Nuclei in Globular Proteins. Journal of Molecular Biology, 2004, 336, 509-525.	4.2	57
68	Chain length is the main determinant of the folding rate for proteins with three-state folding kinetics. Proteins: Structure, Function and Bioinformatics, 2003, 51, 162-166.	2.6	140
69	Contact order revisited: Influence of protein size on the folding rate. Protein Science, 2003, 12, 2057-2062.	7.6	327
70	Common features in structures and sequences of sandwich-like proteins. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14137-14141.	7.1	57
71	Cunning Simplicity of a Hierarchical Folding. Journal of Biomolecular Structure and Dynamics, 2002, 20, 311-313.	3.5	21
72	Threading with chemostructural restrictions method for predicting fold and functionally significant residues: Application to dipeptidylpeptidase IV (DPP-IV). Proteins: Structure, Function and Bioinformatics, 2002, 47, 180-193.	2.6	17

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73	Lecture 9. , 2002, , 103-116.		5
74	α-Helix and β-Hairpin Folding from Experiment, Analytical Theory and Molecular Dynamics Simulations. Current Protein and Peptide Science, 2002, 3, 191-200.	1.4	32
75	Folding of circular permutants with decreased contact order: general trend balanced by protein stability 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 314, 891-900.	4.2	55
76	Folding nuclei in proteins. FEBS Letters, 2001, 489, 113-118.	2.8	72
77	Theoretical Study of a Landscape of Protein Foldingâ^'Unfolding Pathways. Folding Rates at Midtransitionâ€. Biochemistry, 2001, 40, 9957-9961.	2.5	25
78	Folding Nuclei in Proteins. Molecular Biology, 2001, 35, 605-613.	1.3	4
79	Cunning simplicity of protein folding landscapes. Protein Engineering, Design and Selection, 2001, 14, 521-523.	2.1	27
80	Statistical significance of protein structure prediction by threading. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 9978-9983.	7.1	33
81	Derivation and Testing Residue-Residue Mean-Force Potentials for Use in Protein Structure Recognition. , 2000, 143, 155-174.		4
82	Averaging interaction energies over homologs improves protein fold recognition in gapless threading. Proteins: Structure, Function and Bioinformatics, 1999, 35, 353-359.	2.6	23
83	Oleg Borisovich Ptitsyn: July 18, 1929-March 22, 1999. , 1999, 36, 145-146.		0
84	A theoretical search for folding/unfolding nuclei in three-dimensional protein structures. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 11299-11304.	7.1	300
85	Rate of protein folding near the point of thermodynamic equilibrium between the coil and the most stable chain fold: Influence of chain knotting on the rate of folding. Folding & Design, 1998, 3, 67-68.	4.5	20
86	Folding rate dependence on the chain length for RNA-like heteropolymers. Folding & Design, 1998, 3, 69-78.	4.5	12
87	What is the probability of a chance prediction of a protein structure with an rmsd of 6 Ã¥?. Folding & Design, 1998, 3, 141-147.	4.5	185
88	Optimization of Protein Structure on Lattices Using a Self-Consistent Field Approach. Journal of Computational Biology, 1998, 5, 531-538.	1.6	12
89	3D Protein Folds: Homologs Against Errorsâ€"a Simple Estimate Based on the Random Energy Model. Physical Review Letters, 1998, 80, 4823-4825.	7.8	20
90	How Homologs Can Help to Predict Protein Folds Even Though They Cannot Be Predicted for Individual Sequences. Journal of Computational Biology, 1998, 5, 369-376.	1.6	4

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91	Residue-residue mean-force potentials for protein structure recognition. Protein Engineering, Design and Selection, 1997, 10, 865-876.	2.1	48
92	Can protein unfolding simulate protein folding?. Protein Engineering, Design and Selection, 1997, 10, 843-845.	2.1	68
93	Recognition of protein structure on coarse lattices with residue- residue energy functions. Protein Engineering, Design and Selection, 1997, 10, 1123-1130.	2.1	8
94	Protein structure: what is it possible to predict now?. Current Opinion in Structural Biology, 1997, 7, 60-71.	5.7	69
95	S6 permutein shows that the unusual target topology is not responsible for the absence of rigid tertiary structure in de novo protein albebetin. FEBS Letters, 1997, 414, 243-246.	2.8	8
96	Rate of protein folding near the point of thermodynamic equilibrium between the coil and the most stable chain fold. Folding & Design, 1997, 2, 115-121.	4.5	176
97	Lattice modeling: Accuracy of energy calculations. Journal of Computational Chemistry, 1996, 17, 1025-1032.	3.3	5
98	Adjusting potential energy functions for lattice models of chain molecules. , 1996, 25, 379-388.		8
99	Building self-avoiding lattice models of proteins using a self-consistent field optimization. , 1996, 26, 1-8.		9
100	Computer simulation of secondary structure folding of random and â€˜â€˜editedâ€™â€™ RNA chains. Journal of Chemical Physics, 1996, 105, 319-325.	3.0	8
101	Search for the most stable folds of protein chains: II. Computation of stable architectures of Î²-proteins using a self-consistent molecular field theory. Protein Engineering, Design and Selection, 1996, 9, 399-411.	2.1	18
102	Search for the most stable folds of protein chains: I. Application of a self-consistent molecular field theory to a problem of protein three-dimensional structure prediction. Protein Engineering, Design and Selection, 1996, 9, 387-397.	2.1	19
103	Title is missing!. Journal of Computational Chemistry, 1996, 17, 1025.	3.3	0
104	Accurate general method for lattice approximation of three-dimensional structure of a chain molecule. Proteins: Structure, Function and Bioinformatics, 1995, 22, 100-109.	2.6	22
105	Why do protein architectures have boltzmann-like statistics?. Proteins: Structure, Function and Bioinformatics, 1995, 23, 142-150.	2.6	191
106	Perfect temperature for protein structure prediction and folding. Proteins: Structure, Function and Bioinformatics, 1995, 23, 151-162.	2.6	43
107	Constructing Lattice Models of Protein Chains with Side Groups. Journal of Computational Biology, 1995, 2, 527-535.	1.6	13
108	Predicted Î²-structure stability parameters under experimental test. Protein Engineering, Design and Selection, 1995, 8, 207-209.	2.1	11

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109	Folding of chains with random and edited sequences: similarities and differences. Protein Engineering, Design and Selection, 1995, 8, 883-892.	2.1	29
110	Boltzmann-like Statistics of Protein Architectures. Sub-Cellular Biochemistry, 1995, 24, 1-26.	2.4	41
111	A new approach to artificial and modified proteins: theory-based design, synthesis in a cell-free system and fast testing of structural properties by radiolabels. Protein Engineering, Design and Selection, 1994, 7, 1041-1052.	2.1	5
112	Implications of the random characteristics of protein sequences for their three-dimensional structure. Current Opinion in Structural Biology, 1994, 4, 422-428.	5.7	23
113	Computation of biopolymers: A general approach to different problems. BioSystems, 1993, 30, 1-19.	2.0	44
114	Secondary structure of globular proteins at the early and the final stages in protein folding. FEBS Letters, 1993, 334, 265-268.	2.8	50
115	Why are the same protein folds used to perform different functions?. FEBS Letters, 1993, 325, 23-28.	2.8	81
116	Weak points of antiparallel Î²-sheets. How are they filled up in globular proteins?. Protein Engineering, Design and Selection, 1993, 6, 367-372.	2.1	13
117	A new approach to the design of a sequence with the highest affinity for a molecular surface. Protein Engineering, Design and Selection, 1992, 5, 625-628.	2.1	10
118	Search for the stable state of a short chain in a molecular field. Protein Engineering, Design and Selection, 1992, 5, 617-624.	2.1	32
119	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	2.6	26
120	De novo design, synthesis and study of albebetin, a polypeptide with a predetermined three-dimensional structure. Journal of Molecular Biology, 1992, 225, 927-931.	4.2	67
121	A search for the most stable folds of protein chains. Nature, 1991, 351, 497-499.	27.8	140
122	Rate of Î²-structure formation in polypeptides. Proteins: Structure, Function and Bioinformatics, 1991, 9, 23-27.	2.6	54
123	Physical reasons for secondary structure stability: Î±-Helices in short peptides. Proteins: Structure, Function and Bioinformatics, 1991, 10, 287-299.	2.6	85
124	Short alpha-helix stability. Nature, 1990, 345, 300-300.	27.8	13
125	The Classification and Origins of Protein Folding Patterns. Annual Review of Biochemistry, 1990, 59, 1007-1035.	11.1	302
126	The Classification And Origins Of Protein Folding Patterns. Annual Review of Biochemistry, 1990, 59, 1007-1039.	11.1	4

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127	Prediction of protein secondary structure based on physical theory. Histones. Protein Engineering, Design and Selection, 1989, 2, 443-447.	2.1	17
128	Theory of cooperative transitions in protein molecules. I. Why denaturation of globular protein is a first-order phase transition. Biopolymers, 1989, 28, 1667-1680.	2.4	295
129	Theory of cooperative transitions in protein molecules. II. Phase diagram for a protein molecule in solution. Biopolymers, 1989, 28, 1681-1694.	2.4	166
130	The price of lost freedom: entropy of bimolecular complex formation. Protein Engineering, Design and Selection, 1989, 3, 1-3.	2.1	312
131	General architecture of the Î±-helical globule. Journal of Molecular Biology, 1988, 204, 749-769.	4.2	144
132	Prediction of Secondary Structure, Spatial Organization and Distribution of Antigenic Determinants for Hepatitis A Virus Proteins. Journal of Biomolecular Structure and Dynamics, 1987, 5, 447-458.	3.5	2
133	Why do globular proteins fit the limited set of foldin patterns?. Progress in Biophysics and Molecular Biology, 1987, 50, 171-190.	2.9	255
134	Structural model for interferons. FEBS Letters, 1985, 186, 143-148.	2.8	24
135	Theory of protein secondary structure and algorithm of its prediction. Biopolymers, 1983, 22, 15-25.	2.4	257
136	Recognition of signal sequences. FEBS Letters, 1983, 161, 176-179.	2.8	20
137	c I and lexA repressors consist of three cro -like domains. FEBS Letters, 1982, 147, 11-15.	2.8	10
138	Similarities of protein topologies: evolutionary divergence, functional convergence or principles of folding?. Quarterly Reviews of Biophysics, 1980, 13, 339-386.	5.7	193
139	Did the primitive ribosomal RNA code primitive ribosomal protein?. FEBS Letters, 1977, 82, 169-171.	2.8	10
140	Theory of protein molecule self-organization. I. Thermodynamic parameters of local secondary structures in the unfolded protein chain. Biopolymers, 1977, 16, 469-495.	2.4	45
141	Theory of protein molecule self-organization. II. A comparison of calculated thermodynamic parameters of local secondary structures with experiments. Biopolymers, 1977, 16, 497-524.	2.4	54
142	Theory of protein molecule self-organization. III. A calculating method for the probabilities of the secondary structure formation in an unfolded polypeptide chain. Biopolymers, 1977, 16, 525-529.	2.4	34
143	A theory of protein molecule self-organization. Journal of Molecular Biology, 1976, 103, 15-24.	4.2	69
144	Prediction of the three-dimensional structure for ribosomal protein L25. FEBS Letters, 1975, 60, 137-140.	2.8	3

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145	Comparison of predicted and experimentally determined secondary structure of adenyl kinase. Nature, 1974, 250, 140-142.	27.8	190
146	Prediction of the secondary structure of the L7, L12 proteins of the E. coli ribosome. FEBS Letters, 1973, 34, 55-57.	2.8	17
147	Statistical analysis of the correlation among amino acid residues in helical, Î²-stractural and non-regular regions of globular proteins. Journal of Molecular Biology, 1971, 62, 613-624.	4.2	86