

Harold A Scheraga

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328 papers	22,455 citations	71 h-index	140 g-index
344 ext. papers	23,534 ext. citations	4.6 avg, IF	6.62 L-index

#	Paper	IF	Citations
328	Energy parameters in polypeptides. VII. Geometric parameters, partial atomic charges, nonbonded interactions, hydrogen bond interactions, and intrinsic torsional potentials for the naturally occurring amino acids. <i>The Journal of Physical Chemistry</i> , 1975 , 79, 2361-2381		1453
327	Structure of Water and Hydrophobic Bonding in Proteins. I. A Model for the Thermodynamic Properties of Liquid Water. <i>Journal of Chemical Physics</i> , 1962 , 36, 3382-3400	3.9	949
326	Energy parameters in polypeptides. 9. Updating of geometrical parameters, nonbonded interactions, and hydrogen bond interactions for the naturally occurring amino acids. <i>The Journal of Physical Chemistry</i> , 1983 , 87, 1883-1887		902
325	Global optimization of clusters, crystals, and biomolecules. <i>Science</i> , 1999 , 285, 1368-72	33.3	881
324	THE STRUCTURE OF WATER AND HYDROPHOBIC BONDING IN PROTEINS. III. THE THERMODYNAMIC PROPERTIES OF HYDROPHOBIC BONDS IN PROTEINS ^{1,2} . <i>The Journal of Physical Chemistry</i> , 1962 , 66, 1773-1789		830
323	Energy parameters in polypeptides. 10. Improved geometrical parameters and nonbonded interactions for use in the ECEPP/3 algorithm, with application to proline-containing peptides. <i>The Journal of Physical Chemistry</i> , 1992 , 96, 6472-6484		619
322	The structure of water and the thermodynamic properties of aqueous solutions. <i>Journal of Chemical Physics</i> , 1970 , 6, Suppl:487-592	3.9	567
321	Disulfide bonds and protein folding. <i>Biochemistry</i> , 2000 , 39, 4207-16	3.2	487
320	Conformational Analysis of Macromolecules. III. Helical Structures of Polyglycine and Poly-L-Alanine. <i>Journal of Chemical Physics</i> , 1966 , 45, 2091-2101	3.9	391
319	Structure of Water and Hydrophobic Bonding in Proteins. IV. The Thermodynamic Properties of Liquid Deuterium Oxide. <i>Journal of Chemical Physics</i> , 1964 , 41, 680-689	3.9	351
318	Intermolecular potentials from crystal data. 6. Determination of empirical potentials for O-H...O = C hydrogen bonds from packing configurations. <i>The Journal of Physical Chemistry</i> , 1984 , 88, 6231-6233		332
317	METHOD FOR CALCULATION INTERNAL ROTATION BARRIERS. <i>Journal of Chemical Physics</i> , 1965 , 42, 2209-15	3.9	300
316	Conformation of analysis of macromolecules. IV. Helical structures of poly-L-alanine, poly-L-valine, poly-beta-methyl-L-aspartate, poly-gamma-methyl-L-glutamate, and poly-L-tyrosine. <i>Journal of Chemical Physics</i> , 1967 , 46, 4410-26	3.9	285
315	Protein-folding dynamics: overview of molecular simulation techniques. <i>Annual Review of Physical Chemistry</i> , 2007 , 58, 57-83	15.7	278
314	Protein folding. <i>Quarterly Reviews of Biophysics</i> , 1977 , 10, 239-52	7	261
313	Influence of local interactions on protein structure. I. Conformational energy studies of N-acetyl-N'-methylamides of Pro-X and X-Pro dipeptides. <i>Biopolymers</i> , 1977 , 16, 811-43	2.2	247
312	Phase transitions in one dimension and the helix-coil transition in polyamino acids. <i>Journal of Chemical Physics</i> , 1966 , 45, 1456-63	3.9	242

311	Ab initio simulations of protein-folding pathways by molecular dynamics with the united-residue model of polypeptide chains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 2362-7	11.5	230
310	Principal component analysis for protein folding dynamics. <i>Journal of Molecular Biology</i> , 2009 , 385, 312-20	2.5	224
309	Conformational Analysis of Macromolecules. II. The Rotational Isomeric States of the Normal Hydrocarbons. <i>Journal of Chemical Physics</i> , 1966 , 44, 3054-3069	3.9	219
308	Statistical and energetic analysis of side-chain conformations in oligopeptides. <i>International Journal of Peptide and Protein Research</i> , 1983 , 22, 1-15		214
307	Cumulant-based expressions for the multibody terms for the correlation between local and electrostatic interactions in the united-residue force field. <i>Journal of Chemical Physics</i> , 2001 , 115, 2323-2347	3.9	209
306	Analysis of the Contribution of Internal Vibrations to the Statistical Weights of Equilibrium Conformations of Macromolecules. <i>Journal of Chemical Physics</i> , 1969 , 51, 4751-4767	3.9	208
305	Occurrence of a phase transition in nucleic acid models. <i>Journal of Chemical Physics</i> , 1966 , 45, 1464-9	3.9	196
304	Non-Newtonian Viscosity of Solutions of Ellipsoidal Particles. <i>Journal of Chemical Physics</i> , 1955 , 23, 1526-1532	3.5	189
303	Oxidative folding of proteins. <i>Accounts of Chemical Research</i> , 2000 , 33, 805-12	24.3	174
302	Conformational energy studies of beta-sheets of model silk fibroin peptides. I. Sheets of poly(Ala-Gly) chains. <i>Biopolymers</i> , 1991 , 31, 1529-41	2.2	169
301	Modification and optimization of the united-residue (UNRES) potential energy function for canonical simulations. I. Temperature dependence of the effective energy function and tests of the optimization method with single training proteins. <i>Journal of Physical Chemistry B</i> , 2007 , 111, 260-85	3.4	160
300	On the multiple-minima problem in the conformational analysis of polypeptides. II. An electrostatically driven Monte Carlo method--tests on poly(L-alanine). <i>Biopolymers</i> , 1988 , 27, 1283-303	2.2	148
299	Preferred conformation of the tert-butoxycarbonyl-amino group in peptides. <i>International Journal of Peptide and Protein Research</i> , 1980 , 16, 156-72		146
298	Regeneration of bovine pancreatic ribonuclease A. 1. Steady-state distribution. <i>Biochemistry</i> , 1993 , 32, 2671-9	3.2	142
297	Computation of the sterically allowed conformations of peptides. <i>Biopolymers</i> , 1966 , 4, 369-407	2.2	140
296	Influence of water structure and of hydrophobic interactions on the strength of side-chain hydrogen bonds in proteins. <i>Biopolymers</i> , 1963 , 1, 43-69	2.2	136
295	A comparative study of the simulated-annealing and Monte Carlo-with-minimization approaches to the minimum-energy structures of polypeptides: [Met]-enkephalin. <i>Journal of Computational Chemistry</i> , 1991 , 12, 594-605	3.5	135
294	Energy Parameters in Polypeptides. VI. Conformational Energy Analysis of the N-Acetyl N'-Methyl Amides of the Twenty Naturally Occurring Amino Acids. <i>Israel Journal of Chemistry</i> , 1973 , 11, 121-152	3.4	129

293	Prediction of the native conformation of a polypeptide by a statistical-mechanical procedure. I. Backbone structure of enkephalin. <i>Biopolymers</i> , 1985 , 24, 1391-436	2.2	128
292	Conformational analysis of macromolecules. V. Helical structures of poly-L-aspartic acid and poly-L-glutamic acid, and related compounds. <i>Journal of Chemical Physics</i> , 1968 , 49, 2713-26	3.9	127
291	Theoretical determination of sterically allowed conformations of a polypeptide chain by a computer method. <i>Biopolymers</i> , 1965 , 3, 155-184	2.2	126
290	Statistical mechanics of noncovalent bonds in polyamino acids. VIII. Covalent loops in proteins. <i>Biopolymers</i> , 1965 , 3, 379-399	2.2	123
289	Cooperative interactions in single-strand oligomers of adenylic acid. <i>Biopolymers</i> , 1966 , 4, 223-35	2.2	123
288	Molecular dynamics with the united-residue model of polypeptide chains. II. Langevin and Berendsen-bath dynamics and tests on model alpha-helical systems. <i>Journal of Physical Chemistry B</i> , 2005 , 109, 13798-810	3.4	121
287	Use of buildup and energy-minimization procedures to compute low-energy structures of the backbone of enkephalin. <i>Biopolymers</i> , 1985 , 24, 1437-47	2.2	115
286	A fast adaptive multigrid boundary element method for macromolecular electrostatic computations in a solvent. <i>Journal of Computational Chemistry</i> , 1997 , 18, 569-583	3.5	113
285	Determination of net atomic charges using a modified partial equalization of orbital electronegativity method. 1. Application to neutral molecules as models for polypeptides. <i>The Journal of Physical Chemistry</i> , 1990 , 94, 4732-4739		109
284	Deamidation of the asparaginyl-glycyl sequence. <i>International Journal of Peptide and Protein Research</i> , 1986 , 28, 79-84		105
283	Calorimetric measurement of enthalpy change in the isothermal helix-coil transition of poly-L-lysine in aqueous solution. <i>Biopolymers</i> , 1971 , 10, 657-80	2.2	102
282	Molecular dynamics with the united-residue model of polypeptide chains. I. Lagrange equations of motion and tests of numerical stability in the microcanonical mode. <i>Journal of Physical Chemistry B</i> , 2005 , 109, 13785-97	3.4	101
281	Proline-induced constraints in alpha-helices. <i>Biopolymers</i> , 1987 , 26, 1587-600	2.2	100
280	A new force field (ECEPP-05) for peptides, proteins, and organic molecules. <i>Journal of Physical Chemistry B</i> , 2006 , 110, 5025-44	3.4	96
279	Regeneration of bovine pancreatic ribonuclease A: identification of two natively like three-disulfide intermediates involved in separate pathways. <i>Biochemistry</i> , 1998 , 37, 3760-6	3.2	96
278	Coupling of conformational folding and disulfide-bond reactions in oxidative folding of proteins. <i>Biochemistry</i> , 2001 , 40, 9059-64	3.2	95
277	Model for the conformational analysis of hydrated peptides. Effect of hydration on the conformational stability of the terminally blocked residues of the 20 naturally occurring amino acids. <i>Biopolymers</i> , 1979 , 18, 1565-1610	2.2	95
276	Folding and unfolding kinetics of the proline-to-alanine mutants of bovine pancreatic ribonuclease A. <i>Biochemistry</i> , 1996 , 35, 1548-59	3.2	94

275	Mechanism of reductive protein unfolding. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 489-94	17.6	93
274	Role of non-native aromatic and hydrophobic interactions in the folding of hen egg white lysozyme. <i>Biochemistry</i> , 1996 , 35, 13797-807	3.2	93
273	A second right-handed helical structure with the parameters of the Pauling-Corey alpha-helix. <i>Nature</i> , 1967 , 214, 363-5	50.4	92
272	Prodock: Software package for protein modeling and docking. <i>Journal of Computational Chemistry</i> , 1999 , 20, 412-427	3.5	91
271	Formation of local structures in protein folding. <i>Accounts of Chemical Research</i> , 1989 , 22, 70-76	24.3	90
270	Distributions of intramolecular distances in the reduced and denatured states of bovine pancreatic ribonuclease A. Folding initiation structures in the C-terminal portions of the reduced protein. <i>Biochemistry</i> , 2001 , 40, 105-18	3.2	89
269	Molecular simulation study of cooperativity in hydrophobic association. <i>Protein Science</i> , 2000 , 9, 1235-45	6.3	87
268	Preferred conformation of the benzyloxycarbonyl-amino group in peptides. <i>International Journal of Peptide and Protein Research</i> , 1983 , 21, 163-81		86
267	Relation between free energy landscapes of proteins and dynamics. <i>Journal of Chemical Theory and Computation</i> , 2010 , 6, 583-595	6.4	85
266	Calculation of protein conformation by global optimization of a potential energy function. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 204-208	4.2	82
265	Nonrandom distribution of the one-disulfide intermediates in the regeneration of ribonuclease A. <i>Biochemistry</i> , 1996 , 35, 6406-17	3.2	82
264	Exact analytical loop closure in proteins using polynomial equations. <i>Journal of Computational Chemistry</i> , 1999 , 20, 819-844	3.5	81
263	Regeneration of bovine pancreatic ribonuclease A: detailed kinetic analysis of two independent folding pathways. <i>Biochemistry</i> , 1998 , 37, 3767-76	3.2	80
262	Investigation of protein folding by coarse-grained molecular dynamics with the UNRES force field. <i>Journal of Physical Chemistry A</i> , 2010 , 114, 4471-85	2.8	79
261	Application of Multiplexed Replica Exchange Molecular Dynamics to the UNRES Force Field: Tests with alpha and alpha+beta Proteins. <i>Journal of Chemical Theory and Computation</i> , 2009 , 5, 627-640	6.4	78
260	Determination of net atomic charges using a modified partial equalization of orbital electronegativity method. 2. Application to ionic and aromatic molecules as models for polypeptides. <i>The Journal of Physical Chemistry</i> , 1990 , 94, 4740-4746		78
259	Recent progress in the theoretical treatment of protein folding. <i>Biopolymers</i> , 1983 , 22, 1-14	2.2	77
258	Mechanism of fiber assembly: treatment of A β peptide aggregation with a coarse-grained united-residue force field. <i>Journal of Molecular Biology</i> , 2010 , 404, 537-52	6.5	74

257	Optimization of the UNRES Force Field by Hierarchical Design of the Potential-Energy Landscape. 3. Use of Many Proteins in Optimization. <i>Journal of Physical Chemistry B</i> , 2004 , 108, 16950-16959	3.4	70
256	Conformational space annealing by parallel computations: Extensive conformational search of Met-enkephalin and of the 20-residue membrane-bound portion of melittin. <i>International Journal of Quantum Chemistry</i> , 1999 , 75, 255-265	2.1	69
255	Optical activity of single-stranded polydeoxyadenylic and polyriboadenylic acids; dependence of adenine chromophore cotton effects on polymer conformation. <i>Biopolymers</i> , 1969 , 7, 395-409	2.2	69
254	Theory of hydrophobic interactions. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998 , 16, 447-60	3.6	68
253	Conformational analysis of the 20-residue membrane-bound portion of melittin by conformational space annealing. <i>Biopolymers</i> , 1998 , 46, 103-16	2.2	66
252	The thrombin-fibrinogen interaction. <i>Biophysical Chemistry</i> , 2004 , 112, 117-30	3.5	66
251	The nature of the initial step in the conformational folding of disulphide-intact ribonuclease A. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 495-503	17.6	65
250	Optimization of the UNRES Force Field by Hierarchical Design of the Potential-Energy Landscape. 2. Off-Lattice Tests of the Method with Single Proteins. <i>Journal of Physical Chemistry B</i> , 2004 , 108, 16934-16949	3.4	64
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247	Conformations of poly-L-valine in solution. <i>Biopolymers</i> , 1968 , 6, 1551-71	2.2	63
246	An empirical method to calculate average molecular polarizabilities from the dependence of effective atomic polarizabilities on net atomic charge. <i>Journal of the American Chemical Society</i> , 1993 , 115, 2005-2014	16.4	62
245	Protein structure prediction using a combination of sequence homology and global energy minimization I. Global energy minimization of surface loops. <i>Journal of Computational Chemistry</i> , 1990 , 11, 121-151	3.5	62
244	Exploring the parameter space of the coarse-grained UNRES force field by random search: selecting a transferable medium-resolution force field. <i>Journal of Computational Chemistry</i> , 2009 , 30, 2127-35	3.5	61
243	Nature of the unfolded state of ribonuclease A: effect of cis-trans X-Pro peptide bond isomerization. <i>Biochemistry</i> , 1996 , 35, 11719-33	3.2	59
242	Calculation of protein conformation by the build-up procedure. Application to bovine pancreatic trypsin inhibitor using limited simulated nuclear magnetic resonance data. <i>Journal of Biomolecular Structure and Dynamics</i> , 1988 , 5, 705-55	3.6	59
241	Analysis of the structure of ribonuclease A in native and partially denatured states by time-resolved noradiative dynamic excitation energy transfer between site-specific extrinsic probes. <i>Biochemistry</i> , 1995 , 34, 15965-78	3.2	58
240	Regeneration of bovine pancreatic ribonuclease A. 3. Dependence on the nature of the redox reagent. <i>Biochemistry</i> , 1993 , 32, 2690-7	3.2	57

239	Influence of flexibility on the energy contours of dipeptide maps. <i>Biopolymers</i> , 1966 , 4, 709-12	2.2	57
238	Structure of a hydrophobically collapsed intermediate on the conformational folding pathway of ribonuclease A probed by hydrogen-deuterium exchange. <i>Biochemistry</i> , 1996 , 35, 11734-46	3.2	56
237	Empirical solvation models in the context of conformational energy searches: application to bovine pancreatic trypsin inhibitor. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 14, 110-9	4.2	56
236	Lessons from application of the UNRES force field to predictions of structures of CASP10 targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 14936-41	11.5	54
235	On the multiple-minima problem in the conformational analysis of polypeptides. I. Backbone degrees of freedom for a perturbed alpha-helix. <i>Biopolymers</i> , 1987 , 26 Suppl, S33-58	2.2	54
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232	Pattern recognition in the prediction of protein structure. I. Tripeptide conformational probabilities calculated from the amino acid sequence. <i>Journal of Computational Chemistry</i> , 1989 , 10, 770-797	3.5	53
231	Conformational constraints of amino acid side chains in alpha-helices. <i>Biopolymers</i> , 1987 , 26, 1273-86	2.2	53
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229	Molecular theory of the helix-coil transition in polyamino acids. II. Numerical evaluation of s and σ for polyglycine and poly-L-alanine in the absence (for s and σ) and presence (for σ) of solvent. <i>Journal of Chemical Physics</i> , 1970 , 52, 2060-79	3.9	53
228	Effect of hydrophobic bonding on the stability of poly-L-alanine helices in water. <i>Biopolymers</i> , 1963 , 1, 419-429	2.2	52
227	Helix-coil transitions re-visited. <i>Biophysical Chemistry</i> , 2002 , 101-102, 255-65	3.5	51
226	Regeneration of three-disulfide mutants of bovine pancreatic ribonuclease A missing the 65-72 disulfide bond: characterization of a minor folding pathway of ribonuclease A and kinetic roles of Cys65 and Cys72. <i>Biochemistry</i> , 1998 , 37, 4490-501	3.2	51
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224	Kinetics of the Helix-coil transition in polyamino acids. <i>Journal of Chemical Physics</i> , 1966 , 45, 2071-90	3.9	51
223	How main-chains of proteins explore the free-energy landscape in native states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 19708-13	11.5	50
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221	Variable step molecular dynamics: An exploratory technique for peptides with fixed geometry. <i>Journal of Computational Chemistry</i> , 1990 , 11, 468-486	3.5	50
220	Helix-coil transition theory including long-range electrostatic interactions: application to globular proteins. <i>Biopolymers</i> , 1987 , 26, 351-71	2.2	50
219	Regeneration of bovine pancreatic ribonuclease A. 4. Temperature dependence of the regeneration rate. <i>Biochemistry</i> , 1993 , 32, 2698-703	3.2	49
218	Structural characterization of a three-disulfide intermediate of ribonuclease A involved in both the folding and unfolding pathways. <i>Biochemistry</i> , 1994 , 33, 10437-49	3.2	47
217	Standard-geometry chains fitted to X-ray derived structures: Validation of the rigid-geometry approximation. I. Chain closure through a limited search of β -loop conformations. <i>Journal of Computational Chemistry</i> , 1991 , 12, 505-526	3.5	46
216	Prediction of the native conformation of a polypeptide by a statistical-mechanical procedure. III. Probable and average conformations of enkephalin. <i>Biopolymers</i> , 1987 , 26, 1125-62	2.2	46
215	Statistical mechanics of noncovalent bonds in polyamino acids. IX. The two-state theory of protein denaturation. <i>Biopolymers</i> , 1965 , 3, 401-419	2.2	46
214	Effect of side chains on the conformational energy and rotational strength of the n-pi transition for some alpha-helical poly-alpha-amino acids. <i>Biopolymers</i> , 1968 , 6, 1531-50	2.2	46
213	How adequate are one- and two-dimensional free energy landscapes for protein folding dynamics?. <i>Physical Review Letters</i> , 2009 , 102, 238102	7.4	45
212	Circular dichroism evidence for the presence of burst-phase intermediates on the conformational folding pathway of ribonuclease A. <i>Biochemistry</i> , 1996 , 35, 10125-33	3.2	45
211	Communications to the editor: Stable conformations of dipeptides. <i>Biopolymers</i> , 1973 , 12, 2177-83	2.2	45
210	New developments of the electrostatically driven Monte Carlo method: test on the membrane-bound portion of melittin. <i>Biopolymers</i> , 1998 , 46, 117-26	2.2	44
209	Kinetic folding pathway of a three-disulfide mutant of bovine pancreatic ribonuclease A missing the [40-95] disulfide bond. <i>Biochemistry</i> , 1998 , 37, 7561-71	3.2	44
208	Two new structured intermediates in the oxidative folding of RNase A. <i>FEBS Letters</i> , 1999 , 460, 477-9	3.8	44
207	Influence of interatomic interactions on the structure and stability of polypeptides and proteins. <i>Biopolymers</i> , 1981 , 20, 1877-1899	2.2	44
206	Effect of side-chain hydrophobic bonding on the stability of homopolyamino acid alpha-helices: conformational studies of poly-L-leucine in water. <i>Biopolymers</i> , 1970 , 9, 749-64	2.2	44
205	Intramolecular steric effects and hydrogen bonding in regular conformations of polyamino acids. <i>Biopolymers</i> , 1966 , 4, 887-904	2.2	44
204	Molecular dynamics with the United-residue force field: ab initio folding simulations of multichain proteins. <i>Journal of Physical Chemistry B</i> , 2007 , 111, 293-309	3.4	43

203	Macromolecular conformational dynamics in torsional angle space. <i>Journal of Chemical Physics</i> , 1998 , 108, 271-286	3.9	43
202	Kinetic and thermodynamic studies of the folding/unfolding of a tryptophan-containing mutant of ribonuclease A. <i>Biochemistry</i> , 1996 , 35, 12978-92	3.2	42
201	An efficient, differentiable hydration potential for peptides and proteins. <i>Journal of Computational Chemistry</i> , 1996 , 17, 1549-1558	3.5	42
200	Optimizing Potential Functions for Protein Folding. <i>The Journal of Physical Chemistry</i> , 1996 , 100, 14540-14548	4.1	
199	Variable-target-function and build-up procedures for the calculation of protein conformation. Application to bovine pancreatic trypsin inhibitor using limited simulated nuclear magnetic resonance data. <i>Journal of Biomolecular Structure and Dynamics</i> , 1988 , 5, 757-84	3.6	41
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195	Matrix formulation of the transition from a statistical coil to an intramolecular antiparallel beta sheet. <i>Biopolymers</i> , 1984 , 23, 1701-24	2.2	40
194	Acceleration of convergence in Monte Carlo simulations of aqueous solutions using the metropolis algorithm. Hydrophobic hydration of methane. <i>Journal of Computational Chemistry</i> , 1982 , 3, 525-547	3.5	40
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192	Effect of sequence-specific interactions on the stability of helical conformations in polypeptides. <i>Biopolymers</i> , 1988 , 27, 41-58	2.2	39
191	Brownian dynamics simulations of protein folding. <i>Journal of Chemical Physics</i> , 1998 , 108, 287-300	3.9	37
190	Pattern recognition in the prediction of protein structure. II. Chain conformation from a probability-directed search procedure. <i>Journal of Computational Chemistry</i> , 1989 , 10, 798-816	3.5	37
189	Crystal structures of two mutants that have implications for the folding of bovine pancreatic ribonuclease A. <i>Protein Science</i> , 1998 , 7, 1255-8	6.3	36
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187	Can cooperativity in hydrophobic association be reproduced correctly by implicit solvation models?*. <i>International Journal of Quantum Chemistry</i> , 2002 , 88, 41-55	2.1	36
186	Anti-cooperative interactions in single-strand oligomers of deoxyriboadenylic acid. <i>Biopolymers</i> , 1967 , 5, 403-22	2.2	36

185	Performance of protein-structure predictions with the physics-based UNRES force field in CASP11. <i>Bioinformatics</i> , 2016 , 32, 3270-3278	7.2	36
184	Hierarchical energy-based approach to protein-structure prediction: Blind-test evaluation with CASP3 targets. <i>International Journal of Quantum Chemistry</i> , 2000 , 77, 90-117	2.1	35
183	Ion Pair Interactions in Aqueous Solution: Self-Consistent Reaction Field (SCRF) Calculations with Some Explicit Water Molecules. <i>Journal of Physical Chemistry A</i> , 2000 , 104, 6505-6509	2.8	35
182	Influence of local interactions on protein structure. III. Conformational energy studies of N-acetyl-N'-methylamides of Gly-X and X-Gly dipeptides. <i>Biopolymers</i> , 1978 , 17, 1871-1884	2.2	35
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180	Conformational unfolding studies of three-disulfide mutants of bovine pancreatic ribonuclease A and the coupling of proline isomerization to disulfide redox reactions. <i>Biochemistry</i> , 1999 , 38, 2805-15	3.2	34
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177	Helix-random coil transformations in deuterated macromolecules. <i>Annals of the New York Academy of Sciences</i> , 1960 , 84, 608-16	6.5	32
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