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## Dominant forces in protein folding

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2294	Effects of point mutations in a hinge region on the stability, folding, and enzymatic activity of Escherichia coli dihydrofolate reductase. <i>Biochemistry</i> , <b>1991</b> , 30, 7801-9	3.2	36
2293	Extracting hydrophobic free energies from experimental data: relationship to protein folding and theoretical models. <i>Biochemistry</i> , <b>1991</b> , 30, 9686-97	3.2	415
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2291	Alternatively folded states of an immunoglobulin. <i>Biochemistry</i> , <b>1991</b> , 30, 6922-9	3.2	151
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2289	On the role of methionine residues in the sequence-independent recognition of nonpolar protein surfaces. <i>Biochemistry</i> , <b>1991</b> , 30, 6633-6	3.2	214
2288	Improving the thermostability of the neutral protease of Bacillus stearothermophilus by replacing a buried asparagine by leucine. <b>1991</b> , 282, 13-6		19
2287	Temperature-sensitive variants of Saccharomyces cerevisiae iso-1-cytochrome c produced by random mutagenesis of codons 43 to 54. <b>1991</b> , 221, 97-105		6
2286	Role of electrostatic repulsion in the acidic molten globule of cytochrome c. <b>1991</b> , 222, 679-86		134

## (1991-1991)

2285	Generalized protein tertiary structure recognition using associative memory Hamiltonians. <b>1991</b> , 222, 1013-34	65
2284	High resolution structure of an oligomeric eye lens beta-crystallin. Loops, arches, linkers and interfaces in beta B2 dimer compared to a monomeric gamma-crystallin. <b>1991</b> , 222, 1067-83	81
2283	Proper and improper folding of proteins in the cellular environment. <b>1991</b> , 45, 607-35	62
2282	Kinetic analysis of the acid and the alkaline unfolded states of staphylococcal nuclease. <b>1991</b> , 220, 771-8	40
2281	Inclusion Bodies and Recovery of Proteins from the Aggregated State. <b>1991</b> , 1-20	26
2280	Nonclassical hydrophobic effect in membrane binding equilibria. <i>Biochemistry</i> , <b>1991</b> , 30, 9354-9 3.2	178
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2278	Contribution of the hydrophobic effect to protein stability: analysis based on simulations of the Ile-96Ala mutation in barnase. <b>1991</b> , 88, 10880-4	114
2277	Hydrophobic potentials from statistical analysis of protein structures. <b>1991</b> , 202, 20-31	6
2276	Protein engineering to change thermal stability for food enzymes. <b>1991</b> , 19, 655-62	14
2275	Analysis and modulation of protein stability. <b>1991</b> , 2, 551-60	35
2274	Acid denatured apo-cytochrome c is a random coil: evidence from small-angle X-ray scattering and dynamic light scattering. <b>1991</b> , 1078, 289-95	58
2273	Molecular modeling of intramolecular hydrogen bonding in simple oligoamides 1. In vacuo <b>1991</b> , 32, 3613-3616	6
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2271	Differential scanning calorimetry studies of NaCl effect on the inverse temperature transition of some elastin-based polytetra-, polypenta-, and polynonapeptides. <b>1991</b> , 31, 465-75	68
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2269	Molten globule intermediates and protein folding. <b>1991</b> , 19, 221-9	226
2268	Stabilization of the neutral protease of Bacillus stearothermophilus by removal of a buried water molecule. <b>1991</b> , 4, 941-5	23

2267	Influence of the Raman mode interaction on the lasing kinetics of a wide-band ring laser. <b>1991</b> , 21, 407-411	9
2266	Universality in hydrogen-bond networks. <b>1991</b> , 44, R7888-R7890	17
2265	Protein stability and molecular adaptation to extreme conditions. <b>1991</b> , 291-304	6
2264	Isoenthalpic and isoentropic temperatures and the thermodynamics of protein denaturation. <b>1991</b> , 88, 5154-8	96
2263	The protein-folding problem: the native fold determines packing, but does packing determine the native fold?. <b>1991</b> , 88, 4195-9	87
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2261	Probing protein stability with unnatural amino acids. <b>1992</b> , 256, 1798-802	135
2260	Denaturation of stefin B by GuHCl, pH and heat; evidence for molten globule intermediates. <b>1992</b> , 373, 453-8	7
2259	Design, synthesis and structure of an amphipathic peptide with pH-inducible haemolytic activity. <b>1992</b> , 5, 323-31	13
2258	Environment affects amino acid preference for secondary structure. <b>1992</b> , 89, 4462-5	237
2257	Inverse protein folding problem: designing polymer sequences. <b>1992</b> , 89, 4163-7	141
2256	Conformation and fluctuations of free stefin B: a molecular dynamics study. <b>1992</b> , 373, 447-52	
2255	Calculation of the entropy of binary hard sphere mixtures from pair correlation functions. <b>1992</b> , 97, 2153-215	531
2254	Refolding and oriented insertion of a membrane protein into a lipid bilayer. <b>1992</b> , 89, 7457-61	208
2253	Response of a protein structure to cavity-creating mutations and its relation to the hydrophobic effect. <b>1992</b> , 255, 178-83	862
2252	Formulation concerns of protein drugs. <b>1992</b> , 18, 1311-1354	44
2251	Theory of hydrophobicity: transient cavities in molecular liquids. <b>1992</b> , 89, 2995-9	179
2250	Mutational studies of protein structures and their stabilities. <b>1992</b> , 25, 205-50	91

2249	Effects of compact volume and chain stiffness on the conformations of native proteins. <b>1992</b> , 89, 6614-8	42
2248	Truncated staphylococcal nuclease is compact but disordered. <b>1992</b> , 89, 748-52	<sup>1</sup> 74
2247	Use of liquid hydrocarbon and amide transfer data to estimate contributions to thermodynamic functions of protein folding from the removal of nonpolar and polar surface from water.  3.2  Biochemistry, 1992, 31, 3947-55	564
2246	Calculation of solvation interaction energies for protein adsorption on polymer surfaces. <b>1991</b> , 3, 127-47	98
2245	Octan-1-olWater partition coefficients of zwitterionic hamino acids. Determination by centrifugal partition chromatography and factorization into steric/hydrophobic and polar components. <b>1992</b> , 79-84	73
2244	The effect of cavity-filling mutations on the thermostability of Bacillus stearothermophilus neutral protease. <b>1992</b> , 5, 421-6	42
2243	Cloning and expression of the variable regions of mouse myeloma protein MOPC315 in E. coli: recovery of active FV fragments. <b>1992</b> , 29, 21-30	30
2242	Does hydrophobic hydration destabilize protein native structures?. <b>1992</b> , 17, 459-63	26
2241	The mechanism of protein folding. <b>1992</b> , 2, 21-25	9
2240	The amino acid substrate of bovine tyrosine hydroxylase. <b>1992</b> , 21, 191-6	5
2239	Predicting de novo the folded structure of proteins. <b>1992</b> , 2, 402-412	45
2238	The hydrophobic core of Escherichia coli thioredoxin shows a high tolerance to nonconservative single amino acid substitutions. <i>Biochemistry</i> , <b>1992</b> , 31, 11203-9	43
2237	Folding kinetics of proteins and copolymers. <b>1992</b> , 96, 768-780	113
2236	Electrostatics. <b>1992</b> , 2, 223-229	12
2235	Effects of individual oxidants on oven rise and bread properties of Canadian short process bread. <b>1992</b> , 15, 237-251	30
2234	A differential scanning calorimetric study of the thermal unfolding of mutant forms of phage T4 lysozyme. <i>Biochemistry</i> , <b>1992</b> , 31, 10699-702	16
2233	Thermodynamics of structural stability and cooperative folding behavior in proteins. <b>1992</b> , 43, 313-61	474
2232	Extracting information on folding from the amino acid sequence: consensus regions with preferred conformation in homologous proteins. <i>Biochemistry</i> , <b>1992</b> , 31, 10239-49	50

2231	Molecular thermodynamic model to predict the alpha-helical secondary structure of polypeptide chains in solution. <i>Biochemistry</i> , <b>1992</b> , 31, 10591-601	3.2	5
2230	Partitioning of tryptophan side-chain analogs between water and cyclohexane. <i>Biochemistry</i> , <b>1992</b> , 31, 12813-8	3.2	48
2229	Specific divalent cation-induced changes during gelation of .betalactoglobulin. <b>1992</b> , 40, 2092-2097		75
2228	The role of packing interactions in stabilizing folded proteins. <i>Biochemistry</i> , <b>1992</b> , 31, 2842-6	3.2	34
2227	Contributions of the polar, uncharged amino acids to the stability of staphylococcal nuclease: evidence for mutational effects on the free energy of the denatured state. <i>Biochemistry</i> , <b>1992</b> , 31, 5717	7-278	131
2226	Use of a potential of mean force to analyze free energy contributions in protein folding. <i>Biochemistry</i> , <b>1992</b> , 31, 6290-7	3.2	23
2225	The cost of conformational order: entropy changes in molecular associations. <b>1992</b> , 114, 10690-10697		332
2224	Association of lysozyme to phospholipid surfaces and vesicle fusion. <b>1992</b> , 1124, 88-94		26
2223	The folding of an enzyme. II. Substructure of barnase and the contribution of different interactions to protein stability. <b>1992</b> , 224, 783-804		394
2222	Concepts in protein folding. 1992, 307, 10-3		12
2221	Contribution of the hydrophobic effect to globular protein stability. <b>1992</b> , 226, 29-35		206
2220	Prediction of protein folding pathways. <b>1992</b> , 227, 901-16		28
2219	Orthogonal beta beta motifs in proteins. <b>1992</b> , 223, 845-51		19
2218	Design and structural analysis of alternative hydrophobic core packing arrangements in bacteriophage T4 lysozyme. <b>1992</b> , 224, 1143-59		120
2217	Analysis of non-polar regions in proteins. <b>1992</b> , 224, 629-38		15
2216	Structure-derived hydrophobic potential. Hydrophobic potential derived from X-ray structures of globular proteins is able to identify native folds. <b>1992</b> , 224, 725-32		160
2215	An N-terminal fragment of barnase has residual helical structure similar to that in a refolding intermediate. <b>1992</b> , 224, 749-58		83
2214	The folding of an enzyme. VI. The folding pathway of barnase: comparison with theoretical models. <b>1992</b> , 224, 847-59		158

2213	Thermodynamics of unfolding of the alpha-amylase inhibitor tendamistat. Correlations between accessible surface area and heat capacity. <b>1992</b> , 223, 769-79	37
2212	Hydrogen bonding in globular proteins. <b>1992</b> , 226, 1143-59	366
2211	Modeling the effects of mutations on the denatured states of proteins. <b>1992</b> , 1, 201-15	114
2210	Folding protein alpha-carbon chains into compact forms by Monte Carlo methods. <b>1992</b> , 14, 409-20	72
2209	Representation of noncovalent interactions in protein structures. <b>1992</b> , 10, 96-100, 110	6
2208	Statistical mechanics of hydrogen bond networks. <b>1992</b> , 86, 433-442	10
2207	Structural analysis of an outer surface protein from the Lyme disease spirochete, Borrelia burgdorferi, using circular dichroism and fluorescence spectroscopy. <b>1992</b> , 1120, 59-68	19
2206	Effect of cavity-modulating mutations on the stability of Escherichia coli ribonuclease HI. <b>1992</b> , 206, 337-43	23
2205	Pair distribution functions in small systems: implications for protein structure analysis. <b>1992</b> , 32, 3-10	2
2204	The low-temperature heat capacity of solid proteins. <b>1992</b> , 32, 209-18	8
2203	The nature of folded states of globular proteins. <b>1992</b> , 32, 695-709	320
2202	The effects of surface adsorption on the thermal stability of proteins. <b>1992</b> , 40, 8-15	76
2201	High stability to irreversible inactivation at elevated temperatures of enzymes covalently modified by hydrophilic reagents: alpha-Chymotrypsin. <b>1992</b> , 40, 650-62	44
2200	How transferable are hydrogen parameters in molecular mechanics calculations?. <b>1992</b> , 13, 971-978	32
2199	Making sense from antisense: a review of experimental data and developing ideas on senseantisense peptide recognition. <b>1992</b> , 5, 43-54	44
2198	Hydrophobicity and stability for a family of model proteins. <b>1993</b> , 33, 1185-1193	16
2197	Minimization of empirical energy functions in proteins including hydrophobic surface area effects. <b>1993</b> , 14, 510-521	51
2196	Heat capacity of aqueous solutions of monohydric alcohols at subzero temperatures. <b>1993</b> , 46, 27-35	14

2195	UNIFAC model as a heuristic guide for estimating retention in reversed-phase liquid chromatography. <b>1993</b> , 656, 69-79	13
2194	Finding the lowest free energy conformation of a protein is an NP-hard problem: Proof and implications. <b>1993</b> , 55, 1183-1198	28
2193	Packing and hydrophobicity effects on protein folding and stability: effects of beta-branched amino acids, valine and isoleucine, on the formation and stability of two-stranded alpha-helical coiled coils/leucine zippers. <b>1993</b> , 2, 383-94	140
2192	Unnatural amino acid packing mutants of Escherichia coli thioredoxin produced by combined mutagenesis/chemical modification techniques. <b>1993</b> , 2, 395-403	32
2191	Binding of amino acid side chains to preformed cavities: interaction of serine proteinases with turkey ovomucoid third domains with coded and noncoded P1 residues. <b>1993</b> , 2, 786-99	64
2190	Effects of alanine substitutions in alpha-helices of sperm whale myoglobin on protein stability. <b>1993</b> , 2, 1099-105	44
2189	Cross-validation of protein structural class prediction using statistical clustering and neural networks. <b>1993</b> , 2, 1171-82	80
2188	Stabilization of creatinase from Pseudomonas putida by random mutagenesis. <b>1993</b> , 2, 1612-20	56
2187	Calculation of protein backbone geometry from alpha-carbon coordinates based on peptide-group dipole alignment. <b>1993</b> , 2, 1697-714	90
2186	Prediction of protein conformation on the basis of a search for compact structures: test on avian pancreatic polypeptide. <b>1993</b> , 2, 1715-31	131
2185	Local and nonlocal interactions in globular proteins and mechanisms of alcohol denaturation. <b>1993</b> , 2, 2050-65	256
2184	Purification and characterization of beta-structural domains of beta-lactoglobulin liberated by limited proteolysis. <b>1993</b> , 12, 613-25	39
2183	Aromatic-aromatic ring interactions tested in cyclophanes. <b>1993</b> , 3, 263-268	16
2182	Functional expression of D-glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic eubacterium Thermotoga maritima in Escherichia coli. Authenticity and kinetic properties of the recombinant enzyme. <b>1993</b> , 214, 43-50	31
2181	Determinants for the enhanced thermostability of hybrid (1-3,1-4)-beta-glucanases. <b>1993</b> , 216, 829-34	33
2180	HYDRO: a program for protein hydropathy predictions. <b>1993</b> , 41, 121-9	2
2179	Analysis of polypeptides and proteins. <b>1993</b> , 10, 29-90	29
2178	NMR analysis of the residual structure in the denatured state of an unusual mutant of staphylococcal nuclease. <b>1993</b> , 1, 121-34	68

2177	Evidence for an alpha-helical epitope on outer surface protein A from the Lyme disease spirochete, Borrelia burgdorferi: an application of steady-state and time-resolved fluorescence quenching techniques. <b>1993</b> , 1202, 287-96	5
2176	Mechanism-based strategies for protein thermostabilization. <b>1993</b> , 11, 88-95	240
2175	Techniques for assessing the effects of pharmaceutical excipients on the aggregation of porcine growth hormone. <b>1993</b> , 10, 954-62	101
2174	Finding the lowest free energy conformation of a protein is an NP-hard problem: proof and implications. <b>1993</b> , 55, 1183-98	104
2173	Protein design by binary patterning of polar and nonpolar amino acids. <b>1993</b> , 262, 1680-5	631
2172	Compatible solutes of halophilic eubacteria: molecular principles, water-solute interaction, stress protection. <b>1993</b> , 49, 487-496	264
2171	Prediction and analysis of structure, stability and unfolding of thermolysin-like proteases. <b>1993</b> , 7, 367-96	66
2170	Stabilization of Bacillus stearothermophilus neutral protease by introduction of prolines. <b>1993</b> , 317, 89-92	78
2169	Characterization and Refolding of 且actamase Inclusion Bodies in Escherichia coli. <b>1993</b> , 126-139	3
2168	Structure <b>E</b> unction Relationship of Hyperthermophilic Enzymes. <b>1993</b> , 53-67	6
2167	Hydration and heat stability effects on protein unfolding. <b>1993</b> , 59, 237-84	163
2166	Hydrophobic characteristics of folded proteins. <b>1993</b> , 59, 57-103	92
2165	Aspects of protein energetics and dynamics. <b>1993</b> , 60, 73-200	60
2164	Strategies for obtaining stable enzymes. <b>1993</b> , 28, 435-445	48
2163	Hydrogen bonding, hydrophobicity, packing, and protein folding. <b>1993</b> , 22, 381-415	302
2162	Alpha-helix stability and the native state of myoglobin. <i>Biochemistry</i> , <b>1993</b> , 32, 12638-43	26
2161	Folding of the four domains and dimerization are impaired by the Gly446>Glu exchange in human glutathione reductase. Implications for the design of antiparasitic drugs. <i>Biochemistry</i> , <b>1993</b> , 32, 4060-6 <sup>3.2</sup>	109
2160	Improvement of downstream processing of recombinant proteins by means of genetic engineering methods. <b>1993</b> , 11, 31-77	28

2159	Disulfide bond contribution to protein stability: positional effects of substitution in the hydrophobic core of the two-stranded alpha-helical coiled-coil. <i>Biochemistry</i> , <b>1993</b> , 32, 3178-87	3.2	155
2158	Free energy, entropy, and internal energy of hydrophobic interactions: Computer simulations. <b>1993</b> , 98, 6445-6454		244
2157	Microcalorimetry and the molecular recognition of peptides and proteins. 1993, 345, 23-35		30
2156	Characterization of an independent structural unit in apocytochrome b5. <i>Biochemistry</i> , <b>1993</b> , 32, 199-20	73.2	40
2155	Partially structured self-associating states of acidic fibroblast growth factor. <i>Biochemistry</i> , <b>1993</b> , 32, 770	03;:211	50
2154	Acid-induced unfolding and refolding transitions of cytochrome c: a three-state mechanism in H2O and D2O. <i>Biochemistry</i> , <b>1993</b> , 32, 11878-85	3.2	110
2153	A heme c-peptide model system for the resonance Raman study of c-type cytochromes: characterization of the solvent-dependence of peptide-histidine-heme interactions. <i>Biochemistry</i> , <b>1993</b> , 32, 9781-91	3.2	55
2152			4
2151	Intermediate conformational states of apocytochrome c. <i>Biochemistry</i> , <b>1993</b> , 32, 10351-8	3.2	82
2150	Thermodynamics of ligand binding to trp repressor. <i>Biochemistry</i> , <b>1993</b> , 32, 7302-9	3.2	69
2149	Designed replacement of an internal hydration water molecule in BPTI: structural and functional implications of a glycine-to-serine mutation. <i>Biochemistry</i> , <b>1993</b> , 32, 4564-70	3.2	50
2148	Patterns of nonadditivity between pairs of stability mutations in staphylococcal nuclease. <i>Biochemistry</i> , <b>1993</b> , 32, 10131-9	3.2	84
2147	Effects of amino acid substitutions on the pressure denaturation of staphylococcal nuclease as monitored by fluorescence and nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , <b>1993</b> , 32, 5222	- <del>3</del> 2	136
2146	Effect of cavity-creating mutations in the hydrophobic core of chymotrypsin inhibitor 2. <i>Biochemistry</i> , <b>1993</b> , 32, 11259-69	3.2	273
2145	Unfolding of the molten globule state of alpha-lactalbumin studied by 1H NMR. <i>Biochemistry</i> , <b>1993</b> , 32, 13198-203	3.2	38
2144	New insights into sequence recognition process of esperamicin A1 and calicheamicin gamma 11.: origin of their selectivities and "induced fit" mechanism. <i>Biochemistry</i> , <b>1993</b> , 32, 4622-7	3.2	42
2143	Membrane partitioning: distinguishing bilayer effects from the hydrophobic effect. <i>Biochemistry</i> , <b>1993</b> , 32, 6307-12	3.2	201
2142	Destabilizing effects of replacing a surface lysine of cytochrome c with aromatic amino acids: implications for the denatured state. <i>Biochemistry</i> , <b>1993</b> , 32, 183-90	3.2	106

2141	New simulation methods for proteins and DNA. <b>1993</b> , 3, 260-264		2
2140	Strategy and implementation of a system for protein engineering. <b>1993</b> , 28, 41-54		11
2139	pH-dependent thermostabilization of Escherichia coli ribonuclease HI by histidine to alanine substitutions. <b>1993</b> , 28, 117-36		49
2138	Pathways of protein folding. <b>1993</b> , 62, 653-83		447
2137	Molecular chaperone functions of heat-shock proteins. <b>1993</b> , 62, 349-84		1448
2136	Acid stabilization of insulin. <i>Biochemistry</i> , <b>1993</b> , 32, 8075-82	3.2	56
2135	Structural and genetic analysis of protein stability. <b>1993</b> , 62, 139-60		452
2134	Protein foldingwhat's the question?. <b>1993</b> , 90, 439-41		146
2133	The effects of freezing on flesh proteins. <b>1993</b> , 9, 575-610		210
2132	Simulation of water around a model protein helix. 2. The relative contributions of packing, hydrophobicity, and hydrogen bonding. <b>1993</b> , 97, 2991-2999		11
2131	ENVIRON: a software package to compare protein three-dimensional structures with homologous sequences using local structural motifs. <b>1993</b> , 9, 639-45		1
2130	Parameters influencing the productivity of recombinant E. coli cultivations. <b>1993</b> , 48, 53-77		10
2129	To fold or not to fold. <b>1993</b> , 260, 1903-4		88
2128			3
2127	•		25
2126	Acid Stabilization of Insulin. 1993,		
2125	Metal ion-dependent modulation of the dynamics of a designed protein. <b>1993</b> , 261, 879-85		251
2124	Protein core assembly processes. <b>1993</b> , 98, 3475-3487		100

2123	Calculations of the relative free energies of aqueous solvation of several fluorocarbons: A test of the bond potential of mean force correction. <b>1993</b> , 99, 9103-9110	25
2122	Sequence-structure relationships in proteins and copolymers. <b>1993</b> , 48, 2267-2278	80
2121	An analysis of packing in the protein folding problem. <b>1993</b> , 26, 423-98	189
2120	Cooperativity in protein-folding kinetics. <b>1993</b> , 90, 1942-6	414
2119	Protein motif by computer: the perfect Greek key jellyroll designer. <b>1993</b> , 9, 709-22	
2118	Intrinsic stability and extrinsic stabilization of creatinase from Pseudomonas putida. <b>1993</b> , 374, 427-34	7
2117	Application of Systematic Conformational Search to Protein Modeling. <b>1993</b> , 10, 151-174	40
2116	The Protein Folding Problem. <b>1993</b> , 46, 24-32	202
2115	Solvent Exclusion Effect Predicted by the Scaled Particle Theory as an Important Factor of the Hydrophobic Effect. <b>1993</b> , 62, 1782-1793	33
2114	Favored and suppressed patterns of hydrophobic and nonhydrophobic amino acids in protein sequences. <b>1993</b> , 90, 9100-4	17
2113	Kinetics and thermodynamics of folding in model proteins. <b>1993</b> , 90, 6369-72	332
2112	Effects of Surface Mutations on Protein Stability: A role for the Denatured State. <b>1993</b> ,	
2111	Biophysics of Energy Converting Model Proteins. <b>1993</b> , 330, 321	
2110	Engineering A Simplified Dimer: The Interface Domain Of Glutathione Reductase. 1993,	
2109	Methods of computer-aided drug design and their applications to steroids. <b>1993</b> , 21, 29-44	1
2108	Conservative substitutions at internal sites in sperm whale myoglobin reveal correlations with alpha helix propensity. <b>1993</b> ,	
2107	References. <b>1994</b> , 251-265	
2106	Macromolecular crowding and confinement in cells exposed to hypertonicity. <b>1994</b> , 266, C877-92	124

2105	The effect of ion pairs on the thermal stability of D-glyceraldehyde 3-phosphate dehydrogenase from the hyperthermophilic bacterium Thermotoga maritima. <b>1994</b> , 7, 1471-8	34
2104	Protein stability for single substitution mutants and the extent of local compactness in the denatured state. <b>1994</b> , 7, 1209-20	50
2103	Structural basis for the difference in thermodynamic properties between the two cysteine proteinase inhibitors human stefins A and B. <b>1994</b> , 7, 977-84	14
2102	The net energetic contribution of interhelical electrostatic attractions to coiled-coil stability. <b>1994</b> , 7, 1365-72	103
2101	Global statistics of protein sequences: implications for the origin, evolution, and prediction of structure. <b>1994</b> , 23, 407-39	42
2100	Protein side-chain conformational entropy derived from fusion datacomparison with other empirical scales. <b>1994</b> , 7, 149-55	29
2099	A single amino acid substitution can restore the solubility of aggregated colicin A mutants in Escherichia coli. <b>1994</b> , 7, 1495-500	18
2098	Molecular dynamics of conformational substates for a simplified protein model. <b>1994</b> , 101, 5047-5057	36
2097	Folding kinetics of proteinlike heteropolymers. <b>1994</b> , 101, 1519-1528	296
2096	Relative stabilities of biomolecules at high temperatures and pressures. <b>1994</b> , 245, 89-119	17
2095	Hydration and partial compressibility of biological compounds. <b>1994</b> , 51, 89-107; discussion 107-9	223
2094	The effect ofpH on thermal stability of globular proteins. <b>1994</b> , 42, 383-395	11
2093	Amino acids that specify structure through hydrophobic clustering and histidine-aromatic interactions lead to biologically active peptidomimetics. <b>1994</b> , 2, 999-1006	22
2092	The native state of apomyoglobin described by proton NMR spectroscopy: interaction with the paramagnetic probe HyTEMPO and the fluorescent dye ANS. <b>1994</b> , 3, 267-81	61
2091	A role for surface hydrophobicity in protein-protein recognition. <b>1994</b> , 3, 717-29	290
2090	Side-chain entropy and packing in proteins. <b>1994</b> , 3, 997-1009	120
2089	Stability of yeast iso-1-ferricytochrome c as a function of pH and temperature. <b>1994</b> , 3, 1253-60	76
2088	Optimization of the electrostatic interactions in proteins of different functional and folding type. <b>1994</b> , 3, 1556-69	61

2087	Different protein sequences can give rise to highly similar folds through different stabilizing interactions. <b>1994</b> , 3, 1938-44	31
2086	Protein denaturation with guanidine hydrochloride or urea provides a different estimate of stability depending on the contributions of electrostatic interactions. <b>1994</b> , 3, 1984-91	281
2085	Tests for helix-stabilizing interactions between various nonpolar side chains in alanine-based peptides. <b>1994</b> , 3, 1992-7	69
2084	Redesigning the hydrophobic core of a four-helix-bundle protein. <b>1994</b> , 3, 2015-22	120
2083	Analysis of hydrophobicity in the alpha and beta chemokine families and its relevance to dimerization. <b>1994</b> , 3, 2064-72	29
2082	A simplified amino acid potential for use in structure predictions of proteins. <b>1994</b> , 18, 267-80	66
2081	Temperature-induced complementarity as a mechanism for biomolecular assembly. <b>1994</b> , 19, 73-6	20
2080	Molecular basis of cooperativity in protein folding. V. Thermodynamic and structural conditions for the stabilization of compact denatured states. <b>1994</b> , 19, 291-301	116
2079	Solvent-induced organization: a physical model of folding myoglobin. <b>1994</b> , 20, 124-38	14
2078	Learning about protein folding via potential functions. <b>1994</b> , 20, 167-73	23
2077	Polar and nonpolar atomic environments in the protein core: implications for folding and binding. <b>1994</b> , 20, 264-78	74
2076	Lipophilicity of amino acids. <b>1994</b> , 7, 129-45	32
2075	Modelling of peptide and protein structures. <b>1994</b> , 7, 175-202	4
2074	Conformational searches for the global minimum of protein models. <b>1994</b> , 4, 209-227	7
2073	An efficient solvent model for study of hydrophobic phenomena. <b>1994</b> , 227, 215-220	25
2072	A CD study of the alpha-helix nucleation hypothesis. <b>1994</b> , 34, 969-73	3
2071	Phosphophoryn, an "acidic" biomineralization regulatory protein: conformational folding in the presence of Cd(II). <b>1994</b> , 34, 1359-75	26
2070	Globular proteins at solid/liquid interfaces. <b>1994</b> , 2, 517-566	702

	Core-packing constraints, hydrophobicity and protein design. <b>1994</b> , 5, 396-402	52
2068	Spatial and free energy distribution patterns of amino acid residues in water soluble proteins. <b>1994</b> , 51, 327-36	8
2067	How random is a highly denatured protein?. <b>1994</b> , 53, 105-13	79
2066	Protein adsorption on low temperature isotropic carbon. III. Isotherms, competitivity, desorption and exchange of human albumin and fibrinogen. <b>1994</b> , 15, 323-33	55
2065	Thermodynamics of unfolding of the all beta-sheet protein interleukin-1 beta. <i>Biochemistry</i> , <b>1994</b> , 33, 9327-32	45
2064	Determination of hydrophobic hydration in protein unfolding by an intrinsic reference state. <b>1994</b> , 1208, 15-21	4
2063	Volume changes on protein folding. <b>1994</b> , 2, 641-9	491
2062	Proteins under pressure. The influence of high hydrostatic pressure on structure, function and assembly of proteins and protein complexes. <b>1994</b> , 221, 617-30	558
2061	Cold denaturation of the molten globule states of apomyoglobin and a profile for protein folding. <i>Biochemistry</i> , <b>1994</b> , 33, 4903-9	140
2060	Chain condensation in protein folding. <b>1994</b> , 76, 384-8	2
2059	Strategies for the study of cytochrome c structure and function by site-directed mutagenesis. <b>1994</b> , 76, 622-30	17
		17 23
	76, 622-30	·
2058	76, 622-30  The blind watchmaker and rational protein engineering. 1994, 36, 185-220	23
2058	The blind watchmaker and rational protein engineering. <b>1994</b> , 36, 185-220  Ion-Induced Stabilization of the G-DNA Quadruplex: Free Energy Perturbation Studies. <b>1994</b> , 116, 6070-6080	23
2058 2057 2056	The blind watchmaker and rational protein engineering. <b>1994</b> , 36, 185-220  Ion-Induced Stabilization of the G-DNA Quadruplex: Free Energy Perturbation Studies. <b>1994</b> , 116, 6070-6080  Reversibility of thermally induced denaturation of cellular proteins. <b>1994</b> , 720, 65-78	23 119 8
2058 2057 2056 2055	The blind watchmaker and rational protein engineering. 1994, 36, 185-220  Ion-Induced Stabilization of the G-DNA Quadruplex: Free Energy Perturbation Studies. 1994, 116, 6070-6080  Reversibility of thermally induced denaturation of cellular proteins. 1994, 720, 65-78  PolymerBolvent Interactions Studied with Computational Chemistry. 1994, 221-233	23 119 8

2051	Stabilization of intermediate density states in globular proteins by homogeneous intramolecular attractive interactions. <b>1994</b> , 66, 454-66		11
2050	Helix folding simulations with various initial conformations. <b>1994</b> , 66, 1796-803		35
2049	Protein sequence and structure relationship ARMA spectral analysis: application to membrane proteins. <b>1994</b> , 66, 2092-106		13
2048	High-pressure NMR spectroscopy of proteins and membranes. <b>1994</b> , 23, 287-318		162
2047	Amide-Amide and Amide-Water Hydrogen Bonds: Implications for Protein Folding and Stability. <b>1994</b> , 116, 2149-2150		114
2046	Kinetics versus thermodynamics in protein folding. <i>Biochemistry</i> , <b>1994</b> , 33, 7505-9	3.2	219
2045	Symmetries of hydrogen bonds in solution. <b>1994</b> , 266, 1665-8		134
2044	Solvation: from small to macro molecules. <b>1994</b> , 4, 264-268		34
2043	Understanding how proteins fold: the lysozyme story so far. <b>1994</b> , 19, 31-7		325
2042	Properties and origins of protein secondary structure. <b>1994</b> , 49, 3440-3443		46
2041	Chemical Function Queries for 3D Database Search. <b>1994</b> , 34, 1297-1308		179
2040	Exploring conformational space with a simple lattice model for protein structure. <b>1994</b> , 243, 668-82		137
2039	Recombinant single-chain Fv fragments carrying C-terminal cysteine residues: production of bivalent and biotinylated miniantibodies. <b>1994</b> , 31, 1047-58		80
2038	A new tool for studying protein structure and function. <b>1994</b> , 4, 601-607		26
2037	. 1994,		5
2036	Coupling of local folding to site-specific binding of proteins to DNA. <b>1994</b> , 263, 777-84		1400
2035	Molecular nanomachines: physical principles and implementation strategies. <b>1994</b> , 23, 377-405		52
2034	The refolding of human lysozyme: a comparison with the structurally homologous hen lysozyme. <i>Biochemistry</i> , <b>1994</b> , 33, 5867-76	3.2	119

2033	Electrostatic interactions control the parallel and antiparallel orientation of alpha-helical chains in two-stranded alpha-helical coiled-coils. <i>Biochemistry</i> , <b>1994</b> , 33, 3862-71	3.2	177
2032	Importance of environment in determining secondary structure in proteins. <i>Biochemistry</i> , <b>1994</b> , 33, 217	21382	200
2031	NMR Studies of Thermal Denaturation and Cation-Mediated Aggregation of .betaLactoglobulin. <b>1994</b> , 42, 2411-2420		45
2030	Stabilizing and destabilizing effects of placing beta-branched amino acids in protein alpha-helices. <i>Biochemistry</i> , <b>1994</b> , 33, 12022-31	3.2	40
2029	Development of nonpolar surfaces in the folding of Escherichia coli dihydrofolate reductase detected by 1-anilinonaphthalene-8-sulfonate binding. <i>Biochemistry</i> , <b>1994</b> , 33, 15250-8	3.2	56
2028	Solvent-Induced Forces between Two Hydrophilic Groups. <b>1994</b> , 98, 2198-2202		394
2027	Folding of barnase in parts. <i>Biochemistry</i> , <b>1994</b> , 33, 3778-86	3.2	80
2026	Kinetic intermediates in RNA folding. <b>1994</b> , 265, 918-24		310
2025	Transfer-Thermodynamic Quantities and the Hydrophobic Effect. <b>1994</b> , 63, 814-824		6
2024	Controlling the speed of hirudin folding. <b>1994</b> , 300 ( Pt 3), 643-50		66
2023	On the Correlation of Protein Structure with Local Sequence Patterns. <b>1994</b> , 685-703		
2022			
2022	Direct measurement of forces between self-assembled proteins: temperature-dependent exponential forces between collagen triple helices. <b>1994</b> , 91, 276-80		134
	Direct measurement of forces between self-assembled proteins: temperature-dependent exponential forces between collagen triple helices. <b>1994</b> , 91, 276-80  Folded proteins occur frequently in libraries of random amino acid sequences. <b>1994</b> , 91, 2146-50		134 156
	exponential forces between collagen triple helices. <b>1994</b> , 91, 276-80  Folded proteins occur frequently in libraries of random amino acid sequences. <b>1994</b> , 91, 2146-50		
2021	exponential forces between collagen triple helices. <b>1994</b> , 91, 276-80  Folded proteins occur frequently in libraries of random amino acid sequences. <b>1994</b> , 91, 2146-50		156
2021 2020 2019	exponential forces between collagen triple helices. 1994, 91, 276-80  Folded proteins occur frequently in libraries of random amino acid sequences. 1994, 91, 2146-50  Optimal sequence selection in proteins of known structure by simulated evolution. 1994, 91, 5803-7  Chapter 17 Simulated annealing-optimal histogram applications to the protein folding problem.		156 116
2021 2020 2019	Exponential forces between collagen triple helices. 1994, 91, 276-80  Folded proteins occur frequently in libraries of random amino acid sequences. 1994, 91, 2146-50  Optimal sequence selection in proteins of known structure by simulated evolution. 1994, 91, 5803-7  Chapter 17 Simulated annealing-optimal histogram applications to the protein folding problem. 1995, 369-394		156 116 1

2015	Complexity and emergence in drug research. <b>1995</b> , 1-43	12
2014	Fluorescence resolution of the intrinsic tryptophan residues of bovine protein tyrosyl phosphatase. <b>1995</b> , 270, 3809-15	25
2013	Actin-binding proteins-lipid interactions. <b>1995</b> , 169-204	3
2012	Is water structure around hydrophobic groups clathrate-like?. <b>1995</b> , 92, 8308-12	117
2011	Forces of tertiary structural organization in globular proteins. <b>1995</b> , 92, 146-50	171
2010	Periodicity of polar and nonpolar amino acids is the major determinant of secondary structure in self-assembling oligomeric peptides. <b>1995</b> , 92, 6349-53	227
2009	The Thermal Unfolding of Hevein, a Small Disulfide-Rich Protein. <b>1995</b> , 228, 649-652	
2008	Template-Directed Protein Folding into a Metastable State of Increased Activity. <b>1995</b> , 232, 528-535	
2007	Untersuchungen von Struktur und Funktion von Proteinen mit einem erweiterten genetischen Code. <b>1995</b> , 107, 677-690	21
2006	Kooperative Verstfkung elektrostatischer Bindungen durch das Verbergen von Kohlenwasserstoffen. <b>1995</b> , 107, 1644-1646	3
2005	Physical properties of cold-setting gels formed from heat-denatured whey protein isolate. <b>1995</b> , 69, 7-14	81
2004	Kinetics of protein folding: Nucleation mechanism, time scales, and pathways. <b>1995</b> , 36, 83-102	305
2003	Design and characterization of a model alpha beta peptide. <b>1995</b> , 36, 109-20	10
2002	Exploration of compact protein conformations using the guided replication Monte Carlo method. <b>1995</b> , 36, 579-97	4
2001	A molecular mechanics/continuum reaction field investigation of the interactions between polar amino acid side chains in water and organic solvents. <b>1995</b> , 36, 765-780	22
2000	Pressure-induced secondary structure changes of ribonuclease A and ribonuclease S studied by FTIR spectroscopy. <b>1995</b> , 1, 207-216	13
1999	Reduced representation approach to protein tertiary structure prediction: statistical potential and simulated annealing. <b>1995</b> , 172, 13-32	15
1998	Constant temperature simulations of helix folding. <b>1995</b> , 173, 389-400	2

1997	Protein interactions at solid surfaces. <b>1995</b> , 57, 161-227	184
1996	Can contemporary density functional theory yield accurate thermodynamics for hydrogen bonding?. <b>1995</b> , 247, 112-119	47
1995	Enthalpy convergence temperatures: proteins and model compounds. <b>1995</b> , 251, 371-377	7
1994	Computational approaches to study protein unfolding: hen egg white lysozyme as a case study. <b>1995</b> , 21, 196-213	89
1993	Modeling the role of disulfide bonds in protein folding: entropic barriers and pathways. <b>1995</b> , 22, 27-40	72
1992	Empirical evaluation of the influence of side chains on the conformational entropy of the polypeptide backbone. <b>1995</b> , 22, 132-40	55
1991	Optimal local propensities for model proteins. <b>1995</b> , 22, 413-8	57
1990	Local moves: an efficient algorithm for simulation of protein folding. <b>1995</b> , 23, 73-82	58
1989	Relationship of sidechain hydrophobicity and alpha-helical propensity on the stability of the single-stranded amphipathic alpha-helix. <b>1995</b> , 1, 319-29	249
1988	Fuzzy cluster analysis of simple physicochemical properties of amino acids for recognizing secondary structure in proteins. <b>1995</b> , 4, 1178-87	12
1987	The optimization of protein-solvent interactions: thermostability and the role of hydrophobic and electrostatic interactions. <b>1995</b> , 4, 1516-27	150
1986	Interactions in nonnative and truncated forms of staphylococcal nuclease as indicated by mutational free energy changes. <b>1995</b> , 4, 1815-23	10
1985	A statistical mechanical model for hydrogen exchange in globular proteins. <b>1995</b> , 4, 1860-73	100
1984	A preference-based free-energy parameterization of enzyme-inhibitor binding. Applications to HIV-1-protease inhibitor design. <b>1995</b> , 4, 1881-903	121
1983	Binary patterning of polar and nonpolar amino acids in the sequences and structures of native proteins. <b>1995</b> , 4, 2032-9	116
1982	Thermal stability determinants of chicken egg-white lysozyme core mutants: hydrophobicity, packing volume, and conserved buried water molecules. <b>1995</b> , 4, 2050-62	67
1981	Atomic solvation parameters in the analysis of protein-protein docking results. <b>1995</b> , 4, 2087-99	44
1980	Comparison of atomic solvation parametric sets: applicability and limitations in protein folding and binding. <b>1995</b> , 4, 2499-509	78

1979	Chemically crosslinked protein dimers: stability and denaturation effects. <b>1995</b> , 4, 2545-58	16
1978	Crystal structure of recombinant triosephosphate isomerase from Bacillus stearothermophilus. An analysis of potential thermostability factors in six isomerases with known three-dimensional structures points to the importance of hydrophobic interactions. <b>1995</b> , 4, 2594-604	106
1977	Aggregation of a lyophilized pharmaceutical protein, recombinant human albumin: effect of moisture and stabilization by excipients. <b>1995</b> , 13, 493-6	77
1976	Temperature-favoured assembly of collagen is driven by hydrophilic not hydrophobic interactions. <b>1995</b> , 2, 205-10	133
1975	Solvent isotope effect and protein stability. <b>1995</b> , 2, 852-5	155
1974	Structural model for the beta-amyloid fibril based on interstrand alignment of an antiparallel-sheet comprising a C-terminal peptide. <b>1995</b> , 2, 990-8	398
1973	A short linear peptide derived from the N-terminal sequence of ubiquitin folds into a water-stable non-native beta-hairpin. <b>1995</b> , 2, 999-1006	162
1972	Simulating the folding of small proteins by use of the local minimum energy and the free solvation energy yields native-like structures. <b>1995</b> , 13, 312-22	23
1971	SURFNET: a program for visualizing molecular surfaces, cavities, and intermolecular interactions. <b>1995</b> , 13, 323-30, 307-8	754
1970	Engineering thermostability: lessons from thermophilic proteins. <b>1995</b> , 6, 370-4	100
1969	The averaged face growth rates of lysozyme crystals: the effect of temperature. <b>1995</b> , 151, 163-172	62
1968	Salt-induced formation of the molten globule state of apomyoglobin studied by isothermal titration calorimetry. <b>1995</b> , 266, 385-400	11
1967	The extra-stability of thermophilic globular proteins: a thermodynamic approach. 1995, 269-270, 381-392	5
1966	Understanding and increasing protein stability. <b>1995</b> , 1252, 1-14	181
1965	Citrate synthase from the hyperthermophilic Archaeon, Pyrococcus furiosus. <b>1995</b> , 8, 583-92	33
1964	A review of protein engineering for the food industry. <b>1995</b> , 4, 151-66	7
1963	A two state lattice model of membrane proteins: Configuration as a function of sequence. <b>1995</b> , 103, 5091-5101	2
1962	Kinetics at the collapse transition of homopolymers and random copolymers. <b>1995</b> , 103, 4807-4818	112

1961	The hydrophobic nature of GroEL-substrate binding. <b>1995</b> , 270, 1011-4	116
1960	Free energy simulations of the HyHEL-10/HEL antibody-antigen complex. <b>1995</b> , 8, 663-75	8
1959	Thermodynamics of fatty acid binding to fatty acid-binding proteins and fatty acid partition between water and membranes measured using the fluorescent probe ADIFAB. <b>1995</b> , 270, 15076-84	84
1958	Differential scanning calorimetry of proteins. <b>1995</b> , 24, 133-76	51
1957	Epitope mapping and analysis of a growth-enhancing monoclonal antibody by limited tryptic digestion of porcine GH. <b>1995</b> , 145, 169-74	9
1956	Hydrophobic potential by pairwise surface area sum. <b>1995</b> , 8, 437-42	24
1955	Design of copolymeric materials. <b>1995</b> , 28, L387-L393	17
1954	Staphylococcal nuclease: a showcase of m-value effects. <b>1995</b> , 46, 217-47	121
1953	Theoretical Modeling of Electrostatic Effects of Titratable Side Chain Groups on Protein Conformation in a Polar Ionic Solution. 2. pH-Induced Helix-Coil Transition of Poly(L-lysine) in Water and Methanol Ionic Solutions. <b>1995</b> , 99, 7180-7187	38
1952	Extracting hydrophobicity parameters from solute partition and protein mutation/unfolding experiments. <b>1995</b> , 8, 1081-92	22
1951	Mutagenesis of the Regulatory Subunit (RII酮of cAMP-dependent Protein Kinase II厭eveals Hydrophobic Amino Acids That Are Essential for RII即imerization and/or Anchoring RII乖o the Cytoskeleton. <b>1995</b> , 270, 1935-1944	54
1950	The folding characteristics of tryptophanase from Escherichia coli. <b>1995</b> , 117, 384-91	7
1949	Fourier transform infrared spectroscopy investigations of protein structure. <b>1995</b> , 7, 101-43	59
1948	Computer determination of peptide conformations in water: different roads to structure. <b>1995</b> , 92, 3190-3	31
1947	First-principles calculation of the folding free energy of a three-helix bundle protein. <b>1995</b> , 269, 393-6	372
1946	Hydrogen bonds and the pH dependence of ovomucoid third domain stability. <i>Biochemistry</i> , <b>1995</b> , 34, 4724-32	96
1945	Comparison of the refolding of hen lysozyme from dimethyl sulfoxide and guanidinium chloride. <i>Biochemistry,</i> <b>1995</b> , 34, 1714-24	44
1944	Extensive nonrandom structure in reduced and unfolded bovine pancreatic trypsin inhibitor. <i>Biochemistry</i> , <b>1995</b> , 34, 13974-81	60

1943	Energetic contribution of side chain hydrogen bonding to the stability of staphylococcal nuclease. <i>Biochemistry</i> , <b>1995</b> , 34, 13949-60	3.2	80	
1942	Analysis of the mechanism of assembly of cleaved barnase from two peptide fragments and its relevance to the folding pathway of uncleaved barnase. <i>Biochemistry</i> , <b>1995</b> , 34, 1464-8	3.2	31	
1941	A buried polar interaction imparts structural uniqueness in a designed heterodimeric coiled coil. <i>Biochemistry</i> , <b>1995</b> , 34, 8642-8	3.2	285	
1940	The stability of tropomyosin, a two-stranded coiled-coil protein, is primarily a function of the hydrophobicity of residues at the helix-helix interface. <i>Biochemistry</i> , <b>1995</b> , 34, 16797-805	3.2	78	
1939	Calorimetry of proteins and nucleic acids. <b>1995</b> , 5, 682-90		46	
1938	The liquid amide transfer model and the unfolding thermodynamics of small globular proteins. <b>1995</b> , 17, 251-7		13	
1937	Collective variable description of native protein dynamics. <b>1995</b> , 46, 223-50		217	
1936	The peptide backbone plays a dominant role in protein stabilization by naturally occurring osmolytes. <i>Biochemistry</i> , <b>1995</b> , 34, 12884-91	3.2	424	
1935	High resistance of Escherichia coli ribonuclease HI variant with quintuple thermostabilizing mutations to thermal denaturation, acid denaturation, and proteolytic degradation. <i>Biochemistry</i> , <b>1995</b> , 34, 8115-22	3.2	43	
1934	Refined crystal structure of spinach ferredoxin reductase at 1.7 A resolution: oxidized, reduced and 2'-phospho-5'-AMP bound states. <b>1995</b> , 247, 125-45		177	
1933	Structural characterization of the molten globule and native states of apomyoglobin by solution X-ray scattering. <b>1995</b> , 249, 215-28		210	
1932	Contribution of individual side-chains to the stability of BPTI examined by alanine-scanning mutagenesis. <b>1995</b> , 249, 388-97		75	
1931	Atomic environment energies in proteins defined from statistics of accessible and contact surface areas. <b>1995</b> , 249, 675-90		32	
1930	CH/pi interaction in the packing of the adenine ring in protein structures. <b>1995</b> , 251, 9-14		119	
1929	The occurrence of C-HO hydrogen bonds in proteins. <b>1995</b> , 252, 248-62		489	
1928	Recognizing native folds by the arrangement of hydrophobic and polar residues. <b>1995</b> , 252, 709-20		122	
1927	The three-dimensional solution structure of a constrained peptidomimetic in water and in chloroform. Observation of solvent induced hydrophobic cluster. <b>1995</b> , 359, 113-8		5	
1926	Domain interactions stabilize the alternatively folded state of an antibody Fab fragment. <b>1995</b> , 362, 43-	-6	24	

1925 Folding simulations of alanine-b	pased peptides with lysine residues. <b>1995</b> , 68, 826-34		40
1924 Searching for Representations (	to Improve Protein Sequence Fold-Class Prediction. <b>1995</b> , 21, 151-175		
1923 Protein secondary structure pre	ediction. <b>2001</b> , Chapter 2, Unit2.3		1
1922 Investigation of protein unfoldi	ng and stability by computer simulation. <b>1995</b> , 348, 49-59		20
Enthalpic contribution to prote mechanics. <b>1995</b> , 47, 231-306	in stability: insights from atom-based calculations and statistical		146
Energetic origins of specificity of <i>Biochemistry</i> , <b>1995</b> , 34, 8564-75	of ligand binding in an interior nonpolar cavity of T4 lysozyme.	3.2	162
	yrococcus furiosus to environmental changes: implications for the <i>Biochemistry</i> , <b>1995</b> , 34, 9865-73	3.2	54
1918 Energetics of protein structure.	. <b>1995</b> , 47, 307-425		846
<sup>1917</sup> molecule. <b>1995</b> , 8, 13-20	f design: expression and characterization of a first-generation		9
$_{ m 1916}$ other influence the conformation	n partially charged main-chain atoms not hydrogen-bonded to each ons of alpha-helices and antiparallel beta-sheet. A new method for ydrogen bonding groups in proteins includes all the Coulombic		32
1915 Searching for representations t	o improve protein sequence fold-class prediction. <b>1995</b> , 21, 151-175		1
1914 Free energy balance in protein	folding. <b>1995</b> , 46, 27-58		229
1913 Templates in protein de novo d	esign. <b>1995</b> , 41, 197-210		40
1912 Site-directed mutagenesis with	an expanded genetic code. <b>1995</b> , 24, 435-62		166
A simple protein folding algorit 8, 769-78	hm using a binary code and secondary structure constraints. <b>1995</b> ,		92
Entropy-enthalpy compensation 19 <sup>10</sup> 105, 9292-9298	n: Perturbation and relaxation in thermodynamic systems. <b>1996</b> ,		106
	n pathway of transthyretin yields a conformational intermediate rloid. <i>Biochemistry</i> , <b>1996</b> , 35, 6470-82	3.2	499
On the origins of the hydropholosolvents. <b>1996</b> , 71, 600-8	bic effect: observations from simulations of n-dodecane in model		43

1907	Atomic-scale analysis of the solvation thermodynamics of hydrophobic hydration. <b>1996</b> , 71, 1695-706		28
1906	Hydrogen bonding stabilizes globular proteins. <b>1996</b> , 71, 2033-9		249
1905	An engineered penicillin acylase with altered surface charge is more stable in alkaline pH. <b>1996</b> , 799, 61-4		2
1904	The disulfide folding pathway of tick anticoagulant peptide (TAP), a Kunitz-type inhibitor structurally homologous to BPTI. <i>Biochemistry</i> , <b>1996</b> , 35, 11702-9	3.2	61
1903	Temperature dependence of polypeptide partitioning between water and phospholipid bilayers. <i>Biochemistry</i> , <b>1996</b> , 35, 9526-32	3.2	30
1902	Redox-Triggered Secondary Structure Changes in the Aggregated States of a Designed Methionine-Rich Peptide. <b>1996</b> , 118, 12487-12494		74
1901	Coupled folding and site-specific binding of the GCN4-bZIP transcription factor to the AP-1 and ATF/CREB DNA sites studied by microcalorimetry. <i>Biochemistry</i> , <b>1996</b> , 35, 14984-91	3.2	68
1900	Direct determination of the membrane affinities of individual amino acids. <i>Biochemistry</i> , <b>1996</b> , 35, 1803	-9.2	73
1899	Temperature-induced denaturation of ribonuclease S: a thermodynamic study. <i>Biochemistry</i> , <b>1996</b> , 35, 13378-85	3.2	29
1898	Hydrophobic interactions control zymogen activation in the trypsin family of serine proteases. <i>Biochemistry</i> , <b>1996</b> , 35, 4515-23	3.2	96
1897	Testing the correlation between delta A and delta V of protein unfolding using m value mutants of staphylococcal nuclease. <i>Biochemistry</i> , <b>1996</b> , 35, 10234-9	3.2	53
1896	Structural and energetic responses to cavity-creating mutations in hydrophobic cores: observation of a buried water molecule and the hydrophilic nature of such hydrophobic cavities. <i>Biochemistry</i> , <b>1996</b> , 35, 4298-305	3.2	145
1895	Glu46 donates a proton to the 4-hydroxycinnamate anion chromophore during the photocycle of photoactive yellow protein. <i>Biochemistry</i> , <b>1996</b> , 35, 14671-8	3.2	175
1894	Pairwise Gibbs Energy Interaction Parameters for Amino AcidAmide Interactions in Aqueous Solution: A Kinetic Study. <b>1996</b> , 118, 9539-9544		8
1893	Retention Thermodynamics in Hydrophobic Interaction Chromatography. <b>1996</b> , 35, 2964-2981		93
1892	Mechanism of denaturation of bovine serum albumin by dodecyl trimethylammonium bromide. <b>1996</b> , 28, 991-8		31
1891	Thermodynamic stability effects of single peptide bond hydrolysis in protein inhibitors of serine proteinases. <b>1996</b> , 256, 793-802		11
1890	Intermediate states in protein folding. <b>1996</b> , 258, 707-25		261

1889	V35I/I47V gene V protein core mutants. <b>1996</b> , 259, 148-59	20
1888	Local interactions dominate folding in a simple protein model. <b>1996</b> , 259, 988-94	88
1887	Interactions between a helical residue and tertiary structures: helix propensities in small peptides and in native proteins. <b>1996</b> , 261, 279-88	22
1886	Pressure effects on the structure of oligomeric proteins prior to subunit dissociation. <b>1996</b> , 263, 789-99	50
1885	Dominant forces in the recognition of a transient folding intermediate of alpha-lactalbumin by GroEL. <b>1996</b> , 264, 643-9	44
1884	Structural role of a buried salt bridge in the 434 repressor DNA-binding domain. <b>1996</b> , 264, 1002-12	42
1883	Sequence space, folding and protein design. <b>1996</b> , 6, 3-10	141
1882	Engineered disulfide bonds in staphylococcal nuclease: effects on the stability and conformation of the folded protein. <i>Biochemistry</i> , <b>1996</b> , 35, 10328-38	41
1881	Thermal unfolding of beta-lactoglobulin, alpha-lactalbumin, and bovine serum albumin. A thermodynamic approach. <b>1996</b> , 36, 565-601	140
1880	How do proteins acquire their three-dimensional structure and stability?. <b>1996</b> , 83, 544-54	20
1879	Protein Electrostatics. <b>1996</b> , 2, 315-372	24
1878	Thermozymes. <b>1996</b> , 2, 1-83	120
1877	Perspectives for biophysicochemical modifications of enzymes. <b>1995</b> , 7, 1-22	1
1876	Hydrophobicity reinterpreted as ⊞inimisation of the entropy penalty of solvation 1996, 103, 117-124	29
1875	The Metabolic Status of Diapause Embryos of Artemia franciscana (SFB). <b>1996</b> , 69, 49-66	76
1874	. 1996,	79
1873	Computer Methods in Protein Modeling: An Overview. <b>1996</b> , 51-73	
1872	Forces contributing to the conformational stability of proteins. <b>1996</b> , 10, 75-83	542

1871	Stability and folding of ultrastable proteins: eye lens crystallins and enzymes from thermophiles. <b>1996</b> , 10, 84-92	99
1870	The denatured state (the other half of the folding equation) and its role in protein stability. <b>1996</b> , 10, 27-34	361
1869	Strategies for the Design of Novel Proteins. <b>1996</b> , 1-50	3
1868	Direct evidence for modified solvent structure within the hydration shell of a hydrophobic amino acid. <b>1996</b> , 93, 10769-74	78
1867	Roles of electrostatic interaction in proteins. <b>1996</b> , 29, 1-90	238
1866	Structure and stability of hyperstable proteins: glycolytic enzymes from hyperthermophilic bacterium Thermotoga maritima. <b>1996</b> , 48, 181-269	114
1865	An information theory model of hydrophobic interactions. <b>1996</b> , 93, 8951-5	480
1864	Binding of the cellulose-binding domain of exoglucanase Cex from Cellulomonas fimi to insoluble microcrystalline cellulose is entropically driven. <b>1996</b> , 93, 12229-34	154
1863	Glycerol-induced development of catalytically active conformation of Crotalus adamanteus L-amino acid oxidase in vitro. <b>1996</b> , 93, 7546-51	27
1862	The Volume and Compressibility Changes Associated with Protein Denaturation. <b>1996</b> , 25, 723-724	8
1861	Role of hydrophobic interactions and desolvation in determining the structural properties of a model alpha beta peptide. <b>1996</b> , 93, 1135-40	10
1860	A Cubic Monooleintytochrome ctwater Phase: X-ray Diffraction, FT-IR, Differential Scanning Calorimetric, and Electrochemical Studies. <b>1996</b> , 100, 11766-11774	112
1859	Emergence of preferred structures in a simple model of protein folding. <b>1996</b> , 273, 666-9	557
1858	A model of solvation of polypeptide side chains. Application to angiotensin II. <b>1996</b> , 363, 151-165	2
1857	Influence of glycerol on the structure and stability of ferric horse heart myoglobin: a SAXS and circular dichroism study. <b>1996</b> , 1295, 51-8	16
1856	Non-bonded poly(ethylene oxide) polymer-coated column for protein separation by capillary electrophoresis. <b>1996</b> , 731, 273-282	151
1855	Influence of glycerol on the structure and redox properties of horse heart cytochrome c. A circular dichroism and electrochemical study. <b>1996</b> , 15, 599-606	17
1854	Conformational changes of the reactive-centre loop and beta-strand 5A accompany temperature-dependent inhibitor-substrate transition of plasminogen-activator inhibitor 1. <b>1996</b> , 241, 38-46	36

1853	Crystal structure of the bifunctional soybean Bowman-Birk inhibitor at 0.28-nm resolution. Structural peculiarities in a folded protein conformation. <b>1996</b> , 242, 122-31	77
1852	Association tendency of 即actoglobulin AB purified by gel permeation chromatography as determined by dynamic light scattering under quiescent conditions. <b>1996</b> , 10, 323-328	13
1851	Influence of solvation on helix formation of poly-alanine studied by multiple annealing simulations. <b>1996</b> , 370, 33-43	11
1850	Direct electrochemical evidence for an equilibrium intermediate in the guanidine-induced unfolding of cytochrome c. <b>1996</b> , 1298, 102-8	54
1849	Properties of the protein matrix revealed by the free energy of cavity formation. <b>1996</b> , 4, 1517-29	52
1848	The development of tertiary interactions during the folding of a large protein. <b>1996</b> , 1, 145-56	39
1847	Analysis of the effect of local interactions on protein stability. <b>1996</b> , 1, 167-78	61
1846	An NMR study on the beta-hairpin region of barnase. <b>1996</b> , 1, 231-41	20
1845	Local versus nonlocal interactions in protein folding and stabilityan experimentalist's point of view. <b>1996</b> , 1, R71-7	79
1844	Rapid formation of a molten globule intermediate in refolding of alpha-lactalbumin. 1996, 1, 275-87	135
1843	The concept of a random coil. Residual structure in peptides and denatured proteins. <b>1996</b> , 1, R95-106	252
1842	Identification of disulphide bonds in the refolding of bovine pancreatic RNase A. <b>1996</b> , 1, 381-90	14
1841	1H magnetic cross-relaxation between multiple solvent components and rotationally immobilized protein. <b>1996</b> , 35, 497-505	20
1840	Water transfer energetics and solid-like packing of globular proteins. <b>1996</b> , 24, 388-93	8
1839	Patterns in ionizable side chain interactions in protein structures. <b>1996</b> , 24, 439-49	25
1838	Hydrophobic patches on the surfaces of protein structures. <b>1996</b> , 25, 389-97	18
1837	A method for detecting hydrophobic patches on protein surfaces. <b>1996</b> , 26, 192-203	39
1836	Enhanced intramolecular amide-amide hydrogen bonding through cooperativity. <b>1996</b> , 37, 2189-2192	18

1835	Progress towards understanding beta-sheet structure. <b>1996</b> , 4, 739-66	128
1834	A new method of laser desorption mass spectrometry for the study of biological macromolecules. <b>1996</b> , 152, 135-142	77
1833	Comparing theoretical and experimental backbone-dependent sidechain conformational preferences for linear, branched, aromatic and polar residues. <b>1996</b> , 204, 157-171	5
1832	On the complexity of string folding. <b>1996</b> , 71, 217-230	17
1831	Observation of noncovalent complexes using laser-induced liquid beam ionization/desorption. <b>1996</b> , 156, 195-202	41
1830	Theoretical basis for differential scanning calorimetric analysis of multimeric proteins. <b>1996</b> , 62, 95-108	9
1829	Thermodynamics of sequence-specific protein-DNA interactions. <b>1996</b> , 62, 121-39	53
1828	An action principle for biopolymer foldingin vitro: A new perspective on the design of expeditiously-folded RNA molecules. <b>1996</b> , 20, 95-116	
1827	Ontogeny of low molecular weight stress protein p26 during early development of the brine shrimp, Artemia franciscana. <b>1996</b> , 38, 153-160	70
1826	Molecular-size corrections to the strength of the hydrophobic effect: a critical review. <b>1996</b> , 24, 261	12
1825	Folding proteins with a simple energy function and extensive conformational searching. <b>1996</b> , 5, 254-61	70
1824	On the entropy of protein folding. <b>1996</b> , 5, 507-10	66
1823	Protein design automation. <b>1996</b> , 5, 895-903	232
1822	In vivo formation of allosteric aspartate transcarbamoylase containing circularly permuted catalytic polypeptide chains: implications for protein folding and assembly. <b>1996</b> , 5, 1290-300	43
1821	Protein folding in the endoplasmic reticulum: lessons from the human chorionic gonadotropin beta subunit. <b>1996</b> , 5, 1443-52	64
1820	Hydrophobic regions on protein surfaces. Derivation of the solvation energy from their area distribution in crystallographic protein structures. <b>1996</b> , 5, 1676-86	29
1819	Two partially unfolded states of Torpedo californica acetylcholinesterase. <b>1996</b> , 5, 1852-64	19
1818	Perturbations of the denatured state ensemble: modeling their effects on protein stability and folding kinetics. <b>1996</b> , 5, 2343-52	21

1817	Evidence for a three-state model of protein folding from kinetic analysis of ubiquitin variants with altered core residues. <b>1996</b> , 3, 193-205	287
1816	Hydrogen bonding and equilibrium isotope enrichment in histidine-containing proteins. <b>1996</b> , 3, 522-31	28
1815	Proline scanning mutagenesis of a molten globule reveals non-cooperative formation of a protein's overall topology. <b>1996</b> , 3, 682-7	93
1814	Isolation of a local tertiary folding transition in the context of a globally folded RNA. <b>1996</b> , 3, 701-10	55
1813	Thermal Denaturation of Lysozyme in a Cosolvent Studied by NMR. <b>1996</b> , 12, 494-502	5
1812	Native-like beta-hairpin structure in an isolated fragment from ferredoxin: NMR and CD studies of solvent effects on the N-terminal 20 residues. <b>1996</b> , 9, 559-65	63
1811	Role of CD3 gamma in T cell receptor assembly. <b>1996</b> , 132, 299-310	65
1810	Molecular Dynamics Studies of the Properties of Water around Simple Organic Solutes. <b>1996</b> , 100, 11460-114	<b>70</b> 45
1809	Three Extremely Thermostable Proteins from Sulfolobus and a Reappraisal off he Traffic Rules 1996, 377, 505-512	2
1808	Relationship between accessibility and reactivity of Lys, Met and Tyr in subtilisins DY and Carlsberg. <b>1996</b> , 377, 653-9	2
1807	The relative positions of alanine residues in the hydrophobic core control the formation of two-stranded or four-stranded alpha-helical coiled-coils. <b>1996</b> , 9, 353-63	37
1806	CD Spectroscopy and the Helix-Coil Transition in Peptides and Polypeptides. <b>1996</b> , 201-259	40
1805	Gaussian self-consistent method for the kinetics of heteropolymers: A direction in studying the protein folding problem. <b>1996</b> , 53, 3886-3899	19
1804	Kinetics of a Gaussian random copolymer as a prototype for protein folding. <b>1996</b> , 54, 4071-4086	29
1803	A Monte Carlo simulation study on the collapse transition of model polymers: Possible solvent effect and relevance to protein folding. <b>1996</b> , 104, 5304-5310	5
1802	Computational biochemistry of antibodies and T-cell receptors. <b>1996</b> , 49, 149-260	7
1801	Incorporation of non-local interactions in protein secondary structure prediction from the amino acid sequence. <b>1996</b> , 9, 133-42	285
1800	Artificial chaperone-assisted refolding of carbonic anhydrase B. <b>1996</b> , 271, 3478-87	166

1799	Molecular Dynamics/Free Energy Perturbation Studies of the Thermostable V74I Mutant of Ribonuclease HI. <b>1996</b> , 16, 75-85	11	
1798	Hydrophobic regions on protein surfaces: definition based on hydration shell structure and a quick method for their computation. <b>1996</b> , 9, 1121-33	44	
1797	Cumulative stabilizing effects of hydrophobic interactions on the surface of the neutral protease from Bacillus subtilis. <b>1996</b> , 9, 439-45	19	
1796	Modeling DrugReceptor Interactions. <b>1996</b> , 235-336	10	
1795	Are There Water-Bridge-Induced Hydrophilic Interactions?. <b>1996</b> , 100, 6760-6763	7	
1794	A 1.2 ns Molecular Dynamics Simulation of the Ribonuclease T1BEGuanosine Monophosphate Complex. <b>1996</b> , 100, 2480-2488	6	
1793	Effect of Surface Tension on the Stability of Heat-Stressed Proteins: A Molecular Thermodynamic Interpretation. <b>1996</b> , 100, 17400-17405	17	
1792	Response: how much solar radiation do clouds absorb?. <b>1996</b> , 271, 1137-8	51	
1791	Protein folding and association: in vitro studies for self-organization and targeting in the cell. <b>1996</b> , 34, 209-314	50	
1790	Protein structure prediction and potential energy landscape analysis using continuous global minimization. <b>1997</b> ,	2	
1789	Chain growth algorithms for HP-type lattice proteins. 1997,	24	
1788	Discrete Haar transform and protein structure. <b>1997</b> , 15, 489-97	1	
1787	A method for assessing the stability of a membrane protein. <i>Biochemistry</i> , <b>1997</b> , 36, 5884-92	226	5
1786	Refinement and Comparisons of the Crystal Structures of Pig Cytosolic Aspartate Aminotransferase and Its Complex with 2-Methylaspartate. <b>1997</b> , 272, 17293-17302	80	
1785	Amyloid beta-protein fibrillogenesis. Detection of a protofibrillar intermediate. <b>1997</b> , 272, 22364-72	859	9
1784	Introduction of a proline residue into position 31 of the loop of the dimeric 4-alpha-helical protein ROP causes a drastic destabilization. <b>1997</b> , 378, 1141-52	11	
1783	Modelling protein unfolding: hen egg-white lysozyme. <b>1997</b> , 10, 895-903	49	
1782	Importance of a conserved phenylalanine-35 of cytochrome b5 to the protein's stability and redox potential. <b>1997</b> , 10, 575-81	25	

1781	<b>1997</b> , 272, 23011-6	18	3
1780	Assisted protein folding. <b>1997</b> , 272, 3125-8	11	17
1779	Cotranslational folding of globin. <b>1997</b> , 272, 10646-51	11	14
1778	Mechanistic aspects of enzymatic catalysis: lessons from comparison of RNA and protein enzymes. <b>1997</b> , 66, 19-59	23	38
1777	Nanosecond time-resolved spectroscopy of biomolecular processes. <b>1997</b> , 26, 327-55	37	7
1776	Rational protein design: combining theory and experiment. <b>1997</b> , 94, 10015-7	65	5
1775	Allosteric interactions between DNA strands and monovalent cations in DNA quadruplex assembly: thermodynamic evidence for three linked association pathways. <i>Biochemistry</i> , <b>1997</b> , 36, 15428-50	2 57	7
1774	Compressibility and Volume Changes of Lysozyme Due to Guanidine Hydrochloride Denaturation. <b>1997</b> , 26, 1063-1064	17	7
1773	Direct conversion of an oligopeptide from a beta-sheet to an alpha-helix: a model for amyloid formation. <b>1997</b> , 94, 23-8	19	90
1772	Peptides as Models for Understanding Protein Folding. <b>1997</b> , 22, 567-612	3	
1771	Chapter 9 Molecular aspects of steroid receptor/DNA binding. 1997, 1, 241-264		
1771 1770	Chapter 9 Molecular aspects of steroid receptor/DNA binding. <b>1997</b> , 1, 241-264  Effect of Aqueous Alcohol Solutions on the Thermal Transition of Lysozyme: A Calorimetric Study. <b>1997</b> , 101, 8029-8034	53	3
,,	Effect of Aqueous Alcohol Solutions on the Thermal Transition of Lysozyme: A Calorimetric Study.	0	
1770	Effect of Aqueous Alcohol Solutions on the Thermal Transition of Lysozyme: A Calorimetric Study. 1997, 101, 8029-8034  Probing intermolecular main chain hydrogen bonding in serine proteinase-protein inhibitor complexes: chemical synthesis of backbone-engineered turkey ovomucoid third domain.		3
1770 1769	Effect of Aqueous Alcohol Solutions on the Thermal Transition of Lysozyme: A Calorimetric Study. 1997, 101, 8029-8034  Probing intermolecular main chain hydrogen bonding in serine proteinase-protein inhibitor complexes: chemical synthesis of backbone-engineered turkey ovomucoid third domain.  Biochemistry, 1997, 36, 673-9  Heat-Induced Gelation of Globular Proteins. 2. Effect of Environmental Factors on	2 83 52	3
1770 1769 1768 1767	Effect of Aqueous Alcohol Solutions on the Thermal Transition of Lysozyme: A Calorimetric Study. 1997, 101, 8029-8034  Probing intermolecular main chain hydrogen bonding in serine proteinase-protein inhibitor complexes: chemical synthesis of backbone-engineered turkey ovomucoid third domain. <i>Biochemistry</i> , 1997, 36, 673-9  Heat-Induced Gelation of Globular Proteins. 2. Effect of Environmental Factors on Single-Component and Mixed-Protein Gels. 1997, 30, 4855-4862	2 83 52 2 36	3
1770 1769 1768 1767	Effect of Aqueous Alcohol Solutions on the Thermal Transition of Lysozyme: A Calorimetric Study. 1997, 101, 8029-8034  Probing intermolecular main chain hydrogen bonding in serine proteinase-protein inhibitor complexes: chemical synthesis of backbone-engineered turkey ovomucoid third domain.  Biochemistry, 1997, 36, 673-9  Heat-Induced Gelation of Globular Proteins. 2. Effect of Environmental Factors on Single-Component and Mixed-Protein Gels. 1997, 30, 4855-4862  Direct measurement of nucleation and growth rates in lysozyme folding. Biochemistry, 1997, 36, 5108-123.2	2 83 52 2 36	3

1763	Amide backbone and water-related H/D isotope effects on the dynamics of a protein folding reaction. <i>Biochemistry</i> , <b>1997</b> , 36, 5786-94	3.2	79
1762	Conformations, Unfolding, and Refolding of Apomyoglobin in Vacuum: An Activation Barrier for Gas-Phase Protein Folding. <b>1997</b> , 119, 2987-2994		182
1761	Free Energy of Amide Hydrogen Bond Formation in Vacuum, in Water, and in Liquid Alkane Solution. <b>1997</b> , 101, 450-457		134
1760	Hydrophobic Effect, Water Structure, and Heat Capacity Changes. <b>1997</b> , 101, 4343-4348		131
1759	Thermal Gelation of 且actoglobulin AB Purified from Cheddar Whey. 1. Effect of pH on Association As Observed by Dynamic Light Scattering. <b>1997</b> , 45, 2958-2963		21
1758	Special folding pathway to tetramer only through the micelle state of the corticotropin-releasing factor. <i>Biochemistry</i> , <b>1997</b> , 36, 15538-45	3.2	7
1757	An experimental approach to evaluating the role of backbone interactions in proteins using unnatural amino acid mutagenesis. <i>Biochemistry</i> , <b>1997</b> , 36, 11314-22	3.2	106
1756	Stability studies of amino acid substitutions at tyrosine 27 of the staphylococcal nuclease beta-barrel. <i>Biochemistry</i> , <b>1997</b> , 36, 12167-74	3.2	7
1755	Snake venom cardiotoxins-structure, dynamics, function and folding. 1997, 15, 431-63		72
1754	Differences in hydration structure near hydrophobic and hydrophilic amino acids. <b>1997</b> , 73, 2106-15		41
1753	Temperature dependence of histidine ionization constants in myoglobin. <b>1997</b> , 73, 3241-56		33
1752	Influence of surface hydrophilic/hydrophobic balance on enzyme properties. <b>1997</b> , 58, 21-32		36
1751	Proteins: Structure, folding and function. <b>1997</b> , 105-182		1
1750	Temperature Relationships: From Molecules to Biogeography. <b>1997</b> , 1391-1444		9
1749	A reexamination of the hydrophobic effect: Exploring the role of the solvent model in computing the methane than epotential of mean force. <b>1997</b> , 106, 9265-9269		64
1748	The role of phenylalanine 31 in maintaining the conformational stability of ribonuclease P2 from Sulfolobus solfataricus under extreme conditions of temperature and pressure. <i>Biochemistry</i> , <b>1997</b> , 36, 8733-42	3.2	72
1747	Protein/Emulsifier Interactions. <b>1997</b> , 95-146		50
1746	Beta-helical fibrils from a model peptide. <b>1997</b> , 235, 675-9		34

1745	Protein binding versus protein folding: the role of hydrophilic bridges in protein associations. <b>1997</b> , 265, 68-84	218
1744	Determination of atomic desolvation energies from the structures of crystallized proteins. <b>1997</b> , 267, 707-26	433
1743	A histidine variant of yeast iso-1-cytochrome c that strongly affects the energetics of the denatured state. <b>1997</b> , 268, 816-21	33
1742	Three-state model for lysozyme folding: triangular folding mechanism with an energetically trapped intermediate. <b>1997</b> , 270, 294-304	164
1741	Protein thermal stability, hydrogen bonds, and ion pairs. <b>1997</b> , 269, 631-43	580
1740	Kinetics of peptide folding: computer simulations of SYPFDV and peptide variants in water. <b>1997</b> , 272, 423-42	67
1739	Hydrogen bonding interactions between glutamine and asparagine in alpha-helical peptides. <b>1997</b> , 272, 465-73	56
1738	Kinetic role of early intermediates in protein folding. <b>1997</b> , 7, 15-28	300
1737	Protein Structure and the Energetics of Protein Stability. <b>1997</b> , 97, 1251-1268	534
1736	Preferential solvation changes upon lysozyme heat denaturation in mixed solvents. <i>Biochemistry</i> , <b>1997</b> , 36, 9195-9	37
1735	Solvophobic Theory and Normalized Free Energies of Nonpolar Substances in Reversed Phase Chromatography. <b>1997</b> , 101, 5875-5888	60
1734	Protein folding: the endgame. <b>1997</b> , 66, 549-79	170
1733	Solvation: how to obtain microscopic energies from partitioning and solvation experiments. <b>1997</b> , 26, 425-59	79
1732	Protein structure and energy landscape dependence on sequence using a continuous energy function. <b>1997</b> , 4, 227-39	40
1731	Soy Sauce Classification by Geographic Region Based on NIR Spectra and Chemometrics Pattern Recognition. <b>1997</b> , 62, 101-104	24
1730	Physicochemical Changes in Prawns (Machrobrachium rosenbergii) Subjected to Multiple Freeze-Thaw Cycles. <b>1997</b> , 62, 123-127	71
1729	Kinetics of conformational transitions of a single polymer chain. <b>1997</b> , 236, 58-74	11

1727	The Structural Basis of Protein Halophilicity. <b>1997</b> , 117, 307-312	100
1726	Sequence and structural comparison of thermophilic phosphoglycerate kinases with a mesophilic equivalent. <b>1997</b> , 118, 439-51	13
1725	Application of a chemoenzymatic glycosylation method to Ethymotrypsin and Candida rugosa lipase surface modifications. <b>1997</b> , 2, 281-289	7
1724	Crystal structure of a thermostable Bacillus DNA polymerase I large fragment at 2.1 A resolution. <b>1997</b> , 5, 95-108	141
1723	Favourable native-like helical local interactions can accelerate protein folding. <b>1997</b> , 2, 23-33	86
1722	Design of two-helix motifs in peptides: crystal structure of a system of linked helices of opposite chirality and a model helix-linker peptide. <b>1997</b> , 2, 203-10	19
1721	Emerging themes in RNA folding. <b>1997</b> , 2, R65-70	23
1720	Transmuting alpha helices and beta sheets. <b>1997</b> , 2, R71-9	41
1719	Chiral N-substituted glycines can form stable helical conformations. <b>1997</b> , 2, 369-75	151
1718	Purification, structure and in vitro molecular-chaperone activity of Artemia p26, a small heat-shock/alpha-crystallin protein. <b>1997</b> , 243, 225-32	95
1717	Spectroscopic probes of the individual and combined effects of Triton X-100 and chloroform on serum albumins and serum-albumin.bilirubin complexes. <b>1997</b> , 246, 658-64	18
1716	The application of circular dichroism to studies of protein folding and unfolding. <b>1997</b> , 1338, 161-85	376
1715	Non-native architectures in protein design and mimicry. <b>1997</b> , 53, 851-63	55
1714	Classification of the environment of protein residues. <b>1997</b> , 16, 441-7	5
1713	Theory of protein folding: the energy landscape perspective. <b>1997</b> , 48, 545-600	1719
1712	Prediction of folding stability and degradability of the de novo designed protein MB-1 in cow rumen. <b>1997</b> , 66, 83-93	10
1711	The method of frontal polyhedra for conformationally-nonrigid molecules. Quantitative structureActivity relationship in the series of baker triazinesDihydrofolate reductase inhibitors. <b>1997</b> , 31, 147-154	1
1710	Hydrophobic folding units derived from dissimilar monomer structures and their interactions. <b>1997</b> , 6, 24-42	74

1709	Studies of protein-protein interfaces: a statistical analysis of the hydrophobic effect. <b>1997</b> , 6, 53-64	313
1708	Conformational analysis of peptides corresponding to all the secondary structure elements of protein L B1 domain: secondary structure propensities are not conserved in proteins with the same fold. <b>1997</b> , 6, 162-74	42
1707	A desolvation barrier to hydrophobic cluster formation may contribute to the rate-limiting step in protein folding. <b>1997</b> , 6, 347-54	92
1706	Thermal denaturation of iso-1-cytochrome c variants: comparison with solvent denaturation. <b>1997</b> , 6, 657-65	21
1705	Consistency in structural energetics of protein folding and peptide recognition. 1997, 6, 1057-64	45
1704	De novo design of the hydrophobic core of ubiquitin. <b>1997</b> , 6, 1167-78	143
1703	Hydrophobicity regained. <b>1997</b> , 6, 1302-7	160
1702	Hydrophobic folding units at protein-protein interfaces: implications to protein folding and to protein-protein association. <b>1997</b> , 6, 1426-37	101
1701	Mutational analysis of hydrophobic domain interactions in gamma B-crystallin from bovine eye lens. <b>1997</b> , 6, 1529-36	40
1700	Mutational analysis of the BPTI folding pathway: II. Effects of aromatic>leucine substitutions on folding kinetics and thermodynamics. <b>1997</b> , 6, 1563-76	16
1699	Thermodynamic analysis of the effect of selective monodeamidation at asparagine 67 in ribonuclease A. <b>1997</b> , 6, 1682-93	48
1698	Structural motifs at protein-protein interfaces: protein cores versus two-state and three-state model complexes. <b>1997</b> , 6, 1793-805	66
1697	Empirical free energy calculation: comparison to calorimetric data. <b>1997</b> , 6, 1976-84	27
1696	Hydrophobic hydration, hydrophobic forces and protein folding. <b>1997</b> , 238, 113-128	110
1695	Exploring the protein folding funnel landscape. <b>1997</b> , 107, 366-382	15
1694	Thermodynamics of protein unfolding: questions pertinent to testing the validity of the two-state model. <b>1997</b> , 64, 175-97	32
1693	Structure of rabbit muscle phosphoglucomutase refined at 2.4 A resolution. <b>1997</b> , 53, 392-405	34
1692	A fast adaptive multigrid boundary element method for macromolecular electrostatic computations in a solvent. <b>1997</b> , 18, 569-583	113

1691	A united-residue force field for off-lattice protein-structure simulations. I. Functional forms and parameters of long-range side-chain interaction potentials from protein crystal data. <b>1997</b> , 18, 849-873	286
1690	Strength of hydrogen bonds in Helices. <b>1997</b> , 18, 1245-1252	38
1689	Stability of secondary structural elements in a solvent-free environment: the alpha helix. <b>1997</b> , 27, 165-70	58
1688	Mutation matrices and physical-chemical properties: correlations and implications. <b>1997</b> , 27, 336-44	39
1687	Interresidue interactions in protein classes. <b>1997</b> , 27, 360-366	25
1686	Non-randomness in side-chain packing: the distribution of interplanar angles. <b>1997</b> , 29, 370-80	32
1685	Human genome project: Italian contribution. Future directions. <b>1997</b> , 173, 140-3	1
1684	Effect of solvent conditions upon refolding pathways and intermediates for a simple lattice protein. <b>1997</b> , 42, 399-409	16
1683	Design and synthesis of novel nonpolar host peptides for the determination of the 310- and ⊞elix compatibilities of ⊞mino acid buildig blocks: An assessment of ⊞disubstituted glycines. <b>1997</b> , 42, 575-626	23
1682	Effect of three elution buffers on the recovery and structure of monoclonal antibodies. <b>1997</b> , 253, 236-45	35
1681	Monte Carlo Simulations of Guanidinium Acetate and Methylammonium Acetate Ion Pairs in Water. <b>1997</b> , 25, 11-21	9
1680	SulfurAromatic Interactions: A Computational Study of the Dimethyl SulfideBenzene Complex. <b>1997</b> , 25, 213-219	26
1679	Monitoring of Ehelical secondary structures in peptides by reversed-phase HPLC of replacement sets. <b>1997</b> , 352, 365-374	9
1678	The waters of life. <b>1998</b> , 335, 213-240	2
1677	MPSA Short Communications Listing. <b>1998</b> , 17, 505-567	
1676	Partial Molar Volumes of Hydrophobic Compounds <b>I</b> hsight into the Solvation Shell? Part I. <b>1998</b> , 27, 245-254	21
1675	Hydration of Folded and Unfolded Gas-Phase Proteins: Saturation of Cytochrome c and Apomyoglobin. <b>1998</b> , 120, 1327-1328	53
1674	Analysis of the forces which stabilize the active conformation of urokinase-type plasminogen activator. <i>Biochemistry</i> , <b>1998</b> , 37, 2935-40	12

1673	A stable single-layer beta-sheet without a hydrophobic core. <b>1998</b> , 5, 115-9	39
1672	On Levinthal paradoxLand the theory of protein folding. <b>1998</b> , 424, 157-169	6
1671	Intrinsic protein electric fields: basic non-covalent interactions and relationship to protein-induced Stark effects. <b>1998</b> , 1386, 305-30	54
1670	The C4b-binding protein-protein S interaction is hydrophobic in nature. <b>1998</b> , 1388, 181-9	16
1669	De novo design of ⊞elical coiled coils and bundles: models for the development of protein-design principles. <b>1998</b> , 16, 379-389	117
1668	Coupling protein stability and protein function in Escherichia coli CspA. <b>1998</b> , 3, 87-93	66
1667	A simple model for evolution of proteins towards the global minimum of free energy. <b>1998</b> , 3, 389-99	6
1666	Mechanistic comparison of artificial-chaperone-assisted and unassisted refolding of urea-denatured carbonic anhydrase B. <b>1998</b> , 3, 457-68	22
1665	The importance of hydration for the kinetics and thermodynamics of protein folding: simplified lattice models. <b>1998</b> , 3, 523-34	28
1664	Discrete molecular dynamics studies of the folding of a protein-like model. <b>1998</b> , 3, 577-87	255
1663	Hydrophobic interactions of peptides with membrane interfaces. <b>1998</b> , 1376, 339-52	428
1662	Atomic mutations in annexin Vthermodynamic studies of isomorphous protein variants. <b>1998</b> , 253, 1-9	43
1661	The influence of the central region containing residues 19-25 on the aggregation properties and secondary structure of Alzheimer's beta-amyloid peptide. <b>1998</b> , 256, 560-9	28
1660	Influence of Alcohol on Stability of Oil-in-Water Emulsions Containing Sodium Caseinate. <b>1998</b> , 197, 133-41	55
1659	Structural cassette mutagenesis in a de novo designed protein: proof of a novel concept for examining protein folding and stability. <b>1998</b> , 47, 101-23	7
1658	On the role of magnesium ions in RNA stability. <b>1998</b> , 48, 113-35	254
1657	Characterization of the folding pathway of recombinant human macrophage-colony stimulating-factor ¶rhM-CSF ∄by bis-cysteinyl modification and mass spectrometry. <b>1998</b> , 33, 50-62	10
1656	Prediction of the three-dimensional structure of proteins using the electrostatic screening model and hierarchic condensation. <b>1998</b> , 31, 74-96	9

1655	Protein folding simulation with genetic algorithm and supersecondary structure constraints. <b>1998</b> , 31, 247-257	56
1654	Structural investigation of C4b-binding protein by molecular modeling: localization of putative binding sites. <b>1998</b> , 31, 391-405	36
1653	Protein folding mechanisms and the multidimensional folding funnel. <b>1998</b> , 32, 136-158	174
1652	Role of water in plasticity, stability, and action of proteins: the crystal structures of lysozyme at very low levels of hydration. <b>1998</b> , 32, 229-40	77
1651	Can one predict protein stability? An attempt to do so for residue 133 of T4 lysozyme using a combination of free energy derivatives, PROFEC, and free energy perturbation methods. <b>1998</b> , 32, 438-458	20
1650	Multiple conformational states of a new hematopoietic cytokine (megakaryocyte growth and development factor): pH- and urea-induced denaturation. <b>1998</b> , 32, 495-503	5
1649	Intramolecular hydrogen bonding in resonance-stabilized systems. <b>1998</b> , 70, 863-875	16
1648	Prediction of the heat capacity change on thermal denaturation of globular proteins. <b>1998</b> , 321, 23-31	21
1647	Characterizing cavities in model inclusion molecules: a comparative study. 1998, 16, 57-71	9
1646	Influence of pH on lysozyme conformation revealed by dielectric spectroscopy. <b>1998</b> , 12, 1-5	48
1645	Helical protein design. <b>1998</b> , 9, 350-3	15
1644	Hydrophobic core packing and protein design. <b>1998</b> , 2, 675-9	39
1643	The response of T4 lysozyme to large-to-small substitutions within the core and its relation to the hydrophobic effect. <b>1998</b> , 7, 158-77	198
1642	15N backbone dynamics of the S-peptide from ribonuclease A in its free and S-protein bound forms: toward a site-specific analysis of entropy changes upon folding. <b>1998</b> , 7, 389-402	33
1641	Molecular dynamics simulations of hydrophobic collapse of ubiquitin. <b>1998</b> , 7, 860-74	79
1640	The de novo design of a rubredoxin-like Fe site. <b>1998</b> , 7, 1939-46	53
1639	A test of the relationship between sequence and structure in proteins: excision of the heme binding site in apocytochrome b5. <b>1998</b> , 7, 1983-93	15
1638	Probing the contribution of internal cavities to the volume change of protein unfolding under pressure. <b>1998</b> , 7, 2217-22	135

	Determinants of strand register in antiparallel beta-sheets of proteins. <b>1998</b> , 7, 2287-300	163
1636	Unfolding and refolding of dimeric creatine kinase equilibrium and kinetic studies. <b>1998</b> , 7, 2631-41	67
1635	Effect of denaturant and protein concentrations upon protein refolding and aggregation: a simple lattice model. <b>1998</b> , 7, 2642-52	83
1634	A solution SAXS study of Borrelia burgdorferi OspA, a protein containing a single-layer beta-sheet. <b>1998</b> , 7, 2681-3	19
1633	Structure analysis of two CheY mutants: importance of the hydrogen-bond contribution to protein stability. <b>1998</b> , 54, 378-85	8
1632	Thermodynamics of the hydration of non-polar substances. <b>1998</b> , 70, 57-63	14
1631	Contributions of solvent-solvent hydrogen bonding and van der Waals interactions to the attraction between methane molecules in water. <b>1998</b> , 71, 199-204	18
1630	Protein thermostability in extremophiles. <b>1998</b> , 80, 933-41	107
1629	Reversibility of heat-induced conformational changes and surface exposed hydrophobic clusters of beta-lactoglobulin: their role in heat-induced sol-gel state transition. <b>1998</b> , 22, 59-66	65
1628	A Simple Model of Water and the Hydrophobic Effect. <b>1998</b> , 120, 3166-3175	265
1627	The stability of proteins in extreme environments. <b>1998</b> , 8, 738-48	673
1627 1626	Molecular basis of protein functionality with special consideration of cold-set cels derived from	673 471
,	Molecular basis of protein functionality with special consideration of cold-set gels derived from	
1626	Molecular basis of protein functionality with special consideration of cold-set gels derived from heat-denatured whey. <b>1998</b> , 9, 143-151  A descriptive analysis of populations of three-dimensional structures calculated from primary	471
1626 1625	Molecular basis of protein functionality with special consideration of cold-set gels derived from heat-denatured whey. <b>1998</b> , 9, 143-151  A descriptive analysis of populations of three-dimensional structures calculated from primary sequences of proteins by OSIRIS. <b>1998</b> , 5, 351-66	471
1626 1625 1624	Molecular basis of protein functionality with special consideration of cold-set gels derived from heat-denatured whey. 1998, 9, 143-151  A descriptive analysis of populations of three-dimensional structures calculated from primary sequences of proteins by OSIRIS. 1998, 5, 351-66  On the complexity of protein folding. 1998, 5, 423-65  LiquidIliquid Immiscibility in Single-Component Network-Forming Fluids: Model Calculations and	471 5 207
1626 1625 1624 1623	Molecular basis of protein functionality with special consideration of cold-set gels derived from heat-denatured whey. 1998, 9, 143-151  A descriptive analysis of populations of three-dimensional structures calculated from primary sequences of proteins by OSIRIS. 1998, 5, 351-66  On the complexity of protein folding. 1998, 5, 423-65  Liquid Liquid Immiscibility in Single-Component Network-Forming Fluids: Model Calculations and Implications for Polyamorphism in Water. 1998, 37, 3012-3020  Single-tryptophan mutants of monomeric tryptophan repressor: optical spectroscopy reveals	471 5 207

1619	Cooperative Interaction between the Three Strands of a Designed Antiparallel 野heet. <b>1998</b> , 120, 5291-	5300	112
1618	Steady state and time-resolved fluorescence study of residual structures in an unfolded form of yeast phosphoglycerate kinase. <i>Biochemistry</i> , <b>1998</b> , 37, 7444-55	3.2	21
1617	Context-dependent nature of destabilizing mutations on the stability of FKBP12. <i>Biochemistry</i> , <b>1998</b> , 37, 6145-53	3.2	47
1616	Kinetic role of electrostatic interactions in the unfolding of hyperthermophilic and mesophilic rubredoxins. <i>Biochemistry</i> , <b>1998</b> , 37, 3369-76	3.2	104
1615	Helix-stabilizing nonpolar interactions between tyrosine and leucine in aqueous and TFE solutions: 2D-1H NMR and CD studies in alanine-lysine peptides. <i>Biochemistry</i> , <b>1998</b> , 37, 17318-30	3.2	34
1614	Forcing thermodynamically unfolded proteins to fold. <b>1998</b> , 273, 4831-4		299
1613	NMR Evidence for the Reassembly of an <b>知</b> Domain after Cleavage of an <b>Helix:</b> Implications for Protein Design. <b>1998</b> , 120, 7985-7986		17
1612	Thermodynamic and Structural Effects of a Single Backbone Hydrogen Bond Deletion in a Metal-Assembled Helical Bundle Protein. <b>1998</b> , 102, 9975-9980		13
1611	Kinetic refolding of beta-lactoglobulin. Studies by synchrotron X-ray scattering, and circular dichroism, absorption and fluorescence spectroscopy. <b>1998</b> , 275, 149-62		109
1610	An all-atom distance-dependent conditional probability discriminatory function for protein structure prediction. <b>1998</b> , 275, 895-916		383
1609	Molecular dynamics simulation of the unfolding of barnase: characterization of the major intermediate. <b>1998</b> , 275, 677-94		109
1608	Kinetics of lysozyme refolding: structural characterization of a non-specifically collapsed state using time-resolved X-ray scattering. <b>1998</b> , 276, 225-37		70
1607	Contribution of individual residues to formation of the native-like tertiary topology in the alpha-lactalbumin molten globule. <b>1998</b> , 280, 167-74		74
1606	Reversible peptide folding in solution by molecular dynamics simulation. <b>1998</b> , 280, 925-32		340
1605	The single helix in protein L is largely disrupted at the rate-limiting step in folding. <b>1998</b> , 284, 807-15		49
1604	A new method to characterize hydrophobic organization of proteins: application to rational protein engineering of barnase. <b>1998</b> , 15, 673-87		5
1603	Hydrophobic Effects on a Molecular Scale. <b>1998</b> , 102, 10469-10482		307
1602	Determination of the volume changes for pressure-induced transitions of apomyoglobin between the native, molten globule, and unfolded states. <b>1998</b> , 75, 463-70		74

1601	Aspects of weak interactions. <b>1998</b> , 27, 57	157
1600	Thermodynamics of dissolving gaseous argon in different solvents. <b>1998</b> , 76, 437-444	10
1599	Computer simulations with explicit solvent: recent progress in the thermodynamic decomposition of free energies and in modeling electrostatic effects. <b>1998</b> , 49, 531-67	223
1598	Solubility of nonpolar solutes in water: Computer simulations using the CF1 central force model. <b>1998</b> , 109, 7991-8002	22
1597	Influence of Solvent on Aromatic Interactions in Metal Tris-Bipyridine Complexes. <b>1998</b> , 120, 3402-3410	60
1596	Protein hydration and glass transitions. <b>1998</b> , 57-99	4
1595	Protein-lipid interactions. 1998, 385-431	4
1594	Involvement of maize Dof zinc finger proteins in tissue-specific and light-regulated gene expression. <b>1998</b> , 10, 75-89	244
1593	Highly designable protein structures and inter-monomer interactions. <b>1998</b> , 31, 6141-6155	15
1592	Bethe approximation for a semiflexible polymer chain. <b>1998</b> , 58, R5241-R5244	26
1592 1591	Bethe approximation for a semiflexible polymer chain. 1998, 58, R5241-R5244  Collapse of random copolymers. 1998, 108, 9924-9932	26
1591		
1591	Collapse of random copolymers. 1998, 108, 9924-9932  Rigidity of Thermophilic Enzymes. 1998, 15, 277-294	20
1591 1590	Collapse of random copolymers. <b>1998</b> , 108, 9924-9932  Rigidity of Thermophilic Enzymes. <b>1998</b> , 15, 277-294  Stability of preferable structures for a hydrophobic-polar model of protein folding. <b>1998</b> , 57, 3298-3301	20
1591 1590 1589	Collapse of random copolymers. <b>1998</b> , 108, 9924-9932  Rigidity of Thermophilic Enzymes. <b>1998</b> , 15, 277-294  Stability of preferable structures for a hydrophobic-polar model of protein folding. <b>1998</b> , 57, 3298-3301	20 16 16
1591 1590 1589 1588	Collapse of random copolymers. 1998, 108, 9924-9932  Rigidity of Thermophilic Enzymes. 1998, 15, 277-294  Stability of preferable structures for a hydrophobic-polar model of protein folding. 1998, 57, 3298-3301  Fast events in protein folding: the time evolution of primary processes. 1998, 49, 173-202	20 16 16 185
1591 1590 1589 1588	Collapse of random copolymers. 1998, 108, 9924-9932  Rigidity of Thermophilic Enzymes. 1998, 15, 277-294  Stability of preferable structures for a hydrophobic-polar model of protein folding. 1998, 57, 3298-3301  Fast events in protein folding: the time evolution of primary processes. 1998, 49, 173-202  Reduced protein models and their application to the protein folding problem. 1998, 16, 381-96	20 16 16 185

1583	Site-specific analysis of mutational effects in proteins. <b>1998</b> , 51, 59-119	40
1582	THERMAL STABILITY AND SOL-GEL TRANSITIONS OF WHEY AND EGG WHITE PROTEINS. 1998, 145-153	1
1581	On the thermodynamic hypothesis of protein folding. <b>1998</b> , 95, 5545-9	75
1580	Are protein folds atypical?. <b>1998</b> , 95, 4987-90	98
1579	A topologically conserved aliphatic residue in alpha-helix 6 stabilizes the hydrophobic core in domain II of glutathione transferases and is a structural determinant for the unfolding pathway. <b>1998</b> , 336 ( Pt 2), 413-8	10
1578	Hydration for a series of hydrocarbons. <b>1998</b> , 95, 8436-40	55
1577	Brownian dynamics simulations of protein folding: access to milliseconds time scale and beyond. <b>1998</b> , 95, 4288-92	46
1576	Scaling laws for protein folding. <b>1999</b> , 62-71	
1575	A variational approach to the localization transition of heteropolymers at interfaces. <b>1999</b> , 46, 301-306	19
1574	Recognizing misfolded and distorted protein structures by the assumption-based similarity score. <b>1999</b> , 12, 31-40	3
1573	Contribution of amino acid substitutions at two different interior positions to the conformational stability of human lysozyme. <b>1999</b> , 12, 841-50	34
1572	The evolutionary landscape of functional model proteins. <b>1999</b> , 12, 721-6	41
1571	Adaptive Significance of a Small Heat Shock/ECrystallin Protein (p26) in Encysted Embryos of the Brine Shrimp, Artemia franciscana. <b>1999</b> , 39, 836-847	66
1570	Role of structural and sequence information in the prediction of protein stability changes: comparison between buried and partially buried mutations. <b>1999</b> , 12, 549-55	116
1569	Analysis of thermal stabilizing interactions in mesophilic and thermophilic adenylate kinases from the genus Methanococcus. <b>1999</b> , 274, 28453-8	42
1568	Denatured states of tick anticoagulant peptide. Compositional analysis of unfolded scrambled isomers. <b>1999</b> , 274, 123-8	38
1567	Conformation and stability of barley chymotrypsin inhibitor-2 (CI-2) mutants containing multiple lysine substitutions. <b>1999</b> , 12, 967-73	27
1566	Direct kinetic evidence for folding via a highly compact, misfolded state. <b>1999</b> , 274, 26828-37	16

1565	Amino acid composition of protein termini are biased in different manners. <b>1999</b> , 12, 23-30	37
1564	Scaling behavior of stochastic minimization algorithms in a perfect funnel landscape. <b>1999</b> , 59, 938-941	33
1563	Simplified model for the analysis of interaction types in two-stranded coiled-coils. <b>1999</b> , 111, 2311-2321	2
1562	Spatial codes and the hardness of string folding problems. <b>1999</b> , 6, 13-36	8
1561	Designability, thermodynamic stability, and dynamics in protein folding: A lattice model study. <b>1999</b> , 110, 1252-1262	78
1560	Origin of the designability of protein structures. <b>1999</b> , 60, 4696-700	5
1559	C5a receptor activation. Genetic identification of critical residues in four transmembrane helices. <b>1999</b> , 274, 15757-65	112
1558	Protein structure prediction by global optimization of a potential energy function. <b>1999</b> , 96, 5482-5	155
1557	Thermal adaptation analyzed by comparison of protein sequences from mesophilic and extremely thermophilic Methanococcus species. <b>1999</b> , 96, 3578-83	265
1556	Thermodynamic analysis of biomolecular interactions. <b>1999</b> , 3, 557-63	194
1555	Aggregation of polyABIV-1 nucleocapsid protein NCp7 complexes and properties of the aggregates. <b>1999</b> , 152, 263-274	2
1554	The association of 4-(N,N-dimethylamino)benzonitrile and <b>t</b> yclodextrin in dimethyl sulfoxide and N,N-dimethylformamide. <b>1999</b> , 120, 23-28	12
1553	Probing intermolecular backbone H-bonding in serine proteinase-protein inhibitor complexes. <b>1999</b> , 6, 419-27	27
1552	Beta-hairpin and beta-sheet formation in designed linear peptides. <b>1999</b> , 7, 93-103	109
1551	Aggregation of recombinant hepatitis B surface antigen induced in vitro by oxidative stress. <b>1999</b> , 736, 153-66	2
1550	Instability, stabilization, and formulation of liquid protein pharmaceuticals. <b>1999</b> , 185, 129-88	823
1549	Molecular dynamics simulations of the ErbB-2 transmembrane domain within an explicit membrane environment: comparison with vacuum simulations. <b>1999</b> , 76, 35-53	19
1548	Observations on the origin of the non-linear van't Hoff behaviour of polypeptides in hydrophobic environments. <b>1999</b> , 77, 79-97	48

1547	Temperature dependence of the solubility of non-polar gases in water. <b>1999</b> , 78, 21-32	91
1546	Important amino acid properties for enhanced thermostability from mesophilic to thermophilic proteins. <b>1999</b> , 82, 51-67	181
1545	Hydrophobicity of benzene. <b>1999</b> , 82, 69-79	35
1544	Partial molar volumes-insights into molecular structure. <b>1999</b> , 81, 37-45	10
1543	Monte Carlo study of the temperature dependence of the hydrophobic hydration of benzene. <b>1999</b> , 313, 235-240	23
1542	Where U and I meet. <b>1999</b> , 6, 605-8	9
1541	Protein folding as seen from water's perspective. <b>1999</b> , 6, 203-5	12
1540	AcidBase and hydrogen-bonding equilibria in aliphatic amine and carboxylic acid systems in non-aqueous solutions. <b>1999</b> , 401, 317-321	33
1539	Retention models for ions in chromatography. <b>1999</b> , 855, 3-55	184
1538	Relationship between amino acid properties and protein stability: buried mutations. <b>1999</b> , 18, 565-78	66
1537	Structural organization of G-protein-coupled receptors. <b>1999</b> , 13, 325-53	42
1536	Estimating binding constants [The hydrophobic effect and cooperativity. <b>1999</b> , 17, 43-59	29
1535	Solution X-ray scattering as a probe of hydration-dependent structuring of aqueous solutions. <b>1999</b> , 17, 97-118	28
1534	Design of highly stable functional GroEL minichaperones. <b>1999</b> , 8, 2186-93	62
1533	Study of the stability and unfolding mechanism of BBA1 by molecular dynamics simulations at different temperatures. <b>1999</b> , 8, 1292-304	47
1532	Distinguishing between sequential and nonsequentially folded proteins: implications for folding and misfolding. <b>1999</b> , 8, 1591-604	19
1531	Bioconversion of acrylonitrile to acrylamide using a thermostable nitrile hydratase. <b>1999</b> , 77-79, 671-9	25
1530	Generation of recombinant antibodies. <b>1999</b> , 12, 173-201	45

1529	Mitochondrial cytochromes c: a comparative analysis. <b>1999</b> , 4, 824-37	85
1528	Rational design of a more stable yeast iso-1-cytochrome c. <b>1999</b> , 1432, 40-8	17
1527	Stability and folding of domain proteins. <b>1999</b> , 71, 155-241	142
1526	Computational protein design. <b>1999</b> , 7, R105-9	132
1525	Characterization and comparison of protein structures. Part I-characterization. <b>1999</b> , 198, 197-218	8
1524	Thermodynamics of Interaction between Some Cellulose Ethers and SDS by Titration Microcalorimetry. <b>1999</b> , 213, 133-151	34
1523	De novo predictions of the quaternary structure of leucine zippers and other coiled coils. <b>1999</b> , 75, 165-176	4
1522	Thermostability of modified enzymes: a detailed study. <b>1999</b> , 74, 25-32	85
1521	Molecular simulation of the effects of alcohols on peptide structure. <b>1999</b> , 49, 635-45	29
1520	The effect of vicinal polar and charged groups on hydrophobic hydration. <b>1999</b> , 50, 742-50	29
1519	Prediction of protein structure: The problem of fold multiplicity. <b>1999</b> , 37, 199-203	16
1518	Structural and dynamic aspects of 畇lycosidase from mesophilic and thermophilic bacteria by multitryptophanyl emission decay studies. <b>1999</b> , 35, 163-172	9
1517	Use of pair potentials across protein interfaces in screening predicted docked complexes. <b>1999</b> , 35, 364-373	227
1516	Estimates of the loss of main-chain conformational entropy of different residues on protein folding. <b>1999</b> , 36, 332-339	18
1515	Effects of core-packing on the structure, function, and mechanics of a four-helix-bundle protein ROP. <b>1999</b> , 36, 436-46	12
1514	The crystal structure of triosephosphate isomerase (TIM) from Thermotoga maritima: A comparative thermostability structural analysis of ten different TIM structures. <b>1999</b> , 37, 441-453	119
1513	Towards understanding the mechanisms of molecular recognition by computer simulations of ligand-protein interactions. <b>1999</b> , 12, 371-89	32
1512	Hydrophobic hydration: Heat capacity of solvation from computer simulations and from an information theory approximation. <b>1999</b> , 110, 5873-5883	19

1511	Computer simulation of the structural effect of pressure on the hydrophobic hydration of methane. <b>1999</b> , 96, 109-122	51
1510	Thermal denaturation of human gamma-interferon. A calorimetric and spectroscopic study.  Biochemistry, <b>1999</b> , 38, 7865-73	15
1509	Cold-Adapted Organisms. <b>1999</b> ,	22
1508	Evolution of a protein fold in vitro. <b>1999</b> , 284, 325-8	97
1507	Thermodynamics of cavity formation in water and n-hexane using the Widom particle insertion method. <b>1999</b> , 111, 8576-8587	36
1506	Thermal versus guanidine-induced unfolding of ubiquitin. An analysis in terms of the contributions from charge-charge interactions to protein stability. <i>Biochemistry</i> , <b>1999</b> , 38, 8138-49	222
1505	Linkage of proton binding to the thermal unfolding of Sso7d from the hyperthermophilic archaebacterium Sulfolobus solfataricus. <b>1999</b> , 26, 45-53	7
1504	Bioaccumulation of some hazardous metals by solgel entrapped microorganisms. <b>1999</b> , 248, 137-140	78
1503	Membrane protein folding and stability: physical principles. <b>1999</b> , 28, 319-65	1468
1502	Water as Solvent in Organic Synthesis. <b>1999</b> , 1-39	84
	Water as Solvent in Organic Synthesis. <b>1999</b> , 1-39  Determining the Role of Hydration Forces in Protein Folding. <b>1999</b> , 103, 5413-5426	84
1501	Determining the Role of Hydration Forces in Protein Folding. <b>1999</b> , 103, 5413-5426  Conformational equilibria of alkanes in aqueous solution: relationship to water structure near	86
1501 1500 1499	Determining the Role of Hydration Forces in Protein Folding. 1999, 103, 5413-5426  Conformational equilibria of alkanes in aqueous solution: relationship to water structure near hydrophobic solutes. 1999, 77, 645-54  Characterization of solute binding at human serum albumin site II and its geometry using a	86
1501 1500 1499	Determining the Role of Hydration Forces in Protein Folding. 1999, 103, 5413-5426  Conformational equilibria of alkanes in aqueous solution: relationship to water structure near hydrophobic solutes. 1999, 77, 645-54  Characterization of solute binding at human serum albumin site II and its geometry using a biochromatographic approach. 1999, 77, 1206-12	86 42 37
1501 1500 1499 1498	Determining the Role of Hydration Forces in Protein Folding. 1999, 103, 5413-5426  Conformational equilibria of alkanes in aqueous solution: relationship to water structure near hydrophobic solutes. 1999, 77, 645-54  Characterization of solute binding at human serum albumin site II and its geometry using a biochromatographic approach. 1999, 77, 1206-12  Free energy landscapes of encounter complexes in protein-protein association. 1999, 76, 1166-78  Thermodynamics of interactions between amino acid side chains: experimental differentiation of aromatic-aromatic, aromatic-aliphatic, and aliphatic-aliphatic side-chain interactions in water. 1999,	86 42 37 164
1501 1500 1499 1498	Determining the Role of Hydration Forces in Protein Folding. 1999, 103, 5413-5426  Conformational equilibria of alkanes in aqueous solution: relationship to water structure near hydrophobic solutes. 1999, 77, 645-54  Characterization of solute binding at human serum albumin site II and its geometry using a biochromatographic approach. 1999, 77, 1206-12  Free energy landscapes of encounter complexes in protein-protein association. 1999, 76, 1166-78  Thermodynamics of interactions between amino acid side chains: experimental differentiation of aromatic-aromatic, aromatic-aliphatic, and aliphatic-aliphatic side-chain interactions in water. 1999, 76, 2319-28	86 42 37 164 21

1493	Sequential Collapse Model for Protein Folding Pathways. <b>1999</b> , 103, 9749-9758		18
1492	Thermodynamic analysis of unfolding and dissociation in lactose repressor protein. <i>Biochemistry</i> , <b>1999</b> , 38, 6520-8	3.2	42
1491	Contribution of hydrogen bonds to the conformational stability of human lysozyme: calorimetry and X-ray analysis of six Ser> Ala mutants. <i>Biochemistry</i> , <b>1999</b> , 38, 6623-9	3.2	59
1490	Hydrophobic Force Field as a Molecular Alternative to Surface-Area Models. <b>1999</b> , 121, 6299-6305		55
1489	Origins of the Solvent Chain-Length Dependence of Gibbs Free Energies of Transfer. <b>1999</b> , 103, 2977-2	980	13
1488	Multistep denaturation of Borrelia burgdorferi OspA, a protein containing a single-layer beta-sheet. <i>Biochemistry</i> , <b>1999</b> , 38, 4757-67	3.2	33
1487	Hierarchy of the interaction energy distribution in the spatial structure of globular proteins and the problem of domain definition. <b>1999</b> , 17, 133-55		21
1486	Atomic mutations at the single tryptophan residue of human recombinant annexin V: effects on structure, stability, and activity. <i>Biochemistry</i> , <b>1999</b> , 38, 10649-59	3.2	74
1485	Calorimetric examination of high-affinity Src SH2 domain-tyrosyl phosphopeptide binding: dissection of the phosphopeptide sequence specificity and coupling energetics. <i>Biochemistry</i> , <b>1999</b> , 38, 5147-54	3.2	77
1484	An engineered minidomain containing an elastin turn exhibits a reversible temperature-induced IgG binding. <i>Biochemistry</i> , <b>1999</b> , 38, 14897-905	3.2	22
1483	Anhydrous protein ions. <b>1999</b> , 99, 3037-80		301
1482	Effects of core mutations on the folding of a beta-sheet protein: implications for backbone organization in the I-state. <i>Biochemistry</i> , <b>1999</b> , 38, 1377-85	3.2	81
1481	The solution structure of photosystem I accessory protein E from the cyanobacterium Nostoc sp. strain PCC 8009. <i>Biochemistry</i> , <b>1999</b> , 38, 13736-46	3.2	24
1480	Hydrogen bonding and equilibrium protium-deuterium fractionation factors in the immunoglobulin G binding domain of protein G. <i>Biochemistry</i> , <b>1999</b> , 38, 3918-25	3.2	23
1479	Minimization of recombinant human Flt3 ligand aggregation at the Tm plateau: a matter of thermal reversibility. <i>Biochemistry</i> , <b>1999</b> , 38, 5241-7	3.2	51
1478	Vibrational Stark Spectroscopy in Proteins: A Probe and Calibration for Electrostatic Fields. <b>1999</b> , 103, 9813-9817		191
1477	A correlation between the loss of hydrophobic core packing interactions and protein stability. <b>1999</b> , 285, 817-27		60
1476	Molecular dynamics simulations of the hyperthermophilic protein sac7d from Sulfolobus acidocaldarius: contribution of salt bridges to thermostability. <b>1999</b> , 285, 1811-30		105

1475 Crystallographic and calorimetric analysis of peptide binding to OppA protein. <b>1999</b> , 291, 393-415	136
1474 Protein folding: from the levinthal paradox to structure prediction. <b>1999</b> , 293, 283-93	129
1473 De novo protein design. I. In search of stability and specificity. <b>1999</b> , 293, 1161-81	111
The contribution of acidic residues to the conformational stability of common-type acylphosphatase. <b>1999</b> , 363, 349-55	5
beta-glycosidase from the hyperthermophilic archaeon Sulfolobus solfataricus: structure and activity in the presence of alcohols. <b>1999</b> , 126, 545-52	26
Electrostatic interactions affecting the active site of class Sigma glutathione S-transferase. <b>2000</b> , 347, 193	8
Electrostatic interactions affecting the active site of class Sigma glutathione S-transferase. <b>2000</b> , 347, 193-197	26
1468 Osmolyte-induced changes in protein conformational equilibria. <b>2000</b> , 53, 293-307	147
1467 Environment of tryptophan side chains in proteins. <b>2000</b> , 38, 288-300	120
Trans-substitution of the proximal hydrogen bond in myoglobin: II. Energetics, functional consequences, and implications for hemoglobin allostery. <b>2000</b> , 39, 291-308	9
1465 Structural thermodynamics of a random coil protein in guanidine hydrochloride. <b>2000</b> , 41, 44-49	6
1464 Side-chain conformational entropy in protein unfolded states. <b>2000</b> , 40, 443-50	65
Modeling protein density of states: additive hydrophobic effects are insufficient for calorimetric two-state cooperativity. <b>2000</b> , 40, 543-71	123
1462 Mechanism of protein folding. <b>2000</b> , 41, 288-98	60
Exhaustive mutagenesis in silico: Multicoordinate free energy calculations on proteins and peptides. <b>2000</b> , 41, 385-397	58
1460 A Designed 冊airpin Containing a Natural Hydrophobic Cluster. <b>2000</b> , 112, 2420-2423	15
1459 Theoretic information approach to protein stabilization by solvent engineering. <b>2000</b> , 46, 1478-14	189 9
1458 Capillary electroendoosmotic chromatography of peptides. <b>2000</b> , 887, 165-85	59

# (2000-2000)

1457	Contribution of disulfide bonds to the conformational stability and catalytic activity of ribonuclease A. <b>2000</b> , 267, 566-72	124
1456	A DNA ligase from the psychrophile Pseudoalteromonas haloplanktis gives insights into the adaptation of proteins to low temperatures. <b>2000</b> , 267, 3502-12	50
1455	Enthalpic and entropic consequences of the removal of disulfide bridges in ribonuclease A. <b>2000</b> , 364, 165-172	4
1454	On the pH dependence of thermodynamic stability of the mylase inhibitor tendamistat. <b>2000</b> , 345, 59-66	2
1453	The influence of the binding of low molecular weight surfactants on the thermal stability and secondary structure of IgG. <b>2000</b> , 161, 139-150	24
1452	Submicrosecond real-time fluorescence sampling: application to protein folding. 2000, 54, 1-15	51
1451	New perspectives on hydrophobic effects. <b>2000</b> , 258, 349-370	262
1450	A study on the enthalpy-entropy compensation in protein unfolding. <b>2000</b> , 84, 239-51	94
1449	Heat capacity of hydrogen-bonded networks: an alternative view of protein folding thermodynamics. <b>2000</b> , 85, 25-39	125
1448	The effect of mutation at valine-45 on the stability and redox potentials of trypsin-cleaved cytochrome b5. <b>2000</b> , 83, 3-17	18
1447	Discrete reduction of type I collagen thermal stability upon oxidation. <b>2000</b> , 83, 185-95	51
1446	Simple models of the protein folding problem. <b>2000</b> , 288, 31-48	29
1445	Simulations of protein folding. <b>2000</b> , 83-84, 929-931	4
1444	Computational design of an integrin I domain stabilized in the open high affinity conformation. <b>2000</b> , 7, 674-8	111
1443	Design of single-layer beta-sheets without a hydrophobic core. <b>2000</b> , 403, 456-60	54
1442	Lyophilization and development of solid protein pharmaceuticals. 2000, 203, 1-60	847
1441	How do proteins fold?. <b>2000</b> , 28, 76-79	
1440	Structural differences between mesophilic, moderately thermophilic and extremely thermophilic protein subunits: results of a comprehensive survey. <b>2000</b> , 8, 493-504	520

1439	Luxury accommodations: the expanding role of structural plasticity in protein-protein interactions. <b>2000</b> , 8, R137-42	65
1438	Aggregation kinetics of heated whey protein-stabilized emulsions. <b>2000</b> , 14, 155-161	129
1437	Alcohol-induced versus anion-induced states of alpha-chymotrypsinogen A at low pH. <b>2000</b> , 1481, 229-36	43
1436	Hydrophilic framework in proteins?. <b>2000</b> , 19, 93-103	15
1435	Construction of a full three-dimensional model of the transpeptidase domain of Streptococcus pneumoniae PBP2x starting from its Calpha-atom coordinates. <b>2000</b> , 14, 719-30	3
1434	Modeling liquid properties, solvation, and hydrophobicity: A molecular size-based perspective. <b>2000</b> , 19, 19-45	16
1433	Thermodynamic Stability of Ribonuclease B. <b>2000</b> , 61, 363-368	3
1432	CRITICAL REVIEW - Interfacial Behaviour of Wheat Proteins. <b>2000</b> , 31, 195-221	70
1431	The identification of conserved interactions within the SH3 domain by alignment of sequences and structures. <b>2000</b> , 9, 2170-80	140
1430	Nonpolar contributions to conformational specificity in assemblies of designed short helical peptides. <b>2000</b> , 9, 1011-23	4
1429	Charge-charge interactions influence the denatured state ensemble and contribute to protein stability. <b>2000</b> , 9, 1395-8	204
1428	Nonnative intermediate state of acid-stable beta-sheet protein. <b>2000</b> , 33, 253-73	4
1427	EnthalpyEntropy and Cavity Decomposition of Alkane Hydration Free Energies: Numerical Results and Implications for Theories of Hydrophobic Solvation. <b>2000</b> , 104, 6271-6285	289
1426	Parallel cascade identification as a means for automatically classifying protein sequences into structure/function groups. <b>2000</b> , 82, 15-21	8
1425	Enthalpy-entropy compensation in protein unfolding. <b>2000</b> , 45, 1476-1480	4
1424	Halophilic adaptation of enzymes. <b>2000</b> , 4, 91-8	446
1423	Kinetics of the protein folding transition. 2000,	
1422	Anatomy of protein structures: visualizing how a one-dimensional protein chain folds into a three-dimensional shape. <b>2000</b> , 97, 12038-43	68

# (2000-2000)

1421	introducing surface hydrophobic residues. <b>2000</b> , 275, 35723-6	17
1420	Human C4b-binding protein has overlapping, but not identical, binding sites for C4b and streptococcal M proteins. <b>2000</b> , 164, 5328-36	68
1419	Denaturant-induced movement of the transition state of protein folding revealed by high-pressure stopped-flow measurements. <b>2000</b> , 97, 17-22	97
1418	Trifluoroethanol may form a solvent matrix for assisted hydrophobic interactions between peptide side chains. <b>2000</b> , 13, 739-43	96
1417	Deterministic features of side-chain main-chain hydrogen bonds in globular protein structures. <b>2000</b> , 13, 227-38	73
1416	Three-helix-bundle protein in a Ramachandran model. <b>2000</b> , 97, 13614-8	90
1415	Genetic mapping of the human C5a receptor. Identification of transmembrane amino acids critical for receptor function. <b>2000</b> , 275, 35393-401	51
1414	The relationship between sequence and structure in elementary folding units. <b>2000</b> , 53, 49-85	50
1413	Globular state of random copolymers with arbitrary amphiphilicity. <b>2000</b> , 112, 1547-1553	12
1412	Effects of electric charges on hydrophobic forces. II. <b>2000</b> , 62, 6799-809	18
1411	Multiple-sequence information provides protection against mis-specified potential energy functions in the lattice model of proteins. <b>2000</b> , 85, 5242-5	4
1410	Energetic components of cooperative protein folding. <b>2000</b> , 85, 4823-6	89
1409	Comment on "DNA molecular cousin of Schrdinger's cat: a curious example of quantum measurement". <b>2000</b> , 84, 195	1
1408	Hierarchy of regions of amino acid sequence with respect to their role in the protein spatial structure. <b>2000</b> , 7, 183-92	4
1407	Molecular Dynamics Study on Protein and it's Water Structure at High Pressure. 2000, 23, 257-274	10
1406	Temperature dependence of hydrophobic interactions: A mean force perspective, effects of water density, and nonadditivity of thermodynamic signatures. <b>2000</b> , 113, 4683-4700	152
1405	Physics and Chemistry Basis of Biotechnology. <b>2000</b> ,	1
1404	Conformational stability is a determinant of ribonuclease A cytotoxicity. <b>2000</b> , 275, 17463-7	76

1403	Hydrophobic Interactions in Solution: A Nuclear Magnetic Resonance Approach. 2000, 214,	2
1402	Structural changes and interactions involved in the Ca(2+)-triggered stabilization of the cell-bound cell envelope proteinase in Lactococcus lactis subsp. cremoris SK11. <b>2000</b> , 66, 2021-8	16
1401	From DNA sequence to improved functionality: using protein sequence comparisons to rapidly design a thermostable consensus phytase. <b>2000</b> , 13, 49-57	151
1400	Do ultrastable proteins from hyperthermophiles have high or low conformational rigidity?. <b>2000</b> , 97, 2962-4	144
1399	Folding and association of oligomeric and multimeric proteins. <b>2000</b> , 53, 329-401	132
1398	Genetic Engineering. <b>2000</b> ,	
1397	Statistical theory of combinatorial libraries of folding proteins: energetic discrimination of a target structure. <b>2000</b> , 296, 281-94	69
1396	Energetic basis of structural stability in the molten globule state: alpha-lactalbumin. <b>2000</b> , 297, 1259-68	45
1395	Hierarchical unfolding of the alpha-lactalbumin molten globule: presence of a compact intermediate without a unique tertiary fold. <b>2000</b> , 298, 1-6	16
1394	A view of dynamics changes in the molten globule-native folding step by quasielastic neutron scattering. <b>2000</b> , 301, 525-36	53
1393	Influence of mRNA self-structure on hybridization: computational tools for antisense sequence selection. <b>2000</b> , 22, 261-9	11
1392	The thermal stability of immunoglobulin: unfolding and aggregation of a multi-domain protein. <b>2000</b> , 78, 394-404	525
1391	Theoretical studies of the response of a protein structure to cavity-creating mutations. 2000, 78, 1665-71	22
1390	How do proteins fold?. <b>2000</b> , 28, 76-79	1
1389	The three HveA receptor ligands, gD, LT-alpha and LIGHT bind to distinct sites on HveA. <b>2000</b> , 37, 665-73	35
1388	Physicochemical factors in polypeptide and protein purification and analysis by high-performance liquid chromatographic techniques: current status and challenges for the future. <b>2000</b> , 2, 71-235	12
1387	Disulfide bonds and protein folding. <i>Biochemistry</i> , <b>2000</b> , 39, 4207-16 3.2	487
1386	Free Energy, Entropy and Heat Capacity of the Hydrophobic Interaction as a Function of Pressure. <b>2000</b> , 104, 6884-6888	50

## (2000-2000)

1	1385	Stabilization of proteins by enhancement of inter-residue hydrophobic contacts: lessons of T4 lysozyme and barnase. <b>2000</b> , 18, 477-91		8	
1	1384	Contribution of salt bridges near the surface of a protein to the conformational stability. <i>Biochemistry</i> , <b>2000</b> , 39, 12375-81	3.2	97	
1	1383	Estimation of the hydrophobic effect in an antigen-antibody protein-protein interface. <i>Biochemistry</i> , <b>2000</b> , 39, 15375-87	3.2	91	
1	1382	Hydration free energy of hydrophobic solutes studied by a reference interaction site model with a repulsive bridge correction and a thermodynamic perturbation method. <b>2000</b> , 113, 2793-2805		139	
1	1381	Side chain accessibility and dynamics in the molten globule state of alpha-lactalbumin: a (19)F-NMR study. <i>Biochemistry</i> , <b>2000</b> , 39, 372-80	3.2	39	
1	1380	Importance of surrounding residues for protein stability of partially buried mutations. <b>2000</b> , 18, 281-95		37	
1	1379	Barriers in protein folding reactions. <b>2000</b> , 53, 153-207		60	
1	1378	The P5abc peripheral element facilitates preorganization of the tetrahymena group I ribozyme for catalysis. <i>Biochemistry</i> , <b>2000</b> , 39, 2639-51	3.2	57	
1	1377	Design, Synthesis, and Characterization of 4-Ester CI2, a Model for Backbone Hydrogen Bonding in Protein Helices. <b>2000</b> , 122, 12079-12082		58	
1	1376	New peptide labels containing covalently bonded platinum(II) centers as diagnostic biomarkers and biosensors. <b>2000</b> , 2, 3461-4		83	
1	1375	Stepwise formation of alpha-helices during cytochrome c folding. <b>2000</b> , 7, 514-20		128	
1	1374	Thermodynamic stability of the two isoforms of bovine seminal ribonuclease. <i>Biochemistry</i> , <b>2000</b> , 39, 7964-72	3.2	11	
1	1373	Predicting PeptideReceptor, PeptideProtein, and ChaperoneProtein Binding Using Patterns in Amino Acid Hydrophobic Free Energy Sequences 2000, 104, 3953-3959		6	
1	1372	Buried polar interactions and conformational stability in the simian immunodeficiency virus (SIV) gp41 core. <i>Biochemistry</i> , <b>2000</b> , 39, 676-85	3.2	31	
1	1371	Cooperative assembly of a nativelike ubiquitin structure through peptide fragment complexation: energetics of peptide association and folding. <i>Biochemistry</i> , <b>2000</b> , 39, 12355-64	3.2	40	
1	1370	Thermodynamic and structural studies of cavity formation in proteins suggest that loss of packing interactions rather than the hydrophobic effect dominates the observed energetics. <i>Biochemistry</i> , <b>2000</b> , 39, 12365-74	3.2	63	
1	1369	One Water Molecule Stiffens a Protein. <b>2000</b> , 122, 2950-2951		44	
1	1368	On the Solvent Isotope Effect in Hydrophobic Hydration. <b>2000</b> , 104, 9249-9254		33	

1367	Stability and stabilization of globular proteins in solution. <b>2000</b> , 79, 193-203		186
1366	De novo design of helical bundles as models for understanding protein folding and function. <b>2000</b> , 33, 745-54		274
1365	Polar residues in the protein core of Escherichia coli thioredoxin are important for fold specificity. <i>Biochemistry</i> , <b>2001</b> , 40, 10047-53	3.2	35
1364	Insights into the stability of native and partially folded states of ubiquitin: effects of cosolvents and denaturants on the thermodynamics of protein folding. <i>Biochemistry</i> , <b>2001</b> , 40, 10317-25	3.2	37
1363	Characterizing the function of unstructured proteins: Simulations of charged polymers under confinement. <b>2001</b> , 115, 4909-4918		16
1362	Salting-In and Salting-Out of Hydrophobic Solutes in Aqueous Salt Solutions. <b>2001</b> , 105, 6380-6386		149
1361	Computational protein folding: From lattice to all-atom. <b>2001</b> , 40, 297-309		36
1360	Stabilization of hen egg white lysozyme by a cavity-filling mutation. <b>2001</b> , 10, 313-20		46
1359	Physicochemical consequences of the perdeuteriation of glutathione S-transferase from S. japonicum. <b>2001</b> , 10, 572-80		30
1358	Parallel cascade identification and its application to protein family prediction. <b>2001</b> , 91, 35-47		4
			·
1357	Lens crystallins and their microbial homologs: structure, stability, and function. <b>2001</b> , 36, 435-99		126
1357 1356	Lens crystallins and their microbial homologs: structure, stability, and function. <b>2001</b> , 36, 435-99  Optimality of the genetic code with respect to protein stability and amino-acid frequencies. <b>2001</b> , 2, RESEARCH0049		
	Optimality of the genetic code with respect to protein stability and amino-acid frequencies. <b>2001</b> ,		126
1356	Optimality of the genetic code with respect to protein stability and amino-acid frequencies. 2001, 2, RESEARCH0049  Temperature dependence of hydrophobic hydration and entropy convergence in an isotropic		126 128
1356 1355	Optimality of the genetic code with respect to protein stability and amino-acid frequencies. 2001, 2, RESEARCH0049  Temperature dependence of hydrophobic hydration and entropy convergence in an isotropic model of water. 2001, 115, 977-982		126 128 61
1356 1355 1354	Optimality of the genetic code with respect to protein stability and amino-acid frequencies. 2001, 2, RESEARCH0049  Temperature dependence of hydrophobic hydration and entropy convergence in an isotropic model of water. 2001, 115, 977-982  Bovine pancreatic ribonuclease A: oxidative and conformational folding studies. 2001, 341, 189-221		126 128 61 41
1356 1355 1354 1353	Optimality of the genetic code with respect to protein stability and amino-acid frequencies. 2001, 2, RESEARCH0049  Temperature dependence of hydrophobic hydration and entropy convergence in an isotropic model of water. 2001, 115, 977-982  Bovine pancreatic ribonuclease A: oxidative and conformational folding studies. 2001, 341, 189-221  Hydration of Aromatic Hydrocarbons. 2001, 105, 10367-10372  Mutational effects on thermostable superoxide dismutase from Aquifex pyrophilus: understanding		126 128 61 41 60

# (2001-2001)

Formation of the single-layer C-terminal capping globular	r beta-sheet of Borrelia burgdorferi OspA in the absence of the domain. <b>2001</b> , 308, 367-75		8
1348 The alternatively folded state	e of the antibody C(H)3 domain. <b>2001</b> , 309, 1077-85		41
Folding of beta-sheets in me 309, 975-88	mbranes: specificity and promiscuity in peptide model systems. 2001,		44
In silico structural and function 310, 1151-66	onal analysis of the human cytomegalovirus (HHV5) genome. <b>2001</b> ,		40
Four-body potentials reveal phydrophobic core mutations.	protein-specific correlations to stability changes caused by . <b>2001</b> , 311, 625-38		106
1344 Folding of horse cytochrome	c in the reduced state. <b>2001</b> , 312, 1135-60		70
1343 Mutational analysis of hydro	gen bonding residues in the BPTI folding pathway. <b>2001</b> , 313, 639-56		9
1342 Structural determinants of m	nini-protein stability. <b>2001</b> , 29, 16-20		5
1341 Hydrophobic interaction chro	omatography of proteins. <b>2001</b> , 87, 143-59		310
1340 Early events in RNA folding. 2	<b>2001</b> , 52, 751-62		174
1339 Molecular modeling of nucle	ic acid structure: electrostatics and solvation. <b>2001</b> , Chapter 7, Unit 7.9		2
Hyperthermophilic enzymes: 65, 1-43	sources, uses, and molecular mechanisms for thermostability. 2001,		1496
Chirality organization of ferrocharacterization. <b>2001</b> , 123, 6	ocenes bearing podand dipeptide chains: synthesis and structural 68-75		170
Energetics of side chain pack cycles. <i>Biochemistry</i> , <b>2001</b> , 40	ring in staphylococcal nuclease assessed by systematic double mutant 0. 14004-11	3.2	38
1335 Elastomeric polypentapeptid	des cross-linked into matrixes and fibers. <b>2001</b> , 2, 170-9		105
	des cross-linked into matrixes and fibers. <b>2001</b> , 2, 170-9 ons of the rehydration of folded and unfolded cytochrome C ions in the		105
Molecular dynamics simulation vapor phase. <b>2001</b> , 123, 6503	des cross-linked into matrixes and fibers. <b>2001</b> , 2, 170-9 ons of the rehydration of folded and unfolded cytochrome C ions in the		

1331	A Model for Studying Drying at Hydrophobic Interfaces: Structural and Thermodynamic Properties <b>2001</b> , 105, 6745-6753		96
1330	Binding of ferric heme by the recombinant globin from the cyanobacterium Synechocystis sp. PCC 6803. <i>Biochemistry</i> , <b>2001</b> , 40, 6541-52	3.2	36
1329	Swelling Behavior of Erradiation Cross-Linked Elastomeric Polypentapeptide-Based Hydrogels. <b>2001</b> , 34, 4114-4123		67
1328	Solvent size vs cohesive energy as the origin of hydrophobicity. <b>2001</b> , 34, 931-7		100
1327	Polar group burial contributes more to protein stability than nonpolar group burial. <i>Biochemistry</i> , <b>2001</b> , 40, 310-3	3.2	130
1326	Mechanical Properties of Cross-Linked Synthetic Elastomeric Polypentapeptides. <b>2001</b> , 34, 5968-5974		82
1325	Energetics of side chain packing in staphylococcal nuclease assessed by exchange of valines, isoleucines, and leucines. <i>Biochemistry</i> , <b>2001</b> , 40, 13998-4003	3.2	32
1324	Contribution of polar groups in the interior of a protein to the conformational stability. <i>Biochemistry</i> , <b>2001</b> , 40, 4853-8	3.2	44
1323	A comparative study of peptide models of the alpha-domain of alpha-lactalbumin, lysozyme, and alpha-lactalbumin/lysozyme chimeras allows the elucidation of critical factors that contribute to the ability to form stable partially folded states. <i>Biochemistry</i> , <b>2001</b> , 40, 2138-47	3.2	12
1322	Microcalorimetric studies on the interaction mechanism between proteins and hydrophobic solid surfaces in hydrophobic interaction chromatography: effects of salts, hydrophobicity of the sorbent, and structure of the protein. <b>2001</b> , 73, 3875-83		82
1321	Hydrophobic core manipulations in ribonuclease T1. <i>Biochemistry</i> , <b>2001</b> , 40, 10140-9	3.2	13
1320	Role of Topology in the Cooperative Collapse of the Protein Core in the Sequential Collapse Model. Folding Pathway of 且actalbumin and Hen Lysozyme. <b>2001</b> , 105, 2874-2880		11
1319	Cooperativity in amide hydrogen bonding chains: implications for protein-folding models. <b>2001</b> , 123, 4348-9		151
1318	Packing is a key selection factor in the evolution of protein hydrophobic cores. <i>Biochemistry</i> , <b>2001</b> , 40, 15280-9	3.2	64
1317	Design of folded peptides. <b>2001</b> , 101, 3131-52		582
1316	Strength of the NHTTOC and CHTTOC Bonds in Formamide and N-Methylacetamide Dimers. <b>2001</b> , 105, 4963-4968		158
1315	Structural biology of the cell adhesion protein CD2: alternatively folded states and structure-function relation. <b>2001</b> , 2, 1-17		23
1314	Characterizing Cavities in Model Inclusion Fullerenes: A Comparative Study. <b>2001</b> , 2, 72-88		3

1313 Protein Stability. 2001,

1312	Pulsed Electric Field Denaturation of Bovine Alkaline Phosphatase. 2001,	4
1311	Thermostability of proteins from Thermotoga maritima. <b>2001</b> , 334, 438-69	23
1310	Computer simulation of the hydrophobic hydration of concave surfaces. <b>2001</b> , 99, 1289-1298	15
1309	Physicochemical evaluation of protein folds predicted by threading. <b>2001</b> , 30, 1-10	13
1308	Initial protein concentration and residual denaturant concentration strongly affect the batch refolding of hen egg white lysozyme. <b>2001</b> , 6, 410-418	3
1307	Conformational analysis of the nonapeptide leuprorelin using NMR and molecular modeling. <b>2001</b> , 8, 77-87	1
1306	Influence of the oligomeric state of yeast hexokinase isozymes on inactivation and unfolding by urea. <b>2001</b> , 91, 183-90	6
1305	Heat does not come in different colours: entropy-enthalpy compensation, free energy windows, quantum confinement, pressure perturbation calorimetry, solvation and the multiple causes of heat capacity effects in biomolecular interactions. <b>2001</b> , 93, 215-30	278
1304	Selective regulation of gene expression by an orthogonal estrogen receptor-ligand pair created by polar-group exchange. <b>2001</b> , 8, 501-10	22
1303	Can an optimization/scoring procedure in ligand-protein docking be employed to probe drug-resistant mutations in proteins?. <b>2001</b> , 19, 560-70	19
1302	Protein flexibility predictions using graph theory. <b>2001</b> , 44, 150-65	565
1301	Solution structure and dynamics of ribonuclease Sa. <b>2001</b> , 44, 200-11	24
1300	Assembly of a tetrameric alpha-helical bundle: computer simulations on an intermediate-resolution protein model. <b>2001</b> , 44, 376-91	69
1299	Hydrogen-bond disruption probability in proteins by a modified self-consistent harmonic approach. <b>2001</b> , 58, 319-28	6
1298	Effects of hydrogen-bond deletion on peptide helices: structural characterization of depsipeptides containing lactic acid. <b>2001</b> , 59, 276-89	22
1297	Effects of fluorescent probe structure on the dynamics at cysteine-34 within bovine serum albumin: evidence for probe-dependent modulation of the cybotactic region. <b>2001</b> , 59, 502-11	10
1296	A DSC study on the effects of various maltodextrins and sucrose on protein changes in frozen-stored minced blue whiting muscle. <b>2001</b> , 81, 377-384	20

1295	Quantitative comparison of the ability of hydropathy scales to recognize surface beta-strands in proteins. <b>2001</b> , 42, 243-55	49
1294	Entropy calculations on a reversibly folding peptide: changes in solute free energy cannot explain folding behavior. <b>2001</b> , 43, 45-56	85
1293	Ab initio protein structure prediction using physicochemical potentials and a simplified off-lattice model. <b>2001</b> , 43, 186-202	41
1292	Novel features of the interpolymer self-organisation behaviour investigated using covalently linked protoporphyrin IX as fluorescent probe in the macromolecules. <b>2001</b> , 37, 2207-2211	6
1291	Peptide analysis by rapid, orthogonal technologies with high separation selectivities and sensitivities. <b>2001</b> , 29, 159-78	44
1290	Use of surface area computations to describe atom-atom interactions. <b>2001</b> , 15, 521-32	6
1289	Implicit solvation in the self-consistent mean field theory method: sidechain modelling and prediction of folding free energies of protein mutants. <b>2001</b> , 15, 721-40	15
1288	The role of solvent in protein folding and in aggregation. <b>2001</b> , 27, 133-45	28
1287	Modeling hydration water and its role in polymer folding. <b>2001</b> , 27, 243-56	3
1286	Hydrogen-bonding classes in proteins and their contribution to the unfolding reaction. <b>2001</b> , 10, 2075-82	37
1285	NMR of hydrogen bonding in cold-shock protein A and an analysis of the influence of crystallographic resolution on comparisons of hydrogen bond lengths. <b>2001</b> , 10, 1856-68	32
1284	Disulfide bond effects on protein stability: designed variants of Cucurbita maxima trypsin inhibitor-V. <b>2001</b> , 10, 149-60	69
1283	Influence of Glu-376> Gln mutation on enthalpy and heat capacity changes for the binding of slightly altered ligands to medium chain acyl-CoA dehydrogenase. <b>2001</b> , 10, 1822-34	11
1282	A field guide to foldamers. <b>2001</b> , 101, 3893-4012	2004
1281	Purification and conformational properties of a human interferon alpha2b produced in Escherichia coli. <b>2001</b> , 33, 173-82	29
1280	New insights into the thermostability of bacterial ferredoxins: high-resolution crystal structure of the seven-iron ferredoxin from Thermus thermophilus. <b>2001</b> , 6, 663-74	31
1279	Protein flexibility and dynamics using constraint theory. <b>2001</b> , 19, 60-9	103
1278	To charge or not to charge?. <b>2001</b> , 19, 132-5	185

The interrelationships of side-chain and main-chain conformations in proteins. <b>2001</b> , 76, 1-102		168
1276 Predicting properties of intrinsically unstructured proteins. <b>2001</b> , 76, 131-73		59
1275 Structural determinants of mini-protein stability. <b>2001</b> , 29, 16-20		5
Length-dependent stability and strand length limits in antiparallel beta -sheet secondary structure. <b>2001</b> , 98, 12015-20		121
Stabilization of a fibronectin type III domain by the removal of unfavorable electrostatic interactions on the protein surface. <i>Biochemistry</i> , <b>2001</b> , 40, 10326-33	3.2	55
1272 Protein threading by learning. <b>2001</b> , 98, 14350-5		24
The plug domain of FepA, a TonB-dependent transport protein from Escherichia coli, binds its siderophore in the absence of the transmembrane barrel domain. <b>2001</b> , 98, 10676-81		57
1270 Temperature adaptation of enzymes: lessons from laboratory evolution. <b>2000</b> , 55, 161-225		118
1269 Capture of a dimeric intermediate during transthyretin amyloid formation. <b>2001</b> , 276, 39592-9		38
1268 How membranes shape protein structure. <b>2001</b> , 276, 32395-8		255
Analysis of a conserved hydrophobic pocket important for the thermostability of Bacillus pumilus chloramphenicol acetyltransferase (CAT-86). <b>2001</b> , 14, 161-6		6
Are the parameters of various stabilization factors estimated from mutant human lysozymes compatible with other proteins?. <b>2001</b> , 14, 127-34		39
A new scale for side-chain contribution to protein stability based on the empirical stability analysis		39
of mutant proteins. <b>2001</b> , 14, 525-8		
		59
of mutant proteins. <b>2001</b> , 14, 525-8  Osmolytes stabilize ribonuclease S by stabilizing its fragments S protein and S peptide to compact		59 15
of mutant proteins. <b>2001</b> , 14, 525-8  Osmolytes stabilize ribonuclease S by stabilizing its fragments S protein and S peptide to compact folding-competent states. <b>2001</b> , 276, 28789-98		
of mutant proteins. <b>2001</b> , 14, 525-8  Osmolytes stabilize ribonuclease S by stabilizing its fragments S protein and S peptide to compact folding-competent states. <b>2001</b> , 276, 28789-98  A minimalist model protein with multiple folding funnels. <b>2001</b> , 98, 9074-9		15

1259	Molecular mimetics of Neisseria meningitidis serogroup B polysaccharide. <b>2001</b> , 20, 201-20	23
1258	Stabilization of protein structure. <b>2001</b> , 168, 1-16	10
1257	Statistical mechanics of solvophobic aggregation: Additive and cooperative effects. <b>2001</b> , 115, 3424-3431	16
1256	Sequence rotation in N-dimensional space and the folding of hydrophobic protein models: Surpassing the diagonal unfolded state approximation. <b>2001</b> , 114, 570	7
1255	Thermodynamic implications of confinement for a waterlike fluid. <b>2001</b> , 114, 2401-2418	137
1254	Cold-Adapted Enzymes. <b>2001</b> , 177-196	5
1253	Evolution of functional model proteins. <b>2001</b> , 115, 1935-1942	30
1252	Model for the hydration of nonpolar compounds and polymers. <b>2001</b> , 64, 051805	5
1251	Anti-cooperativity in hydrophobic interactions: A simulation study of spatial dependence of three-body effects and beyond. <b>2001</b> , 115, 1414-1421	42
1250	Thermodynamically important contacts in folding of model proteins. <b>2001</b> , 63, 032901	8
1249	Folding simulations of a three-dimensional protein model with a nonspecific hydrophobic energy function. <b>2001</b> , 64, 011912	11
1248	Quantifying the accessible surface area of protein residues in their local environment. <b>2002</b> , 15, 659-67	90
1247	Statistical geometry of packing defects of lattice chain polymer from enumeration and sequential Monte Carlo method. <b>2002</b> , 117, 3511-3521	36
1246	Grouping of residues based on their contact interactions. <b>2002</b> , 65, 041911	11
1245	A study of water water interactions in hydrophobic association by a molecular dynamics simulation with an optimized umbrella sampling method. <b>2002</b> , 116, 6725-6730	14
1244	Influence of the hydrophobic face width on the degree of association of coiledfloil proteins. <b>2002</b> , 117, 10321-10328	3
1243	A first-order transition in the charge-induced conformational changes of polymers. <b>2002</b> , 116, 9964-9974	5
1242	Protein unfolding: rigidity lost. <b>2002</b> , 99, 3540-5	227

Roles of mutation and recombination in the evolution of protein thermodynamics. <b>2002</b> , 99, 10382-7	56
Role of interfacial hydrophobic residues in the stabilization of the leucine zipper structures of the transcription factors c-Fos and c-Jun. <b>2002</b> , 277, 23-31	31
1239 FlgM gains structure in living cells. <b>2002</b> , 99, 12681-4	265
Structure and stability of an acidic fibroblast growth factor from Notophthalmus viridescens. <b>2002</b> , 277, 46424-32	22
Helicogenicity of solvents in the conformational equilibrium of oligo(m-phenylene ethynylene)s: implications for foldamer research. <b>2002</b> , 99, 5053-7	116
1236 Toward predicting protein topology: an approach to identifying beta hairpins. <b>2002</b> , 99, 11157-62	41
An alanine-zipper structure determined by long range intermolecular interactions. <b>2002</b> , 277, 48708-13	14
1234 Key interactions in neocarzinostatin, a protein of the immunoglobulin fold family. <b>2002</b> , 15, 861-9	9
A procedure for detection and quantitation of cavity volumes proteins. Application to measure the strength of the hydrophobic driving force in protein folding. <b>2002</b> , 277, 31345-53	41
Recent Advances in the Description of the Structure of Water, the Hydrophobic Effect, and the Like-Dissolves-Like Rule. <b>2002</b> , 59-90	1
The human complement regulator factor H binds pneumococcal surface protein PspC via short consensus repeats 13 to 15. <b>2002</b> , 70, 5604-11	76
1230 The Early Stage of a Hairpin Folding: The Role of Water Molecules. <b>2002</b> , 49, 783-789	1
1229 Flexible and Rigid Regions in Proteins. <b>2002</b> , 357-384	12
1228 Properties of Extremophilic Enzymes and Their Importance in Food Science and Technology. <b>2002</b> ,	
Structural bioinformatics: methods, concepts and applications to blood coagulation proteins. <b>2002</b> , 3, 341-64	16
1226 Structural features and dynamics of protein unfolding. <b>2002</b> , 19, 7-16	
1225 Peptide pinwheels. <b>2002</b> , 124, 1154-5	16
Stress-induced aggregation profiles of GST-alpha-synuclein fusion proteins: role of the C-terminal acidic tail of alpha-synuclein in protein thermosolubility and stability. <i>Biochemistry</i> , <b>2002</b> , 41, 4137-46	.2 46

1223	A Simple Statistical Mechanical Model of Water. <b>2002</b> , 106, 11829-11842		56
1222	Enthalpy and Entropy Decomposition of Free-Energy Changes for Side-Chain Conformations of Aspartic Acid and Asparagine in Acidic, Neutral, and Basic Aqueous Solutions. <b>2002</b> , 106, 12336-12343		23
1221	Exploring Structure and Energetics of a Helix-Forming Oligomer by Molecular Modeling and Molecular Dynamics Simulation Methods: Dynamics of Water in a Hydrophobic Nanotube. <b>2002</b> , 106, 11343-11350		7
1220	Noncovalent Interactions between Unsolvated Peptides 2002, 106, 9655-9664		28
1219	Contribution of hydrogen bonding to protein stability estimated from isotope effects. <i>Biochemistry</i> , <b>2002</b> , 41, 2120-9	3.2	43
1218	pi-Ligands for generating transition metal-peptide complexes: coordination of amino acid derivatives to tungsten utilizing alkyne ligands. <b>2002</b> , 4, 2917-20		17
1217	Mechanism of formation of a productive molten globule form of barstar. <i>Biochemistry</i> , <b>2002</b> , 41, 1710-6	3.2	50
1216	Nonlinear signal analysis methods in the elucidation of protein sequence-structure relationships. <b>2002</b> , 102, 1471-92		93
1215	Differences between the Sequential Collapse Folding Pathways of Apoleghemoglobin and Apomyoglobin. <b>2002</b> , 106, 4818-4822		7
1214	The roles of coenzyme A in the pyruvate:ferredoxin oxidoreductase reaction mechanism: rate enhancement of electron transfer from a radical intermediate to an iron-sulfur cluster. <i>Biochemistry</i> , <b>2002</b> , 41, 9921-37	3.2	47
1213	Binding Behavior of Crystalline and Noncrystalline Phases: Evaluation of the Enthalpic and Entropic Contributions to the Separation Selectivity of Nonpolar Solutes with a Novel Chromatographic Sorbent. <b>2002</b> , 106, 11936-11950		26
1212	Quasichemical Lattice Fluid Model for Water and Hydrophobic Solvation. <b>2002</b> , 106, 12282-12290		11
1211	Maximal stabilities of reversible two-state proteins. <i>Biochemistry</i> , <b>2002</b> , 41, 5359-74	3.2	79
1210	Protein stabilization by urea and guanidine hydrochloride. <i>Biochemistry</i> , <b>2002</b> , 41, 13386-94	3.2	131
1209	Structures of apolipoprotein A-II and a lipid-surrogate complex provide insights into apolipoprotein-lipid interactions. <i>Biochemistry</i> , <b>2002</b> , 41, 11681-91	3.2	31
1208	A View of the Hydrophobic Effect. <b>2002</b> , 106, 521-533		696
1207	Understanding protein folding with energy landscape theory. Part I: Basic concepts. <b>2002</b> , 35, 111-67		163
1206	Hydrophobic effects and modeling of biophysical aqueous solution interfaces. <b>2002</b> , 102, 2671-92		333

1205	Protein formulation and fill-finish operations. <b>2002</b> , 8, 55-84		65
1204	Lattice polymers with hydrogen bondlike interactions. <b>2002</b> , 117, 10360-10369		13
1203	Bethe approximation for a hydrophobic-polar random copolymer. <b>2002</b> , 66, 031803		5
1202	Hydrophobic/hydrophilic solvation: inferences from Monte Carlo simulations and experiments. <b>2002</b> , 100, 2773-2792		37
1201	Reversible stretching of random heteropolymers. <b>2002</b> , 65, 056110		20
1200	Lyophilization and the Thermostability of Vaccines. <b>2002</b> , 1, 91-104		43
1199	Carboxylates stacked over aromatic rings promote salt bridge formation in water. <b>2002</b> , 124, 442-9		54
1198	Elucidation of factors responsible for enhanced thermal stability of proteins: a structural genomics based study. <i>Biochemistry</i> , <b>2002</b> , 41, 8152-61	3.2	217
1197	Enthalpy and entropy contributions to the pressure dependence of hydrophobic interactions. <b>2002</b> , 116, 2480-2486		79
1196	Rational Design of Stable Protein Formulations. 2002,		28
1196 1195	Rational Design of Stable Protein Formulations. 2002,  Amino Acid Side-chain Hydrophobicity. 2002,		28
1195			
1195	Amino Acid Side-chain Hydrophobicity. <b>2002</b> ,		6
1195	Amino Acid Side-chain Hydrophobicity. 2002,  Mechanism of fast protein folding. 2002, 71, 783-815	3.2	6
1195 1194 1193	Amino Acid Side-chain Hydrophobicity. 2002,  Mechanism of fast protein folding. 2002, 71, 783-815  Mechanical Response of Random Heteropolymers. 2002, 35, 4429-4436  Structural evidence for a dominant role of nonpolar interactions in the binding of a	3.2	6 106 16
1195 1194 1193 1192 1191	Amino Acid Side-chain Hydrophobicity. 2002,  Mechanism of fast protein folding. 2002, 71, 783-815  Mechanical Response of Random Heteropolymers. 2002, 35, 4429-4436  Structural evidence for a dominant role of nonpolar interactions in the binding of a transport/chemosensory receptor to its highly polar ligands. <i>Biochemistry</i> , 2002, 41, 706-12  Size and temperature dependence of hydrocarbon solubility in concentrated aqueous solutions of	3.2	6 106 16
1195 1194 1193 1192 1191	Amino Acid Side-chain Hydrophobicity. 2002,  Mechanism of fast protein folding. 2002, 71, 783-815  Mechanical Response of Random Heteropolymers. 2002, 35, 4429-4436  Structural evidence for a dominant role of nonpolar interactions in the binding of a transport/chemosensory receptor to its highly polar ligands. <i>Biochemistry</i> , 2002, 41, 706-12  Size and temperature dependence of hydrocarbon solubility in concentrated aqueous solutions of urea and guanidine hydrochloride. 2002, 80, 388-400	3.2	6 106 16 60

1187	New stochastic strategy to analyze helix folding. <b>2002</b> , 82, 1123-32	35
1186	Proteins wriggle. <b>2002</b> , 82, 2665-70	17
1185	Redox properties of Met(35) in neurotoxic beta-amyloid peptide. A molecular modeling study. <b>2002</b> , 15, 408-18	59
1184	On the dissection of the unfolding reaction by the dissolution thermodynamics of N-alkyl amides. <b>2002</b> , 31, 103-9	3
1183	How ions affect the structure of water. <b>2002</b> , 124, 12302-11	569
1182	Detecting Native Protein Folds among Large Decoy Sets with the OPLS All-Atom Potential and the Surface Generalized Born Solvent Model. <b>2002</b> , 459-486	2
1181	. 2002,	8
1180	Compressibility of protein transitions. <b>2002</b> , 1595, 48-70	131
1179	Revisiting volume changes in pressure-induced protein unfolding. <b>2002</b> , 1595, 201-9	342
1178	Reductive unfolding and oxidative refolding of a Bowman-Birk inhibitor from horsegram seeds (Dolichos biflorus): evidence for "hyperreactive" disulfide bonds and rate-limiting nature of disulfide isomerization in folding. <b>2002</b> , 1597, 280-91	47
1177	Rational design of a more stable penicillin G acylase against organic cosolvent. <b>2002</b> , 18, 285-290	21
1176	Molekulare Chaperone: zellulæ Maschinen fādie Proteinfaltung. <b>2002</b> , 114, 1142-1158	12
1175	AnsEze zur Beschreibung und Vorhersage der BindungsaffinitEniedermolekularer Liganden an makromolekulare Rezeptoren. <b>2002</b> , 114, 2764-2798	34
1174	Molecular chaperonescellular machines for protein folding. <b>2002</b> , 41, 1098-113	322
1173	Approaches to the description and prediction of the binding affinity of small-molecule ligands to macromolecular receptors. <b>2002</b> , 41, 2644-76	595
1172	Importance of mutant position in Ramachandran plot for predicting protein stability of surface mutations. <b>2002</b> , 64, 210-20	38
1171	Application of a chaperone-based refolding method to two- and three-dimensional off-lattice protein models. <b>2002</b> , 64, 146-60	15
1170	Extreme stability of helices formed by water-soluble poly-N-substituted glycines (polypeptoids) with alpha-chiral side chains. <b>2002</b> , 63, 12-20	132

# (2002-2002)

1169	The SGB/NP hydration free energy model based on the surface generalized born solvent reaction field and novel nonpolar hydration free energy estimators. <b>2002</b> , 23, 517-29	212
1168	Origins of gene, genetic code, protein and life: comprehensive view of life systems from a GNC-SNS primitive genetic code hypothesis. <b>2002</b> , 27, 165-86	47
1167	Structural characterization of monomeric folding intermediates of recombinant human macrophage-colony stimulating factor beta (rhM-CSFbeta) by chemical trapping, chromatographic separation and mass spectrometric peptide mapping. <b>2002</b> , 782, 393-404	6
1166	Thermostabilization of cellulosomal endoglucanase EngB from Clostridium cellulovorans by in vitro DNA recombination with non-cellulosomal endoglucanase EngD. <b>2002</b> , 45, 617-26	60
1165	Stepwise adaptations of citrate synthase to survival at life's extremes. From psychrophile to hyperthermophile. <b>2002</b> , 269, 6250-60	57
1164	The metal site as a template for the metalloprotein structure formation. <b>2002</b> , 88, 77-86	22
1163	Methinks it is like a folding curve. <b>2002</b> , 101-102, 167-71	11
1162	Entropy calculations on the molten globule state of a protein: side-chain entropies of alpha-lactalbumin. <b>2002</b> , 46, 215-24	55
1161	Can cooperativity in hydrophobic association be reproduced correctly by implicit solvation models?*. <b>2002</b> , 88, 41-55	36
1160	Exploratory studies of ab initio protein structure prediction: multiple copy simulated annealing, AMBER energy functions, and a generalized born/solvent accessibility solvation model. <b>2002</b> , 46, 128-46	57
1159	Identifying proteins of high designability via surface-exposure patterns. 2002, 47, 295-304	11
1158	Interhelical hydrogen bonds and spatial motifs in membrane proteins: polar clamps and serine zippers. <b>2002</b> , 47, 209-18	141
1157	Comparative structural analysis of psychrophilic and meso- and thermophilic enzymes. <b>2002</b> , 47, 236-49	134
1156	Ab initio prediction of protein structure using LINUS. <b>2002</b> , 47, 489-95	55
1155	Anti-cooperativity and cooperativity in hydrophobic interactions: Three-body free energy landscapes and comparison with implicit-solvent potential functions for proteins. <b>2002</b> , 48, 15-30	77
1154	Non-native interactions, effective contact order, and protein folding: a mutational investigation with the energetically frustrated hydrophobic model. <b>2002</b> , 49, 167-80	26
1153	Distinguishing native conformations of proteins from decoys with an effective free energy estimator based on the OPLS all-atom force field and the Surface Generalized Born solvent model. <b>2002</b> , 48, 404-22	117
1152	Stability scale and atomic solvation parameters extracted from 1023 mutation experiments. <b>2002</b> , 49, 483-92	68

1151	Hydrophobic core packing in the SH3 domain folding transition state. <b>2002</b> , 9, 126-30	135
1150	Engineering selectivity and discrimination into ligand-receptor interfaces. <b>2002</b> , 9, 17-23	37
1149	Toward the synthesis of artificial proteins: the discovery of an amphiphilic helical peptoid assembly. <b>2002</b> , 9, 647-54	103
1148	Analysis of the pi-pi stacking interactions between the aminoglycoside antibiotic kinase APH(3')-IIIa and its nucleotide ligands. <b>2002</b> , 9, 1209-17	69
1147	Folding pathway of apo-metallothionein induced by Zn2+, Cd2+ and Co2+. <b>2002</b> , 88, 144-52	76
1146	Salt effects on the interaction of an amphiphilic model molecule with immobilized phosphatidylcholine monolayers. <b>2002</b> , 977, 185-92	6
1145	Design of an optimal Chebyshev-expanded discrimination function for globular proteins. <b>2002</b> , 11, 2010-21	20
1144	An improved hydrogen bond potential: impact on medium resolution protein structures. <b>2002</b> , 11, 1415-23	99
1143	Reversible denaturation behavior of immobilized glucose oxidase. <b>2002</b> , 102-103, 471-80	7
1142	Physical stability of proteins in aqueous solution: mechanism and driving forces in nonnative protein aggregation. <b>2003</b> , 20, 1325-36	1032
1141	Contribution of the dimeric state to the thermal stability of the flavoprotein D-amino acid oxidase. <b>2003</b> , 12, 1018-29	38
1140	Equilibrium and kinetic studies on folding of canine milk lysozyme. <b>2003</b> , 12, 609-19	11
1139	Folding specificity induced by loop stiffness. <b>2003</b> , 12, 1473-82	8
1138	Recognition of adenosine triphosphate binding sites using parallel cascade system identification. <b>2003</b> , 31, 462-70	5
1137	Mechanisms of aggregate formation and carbohydrate excipient stabilization of lyophilized humanized monoclonal antibody formulations. <b>2003</b> , 5, E10	118
1136	Enzymic, spectroscopic and calorimetric studies of a recombinant dextranase expressed in Pichia pastoris. <b>2003</b> , 38, 211-21	5
1135	Possible mechanism for cold denaturation of proteins at high pressure. <b>2003</b> , 91, 138103	85
1134	Probing folding free energy landscape of small proteins through minimalistic models: Folding of HP-36 and 軸myloid. <b>2003</b> , 115, 621-636	3

1133	Theoretical studies of the conformational behavior of chain molecules containing polar groups: simulations of a poly(vinylidene fluoride) model. <b>2003</b> , 9, 379-89	6
1132	Protein thermostability: structure-based difference of residual properties between thermophilic and mesophilic proteins. <b>2003</b> , 26, 257-264	20
1131	BindungsaffinitEen von Wirt-Gast-, Protein-Ligand- und Protein-Bergangszustands-Komplexen. <b>2003</b> , 115, 5020-5046	71
1130	Binding and catalysis: a thermodynamic study on a catalytic antibody system. <b>2003</b> , 4, 537-40	5
1129	Binding affinities of host-guest, protein-ligand, and protein-transition-state complexes. <b>2003</b> , 42, 4872-97	442
1128	On the nature of the forces controlling selectivity in the high performance capillary electrochromatographic separation of peptides. <b>2003</b> , 71, 429-53	20
1127	Spectroscopic investigation on gel-forming beta-sheet assemblage of peptide derivatives. <b>2003</b> , 70, 346-54	40
1126	Hydrophobic tendencies of polar groups as a major force in molecular recognition. 2003, 70, 492-6	25
1125	Local sequence information in cellular retinoic acid-binding protein I: specific residue roles in beta-turns. <b>2003</b> , 71, 638-51	13
1124	Raman OD stretching spectral differences between aqueous and alcoholic tetraalkylammonium chloride solutions. <b>2003</b> , 379, 216-222	9
1123	Relating contact order to the rate of cooperative collapse in the sequential collapse model for protein folding pathways. <b>2003</b> , 376, 612-617	6
1122	Potentiometric investigation of acid dissociation and anionic homoconjugation equilibria of substituted phenols in dimethyl sulfoxide. <b>2003</b> , 35, 1645-1655	10
1121	Determination of minor conformational changes of a doxorubicin-peptide conjugate under chromatographic conditions. <b>2003</b> , 983, 73-82	5
1120	Evaluation of methods for measuring amino acid hydrophobicities and interactions. 2003, 1000, 637-55	84
1119	Block structure and stability of the genetic code. <b>2003</b> , 222, 177-88	24
1118	Approximate protein folding in the HP side chain model on extended cubic lattices. 2003, 127, 163-177	10
1117	Hydration water dynamics of a completely hydrophobic oligopeptide. 2003, 292, 235-245	31
1116	Volumetric effects of ionization of amino and carboxyl termini of alpha,omega-aminocarboxylic acids. <b>2003</b> , 104, 21-36	16

1115	Effect of trifluoroethanol on the conformational stability of a hyperthermophilic esterase: a CD study. <b>2003</b> , 104, 407-15	10
1114	Entropy convergence in hydrophobic hydration: a scaled particle theory analysis. <b>2003</b> , 105, 241-50	46
1113	Hydration of krypton and consideration of clathrate models of hydrophobic effects from the perspective of quasi-chemical theory. <b>2003</b> , 105, 323-38	45
1112	Analysis of thermal hysteresis protein hydration using the random network model. <b>2003</b> , 105, 195-209	46
1111	Hydrophobic hydrophilic phenomena in biochemical processes. <b>2003</b> , 105, 183-93	23
1110	A simple analytical model of water. <b>2003</b> , 105, 449-59	21
1109	Long proteins with unique optimal foldings in the H-P model. <b>2003</b> , 25, 139-159	10
1108	Forming process of folded drop surface covered by human serum albumin, <code>#actoglobulin</code> and <code>#casein</code> , respectively, at the chloroform/water interface. <b>2003</b> , 215, 25-32	23
1107	Molecular dynamics simulation reveals a surface salt bridge forming a kinetic trap in unfolding of truncated Staphylococcal nuclease. <b>2003</b> , 50, 507-15	23
1106	Thermal unfolding simulations of apo-calmodulin using leap-dynamics. <b>2003</b> , 50, 648-56	16
1105	Non-intertwined binary patterns of hydrophobic/nonhydrophobic amino acids are considerably better markers of regular secondary structures than nonconstrained patterns. <b>2003</b> , 51, 236-44	19
1104	Contact order dependent protein folding rates: kinetic consequences of a cooperative interplay between favorable nonlocal interactions and local conformational preferences. <b>2003</b> , 52, 524-33	68
1103	Simple two-state protein folding kinetics requires near-levinthal thermodynamic cooperativity. <b>2003</b> , 52, 510-23	61
1102	Phenomenological similarities between protein denaturation and small-molecule dissolution: Insights into the mechanism driving the thermal resistance of globular proteins. <b>2004</b> , 54, 323-32	10
1101	Quantifying the effect of burial of amino acid residues on protein stability. <b>2004</b> , 54, 315-22	96
1100	Mimicry of dimerization by synthetic peptides designed to target homologous regions of proteins. <b>2003</b> , 3, 317-24	3
1099	Factors influencing the thermal stability of buried protein mutants. 2003, 44, 4061-4066	8
1098	Effect of phase ratio on van't Hoff analysis in reversed-phase liquid chromatography, and phase-ratio-independent estimation of transfer enthalpy. <b>2003</b> , 1003, 101-11	151

Aggregation kinetics of bovine serum albumin studied by FTIR spectroscopy and light scattering. **2003**,

The Structure of Dilute Clusters of Methane and Water by ab Initio Quantum Mechanical Calculations. <b>2003</b> , 107, 2289-2295	17
Temperature range of thermodynamic stability for the native state of reversible two-state proteins. <i>Biochemistry</i> , <b>2003</b> , 42, 4864-73	3.2 39
1094 Hydrophobic Interaction Model for Upper and Lower Critical Solution Temperatures. <b>2003</b> , 36, 5845-5853	3 35
Study of Pair Contact Formation among Hydrophobic Residues in a Model HP-36 Protein: Relationship between Contact Order Parameter and Rate of Folding and Collapse. <b>2003</b> , 107, 11768-117	73 <sup>10</sup>
Stabilization of beta-hairpin peptides by salt bridges: role of preorganization in the energetic contribution of weak interactions. <b>2003</b> , 125, 9038-47	89
1091 Helix-turn-helix motifs in unsolvated peptides. <b>2003</b> , 125, 7186-7	24
Noncovalent Interactions between Unsolvated Peptides: Dissociation of Helical and Globular Peptide Complexes. <b>2003</b> , 107, 14529-14536	15
Water-Mediated Three-Particle Interactions between Hydrophobic Solutes: Size, Pressure, and Salt Effects. <b>2003</b> , 107, 612-617	51
Comparative analysis of two different amide-to-ester bond mutations in the beta-sheet of 4-oxalocrotonate tautomerase. <i>Biochemistry</i> , <b>2003</b> , 42, 6620-30	3.2 15
Molecular Simulation Study of the Potentials of Mean Force for the Interactions between Models of Like-Charged and between Charged and Nonpolar Amino Acid Side Chains in Water. <b>2003</b> , 107, 13496-	-13504 <sup>31</sup>
Determination of the Potentials of Mean Force for Rotation about CEEVirtual Bonds in 1086 Polypeptides from the ab Initio Energy Surfaces of Terminally Blocked Glycine, Alanine, and Proline <b>2003</b> , 107, 8035-8046	58
1085 Cages of Water Coordinating Kr in Aqueous Solution. <b>2003</b> , 107, 11267-11270	9
$_{1084}$ The jigsaw puzzle model: search for conformational specificity in protein interiors. <b>2003</b> , 333, 211-26	31
The relationship between conservation, thermodynamic stability, and function in the SH3 domain hydrophobic core. <b>2003</b> , 333, 641-55	56
Kinetics of Irreversible Protein Aggregation: Analysis of Extended Lumry <b>E</b> yring Models and Implications for Predicting Protein Shelf Life. <b>2003</b> , 107, 1194-1207	132
1081 Heat Capacity Change of the Hydrophobic Interaction. <b>2003</b> , 107, 9853-9857	34
$_{ m 1080}$ Structural details, pathways, and energetics of unfolding apomyoglobin. <b>2003</b> , 325, 555-67	50

1079	Computational simulation of the statistical properties of unfolded proteins. 2003, 326, 1615-33	107
1078	Testing the relationship between foldability and the early folding events of dihydrofolate reductase from Escherichia coli. <b>2003</b> , 328, 273-88	25
1077	Prudent modeling of core polar residues in computational protein design. 2003, 329, 611-22	38
1076	Insights into protein-protein binding by binding free energy calculation and free energy decomposition for the Ras-Raf and Ras-RalGDS complexes. <b>2003</b> , 330, 891-913	924
1075	Structures of thermophilic and mesophilic adenylate kinases from the genus Methanococcus. <b>2003</b> , 330, 1087-99	56
1074	A large scale test of computational protein design: folding and stability of nine completely redesigned globular proteins. <b>2003</b> , 332, 449-60	256
1073	Thermodynamic analysis of the contributions of the copper ion and the disulfide bridge to azurin stability: synergism among multiple depletions. <b>2003</b> , 414, 121-7	9
1072	Structurally homologous all beta-barrel proteins adopt different mechanisms of folding. <b>2003</b> , 85, 459-72	15
1071	The hydrophobic effect. <b>2003</b> , 5, 3085	235
1070	Cooperativity in Amide Hydrogen Bonding Chains. Relation between Energy, Position, and H-Bond Chain Length in Peptide and Protein Folding Models. <b>2003</b> , 107, 10389-10395	145
1069	Effect of Temperature on Hydrophobic Interaction between Proteins and Hydrophobic Adsorbents: Studies by Isothermal Titration Calorimetry and the van't Hoff Equation. <b>2003</b> , 19, 9395-9403	108
1068	Three-dimensional functional model proteins: Structure function and evolution. <b>2003</b> , 119, 3453-3460	19
1067	NCI: A server to identify non-canonical interactions in protein structures. <b>2003</b> , 31, 3345-8	56
1066	Ab initio study of CdEhiol complexes: application to the modelling of the metallothionein active site. <b>2003</b> , 5, 3762-3767	21
1065	The contribution of polar group burial to protein stability is strongly context-dependent. <b>2003</b> , 278, 31790-5	53
1064	In search of the energetic role of peptide hydrogen bonds. <b>2003</b> , 278, 17581-8	102
1063	Correlation between rate of folding, energy landscape, and topology in the folding of a model protein HP-36. <b>2003</b> , 118, 4733-4747	44
1062	Compact phases of polymers with hydrogen bonding. <b>2003</b> , 67, 021805	7

1	.061	Network rigidity at finite temperature: relationships between thermodynamic stability, the nonadditivity of entropy, and cooperativity in molecular systems. <b>2003</b> , 68, 061109	41
1	.060	Computer simulation of the hydrophobic hydration of convex surfaces of large radius. <b>2003</b> , 101, 3121-3128	8
1	.059	Structural basis for thermostability of beta-glycosidase from the thermophilic eubacterium Thermus nonproteolyticus HG102. <b>2003</b> , 185, 4248-55	21
1	.058	Detection of an intermediate during unfolding of bacterial cell division protein FtsZ: loss of functional properties precedes the global unfolding of FtsZ. <b>2003</b> , 278, 21336-43	33
1	.057	Identification of a COOH-terminal segment involved in maturation and stability of human ether-a-go-go-related gene potassium channels. <b>2003</b> , 278, 40105-12	45
1	.056	Crystal structure of D-Hydantoinase from Burkholderia pickettii at a resolution of 2.7 Angstroms: insights into the molecular basis of enzyme thermostability. <b>2003</b> , 185, 4038-49	63
1	.055	Conservation of Hydrophobic and Hydrophilic Residues in Four-Helix Bundle. <b>2003</b> , 20, 1883-1886	7
1	.054	Protein Folding. 2003,	
1	.053	. 2003,	24
1	.052	Protein folding: search for basic physical models. <b>2003</b> , 3, 623-35	3
1	.051	Combinatorial Problems on Strings with Applications to Protein Folding. <b>2004</b> , 369-378	7
1	.050	Hairpin Formation in Polynucleotides: A Simple Folding Problem?. <b>2004</b> , 99-147	1
1	.049	The Kirkwood-Buff theory and the effect of cosolvents on biochemical reactions. <b>2004</b> , 121, 9147-55	95
1	.048	Two-dimensional lattice-fluid model with waterlike anomalies. <b>2004</b> , 69, 061502	23
1	.047	Model study of protein unfolding by interfaces. <b>2004</b> , 69, 021907	16
1	046	A computer simulation study of water drying at the interface of protein chains. <b>2004</b> , 121, 1969-77	9
1	.045	Thermodynamic anomalies in a lattice model of water. <b>2004</b> , 121, 11856-66	26
1	.044	A coarse-grained model and associated lattice Monte Carlo simulation of the coil-helix transition of a homopolypeptide. <b>2004</b> , 120, 3467-74	16

1043	Predicting protein folding pathways. <b>2004</b> , 20 Suppl 1, i386-93	15
1042	Probing the role of tryptophans in Aequorea victoria green fluorescent proteins with an expanded genetic code. <b>2004</b> , 385, 191-202	36
1041	Biomolecular cryocrystallography: structural changes during flash-cooling. <b>2004</b> , 101, 4793-8	153
1040	Ultrafast hydration dynamics in protein unfolding: human serum albumin. <b>2004</b> , 101, 13411-6	107
1039	Water and proteins: a love-hate relationship. <b>2004</b> , 101, 3325-6	134
1038	Close agreement between the orientation dependence of hydrogen bonds observed in protein structures and quantum mechanical calculations. <b>2004</b> , 101, 6946-51	211
1037	MoViES: molecular vibrations evaluation server for analysis of fluctuational dynamics of proteins and nucleic acids. <b>2004</b> , 32, W679-85	13
1036	Elastic coupling of integral membrane protein stability to lipid bilayer forces. <b>2004</b> , 101, 4065-70	196
1035	Disulfide bonds, their stereospecific environment and conservation in protein structures. <b>2004</b> , 17, 795-808	103
1034	Alcohol-mediated error-prone PCR. <b>2004</b> , 23, 789-95	8
1034	Alcohol-mediated error-prone PCR. <b>2004</b> , 23, 789-95  Searching for folded proteins in vitro and in silico. <b>2004</b> , 271, 1615-22	23
1033		
1033	Searching for folded proteins in vitro and in silico. <b>2004</b> , 271, 1615-22  Context-dependent contributions of backbone hydrogen bonding to beta-sheet folding energetics.	23
1033	Searching for folded proteins in vitro and in silico. <b>2004</b> , 271, 1615-22  Context-dependent contributions of backbone hydrogen bonding to beta-sheet folding energetics. <b>2004</b> , 430, 101-5	23
1033	Searching for folded proteins in vitro and in silico. <b>2004</b> , 271, 1615-22  Context-dependent contributions of backbone hydrogen bonding to beta-sheet folding energetics. <b>2004</b> , 430, 101-5  Ageing and vision: structure, stability and function of lens crystallins. <b>2004</b> , 86, 407-85	23 239 627
1033 1032 1031	Searching for folded proteins in vitro and in silico. 2004, 271, 1615-22  Context-dependent contributions of backbone hydrogen bonding to beta-sheet folding energetics. 2004, 430, 101-5  Ageing and vision: structure, stability and function of lens crystallins. 2004, 86, 407-85  Constraint Logic Programming approach to protein structure prediction. 2004, 5, 186  Protein folding, misfolding, and aggregation. Formation of inclusion bodies and aggresomes. 2004,	23 239 627 42
1033 1032 1031 1030	Searching for folded proteins in vitro and in silico. 2004, 271, 1615-22  Context-dependent contributions of backbone hydrogen bonding to beta-sheet folding energetics. 2004, 430, 101-5  Ageing and vision: structure, stability and function of lens crystallins. 2004, 86, 407-85  Constraint Logic Programming approach to protein structure prediction. 2004, 5, 186  Protein folding, misfolding, and aggregation. Formation of inclusion bodies and aggresomes. 2004, 69, 971-84  Defining the minimum size of a hydrophobic cluster in two-stranded alpha-helical coiled-coils:	23 239 627 42

### (2004-2004)

1025	Salt-dependent studies of NADP-dependent isocitrate dehydrogenase from the halophilic archaeon Haloferax volcanii. <b>2004</b> , 8, 377-84	24
1024	Some like it cold: biocatalysis at low temperatures. <b>2004</b> , 28, 25-42	306
1023	Importance of hydrophobic cluster formation through long-range contacts in the folding transition state of two-state proteins. <b>2004</b> , 55, 1023-35	14
1022	Strategy for supplementing structure calculations using limited data with hydrophobic distance restraints. <b>2004</b> , 56, 117-29	3
1021	Designing proteins from the inside out. <b>2004</b> , 56, 1-10	31
1020	Fast accurate evaluation of protein solvent exposure. <b>2004</b> , 57, 565-76	22
1019	Kinetics of folding and unfolding of goat alpha-lactalbumin. <b>2004</b> , 57, 345-56	14
1018	The hairpin ribozyme. <b>2004</b> , 73, 71-8	54
1017	NMR solution structure of a highly stable de novo heterodimeric coiled-coil. <b>2004</b> , 75, 367-75	60
1016	AGBNP: an analytic implicit solvent model suitable for molecular dynamics simulations and high-resolution modeling. <b>2004</b> , 25, 479-99	294
1015	Protein stabilization by salt bridges: concepts, experimental approaches and clarification of some misunderstandings. <b>2004</b> , 17, 1-16	212
1014	Coiled coil domains: stability, specificity, and biological implications. <b>2004</b> , 5, 170-6	521
1013	The polar hydrophobicity of fluorinated compounds. <b>2004</b> , 5, 622-7	343
1012	Chiral Molecular Self-Assembly. <b>2004</b> , 281-372	14
1011	Analysis of protein folding and function using backbone modified proteins. <b>2004</b> , 32, 438-49	38
1010	Hydrophobic interaction chromatography correctly refolding proteins assisted by glycerol and urea gradients. <b>2004</b> , 1061, 193-9	38
1009	How a repulsive charge distribution becomes attractive and stabilized by a polarizable protein dielectric. <b>2004</b> , 668, 65-73	4
1008	Mesoscopic analysis of conformational and entropic contributions to nonspecific adsorption of HP copolymer chains using dynamic Monte Carlo simulations. <b>2004</b> , 275, 458-69	11

1007	Physics of protein folding. 2004, 1, 23-56	79
1006	Energetics of protein thermodynamic cooperativity: contributions of local and nonlocal interactions. <b>2004</b> , 45, 623-632	20
1005	Studies on interpolymer self-organisation behaviour of protoporphyrin IX bound poly(carboxylic acid)s with complimentary polymers by means of fluorescence techniques. <b>2004</b> , 40, 2291-2303	15
1004	Exploring the effects of hydrogen bonding and hydrophobic interactions on the foldability and cooperativity of helical proteins using a simplified atomic model. <b>2004</b> , 307, 187-199	20
1003	Complex formation in aqueous medium of partially hydrolysed oat cereal proteins with sodium stearoyl-2 lactylate (SSL) lipid surfactant and implications for bile acids activity. <b>2004</b> , 35, 175-84	17
1002	The hydrophobic effect and the excess free energy of solvation. <b>2004</b> , 392, 456-459	6
1001	Large gain in translational entropy of water is a major driving force in protein folding. <b>2004</b> , 399, 342-348	82
1000	Aggregation kinetics of bovine serum albumin studied by FTIR spectroscopy and light scattering. <b>2004</b> , 107, 175-87	234
999	The non-polar solvent potential of mean force for the dimerization of alanine dipeptide: the role of solute-solvent van der Waals interactions. <b>2004</b> , 109, 251-60	31
998	Proton dependence of tobacco mosaic virus dissociation by pressure. <b>2004</b> , 111, 53-61	23
997	Experiment-guided thermodynamic simulations on reversible two-state proteins: implications for protein thermostability. <b>2004</b> , 111, 235-46	17
996	Sequential Collapse Folding Pathway of Staphylococcal Nuclease: Entropic Activation Barriers to Hydrophobic Collapse of the Protein Core. <b>2004</b> , 108, 8023-8030	2
995	Reversal of negative charges on the surface of Escherichia coli thioredoxin: pockets versus protrusions. <i>Biochemistry</i> , <b>2004</b> , 43, 3835-43	5
994	7 Computational protein design and discovery. <b>2004</b> , 100, 195-236	7
993	Protein hydration dynamics in solution: a critical survey. <b>2004</b> , 359, 1207-23; discussion 1223-4, 1323-8	419
992	Estimating hydration changes upon biomolecular reactions from osmotic stress, high pressure, and preferential hydration experiments. <b>2004</b> , 101, 1195-9	168
991	Interplay of secondary structures and side-chain contacts in the denatured state of BBA1. <b>2004</b> , 121, 2412-21	19
990	Protein structure, stability and solubility in water and other solvents. <b>2004</b> , 359, 1225-34; discussion 1234-5	259

### (2004-2004)

989	<b>2004</b> , 5, 758-67	54
988	Microcapsule assembly of human serum albumin at the liquid/liquid interface by the pendent drop technique. <b>2004</b> , 20, 8401-3	36
987	Single-site mutation and secondary structure stability: an isodesmic reaction approach. The case of unnatural amino acid mutagenesis Ala>Lac. <b>2004</b> , 69, 3250-61	13
986	Elimination of a misfolded folding intermediate by a single point mutation. <i>Biochemistry</i> , <b>2004</b> , 43, 3357-67	38
985	Cause of hydration/dehydration in condensed organic materials: synthesis of hydrophobic pores. <b>2004</b> , 6, 877-80	7
984	A protein folding degree measure and its dependence on crystal packing, protein size, secondary structure, and domain structural class. <b>2004</b> , 44, 1238-50	15
983	Cooperative motions of protein and hydration water molecules: molecular dynamics study of scytalone dehydratase. <b>2004</b> , 126, 13132-9	12
982	Three-body interactions improve the prediction of rate and mechanism in protein folding models. <b>2004</b> , 101, 15088-93	85
981	Fs-21 Peptides Can Form Both Single Helix and Helix Turn Helix. 2004, 108, 7479-7489	34
980	Simulated evolution of emergent chiral structures in polyalanine. <b>2004</b> , 126, 14459-67	26
979	Hydration of enzyme in nonaqueous media is consistent with solvent dependence of its activity. <b>2004</b> , 87, 812-21	200
978	Pressure denaturation of staphylococcal nuclease studied by neutron small-angle scattering and molecular simulation. <b>2004</b> , 87, 3479-92	70
977	Thermodynamics of denaturant-induced unfolding of a protein that exhibits variable two-state denaturation. <i>Biochemistry</i> , <b>2004</b> , 43, 13357-69	64
976	Thermodynamics of core hydrophobicity and packing in the hyperthermophile proteins Sac7d and Sso7d. <i>Biochemistry</i> , <b>2004</b> , 43, 2840-53	32
975	Urea-induced sequential unfolding of fibronectin: a fluorescence spectroscopy and circular dichroism study. <i>Biochemistry</i> , <b>2004</b> , 43, 1724-35	36
974	Reduced amino acid alphabet is sufficient to accurately recognize intrinsically disordered protein. <b>2004</b> , 576, 348-52	102
973	Role of weak interactions in thermal stability of proteins. <b>2004</b> , 325, 1082-9	34
972	Eight-residue Abeta peptides inhibit the aggregation and enzymatic activity of Abeta42. <b>2004</b> , 120, 227-36	24

971	Relation between protein stability, evolution and structure, as probed by carboxylic acid mutations. <b>2004</b> , 336, 313-8	50
970	Can contact potentials reliably predict stability of proteins?. <b>2004</b> , 336, 1223-38	64
969	Estimating the prevalence of protein sequences adopting functional enzyme folds. 2004, 341, 1295-315	36
968	Analysis of anisotropic side-chain packing in proteins and application to high-resolution structure prediction. <b>2004</b> , 342, 651-64	40
967	Water as a conformational editor in protein folding. <b>2004</b> , 343, 1125-33	26
966	Replacement of staphylococcal nuclease hydrophobic core residues with those from thermophilic homologues indicates packing is improved in some thermostable proteins. <b>2004</b> , 344, 271-80	22
965	Binding of phlorizin to the C-terminal loop 13 of the Na(+)/glucose cotransporter does not depend on the [560-608] disulfide bond. <b>2004</b> , 425, 58-64	4
964	Heat Capacity Changes Accompanying Micelle Formation upon Burial of Hydrophobic Tail of Nonionic Surfactants. <b>2004</b> , 108, 19096-19098	27
963	Cooperativity principles in protein folding. <b>2004</b> , 380, 350-79	157
962	Protein thermostability: structure-based difference of amino acid between thermophilic and mesophilic proteins. <b>2004</b> , 111, 269-77	86
961	Entropic Contributions in Cosolvent Binding to Hydrophobic Solutes in Water. 2004, 108, 1056-1064	76
960	Rational design of solution additives for the prevention of protein aggregation. <b>2004</b> , 87, 1631-9	90
959	Nanoscale hydrophobic interaction and nanobubble nucleation. <b>2004</b> , 93, 185701	88
958	On hydrophobicity and conformational specificity in proteins. <b>2004</b> , 86, 23-30	23
957	Conformational conversion of proteins due to mutation. <b>2004</b> , 67, 491-497	4
956	Inverse protein folding in 2D HP model.	
955	The roles of disulphide and non-covalent bonding in the functional properties of heat-induced whey protein gels. <b>2004</b> , 71, 330-9	83
954	Configurational Entropy of Proteins: Covariance Matrix versus Cumulative Distribution Calculations. <b>2004</b> , 51, 1209-1219	3

953	Protein Conformational Transitions as Seen from the Solvent: Magnetic Relaxation Dispersion Studies of Water, Co-solvent, and Denaturant Interactions with Nonnative Proteins. 201-246	3
952	Protein-Protein Docking Methods. <b>2005</b> , 115-146	11
951	Predicting Free Energy Changes of Mutations in Proteins. 343-376	
950	Thermal Unfolding of Proteins Studied by Calorimetry. 70-98	2
949	Pressure-Temperature Phase Diagrams of Proteins. 99-126	8
948	Weak Interactions in Protein Folding: Hydrophobic Free Energy, van der Waals Interactions, Peptide Hydrogen Bonds, and Peptide Solvation. 127-162	4
947	A new amphipathy scale I. Determination of the scale from molecular dynamics data. <b>2005</b> , 1747, 35-46	10
946	Hydration of tetrahydrofuran derived from FTIR spectroscopy. <b>2005</b> , 734, 183-190	33
945	Distinct roles of conventional non-covalent and cation[Interactions in protein stability. 2005, 46, 983-990	15
944	Partition function zeros of the two-dimensional HP model for protein folding. <b>2005</b> , 350, 45-51	17
943	Stochastic strategy to analyze protein folding. <b>2005</b> , 353, 353-364	10
942	Solvent dependent selective alkylation of a bis(sulfonamide) for the synthesis of a DNA-binding chiral polyamine. <b>2005</b> , 46, 2783-2787	6
941	On the hydration heat capacity change of benzene. <b>2005</b> , 116, 137-44	9
940	Binding behaviour and conformational properties of globular proteins in the presence of immobilised non-polar ligands used in reversed-phase liquid chromatography. <b>2005</b> , 1079, 173-86	14
939	Relative importance of secondary structure and solvent accessibility to the stability of protein mutants. A case study with amino acid properties and energetics on T4 and human lysozymes. <b>2005</b> , 29, 25-35	24
938	Computational methods for protein design and protein sequence variability: biased Monte Carlo and replica exchange. <b>2005</b> , 401, 205-210	33
937	Monte Carlo simulations of flexible molecules in a static electric field: electric dipole and conformation. <b>2005</b> , 401, 1-6	11
936	Protein-water displacement distributions. <b>2005</b> , 1749, 173-86	164

935	Role of the disulphide bridge in folding, stability and function of porcine odorant binding protein: spectroscopic equilibrium studies on C63A/C155A double mutant. <b>2005</b> , 1750, 30-9	11
934	Early stages of salmon calcitonin aggregation: effect induced by ageing and oxidation processes in water and in the presence of model membranes. <b>2005</b> , 1750, 134-45	31
933	Morphological aspects of oligomeric protein structures. <b>2005</b> , 89, 9-35	61
932	Adsorption of amyloid beta-peptide at polymer surfaces: a neutron reflectivity study. <b>2005</b> , 6, 2527-34	37
931	Gold glyconanoparticles as probes to explore the carbohydrate-mediated self-recognition of marine sponge cells. <b>2005</b> , 6, 828-31	53
930	Predicting Protein Retention Time in Hydrophobic Interaction Chromatography. 2005, 28, 1326-1334	9
929	On the influence of charged side chains on the folding-unfolding equilibrium of beta-peptides: a molecular dynamics simulation study. <b>2005</b> , 11, 7276-93	23
928	Role of mutational bias and natural selection on genome-wide nucleotide bias in prokaryotic organisms. <b>2005</b> , 81, 11-8	21
927	Potentiometric investigations of molecular heteroconjugation equilibria of substituted phenol+n-butylamine systems in dimethyl sulfoxide. <b>2005</b> , 37, 778-782	2
926	Studies on (acid+base) equilibria in substituted (phenol+n-butylamine) systems in acetonitrile. <b>2005</b> , 37, 810-813	3
925	Hydrogen bonding in aromatic formamides. <b>2005</b> , 35, 723-729	4
924	Crystal structure model based on the analysis of hydrophilic-hydrophobic ratio in molecules. Isosteviol derivatives. <b>2005</b> , 46, S195-S201	8
923	Thermal Aggregation of Methyl Cellulose in Aqueous Solution: A Thermodynamic Study and Protein Partitioning Behaviour. <b>2005</b> , 12, 293-304	7
922	Electronic properties of amino acid side chains: quantum mechanics calculation of substituent effects. <b>2005</b> , 5, 2	36
921	Geometric cooperativity and anticooperativity of three-body interactions in native proteins. <b>2005</b> , 60, 46-65	34
920	Statistical and molecular dynamics studies of buried waters in globular proteins. <b>2005</b> , 60, 450-63	92
919	Statistical characterization of salt bridges in proteins. <b>2005</b> , 60, 732-9	56
918	Molecular dynamics study on the folding and metallation of the individual domains of metallothionein. <b>2006</b> , 62, 159-72	35

## (2005-2006)

917	The thermal adaptation of the nitrogenase Fe protein from thermophilic Methanobacter thermoautotrophicus. <b>2006</b> , 62, 450-60	6
916	Hydrogen bonding increases packing density in the protein interior. <b>2006</b> , 63, 278-82	34
915	Proteins. <b>2005</b> ,	1
914	Alcohol- and Salt-induced Partially Folded Intermediates. 884-915	4
913	Concurrent Association and Folding of Small Oligomeric Proteins. 965-997	2
912	Folding of Membrane Proteins. 998-1031	O
911	Paradigm Changes from Unboiling an Egglto Bynthesizing a Rabbit[12-31	
910	Folding and Association of Multi-domain and Oligomeric Proteins. 32-72	
909	Hybrid Evolutionary Algorithms for Protein Structure Prediction under the HPNX Model. <b>2005</b> , 525-534	3
908	. 2005,	23
907	Macromolecular Forces. 2005, 71-87	
906	Protein folding cooperativity: basic insights from minimalist models. <b>2005</b> , 12, 223-8	4
906	Hierarchical docking of databases of multiple ligand conformations. <b>2005</b> , 5, 739-49	120
905	Hierarchical docking of databases of multiple ligand conformations. <b>2005</b> , 5, 739-49  Comparison of Hsc70 orthologs from polar and temperate notothenioid fishes: differences in	120
905	Hierarchical docking of databases of multiple ligand conformations. <b>2005</b> , 5, 739-49  Comparison of Hsc70 orthologs from polar and temperate notothenioid fishes: differences in prevention of aggregation and refolding of denatured proteins. <b>2005</b> , 288, R1195-202	120
905 904 903	Hierarchical docking of databases of multiple ligand conformations. 2005, 5, 739-49  Comparison of Hsc70 orthologs from polar and temperate notothenioid fishes: differences in prevention of aggregation and refolding of denatured proteins. 2005, 288, R1195-202  Molecular and Cellular Signaling. 2005,	120 33

899	The Biologist's Forum: Thermostability of proteins. <b>2005</b> , 76, 22-27	4
898	A simple hydrophobicity-based score for profiling protein structures. <b>2005</b> , 17, S1595-S1606	4
897	Engineering Proteins for Stability and Efficient Folding. 1281-1333	1
896	Molecular simulation of surfactant-assisted protein refolding. <b>2005</b> , 122, 134902	12
895	Thermodynamic anomalies in a lattice model of water: solvation properties. <b>2005</b> , 123, 24506	8
894	Molecular simulation of polymer assisted protein refolding. <b>2005</b> , 123, 134903	4
893	Large-scale molecular-dynamics simulation of nanoscale hydrophobic interaction and nanobubble formation. <b>2005</b> , 123, 204707	46
892	Self-similarity and protein chains. <b>2005</b> , 71, 012901	22
891	Structure-approximating inverse protein folding problem in the 2D HP model. <b>2005</b> , 12, 1328-45	23
890	Statistical theory for protein ensembles with designed energy landscapes. <b>2005</b> , 123, 154908	19
889	The role of electrostatic interaction in triggering the unraveling of stable helix 1 in normal prion protein. A molecular dynamics simulation investigation. <b>2005</b> , 22, 563-70	9
888	Cooperative water filling of a nonpolar protein cavity observed by high-pressure crystallography and simulation. <b>2005</b> , 102, 16668-71	168
887	Proteomics and Protein-Protein Interactions. 2005,	10
886	Hydrophobic hydration from small to large lengthscales: Understanding and manipulating the crossover. <b>2005</b> , 102, 9475-80	255
885	SRide: a server for identifying stabilizing residues in proteins. <b>2005</b> , 33, W303-5	95
884	Role of arginine in the stabilization of proteins against aggregation. <i>Biochemistry</i> , <b>2005</b> , 44, 4919-25 3.2	192
883	Matrix assisted refolding of proteins by ion exchange chromatography. <b>2005</b> , 117, 83-97	37
882	Water's hydrogen bonds in the hydrophobic effect: a simple model. <b>2005</b> , 109, 23611-7	45

## (2005-2005)

881	Fundamentals of Reversed Phase Chromatography: Thermodynamic and Exothermodynamic Treatment. <b>2005</b> , 28, 965-1054	46
880	Topology-dependent protein folding rates analyzed by a stereochemical model. <b>2005</b> , 123, 154906	5
879	Folding of small proteins: a matter of geometry?. <b>2005</b> , 103, 2903-2910	1
878	From Hydrophobic to Hydrophilic Solvation: An Application to Hydration of Benzene. <b>2005</b> , 1, 643-52	60
877	A computational pathway for bracketing native-like structures fo small alpha helical globular proteins. <b>2005</b> , 7, 2364-75	50
876	RNA and protein folding: common themes and variations. <i>Biochemistry</i> , <b>2005</b> , 44, 4957-70 3.2	226
875	Electrostatics of Proteins: Principles, Models and Applications. 163-200	2
874	Backbone-Backbone H-Bonds Make Context-Dependent Contributions to Protein Folding Kinetics and Thermodynamics: Lessons from Amide-to-Ester Mutations. <b>2005</b> , 72, 39-78	53
873	Comment on "Entropy/enthalpy compensation: hydrophobic effect, micelles and protein complexes" by E. Fisicaro, C. Compari and A. Braibanti, Phys. Chem. Chem. Phys., 2004, 6, 4156. <b>2005</b> , 7, 1322-3; discussion 1324-5	6
872	Molecular assembly of biomimetic microcapsules. <b>2005</b> , 1, 259-264	79
871	Dynamics of water trapped between hydrophobic solutes. <b>2005</b> , 109, 6422-9	150
870	On the salt-induced stabilization of pair and many-body hydrophobic interactions. <b>2005</b> , 109, 642-51	113
869	Communication of stabilizing energy between substructures of a protein. <i>Biochemistry</i> , <b>2005</b> , 44, 2349-5 <del>9</del> .2	32
868	Predicting the energetics of osmolyte-induced protein folding/unfolding. 2005, 102, 15065-8	351
867	Molecular dynamics simulations of helix-forming, amine-functionalized m-poly(phenyleneethynylene)s. <b>2005</b> , 109, 7548-56	19
866	Protein folding on the hexagonal lattice in the HP model. <b>2005</b> , 3, 19-34	22
865	Local density profiles are coupled to solute size and attractive potential for nanoscopic hydrophobic solutes. <b>2005</b> , 31, 457-463	35
864	Protein structure and dynamics from single-molecule fluorescence resonance energy transfer. <b>2005</b> , 109, 1626-34	17

863	Switching the Properties of Polyelectrolyte Brushes via ⊞ydrophobic Collapse□ <b>2005</b> , 38, 10192-10199	170
862	Denaturation and aggregation of three alpha-lactalbumin preparations at neutral pH. <b>2005</b> , 53, 3182-90	69
861	Are solvation free energies of homogeneous helical peptides additive?. 2005, 109, 19000-7	20
860	Dye-Assisted Structural Modulation of Hydrogen-Bonded Binary Supramolecular Polymers. <b>2005</b> , 17, 4392-4398	58
859	Structural transformation of apocytochrome c induced by alternating copolymers of maleic acid and alkene. <b>2005</b> , 6, 2748-55	14
858	Solvophobic and steric effects of side groups on polymer folding: molecular modeling studies of amine-functionalized m-poly(phenyleneethynylene) foldamers in aqueous solution. <b>2005</b> , 109, 19952-9	17
857	On the mechanism of hydrophobic association of nanoscopic solutes. <b>2005</b> , 127, 3556-67	268
856	Helix, sheet, and polyproline II frequencies and strong nearest neighbor effects in a restricted coil library. <i>Biochemistry</i> , <b>2005</b> , 44, 9691-702	150
855	Entropic stabilization of isolated beta-sheets. <b>2005</b> , 127, 4675-9	39
854	On the intactness of hydrogen bonds around nonpolar solutes dissolved in water. <b>2005</b> , 109, 8103-7	40
853	Attempts to delineate the relative contributions of changes in hydrophobicity and packing to changes in stability of ribonuclease S mutants. <i>Biochemistry</i> , <b>2005</b> , 44, 5923-30	8
852	Structural and energetic consequences of mutations in a solvated hydrophobic cavity. <b>2005</b> , 346, 307-18	24
851	Comprehensive analysis of protein folding activation thermodynamics reveals a universal behavior violated by kinetically stable proteases. <b>2005</b> , 347, 355-66	49
850	Desolvation is a likely origin of robust enthalpic barriers to protein folding. <b>2005</b> , 349, 872-89	73
849	Specifically collapsed intermediate in the early stage of the folding of ribonuclease A. <b>2005</b> , 350, 349-62	41
848	Stabilization of the ribosomal protein S6 by trehalose is counterbalanced by the formation of a putative off-pathway species. <b>2005</b> , 351, 402-16	20
847	Fine structure analysis of a protein folding transition state; distinguishing between hydrophobic stabilization and specific packing. <b>2005</b> , 354, 693-705	48
846	Dependence of the size of the initially collapsed form during the refolding of barstar on denaturant concentration: evidence for a continuous transition. <b>2005</b> , 353, 704-18	48

# (2006-2005)

845	Sterics and solvation winnow accessible conformational space for unfolded proteins. <b>2005</b> , 353, 873-87	40
844	Importance of main-chain hydrophobic free energy to the stability of thermophilic proteins. <b>2005</b> , 35, 211-20	21
843	Fluorimetric study of the artificial chaperone-assisted renaturation of carbonic anhydrase: a kinetic analysis. <b>2005</b> , 36, 191-7	13
842	Adaptation to extreme environments: macromolecular dynamics in complex systems. <b>2005</b> , 1724, 404-10	38
841	Relevance of Frank's solvent classification as typically aqueous and typically non-aqueous to activities of firefly luciferase, alcohol dehydrogenase, and alpha-chymotrypsin in aqueous binaries. <b>2005</b> , 433, 454-65	15
840	pH dependence thermal stability of a chymotrypsin inhibitor from Schizolobium parahyba seeds. <b>2005</b> , 88, 3509-17	12
839	Folding Trp-cage to NMR resolution native structure using a coarse-grained protein model. <b>2005</b> , 88, 147-55	125
838	Elucidating protein thermodynamics from the three-dimensional structure of the native state using network rigidity. <b>2005</b> , 88, 903-15	42
837	Comparing folding codes in simple heteropolymer models of protein evolutionary landscape: robustness of the superfunnel paradigm. <b>2005</b> , 88, 118-31	35
836	Prediction of protein thermostability with a direction- and distance-dependent knowledge-based potential. <b>2005</b> , 14, 2682-92	45
835	Osmolyte trimethylamine-N-oxide does not affect the strength of hydrophobic interactions: origin of osmolyte compatibility. <b>2005</b> , 89, 858-66	130
834	Translational-entropy gain of solvent upon protein folding. <b>2005</b> , 89, 2701-10	128
833	Coarse-grained strategy for modeling protein stability in concentrated solutions. 2005, 89, 2372-84	38
832	Structure-based design of novel Chk1 inhibitors: insights into hydrogen bonding and protein-ligand affinity. <b>2005</b> , 48, 4332-45	88
831	A knowledge-based energy function for protein-ligand, protein-protein, and protein-DNA complexes. <b>2005</b> , 48, 2325-35	236
830	Water mediation in protein folding and molecular recognition. <b>2006</b> , 35, 389-415	768
829	Beta-silks: enhancing and controlling aggregation. <b>2006</b> , 73, 17-53	34
828	Closed-Loop Phase Behavior for Weakly Interacting Block Copolymers. <b>2006</b> , 39, 5926-5930	15

827	Solvation forces between colloidal nanoparticles: directed alignment. <b>2006</b> , 73, 020401	45
826	An antiparallel alpha-helical coiled-coil model system for rapid assessment of side-chain recognition at the hydrophobic interface. <b>2006</b> , 128, 16444-5	49
825	Molecular simulation studies of water physisorption in zeolites. <b>2006</b> , 8, 5396-406	116
824	Molecular studies of the structural properties of hydrogen gas in bulk water. <b>2006</b> , 32, 269-278	19
823	Fuzzy-oil-drop hydrophobic force fielda model to represent late-stage folding (in silico) of lysozyme. <b>2006</b> , 23, 519-28	21
822	Recent progress in understanding hydrophobic interactions. <b>2006</b> , 103, 15739-46	693
821	Hydrophobic contribution of amino acids in peptides measured by hydrophobic interaction chromatography. <b>2006</b> , 110, 9148-54	5
820	Extraction and partial characterization of proteolytic activities from the cell surface of Lactobacillus helveticus Zuc2. <b>2006</b> , 89, 3800-9	28
819	Enhancement of protein thermal stability: toward the design of robust proteins for bionanotechnological applications. <b>2006</b> , 117-139	3
818	Thermodynamics of hydrogen bonding in hydrophilic and hydrophobic media. <b>2006</b> , 110, 4393-8	323
818	Thermodynamics of hydrogen bonding in hydrophilic and hydrophobic media. <b>2006</b> , 110, 4393-8  Stabilization of E. coli Ribonuclease HI by the 'stability profile of mutant protein' (SPMP)-inspired random and non-random mutagenesis. <b>2006</b> , 124, 512-22	323
	Stabilization of E. coli Ribonuclease HI by the 'stability profile of mutant protein' (SPMP)-inspired	
	Stabilization of E. coli Ribonuclease HI by the 'stability profile of mutant protein' (SPMP)-inspired random and non-random mutagenesis. <b>2006</b> , 124, 512-22	1
817 816	Stabilization of E. coli Ribonuclease HI by the 'stability profile of mutant protein' (SPMP)-inspired random and non-random mutagenesis. <b>2006</b> , 124, 512-22  Protein Structure and Folding in the Gas Phase: Ubiquitin and Cytochrome c. <b>2006</b> , 177-212	1
817 816 815	Stabilization of E. coli Ribonuclease HI by the 'stability profile of mutant protein' (SPMP)-inspired random and non-random mutagenesis. 2006, 124, 512-22  Protein Structure and Folding in the Gas Phase: Ubiquitin and Cytochrome c. 2006, 177-212  Protein-solvent interactions. 2006, 106, 1616-23  Coarse-grained strategy for modeling protein stability in concentrated solutions. II: phase behavior.	1 16 119
817 816 815	Stabilization of E. coli Ribonuclease HI by the 'stability profile of mutant protein' (SPMP)-inspired random and non-random mutagenesis. 2006, 124, 512-22  Protein Structure and Folding in the Gas Phase: Ubiquitin and Cytochrome c. 2006, 177-212  Protein-solvent interactions. 2006, 106, 1616-23  Coarse-grained strategy for modeling protein stability in concentrated solutions. II: phase behavior. 2006, 90, 1949-60	1 16 119 33
817 816 815 814 813	Stabilization of E. coli Ribonuclease HI by the 'stability profile of mutant protein' (SPMP)-inspired random and non-random mutagenesis. 2006, 124, 512-22  Protein Structure and Folding in the Gas Phase: Ubiquitin and Cytochrome c. 2006, 177-212  Protein-solvent interactions. 2006, 106, 1616-23  Coarse-grained strategy for modeling protein stability in concentrated solutions. II: phase behavior. 2006, 90, 1949-60  Heteropolymer collapse theory for protein folding in the pressure-temperature plane. 2006, 91, 2427-35  Role of protein cavities on unfolding volume change and on internal dynamics under pressure. 2006	1 16 119 33 33

## (2016-2006)

809	Side chain dynamics and alternative hydrogen bonding in the mechanism of protein thermostabilization. <b>2006</b> , 24, 255-62	16
808	Investigation of Salt Bridge Stability in a Generalized Born Solvent Model. <b>2006</b> , 2, 115-27	103
807	Quantitative description of the hydrophobic effect: the enthalpic contribution. <b>2006</b> , 110, 9298-303	34
806	Insight into heme protein redox potential control and functional aspects of six-coordinate ligand-sensing heme proteins from studies of synthetic heme peptides. <b>2006</b> , 45, 9985-10001	47
805	Design of functional ferritin-like proteins with hydrophobic cavities. <b>2006</b> , 128, 6611-9	52
804	Calorimetric dissection of colicin DNaseimmunity protein complex specificity. <i>Biochemistry</i> , <b>2006</b> , 45, 3243-54	30
803	Amide-to-E-olefin versus amide-to-ester backbone H-bond perturbations: Evaluating the O-O repulsion for extracting H-bond energies. <b>2006</b> , 128, 15948-9	36
802	AUC-Maximized Deep Convolutional Neural Fields for Protein Sequence Labeling. <b>2016</b> , 9852, 1-16	17
801	The effect of urea and taurine osmolytes on hydrophobic association and solvation of methane and neopentane molecules. <b>2016</b> , 223, 660-671	1
800	Multivalent bonds in self-assembled bundles of ultrathin gold nanowires. <b>2016</b> , 18, 27165-27169	24
799	Anomalous Dynamics of Water Confined in Protein-Protein and Protein-DNA Interfaces. <b>2016</b> , 7, 3967-3972	25
798	Solid acetone structure dependence on pressure: a new fibre textured thin film crystallographic structure studied by grazing-incidence X-ray diffraction. <b>2016</b> , 18, 8220-8228	1
797	Computational Repacking of HIF-2ECavity Replaces Water-Based Stabilized Core. <b>2016</b> , 24, 1918-1927	5
796	Electrostatic Contributions to Protein Quinary Structure. <b>2016</b> , 138, 13139-13142	52
795	Optimization of Spray Drying Conditions for Yield, Particle Size and Biological Activity of Thermally Stable Viral Vectors. <b>2016</b> , 33, 2763-76	37
794	Excipients Used in Biotechnology Products. <b>2016</b> , 145-198	3
793	Molecular basis of the osmolyte effect on protein stability: a lesson from the mechanical unfolding of lysozyme. <b>2016</b> , 473, 3705-3724	14
792	Peptide binding landscapes: Specificity and homophilicity across sequence space in a lattice model. <b>2016</b> , 94, 042405	

791	Electrostatic effects on the folding stability of FKBP12. <b>2016</b> , 29, 301-308	5
790	On the structural denaturation of biological analytes in trapped ion mobility spectrometry - mass spectrometry. <b>2016</b> , 141, 3722-30	64
7 <sup>8</sup> 9	The temperature dependence of the Hofmeister series: thermodynamic fingerprints of cosolute-protein interactions. <b>2016</b> , 18, 29698-29708	45
788	Testing the limits of synthon engineering: salts of salicylic and sulfosalicylic acid with nucleobases and derivatives. <b>2016</b> , 18, 7573-7579	17
787	Thermodynamic Perturbation Theory for Associating Molecules. <b>2016</b> , 1-47	3
786	Entropically Driven Self-Assembly of Bolaamphiphilic Perylene Dyes in Water. <b>2016</b> , 55, 12094-8	59
785	Salt Effect Accelerates Site-Selective Cysteine Bioconjugation. <b>2016</b> , 2, 637-646	28
784	Entropically Driven Self-Assembly of Bolaamphiphilic Perylene Dyes in Water. <b>2016</b> , 128, 12273-12277	23
783	Studying the role of cooperative hydration in stabilizing folded protein states. <b>2016</b> , 196, 394-406	12
782	Application of the Kinetic Nucleation Theory to Protein Folding. <b>2016</b> , 229-366	
782 781	Application of the Kinetic Nucleation Theory to Protein Folding. 2016, 229-366  n-> Interactions Are Competitive with Hydrogen Bonds. 2016, 18, 3614-7	29
		29 16
781	n->鬥 Interactions Are Competitive with Hydrogen Bonds. <b>2016</b> , 18, 3614-7	. (
781 780	n-> Interactions Are Competitive with Hydrogen Bonds. 2016, 18, 3614-7  GdnHCl-induced unfolding intermediate in the mitochondrial carbonic anhydrase VA. 2016, 91, 1151-60  Macromolecular Crowding Facilitates the Conformational Transition of on-Pathway Molten Globule	16
781 780 779	n-> Interactions Are Competitive with Hydrogen Bonds. 2016, 18, 3614-7  GdnHCl-induced unfolding intermediate in the mitochondrial carbonic anhydrase VA. 2016, 91, 1151-60  Macromolecular Crowding Facilitates the Conformational Transition of on-Pathway Molten Globule States of the Prion Protein. 2016, 120, 11093-11101	16
781 780 779 778	n-> Interactions Are Competitive with Hydrogen Bonds. 2016, 18, 3614-7  GdnHCl-induced unfolding intermediate in the mitochondrial carbonic anhydrase VA. 2016, 91, 1151-60  Macromolecular Crowding Facilitates the Conformational Transition of on-Pathway Molten Globule States of the Prion Protein. 2016, 120, 11093-11101  A prevalent intraresidue hydrogen bond stabilizes proteins. 2016, 12, 1084-1088	16 4 66
781 780 779 778	n-> Interactions Are Competitive with Hydrogen Bonds. 2016, 18, 3614-7  GdnHCl-induced unfolding intermediate in the mitochondrial carbonic anhydrase VA. 2016, 91, 1151-60  Macromolecular Crowding Facilitates the Conformational Transition of on-Pathway Molten Globule States of the Prion Protein. 2016, 120, 11093-11101  A prevalent intraresidue hydrogen bond stabilizes proteins. 2016, 12, 1084-1088  Protein thermostability engineering. 2016, 6, 115252-115270  Various nanoparticle morphologies and surface properties of waterborne polyurethane controlled	16 4 66 62

# (2016-2016)

773	Role of von Willebrand FactorA1 Domain Variants P1266L, H1268D, C1272R, and C1272F in VWD: A Molecular Modeling and Simulation Analysis Approach. <b>2016</b> , 102, 299-330	О
772	Spectroscopic Monitoring of Mechanical Forces during Protein Folding by using Molecular Force Probes. <b>2016</b> , 17, 1486-92	10
771	Influence of precipitating agents on thermodynamic parameters of protein crystallization solutions. <b>2016</b> , 105, 642-52	2
770	Selective Uptake and Refolding of Globular Proteins in Coacervate Microdroplets. <b>2016</b> , 32, 5881-9	57
769	Allosterism and Structure in Thermally Activated Transient Receptor Potential Channels. 2016, 45, 371-98	39
768	Structural basis of urea-induced unfolding: Unraveling the folding pathway of hemochromatosis factor E. <b>2016</b> , 91, 1051-61	20
767	Purification and structural characterization of Mce4A from Mycobacterium tuberculosis. <b>2016</b> , 93, 235-241	9
766	Point mutation Gln121-Arg increased temperature optima of Bacillus lipase (1.4 subfamily) by fifteen degrees. <b>2016</b> , 88, 507-14	7
765	Applications of pressure perturbation calorimetry to study factors contributing to the volume changes upon protein unfolding. <b>2016</b> , 1860, 1036-1042	5
764	Aromatic Side Chain Water-to-Lipid Transfer Free Energies Show a Depth Dependence across the Membrane Normal. <b>2016</b> , 138, 7946-50	29
763	Information and redundancy in the burial folding code of globular proteins within a wide range of shapes and sizes. <b>2016</b> , 84, 515-31	2
762	Interplay between binding affinity and kinetics in protein-protein interactions. 2016, 84, 920-33	9
761	Expression Characterization of Stress Genes Under High and Low Temperature Stresses in the Pacific Oyster, Crassostrea gigas. <b>2016</b> , 18, 176-88	47
760	Reorientation Motion and Preferential Interactions of a Peptide in Denaturants and Osmolyte. <b>2016</b> , 120, 3089-99	17
759	The influence of putrescine on the structure, enzyme activity and stability of £hymotrypsin. <b>2016</b> , 6, 29264-29278	29
758	Thermal properties of milk fat, xanthine oxidase, caseins and whey proteins in pulsed electric field-treated bovine whole milk. <b>2016</b> , 207, 34-42	36
757	Topological constraints and modular structure in the folding and functional motions of GlpG, an intramembrane protease. <b>2016</b> , 113, 2098-103	16
756	Percutaneous delivery of Emelanocyte-stimulating hormone for the treatment of imiquimod-induced psoriasis. <b>2016</b> , 24, 537-47	11

755	Reconciling the understanding of 'hydrophobicity' with physics-based models of proteins. <b>2016</b> , 28, 083003	12
754	The effect of monovalent cations on the collective dynamics of water and on a model protein. <b>2016</b> , 215, 197-203	11
753	Cooperativity in Noncovalent Interactions. <b>2016</b> , 116, 2775-825	515
75 <sup>2</sup>	Protein stability: a crystallographer's perspective. <b>2016</b> , 72, 72-95	98
751	Fluid transition layer between rigid solute and liquid solvent: is there depletion or enrichment?. <b>2016</b> , 18, 7888-902	1
750	Pair correlations that link the hydrophobic and Hofmeister effects. <b>2016</b> , 18, 14949-59	5
749	Long-ranged contributions to solvation free energies from theory and short-ranged models. <b>2016</b> , 113, 2819-26	37
748	Membrane Protein Folding and Structure. <b>2016</b> , 303-331	
747	An active site rearrangement within the Tetrahymena group I ribozyme releases nonproductive interactions and allows formation of catalytic interactions. <b>2016</b> , 22, 32-48	5
746	Importance of Hydrophilic Hydration and Intramolecular Interactions in the Thermodynamics of Helix-Coil Transition and Helix-Helix Assembly in a Deca-Alanine Peptide. <b>2016</b> , 120, 69-76	20
745	Base-Free Photoredox/Nickel Dual-Catalytic Cross-Coupling of Ammonium Alkylsilicates. <b>2016</b> , 138, 475-8	211
744	A Chemical Perspective on Allostery. <b>2016</b> , 116, 6488-502	54
743	Spectroscopic and MD simulation studies on unfolding processes of mitochondrial carbonic anhydrase VA induced by urea. <b>2016</b> , 34, 1987-97	19
742	Gelation of carrageenan: Effects of sugars and polyols. <b>2016</b> , 54, 284-292	52
741	Thermodynamic investigations of protein's behaviour with ionic liquids in aqueous medium studied by isothermal titration calorimetry. <b>2016</b> , 1860, 1017-1025	11
740	Role of cytochrome b5 in the modulation of the enzymatic activities of cytochrome P450 17Hydroxylase/17,20-lyase (P450 17A1). <b>2017</b> , 170, 2-18	23
739	Binding of small molecules at interface of protein-protein complex - A newer approach to rational drug design. <b>2017</b> , 24, 379-388	11
738	Phase Behavior and Self-Assembly of Perfectly Sequence-Defined and Monodisperse Multiblock Copolypeptides. <b>2017</b> , 18, 599-609	37

# (2017-2017)

737	Conformational dynamics and self-association of intrinsically disordered Huntingtin exon 1 in cells. <b>2017</b> , 19, 10738-10747	18
736	Trimethylamine -oxide stabilizes proteins via a distinct mechanism compared with betaine and glycine. <b>2017</b> , 114, 2479-2484	92
735	Thermodynamic properties of amyloid fibrils in equilibrium. <b>2017</b> , 231, 155-160	7
734	Optical methods for measuring DNA folding. <b>2017</b> , 31, 1730001	1
733	The functional and structural stabilization of trypsin by sucrose. <b>2017</b> , 99, 343-349	31
732	Computational Modeling in Bioprocess Development. <b>2017</b> , 177-225	1
731	Quantum mechanical electronic structure calculation reveals orientation dependence of hydrogen bond energy in proteins. <b>2017</b> , 85, 1046-1055	3
730	Perplexing cooperative folding and stability of a low-sequence complexity, polyproline 2 protein lacking a hydrophobic core. <b>2017</b> , 114, 2241-2246	21
729	Supermacroporous hydrophobic affinity sorbents for penicillin acylase purification. 2017, 54, 71-79	9
728	Hydrogen bonds in the vicinity of the special pair of the bacterial reaction center probed by hydrostatic high-pressure absorption spectroscopy. <b>2017</b> , 231, 27-33	10
727	Effects of high pressure processing on protein fractions of blue crab (Callinectes sapidus) meat. <b>2017</b> , 41, 323-329	47
726	A general method for the derivation of the functional forms of the effective energy terms in coarse-grained energy functions of polymers. I. Backbone potentials of coarse-grained polypeptide chains. <b>2017</b> , 146, 124106	31
725	Synergistic effects of fibronectin and bone morphogenetic protein on the bioactivity of titanium metal. <b>2017</b> , 105, 2485-2498	13
724	Temperature-Induced, Selective Assembly of Supramolecular Colloids in Water. <b>2017</b> , 2, 1720-1730	5
723	Predicting Protein Interactions of Concentrated Globular Protein Solutions Using Colloidal Models. <b>2017</b> , 121, 4756-4767	32
722	Thermal Aggregation of Bovine Serum Albumin in Conventional Buffers: An Insight into Molecular Level Interactions. <b>2017</b> , 46, 831-848	17
721	Theory and Electrochemistry of Cytochrome c. <b>2017</b> , 121, 4958-4967	28
720	Water structure around hydrophobic amino acid side chain analogs using different water models. <b>2017</b> , 146, 225104	15

719	Characterization of highly concentrated antibody solution - A toolbox for the description of protein long-term solution stability. <b>2017</b> , 9, 1169-1185	33
718	Breaking the color barrier - a multi-selective antibody reporter offers innovative strategies of fluorescence detection. <b>2017</b> , 130, 2644-2653	4
717	A simple and facile NMR method for the determination of hydrogen bonding by amide NH protons in protein models and other compounds. <b>2017</b> , 41, 6064-6066	11
716	Imprinted micelles for chiral recognition in water: shape, depth, and number of recognition sites. <b>2017</b> , 15, 4851-4858	18
715	Packing in protein cores. <b>2017</b> , 29, 293001	14
714	Impact of Hydrogen Bonding on the Susceptibility of Peptides to Oxidation. <b>2017</b> , 12, 1485-1489	6
713	Development of a candidate stabilizing formulation for bulk storage of a double mutant heat labile toxin (dmLT) protein based adjuvant. <b>2017</b> , 35, 5471-5480	10
712	Principles for Tuning Hydrophobic Ligand-Receptor Binding Kinetics. <b>2017</b> , 13, 3012-3019	11
711	Real-time monitoring of hydrophobic aggregation reveals a critical role of cooperativity in hydrophobic effect. <b>2017</b> , 8, 15639	47
710	High-pressure modulation of the structure of the bacterial photochemical reaction center at physiological and cryogenic temperatures. <b>2017</b> , 50, 144006	5
709	Protein-gold nanoparticle interactions and their possible impact on biomedical applications. <b>2017</b> , 55, 13-27	91
708	The Solution Assembly of Biological Molecules Using Ion Mobility Methods: From Amino Acids to Amyloid Protein. <b>2017</b> , 10, 365-386	36
707	Role of local and nonlocal interactions in folding and misfolding of globular proteins. 2017, 146, 065102	5
706	Biocompatibility of ionic liquids towards protein stability: A comprehensive overview on the current understanding and their implications. <b>2017</b> , 96, 611-651	63
705	Strategy for assessment of the colloidal and biological stability of H1N1 influenza A viruses. <b>2017</b> , 517, 80-87	3
704	Infectious bronchitis vaccine virus detection and part-S1 genetic variation following single or dual inoculation in broiler chicks. <b>2017</b> , 46, 309-318	3
703	Automated protein design: Landmarks and operational principles. 2017, 125, 24-35	9
702	Simple Physics-Based Analytical Formulas for the Potentials of Mean Force of the Interaction of Amino Acid Side Chains in Water. VII. Charged-Hydrophobic/Polar and Polar-Hydrophobic/Polar Side Chains. <b>2017</b> , 121, 379-390	16

701	Role of Urea-Aromatic Stacking Interactions in Stabilizing the Aromatic Residues of the Protein in Urea-Induced Denatured State. <b>2017</b> , 139, 14931-14946	36
700	Synthetic polypeptides: from polymer design to supramolecular assembly and biomedical application. <b>2017</b> , 46, 6570-6599	193
699	Proton Network Flexibility Enables Robustness and Large Electric Fields in the Ketosteroid Isomerase Active Site. <b>2017</b> , 121, 9807-9815	25
698	Molecular mechanism of reflectind tunable biophotonic control: Opportunities and limitations for new optoelectronics. <b>2017</b> , 5, 104801	15
697	Statistical thermodynamics unveils the dissolution mechanism of cellobiose. <b>2017</b> , 19, 23106-23112	7
696	Miniprotein Design: Past, Present, and Prospects. <b>2017</b> , 50, 2085-2092	46
695	Analytical theory of the hydrophobic effect of solutes in water. <b>2017</b> , 96, 032101	10
694	Emerging Concepts in TCR Specificity: Rationalizing and (Maybe) Predicting Outcomes. <b>2017</b> , 199, 2203-2213	43
693	The Hydrophobic Effect and the Role of Cosolvents. <b>2017</b> , 121, 9986-9998	70
692	Scrutiny of electrostatic-driven conformational ordering of polypeptide chains in DMSO: a study with a model oligopeptide. <b>2017</b> , 7, 27981-27991	5
691	A protein folding model using the face-centered cubic lattice model. 2017,	О
690	A tensegrity model for hydrogen bond networks in proteins. <b>2017</b> , 3, e00307	2
689	Pairwise Hydrophobicity at Low Temperature: Appearance of a Stable Second Solvent-Separated Minimum with Possible Implication in Cold Denaturation. <b>2017</b> , 121, 7016-7026	16
688	Modulation of polypeptide conformation through donor-acceptor transformation of side-chain hydrogen bonding ligands. <b>2017</b> , 8, 92	33
687	Intramolecular Interactions Overcome Hydration to Drive the Collapse Transition of Gly. 2017, 121, 8078-8084	22
686	Global analysis of protein folding using massively parallel design, synthesis, and testing. <b>2017</b> , 357, 168-175	241
685	Plasticity in the Oxidative Folding Pathway of the High Affinity Nerita Versicolor Carboxypeptidase Inhibitor (NvCI). <b>2017</b> , 7, 5457	3
684	Influences of lone-pair electrons on directionality of hydrogen bonds formed by hydrophilic amino acid side chains in molecular dynamics simulation. <b>2017</b> , 7, 15859	13

683	Implicit Solvation Using the Superposition Approximation (IS-SPA): An Implicit Treatment of the Nonpolar Component to Solvation for Simulating Molecular Aggregation. <b>2017</b> , 13, 5911-5924	5
682	A Hybrid Evolutionary Algorithm for Protein Structure Prediction Using the Face-Centered Cubic Lattice Model. <b>2017</b> , 628-638	5
681	Hydrophobic interaction chromatography. <b>2017</b> , 171-190	3
680	The stabilization of biopharmaceuticals: current understanding and future perspectives. <b>2017</b> , 47, 475-496	14
679	Entropy in molecular recognition by proteins. <b>2017</b> , 114, 6563-6568	96
678	Structure optimisation by thermal cycling for the hydrophobic-polar lattice model of protein folding. <b>2017</b> , 226, 639-649	3
677	Improving prediction of burial state of residues by exploiting correlation among residues. <b>2017</b> , 18, 70	3
676	Characterization of folding intermediates during urea-induced denaturation of human carbonic anhydrase II. <b>2017</b> , 95, 881-887	19
675	Spectroscopic insight into the interaction of bovine serum albumin with imidazolium-based ionic liquids in aqueous solution. <b>2017</b> , 32, 695-705	26
674	Important amino acid residues involved in folding and binding of protein-protein complexes. <b>2017</b> , 94, 438-444	11
673	Comparative thermal unfolding study of psychrophilic and mesophilic subtilisin-like serine proteases by molecular dynamics simulations. <b>2017</b> , 35, 1500-1517	16
672	Production, purification, and characterization of metalloprotease from Candida kefyr 41 PSB. <b>2017</b> , 94, 106-113	13
671	Basic units of protein structure, folding, and function. <b>2017</b> , 128, 85-99	20
670	Random-phase-approximation theory for sequence-dependent, biologically functional liquid-liquid phase separation of intrinsically disordered proteins. <b>2017</b> , 228, 176-193	73
669	Adaptive thermostability of light-harvesting complexes in marine picocyanobacteria. 2017, 11, 112-124	18
668	Conformational disorder and solvation properties of the key-residues of a protein in water-ethanol mixed solutions. <b>2017</b> , 19, 32636-32646	2
667	The T3 Method (面3 It!) Transcribe -> Translate -> Transform. <b>2017</b> , 79, 257-271	
666	Are Directed Evolution Approaches Efficient in Exploring Nature Potential to Stabilize a Lipase in Organic Cosolvents?. <b>2017</b> , 7, 142	26

66	Single-molecule force spectroscopy of protein-membrane interactions. <b>2017</b> , 6,	35
66	2.3 Peptoids: Synthesis, Characterization, and Nanostructures. <b>2017</b> , 41-66	O
66	Intrinsically disordered proteins: structural and functional dynamics. <b>2017</b> , Volume 8, 7-16	5
66	Outer membrane protein folding from an energy landscape perspective. <b>2017</b> , 15, 123	43
66	Molecular Docking of Interaction between E-Cadherin Protein and Conformational Structure of Cyclic Peptide ADTC3 (Ac-CADTPC-NH2) Simulated on 20 ns. <b>2017</b> , 20, 30-36	4
66	Cosolvent Effects on Polymer Hydration Drive Hydrophobic Collapse. <b>2018</b> , 122, 3587-3595	21
65	Measuring a frequency spectrum for single-molecule interactions with a confined nanopore. <b>2018</b> , 210, 87-99	23
65	Amyloid-Polymorphie in der Energielandschaft der Faltung und Aggregation von Proteinen. <b>2018</b> , 130, 8502-8515	12
65	A network of conformational transitions in an unfolding process of HP-35 revealed by high-temperature MD simulation and a Markov state model. <b>2018</b> , 27, 018701	1
65	Effects of Trimethylamine- N-oxide (TMAO) on Hydrophobic and Charged Interactions. <b>2018</b> , 122, 5557-5566	5 14
65	Agar-agar immobilization: An alternative approach for the entrapment of protease to improve the catalytic efficiency, thermal stability and recycling efficiency. <b>2018</b> , 111, 917-922	13
65	Hydration dynamics of a lipid membrane: Hydrogen bond networks and lipid-lipid associations. <b>2018</b> , 148, 094901	20
65	Foldamer Tertiary Structure through Sequence-Guided Protein Backbone Alteration. <b>2018</b> , 51, 1220-1228	38
65	Approximation Algorithms for Protein Folding in the Hydrophobic-Polar Model on 3D Hexagonal Prism Lattice. <b>2018</b> , 25, 487-498	1
65	On the molecular origin of the cooperative coil-to-globule transition of poly(N-isopropylacrylamide) in water. <b>2018</b> , 20, 9997-10010	66
65	50 Hydrogen bonding between hydrides of the upper-right part of the periodic table. <b>2018</b> , 507, 34-43	2
		3
62	The application of STEP-technology of for particle and protein dispersion detection studies in	9
62	The application of STEP-technology for particle and protein dispersion detection studies in biopharmaceutical research. <b>2018</b> , 543, 257-268	

647	Protein folding, misfolding and aggregation: A tale of constructive to destructive assembly. <b>2018</b> , 112, 217-229	12
646	Coiled coil protein origami: from modular design principles towards biotechnological applications. <b>2018</b> , 47, 3530-3542	48
645	Measuring Entropy in Molecular Recognition by Proteins. <b>2018</b> , 47, 41-61	45
644	Principles of Protein Stability and Their Application in Computational Design. 2018, 87, 105-129	106
643	Hydration Behavior along the Folding Pathways of Trpzip4, Trpzip5 and Trpzip6. 2018, 122, 1560-1572	5
642	The effects of biological buffers TRIS, TAPS, TES on the stability of lysozyme. <b>2018</b> , 112, 720-727	8
641	Fuzzy Logic Augmentation of Neural and Optimization Algorithms: Theoretical Aspects and Real Applications. <b>2018</b> ,	1
640	Collapse Transitions of Proteins and the Interplay Among Backbone, Sidechain, and Solvent Interactions. <b>2018</b> , 47, 19-39	58
639	Comparative Study of Computational Strategies for Protein Structure Prediction. 2018, 449-459	1
638	Glutamate Induced Thermal Equilibrium Intermediate and Counteracting Effect on Chemical Denaturation of Proteins. <b>2018</b> , 122, 1132-1144	10
637	Free energy calculations on the stability of the 14-3-3[protein. 2018, 1866, 442-450	7
636	Unified understanding of folding and binding mechanisms of globular and intrinsically disordered proteins. <b>2018</b> , 10, 163-181	22
635	Electrostatic Interactions in Protein Structure, Folding, Binding, and Condensation. 2018, 118, 1691-1741	290
634	System-Size Dependence of Electrolyte Activity Coefficients in Molecular Simulations. <b>2018</b> , 122, 3330-3338	12
633	A novel cold-adapted esterase from Enterobacter cloacae: Characterization and improvement of its activity and thermostability via the site of Tyr193Cys. <b>2018</b> , 17, 45	7
632	Mimicking a p53-MDM2 interaction based on a stable immunoglobulin-like domain scaffold. <b>2018</b> , 86, 802-812	1
631	High-Pressure Scanning Microcalorimetry - A New Method for Studying Conformational and Phase Transitions. <b>2018</b> , 83, S134-S145	2
630	Poly(lactic-co-glycolic acid) devices: Production and applications for sustained protein delivery. <b>2018</b> , 10, e1516	24

629	Random heteropolymers preserve protein function in foreign environments. 2018, 359, 1239-1243	126
628	Generating intrinsically disordered protein conformational ensembles from a Markov chain. <b>2018</b> , 148, 105102	3
627	One Peptide Reveals the Two Faces of Helix Unfolding-Folding Dynamics. 2018, 122, 3790-3800	6
626	Defining the Structure of a Protein-Spherical Nucleic Acid Conjugate and Its Counterionic Cloud. <b>2018</b> , 4, 378-386	19
625	Effects of localized interactions and surface properties on stability of protein-based therapeutics. <b>2018</b> , 70, 609-624	7
624	Transcriptome sequencing of an Antarctic microalga, Chlorella sp. (Trebouxiophyceae, Chlorophyta) subjected to short-term ultraviolet radiation stress. <b>2018</b> , 30, 87-99	18
623	Shielding effect in protein folding. <b>2018</b> , 79, 118-132	4
622	A mechanistic insight into protein-ligand interaction, folding, misfolding, aggregation and inhibition of protein aggregates: An overview. <b>2018</b> , 106, 1115-1129	32
621	Mechanism and Dynamics of Long-Term Stability of Cytochrome c Conferred by Long-Chain Imidazolium Ionic Liquids at Low Concentration. <b>2018</b> , 6, 803-815	36
620	Water's Thermal Pressure Drives the Temperature Dependence of Hydrophobic Hydration. <b>2018</b> , 122, 3620-3625	6
619	Synthesis of Trifluoromethyl Tetrafluoro-🗗-sulfanyl-Substituted Alkenes, Ketones, and Acids: Polar Hydrophobic Building Blocks. <b>2018</b> , 2018, 772-780	7
618	Protein crystal quality oriented disulfide bond engineering. <b>2018</b> , 9, 659-663	10
617	Neutron Imaging and Electrochemical Characterization of a Glucose Oxidase-Based Enzymatic Electrochemical Cell. <b>2018</b> , 15,	0
616	Complex Dynamics of Water in Protein Confinement. <b>2018</b> , 122, 3418-3425	11
615	Synthesis and comparison of crosslinked peptide nanoparticles based on diphenylalanine derivatives. <b>2018</b> , 135, 45930	1
614	Practical insights on enzyme stabilization. <b>2018</b> , 38, 335-350	110
613	Identification and characterization of functional single nucleotide polymorphisms (SNPs) in Axin 1 gene: a molecular dynamics approach. <b>2018</b> , 76, 173-185	6
612	Insight into the functional and structural transition of garlic phytocystatin induced by urea and guanidine hydrochloride: A comparative biophysical study. <b>2018</b> , 106, 20-29	8

611	Probing the Interaction between Cyclic ADTC1 Ac-CADTPPVC-NH2) Peptide with EC1-EC2 domain of E-cadherin using Molecular Docking Approach. <b>2018</b> , 349, 012050	1
610	Exploring the pH-Induced Functional Phase Space of Human Serum Albumin by EPR Spectroscopy. <b>2018</b> , 4, 47	14
609	Stapling of two PEGylated side chains increases the conformational stability of the WW domain via an entropic effect. <b>2018</b> , 16, 8933-8939	6
608	Estabilidad termodinfinica de protefias. <b>2018</b> , 29, 3	
607	MELD IMD Folds Nonthreadables, Giving Native Structures and Populations. 2018, 14, 6734-6740	9
606	Peptoid applications in biomedicine and nanotechnology. <b>2018</b> , 183-213	12
605	Why Does RNA Collapse? The Importance of Water in a Simulation Study of Helix-Junction-Helix Systems. <b>2018</b> , 140, 16948-16951	13
604	Direct measurement of the electrostatic image force of a levitated charged nanoparticle close to a surface. <b>2018</b> , 98,	18
603	n->∄ Interactions Modulate the Properties of Cysteine Residues and Disulfide Bonds in Proteins. <b>2018</b> , 140, 17606-17611	25
602	Entropic effect implication for change in polymer coils swelling state in the demixing enthalpy recovery of aqueous poly(vinyl methyl ether) solutions. <b>2018</b> , 57, 142	
601	Extended coarse-grained dipole model for polar liquids: Application to bulk and confined water. <b>2018</b> , 98,	10
600	Exploring life: answer set programming in bioinformatics. <b>2018</b> , 359-412	1
599	Predicting the location of the non-local contacts in synuclein. <b>2018</b> , 1866, 1201-1208	4
598	Interaction Studies Between Cyclic Peptide ADT-C3 (Ac-CADTPC-NH2) with E-Cadherin Protein using the Molecular Docking Method Simulated on 120ns. <b>2018</b> , 21, 85-91	
597	Interfacing enzymes with silicon nanocrystals through the thiol-ene reaction. 2018, 10, 18706-18719	15
596	Molecular Docking of Phenylethylamine and CGP54626 to an Extracellular Domain of the GABAB-Receptor. <b>2018</b> , 50, 230-242	1
595	Protein stabilization with retained function of monellin using a split GFP system. 2018, 8, 12763	3
594	Generating Intrinsically Disordered Protein Conformational Ensembles from a Database of Ramachandran Space Pair Residue Probabilities Using a Markov Chain. <b>2018</b> , 122, 9087-9101	9

593	Origami Biosystems: 3D Assembly Methods for Biomedical Applications. <b>2018</b> , 2, 1800230	39
592	Stability Testing Considerations for Biologicals and Biotechnology Products. 2018, 335-347	
591	Methods for Stability Testing of Pharmaceuticals. 2018,	3
590	Computational design of thermostable mutants for cephalosporin C acylase from Pseudomonas strain SE83. <b>2018</b> , 116, 112-121	5
589	Tighter Ligand Binding Can Compensate for Impaired Stability of an RNA-Binding Protein. <b>2018</b> , 13, 1499-1505	4
588	Selected Publications of Ken A. Dill. <b>2018</b> , 122, 5269-5277	1
587	Correlating interfacial water dynamics with protein-protein interaction in complex of GDF-5 and BMPRI receptors. <b>2018</b> , 240, 50-62	3
586	Functional Role of Solvent Entropy and Conformational Entropy of Metal Binding in a Dynamically Driven Allosteric System. <b>2018</b> , 140, 9108-9119	17
585	Modeling protein folding in vivo. <b>2018</b> , 13, 13	14
584	Cooperative fibril model: Native, amyloid-like fibril and unfolded states of proteins. <b>2018</b> , 511, 154-165	3
583	Hybrid DFT study on non-covalent interactions and their influence on pK's of magnesium-carboxylate complexes. <b>2018</b> , 85, 13-24	5
582	Study of distance dependence of hydrophobic force between two graphene-like walls and a signature of pressure induced structure formation in the confined water. <b>2018</b> , 149, 044502	7
581	Nanotechnological Strategies for Protein Delivery. <b>2018</b> , 23,	33
580	Changing relations between proteins and osmolytes: a choice of nature. <b>2018</b> , 20, 20315-20333	23
579	Roles of membrane protein damage and intracellular protein damage in death of bacteria induced by atmospheric-pressure air discharge plasmas <b>2018</b> , 8, 21139-21149	14
578	Kinetic Trapping of Folded Proteins Relative to Aggregates under Physiologically Relevant Conditions. <b>2018</b> , 122, 7682-7698	11
577	Proteasesgeneral aspects. <b>2018</b> , 257-266	0
576	Solvent- and Heat-Dependent Binding Behaviors of HMeQ[6] with Alkyldiammonium Ions. <b>2018</b> , 3, 9211-9217	3

575	Interconverting Hydrogen-Bonding and Weak n -> 전 Interactions in Aqueous Solution: A Direct Spectroscopic Evidence. <b>2018</b> , 9, 5425-5429	9
574	PEGylation may reduce allergenicity and improve gelling properties of protein isolate from black kidney bean (Phaseolus vulgaris L.). <b>2018</b> , 25, 83-90	9
573	Helical Propensity Affects the Conformational Properties of the Denatured State of Cytochrome c'. <b>2018</b> , 114, 311-322	
57 <sup>2</sup>	Signature of Pareto optimization in the Escherichia coli proteome. <b>2018</b> , 8, 9141	6
571	Improved Fluorescence Methods for High-Throughput Protein Formulation Screening. 2018, 23, 516-528	11
570	Kinetic analysis of the multistep aggregation pathway of human transthyretin. <b>2018</b> , 115, E6201-E6208	16
569	The mechanism of salt effects on starch gelatinization from a statistical thermodynamic perspective. <b>2019</b> , 87, 593-601	18
568	Cytotoxic species in amyloid-associated diseases: Oligomers or mature fibrils. <b>2019</b> , 118, 333-369	9
567	Advances in protein structure prediction and design. <b>2019</b> , 20, 681-697	215
566	Dynamic properties of aqueous electrolyte solutions from non-polarisable, polarisable, and scaled-charge models. <b>2019</b> , 117, 3538-3549	17
565	Transcriptome sequencing of a toxic dinoflagellate, Karenia mikimotoi subjected to stress from solar ultraviolet radiation. <b>2019</b> , 88, 101640	6
564	Individual and combined effects of urea and trimethylamine N-oxide (TMAO) on protein structures. <b>2019</b> , 293, 111443	5
563	Forecasting the upper bound free energy difference between protein native-like structures. <b>2019</b> , 533, 122053	5
562	Explicit Characterization of the Free Energy Landscape of pKID-KIX Coupled Folding and Binding. <b>2019</b> , 5, 1342-1351	13
561	Molecular folding science. <b>2019</b> , 110, e23314	2
560	Pearl-Necklace-Like Local Ordering Drives Polypeptide Collapse. <b>2019</b> , 52, 5491-5498	5
559	Novel Heat-Promoted Folding Dynamics of the yybP-ykoY Manganese Riboswitch: Kinetic and Thermodynamic Studies at the Single-Molecule Level. <b>2019</b> , 123, 5412-5422	7
558	Purification and biochemical characterization of a novel thermostable protease from the oyster mushroom Pleurotus sajor-caju strain CTM10057 with industrial interest. <b>2019</b> , 19, 43	17

557	Spatially Heterogeneous Water Properties at Disordered Surfaces Decrease the Hydrophobicity of Nonpolar Self-Assembled Monolayers. <b>2019</b> , 10, 3991-3997	13
556	Folding Free Energy Landscape of Ordered and Intrinsically Disordered Proteins. <b>2019</b> , 9, 14927	19
555	Hydrogen bonding in the complexes formed by arsine and H-X molecules: A theoretical study. <b>2019</b> , 735, 136767	4
554	Enhancing the Biocatalytic Activity ofl-Asparaginase Using Aqueous Solutions of Cholinium-Based Ionic Liquids. <b>2019</b> , 7, 19720-19731	9
553	Phase behavior of blocky charge lattice polymers: Crystals, liquids, sheets, filaments, and clusters. <b>2019</b> , 100, 052404	13
552	Ligand Binding Induces Agonistic-Like Conformational Adaptations in Helix 12 of Progesterone Receptor Ligand Binding Domain. <b>2019</b> , 7, 315	3
551	Structure Based Prediction of Neoantigen Immunogenicity. <b>2019</b> , 10, 2047	34
550	Stabilization of HSV-2 viral vaccine candidate by spray drying. <b>2019</b> , 569, 118615	14
549	Structural Prediction and Inverse Design by a Strongly Correlated Neural Network. <b>2019</b> , 123, 108002	7
548	DMSO hydration redefined: Unraveling the hydrophobic hydration of solutes with a mixed hydrophilicBydrophobic characteristic. <b>2019</b> , 294, 111661	7
547	The secondary structure of a heptapeptide containing trifluoromethyl-Etetrafluorosulfanyl substituted amino acids. <b>2019</b> , 17, 8079-8082	3
546	Sequential and Environmental Dependence of Conformation in a Small Opioid Peptide. <b>2019</b> , 84, 13299-133	120
545	A topology-based investigation of protein interaction sites using Hydrophobic Cluster Analysis. <b>2019</b> , 167, 68-80	3
544	Observation of a weak intra-residue C5 hydrogen-bond in a dipeptide containing Gly-Pro sequence. <b>2019</b> , 151, 104309	5
543	Do soft anions promote protein denaturation through binding interactions? A case study using ribonuclease A <b>2019</b> , 9, 3416-3428	8
542	A grid-based algorithm in conjunction with a gaussian-based model of atoms for describing molecular geometry. <b>2019</b> , 40, 1290-1304	2
541	Structural Perspective on Revealing and Altering Molecular Functions of Genetic Variants Linked with Diseases. <b>2019</b> , 20,	13
540	A Shift in Aggregation Avoidance Strategy Marks a Long-Term Direction to Protein Evolution. <b>2019</b> , 211, 1345-1355	11

539	Thermodynamically driven assemblies and liquid-liquid phase separations in biology. <b>2019</b> , 15, 1135-1154	48
538	Quantifying the Strength of a Salt Bridge by Neutron Scattering and Molecular Dynamics. <b>2019</b> , 10, 3254-325	59 11
537	Aggregation rate of amyloid beta peptide is controlled by beta-content in monomeric state. <b>2019</b> , 150, 225101	16
536	Unfolded states under folding conditions accommodate sequence-specific conformational preferences with random coil-like dimensions. <b>2019</b> , 116, 12301-12310	28
535	Deciphering the intrinsic properties of fungal proteases in optimizing phytopathogenic interaction. <b>2019</b> , 711, 143934	3
534	Probing the Transition State in Enzyme Catalysis by High-Pressure NMR Dynamics. <b>2019</b> , 2, 726-734	14
533	Secondary Forces in Protein Folding. <b>2019</b> , 14, 1677-1686	44
532	General Method for Peptide Recognition in Water through Bioinspired Complementarity. <b>2019</b> , 31, 4889-489	<b>)6</b> 20
531	Charge-Preserving Atom Transfer Radical Polymerization Initiator Rescues the Lost Function of Negatively Charged Protein-Polymer Conjugates. <b>2019</b> , 20, 2392-2405	15
530	Nucleic Acid Nanotechnology. <b>2019</b> , 13-34	1
530 529	Nucleic Acid Nanotechnology. <b>2019</b> , 13-34  Crowding Differential Evolution for Protein Structure Prediction. <b>2019</b> , 193-203	3
529	Crowding Differential Evolution for Protein Structure Prediction. <b>2019</b> , 193-203  The Protein Role in Substrate Positioning and Reactivity for Biosynthetic Enzyme Complexes: The	3
529 528	Crowding Differential Evolution for Protein Structure Prediction. 2019, 193-203  The Protein Role in Substrate Positioning and Reactivity for Biosynthetic Enzyme Complexes: The Case of SyrB2/SyrB1. 2019, 9, 4930-4943  The Cold Thermal Response of an Amyloid Oligomer Differs from Typical Globular Protein Cold	3
529 528 527	Crowding Differential Evolution for Protein Structure Prediction. 2019, 193-203  The Protein Role in Substrate Positioning and Reactivity for Biosynthetic Enzyme Complexes: The Case of SyrB2/SyrB1. 2019, 9, 4930-4943  The Cold Thermal Response of an Amyloid Oligomer Differs from Typical Globular Protein Cold Denaturation. 2019, 10, 2453-2457	3 15 9
529 528 527 526	Crowding Differential Evolution for Protein Structure Prediction. 2019, 193-203  The Protein® Role in Substrate Positioning and Reactivity for Biosynthetic Enzyme Complexes: The Case of SyrB2/SyrB1. 2019, 9, 4930-4943  The Cold Thermal Response of an Amyloid Oligomer Differs from Typical Globular Protein Cold Denaturation. 2019, 10, 2453-2457  Structure of proteins: Evolution with unsolved mysteries. 2019, 149, 160-172	3 15 9
529 528 527 526 525	Crowding Differential Evolution for Protein Structure Prediction. 2019, 193-203  The Protein Role in Substrate Positioning and Reactivity for Biosynthetic Enzyme Complexes: The Case of SyrB2/SyrB1. 2019, 9, 4930-4943  The Cold Thermal Response of an Amyloid Oligomer Differs from Typical Globular Protein Cold Denaturation. 2019, 10, 2453-2457  Structure of proteins: Evolution with unsolved mysteries. 2019, 149, 160-172  End-to-End Differentiable Learning of Protein Structure. 2019, 8, 292-301.e3	3 15 9 8 169

521	Stabilizing osmolytes' effects on the structure, stability and function of tc-tenecteplase: A one peptide bond digested form of tenecteplase. <b>2019</b> , 130, 863-877	2
520	Preferential adsorption to air-water interfaces: a novel cryoprotective mechanism for LEA proteins. <b>2019</b> , 476, 1121-1135	9
519	Studies of the Effect of Urea on PEG-4000 Polymer Water Interactions at 298.15 K. <b>2019</b> , 64, 2341-2349	1
518	Single-Conformation Spectroscopy of Capped Aminoisobutyric Acid Dipeptides: The Effect of C-Terminal Cap Chromophores on Conformation. <b>2019</b> , 123, 4178-4187	6
517	Structure of water confined between two parallel graphene plates. <b>2019</b> , 150, 124703	26
516	Computational Investigation of the Effect of Pressure on Protein Stability. <b>2019</b> , 10, 1894-1899	7
515	Theoretical analysis on thermodynamic stability of chignolin. <b>2019</b> , 9, 5186	9
514	Protein corona formed on silver nanoparticles in blood plasma is highly selective and resistant to physicochemical changes of the solution. <b>2019</b> , 6, 1089-1098	36
513	Thermodynamics of protein folding: methodology, data analysis and interpretation of data. <b>2019</b> , 48, 305-316	9
512	Biophysical Spandrels form a Hot-Spot for Kosmotropic Mutations in Bacteriophage Thermal Adaptation. <b>2019</b> , 87, 27-36	О
511	Dihedral Angle Calculations To Elucidate the Folding of Peptides through Its Main Mechanical Forces. <i>Biochemistry</i> , <b>2019</b> , 58, 1032-1037	3
510	Hydrophilicity of the hydrophobic group: Effect of cosolvents and ions. <b>2019</b> , 280, 389-398	5
509	Ice-Binding Protein from Inhibits Ice Crystal Growth in Highly Alkaline Solutions. 2019, 11,	5
508	Void distributions reveal structural link between jammed packings and protein cores. <b>2019</b> , 99, 022416	7
507	EFFECT OF SOLVENTS ON CHEMICAL REACTIONS AND REACTIVITY. <b>2019</b> , 765-850	
506	Thermodynamic properties of amyloid fibrils: A simple model of peptide aggregation. <b>2019</b> , 489, 104-110	1
505	Molecular dynamics simulations suggest stabilizing mutations in a de novo designed <b>protein. 2019</b> , 32, 317-329	4
504	Elucidating the Nature of Interactions in Collagen Triple-Helix Wrapping. 2019, 10, 7644-7649	5

503	On the Nonaggregation of Normal Adult Hemoglobin and the Aggregation of Sickle Cell Hemoglobin. <b>2019</b> , 123, 10735-10745	1
502	Highly thermostable carboxylic acid reductases generated by ancestral sequence reconstruction. <b>2019</b> , 2, 429	13
501	Impact of polypeptide sequence on thermal properties for diblock, random, and alternating copolymers containing a stoichiometric mixture of glycine and valine. <b>2019</b> , 161, 197-204	7
500	Understanding contact patterns of protein structures from protein contact map and investigation of unique patterns in the globin-like folded domains. <b>2019</b> , 120, 9877-9886	4
499	The aqueous environment as an active participant in the protein folding process. 2019, 87, 227-239	5
498	Unveiling the n->Ħ interactions in dipeptides. <b>2019</b> , 2,	18
497	A systematic study of minima in alanine dipeptide. <b>2019</b> , 40, 297-309	15
496	Enzymes in Sweeteners Production. <b>2019</b> , 151-179	1
495	Effect of external electric field on the solvent forces in hydrophilic solutes. 2019, 518, 47-57	
494	Green Bio-processes. 2019,	3
494 493	Green Bio-processes. 2019,  Superfunneled Energy Landscape of Protein Evolution Unifies the Principles of Protein Evolution, Folding, and Design. 2019, 122, 018103	3 5
	Superfunneled Energy Landscape of Protein Evolution Unifies the Principles of Protein Evolution,	
493	Superfunneled Energy Landscape of Protein Evolution Unifies the Principles of Protein Evolution, Folding, and Design. <b>2019</b> , 122, 018103  Molecular Order Affects Interfacial Water Structure and Temperature-Dependent Hydrophobic	5
493 492	Superfunneled Energy Landscape of Protein Evolution Unifies the Principles of Protein Evolution, Folding, and Design. 2019, 122, 018103  Molecular Order Affects Interfacial Water Structure and Temperature-Dependent Hydrophobic Interactions between Nonpolar Self-Assembled Monolayers. 2019, 35, 2078-2088  Principles of Inter-Amino-Acid Recognition Revealed by Binding Energies between Homogeneous	26
493 492 491	Superfunneled Energy Landscape of Protein Evolution Unifies the Principles of Protein Evolution, Folding, and Design. 2019, 122, 018103  Molecular Order Affects Interfacial Water Structure and Temperature-Dependent Hydrophobic Interactions between Nonpolar Self-Assembled Monolayers. 2019, 35, 2078-2088  Principles of Inter-Amino-Acid Recognition Revealed by Binding Energies between Homogeneous Oligopeptides. 2019, 5, 97-108  4-Hydroxyphenylpyruvate Dioxygenase Thermolability Is Responsible for Temperature-Dependent	5 26 16
493 492 491 490	Superfunneled Energy Landscape of Protein Evolution Unifies the Principles of Protein Evolution, Folding, and Design. 2019, 122, 018103  Molecular Order Affects Interfacial Water Structure and Temperature-Dependent Hydrophobic Interactions between Nonpolar Self-Assembled Monolayers. 2019, 35, 2078-2088  Principles of Inter-Amino-Acid Recognition Revealed by Binding Energies between Homogeneous Oligopeptides. 2019, 5, 97-108  4-Hydroxyphenylpyruvate Dioxygenase Thermolability Is Responsible for Temperature-Dependent Melanogenesis in Aeromonas salmonicida subsp 2019, 85,  Increased sequence hydrophobicity reduces conformational specificity: A mutational case study of	5 26 16
493 492 491 490 489	Superfunneled Energy Landscape of Protein Evolution Unifies the Principles of Protein Evolution, Folding, and Design. 2019, 122, 018103  Molecular Order Affects Interfacial Water Structure and Temperature-Dependent Hydrophobic Interactions between Nonpolar Self-Assembled Monolayers. 2019, 35, 2078-2088  Principles of Inter-Amino-Acid Recognition Revealed by Binding Energies between Homogeneous Oligopeptides. 2019, 5, 97-108  4-Hydroxyphenylpyruvate Dioxygenase Thermolability Is Responsible for Temperature-Dependent Melanogenesis in Aeromonas salmonicida subsp 2019, 85,  Increased sequence hydrophobicity reduces conformational specificity: A mutational case study of the Arc repressor protein. 2019, 87, 23-33	5 26 16 1

485	Universal and simple method for facile fabrication of sustainable high internal phase emulsions solely using meat protein particles with various pH values. <b>2020</b> , 100, 105444		17
484	Study of alkaline phosphatase interaction with putrescine using multi-spectroscopic and docking methods. <b>2020</b> , 185, 110509		4
483	Combined in vitro and in silico analyses of missense mutations in GNPTAB provide new insights into the molecular bases of mucolipidosis II and III alpha/beta. <b>2020</b> , 41, 133-139		2
482	Protein Nanotechnology. <b>2020</b> ,		2
481	Evolutionary conservation and structural localizations suggest a physical trace of metabolism's progressive geochronological emergence. <b>2020</b> , 38, 3700-3719		3
480	Conformation changes of albumin and lysozyme on electrospun TiO nanofibers and its effects on MSC behaviors. <b>2020</b> , 185, 110604		9
479	Differential scanning calorimetry in the biopharmaceutical sciences. <b>2020</b> , 311-332		O
478	Temporal changes in postprandial intragastric pH: Comparing measurement methods, food structure effects, and kinetic modelling. <b>2020</b> , 128, 108784		10
477	Recent advances in shear-thinning and self-healing hydrogels for biomedical applications. <b>2020</b> , 137, 48668		80
476	ReaxFF molecular dynamics simulations on the structure and dynamics of electrolyte water systems at ambient temperature. <b>2020</b> , 172, 109349		9
475	Activity Coefficients and Solubility of CaCl2 from Molecular Simulations. <b>2020</b> , 65, 337-348		9
474	Critical considerations in the formulation development of parenteral biologic drugs. <b>2020</b> , 25, 574-581		14
473	Temperature of maximum density of proteins in water: £Chymotrypsin and bovine serum albumin. <b>2020</b> , 142, 106008		4
472	Hydrophobicity of small alkane molecules (propane dimer) in solvents: a classical molecular dynamics study. <b>2020</b> , 17, 1-12		O
471	Finding the generalized molecular principles of protein thermal stability. <b>2020</b> , 88, 788-808		19
470	Computational approach and electrochemical measurements for protein detection with MIP-based sensor. <b>2020</b> , 151, 111978		20
469	Molecular Dynamics Simulations of the Hypoxia-Inducible Factor PAS-B Domain Confirm That Internally Bound Water Molecules Function To Stabilize the Protein Core for Ligand Binding.  Biochemistry, <b>2020</b> , 59, 450-459	.2	2
468	Spectroscopic Signature of the Steric Strains in an RNase HI Cavity-Filling Destabilized Mutant Protein. <b>2020</b> , 124, 91-100		4

467	Do sequence neighbours of intrinsically disordered regions promote structural flexibility in intrinsically disordered proteins?. <b>2020</b> , 209, 107428	2
466	Structure, rheology and functionality of whey protein emulsion gels: Effects of double cross-linking with transglutaminase and calcium ions. <b>2020</b> , 102, 105569	49
465	PEGylation near a Patch of Nonpolar Surface Residues Increases the Conformational Stability of the WW Domain. <b>2020</b> , 85, 1725-1730	О
464	Self-Assembly and Neurotoxicity of Amyloid (21-40) Peptide Fragment: The Regulatory Role of GxxxG Motifs. <b>2020</b> , 15, 293-301	12
463	Functionalized TiO Nanotube-Based Electrochemical Biosensor for Rapid Detection of SARS-CoV-2. <b>2020</b> , 20,	76
462	The hydrophobic effect: is water afraid, or just not that interested?. <b>2020</b> , 6, 1	4
461	Protein conformational entropy is not slaved to water. <b>2020</b> , 10, 17587	1
460	Funneled energy landscape unifies principles of protein binding and evolution. <b>2020</b> , 117, 27218-27223	5
459	Cooperative unfolding of a single-layer 點heet protein, CPAP G-box. <b>2020</b> , 526, 105-109	1
458	Correlation among hydrophobic aromatic and aliphatic residues in the six enzyme classes. <b>2020</b> , 13, 209	Ο
457	Computational study of noncovalent interactions within the various complexes of para aminosalicylic acid and Cr2+, Mn+, Fe2+, Co+, Ni2+, Cu+, Zn2+ cations: exploration of the enhancing effect of the cationInteraction on the intramolecular hydrogen bond. 2020, 139, 1	2
456	Robust folding of a de novo designed ideal protein even with most of the core mutated to valine. <b>2020</b> , 117, 31149-31156	8
455	A Geometric Definition of Short to Medium Range Hydrogen-Mediated Interactions in Proteins. <b>2020</b> , 25,	3
454	Hydrophilic Interactions Dominate the Inverse Temperature Dependence of Polypeptide Hydration Free Energies Attributed to Hydrophobicity. <b>2020</b> , 11, 9965-9970	4
453	Quantifications of Oleocolloid Matrices Made of Whey Protein and Oleogels. 2020, 9,	6
452	Structural impact due to PPQEE deletion in multiple cancer associated protein - Integrin <b>¥</b> : An In silico exploration. <b>2020</b> , 198, 104216	3
451	Interdiction of Protein Folding for Therapeutic Drug Development in SARS CoV-2. <b>2020</b> , 124, 8201-8208	7
450	Insights into amyotrophic lateral sclerosis linked Pro525Arg mutation in the fused in sarcoma protein through analysis and molecular dynamics simulation. <b>2021</b> , 39, 5963-5976	3

449	Using physical features of protein core packing to distinguish real proteins from decoys. <b>2020</b> , 29, 1931-1944	1
448	Small crowder interactions can drive hydrophobic polymer collapse as well as unfolding. <b>2020</b> , 22, 18091-1810	ጋኂ
447	EGlutamyltranspeptidase from Bacillus amyloliquefaciens: transpeptidation activity enhancement and L-theanine production. <b>2020</b> , 140, 109644	6
446	Predicting Hydrophobicity by Learning Spatiotemporal Features of Interfacial Water Structure: Combining Molecular Dynamics Simulations with Convolutional Neural Networks. <b>2020</b> , 124, 9103-9114	13
445	Experimentally determined strengths of favorable and unfavorable interactions of amide atoms involved in protein self-assembly in water. <b>2020</b> , 117, 27339-27345	4
444	An able-cryoprotectant and a moderate denaturant: distinctive character of ethylene glycol on protein stability. <b>2020</b> , 1-13	1
443	Drug Stability and Chemical Kinetics. <b>2020</b> ,	1
442	Helix-Coil Transition at a Glycine Following a Nascent ⊞elix: A Synergetic Guidance Mechanism for Helix Growth. <b>2020</b> , 124, 7478-7490	3
441	Tube to ribbon transition in a self-assembling model peptide system. <b>2020</b> , 22, 18320-18327	7
440	Protein structure prediction in an atomic model with differential evolution integrated with the crowding niching method. <b>2020</b> , 1	4
439	Harnessing Environmental Ca for Extracellular Protein Thermostabilization. <i>Biochemistry</i> , <b>2020</b> , 59, 3725 <sub>3</sub> 3740	0 0
438	Increasing protein stability by engineering the n -> 🖰 interaction at the 毗urn. <b>2020</b> , 11, 9480-9487	9
437	Harnessing Noncovalent Interactions to Drive Single-Chain Nanoparticle Formation. <b>2020</b> , 53, 8141-8143	2
436	Cellular Control of Viscosity Counters Changes in Temperature and Energy Availability. <b>2020</b> , 183, 1572-1585.	e16
435	Effect of Homochirality of Dipeptide to Polymers' Degradation. 2020, 12,	O
434	New Insight into Mechanisms of Protein Adaptation to High Temperatures: A Comparative Molecular Dynamics Simulation Study of Thermophilic and Mesophilic Subtilisin-Like Serine Proteases. <b>2020</b> , 21,	8
433	Net Charge and Nonpolar Content Guide the Identification of Folded and Prion Proteins.  Biochemistry, 2020, 59, 1881-1895  3.2	1
432	Helical polymers for biological and medical applications. <b>2020</b> , 4, 291-310	36

431	Folding-Unfolding Dynamics of pH-Assisted Structures of S-Peptide. <b>2020</b> , 5, 5748-5755	1
430	Interaction of Water at the Hydrophobic Interface of Alkyl Group of Alcohol with p-Nitro-Aniline Charge Transfer State. <b>2020</b> , 5, 3655-3660	O
429	Effect of linker on the binding free energy of stapled p53/HDM2 complex. <b>2020</b> , 15, e0232613	1
428	The labilelthemical bond: A perspective on mechanochemistry in polymers. 2020, 202, 122639	19
427	Protein aggregation and immunogenicity of biotherapeutics. <b>2020</b> , 585, 119523	15
426	Associative interactions between pullulan and negatively charged bovine serum albumin in physiological saline solutions. <b>2020</b> , 246, 116630	4
425	Position-coded multivalent peptide-peptide interactions revealed by tryptophan-scanning mutagenesis. <b>2020</b> , 26, e3273	2
424	Volume and compressibility changes on mixing solutions of alkali halides/sodium acetate with sodium salt of butyric acid at 298.15 K: Understanding like charge ionic (anion⊞nion) interactions in water. <b>2020</b> , 315, 113654	4
423	Self-Assembly of Model Amphiphilic Peptides in Nonaqueous Solvents: Changing the Driving Force for Aggregation Does Not Change the Fibril Structure. <b>2020</b> , 36, 8451-8460	4
422	Comparative studies on ion-pair energetic, distribution among three domains of life: Archaea, eubacteria, and eukarya. <b>2020</b> , 88, 865-873	О
421	Biomolecular interactions of selected buffers with hemoglobin. <b>2020</b> , 142, 2003-2013	0
420	The influence of alkylation on the photophysical properties of BODIPYs and their labeling in blood plasma proteins. <b>2020</b> , 304, 112717	10
419	Mechanistic Insights into Protein Stability and Self-aggregation in GLUT1 Genetic Variants Causing GLUT1-Deficiency Syndrome. <b>2020</b> , 253, 87-99	7
418	Volumetric studies of solvation of carboxylic acids in aqueous, carbon tetrachloride, methanolic and methanolic-urea binary solutions at 298.15 K. <b>2020</b> , 304, 112658	
417	Protein unfolding by SDS: the microscopic mechanisms and the properties of the SDS-protein assembly. <b>2020</b> , 12, 5422-5434	15
416	The VES KM: a pathway for protein folding in vivo. <b>2020</b> , 92, 179-191	1
415	SAXSDom: Modeling multidomain protein structures using small-angle X-ray scattering data. <b>2020</b> , 88, 775-787	5
414	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. <b>2020</b> , 132, 11201-11207	3

## (2021-2020)

413	Thermodynamic Unfolding and Aggregation Fingerprints of Monoclonal Antibodies Using Thermal Profiling. <b>2020</b> , 37, 78		2
412	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. <b>2020</b> , 59, 11108-11114		9
411	Experimentally-driven protein structure modeling. <b>2020</b> , 220, 103777		14
410	Mass Spectrometry-Based Protein Footprinting for Higher-Order Structure Analysis: Fundamentals and Applications. <b>2020</b> , 120, 4355-4454		56
409	The role of water in the primary nucleation of protein amyloid aggregation. <b>2021</b> , 269, 106520		13
408	The enthalpies of dilution of some dipeptides in water at 298.15 K. <b>2021</b> , 154, 106338		1
407	Studies of osmotic and activity coefficient properties of aqueous solutions of triethylammonium formate and triethylammonium glycolate protic ionic liquids at 298.15 K. <b>2021</b> , 324, 115143		4
406	Effect of pH on the activity of ice-binding protein from Marinomonas primoryensis. <b>2021</b> , 25, 1-13		2
405	Predicting Hot Spot Residues at Protein-DNA Binding Interfaces Based on Sequence Information. <b>2021</b> , 13, 1-11		3
404	Solvent Induced Effects on Protein Folding. <b>2021</b> , 69-91		
403	The Origin of Protein. <b>2021</b> , 21-60		
402	The Challenge of Environment-Friendly Adhesives for Bio-Composites. <b>2021</b> , 195-229		2
401	Exploring the Evolutionary History of Kinetic Stability in the £ytic Protease Family. <i>Biochemistry</i> , <b>2021</b> , 60, 170-181	2	Ο
400	The Origin of Life. <b>2021</b> , 193-227		
400 399	The Origin of Life. <b>2021</b> , 193-227  Review of the current state of protein aggregation inhibition from a materials chemistry perspective: special focus on polymeric materials. <b>2021</b> , 2, 1139-1176		23
	Review of the current state of protein aggregation inhibition from a materials chemistry		23
399	Review of the current state of protein aggregation inhibition from a materials chemistry perspective: special focus on polymeric materials. <b>2021</b> , 2, 1139-1176  The driving force for co-translational protein folding is weaker in the ribosome vestibule due to		

395	The role of the intramolecular interactions in the structural behavior of biomolecules: Insights from rotational spectroscopy. <b>2021</b> , 93-141	3
394	Contributions of topological polar-polar contacts to achieve better folding stability of 2D/3D HP lattice proteins: An in silico approach. <b>2021</b> , 8, 291-306	1
393	Three-component radical homo Mannich reaction. <b>2021</b> , 12, 1006	6
392	Tim4 recognizes carbon nanotubes and mediates phagocytosis leading to granuloma formation. <b>2021</b> , 34, 108734	6
391	Spectroscopic Analysis of the Interaction between Silver Nanoparticles and Trypsin. 2021, 88, 153-165	2
390	Optimal proteome allocation and the temperature dependence of microbial growth laws. <b>2021</b> , 7, 14	2
389	Composition-dependent multivalency of peptide-peptide interactions revealed by tryptophan-scanning mutagenesis. <b>2021</b> , 27, e3310	3
388	Cross-Talk between Overlap Interactions in Biomolecules: A Case Study of the -Turn Motif. <b>2021</b> , 26,	O
387	Methane Clathrate Formation is Catalyzed and Kinetically Inhibited by the Same Molecule: Two Facets of Methanol. <b>2021</b> , 125, 4162-4168	1
386	An efficient alpha helix model and simulation framework for stationary electrostatic interaction force estimation. <b>2021</b> , 11, 9053	
385	Principles that rule the calculation of dihedral angles in secondary structures: the cases of an Ehelix and a Scheet. <b>2021</b> , 1229, 129802	
384	Genetic diversity of the LILRB1 and LILRB2 coding regions in an admixed Brazilian population sample. <b>2021</b> ,	
383	A Peptides Prediction Methodology for Tertiary Structure Based on Simulated Annealing. <b>2021</b> , 26, 39	1
382	Lipid Bilayer Induces Contraction of the Denatured State Ensemble of a Helical-Bundle Membrane Protein.	
381	Interaction-Deletion: A Composite Energy Method for the Optimization of Molecular Systems Selectively Removing Specific Nonbonded Interactions. <b>2021</b> , 125, 4668-4682	
380	Two-distinct polymer ubiquitin conjugates by photochemical grafting-from. <b>2021</b> , 222, 2100091	1
379	Pharmaceutical protein solids: Drying technology, solid-state characterization and stability. <b>2021</b> , 172, 211-233	7
378	Resurrection of Ancestral Malate Dehydrogenases Reveals the Evolutionary History of Halobacterial Proteins: Deciphering Gene Trajectories and Changes in Biochemical Properties. <b>2021</b> , 38, 3754-3774	2

## (2021-2021)

377	Self-consistent dielectric functions of materials: Toward accurate computation of Casimir-van der Waals forces. <b>2021</b> , 7,	4
376	Effect of pH and urea on the proteins secondary structure at the water/air interface and in solution. <b>2021</b> , 590, 38-49	7
375	A PROSS-designed extensively mutated estrogen receptor Bariant displays enhanced thermal stability while retaining native allosteric regulation and structure. <b>2021</b> , 11, 10509	2
374	A Structural Model for the Ligand Binding of Pneumococcal Serotype 3 Capsular Polysaccharide-Specific Protective Antibodies. <b>2021</b> , 12, e0080021	3
373	Large Stabilization Effects by Intramolecular Beryllium Bonds in -Benzene Derivatives. <b>2021</b> , 26,	О
372	Natural microbial polysaccharides as effective factors for modification of the catalytic properties of fungal cellobiose dehydrogenase. <b>2021</b> , 203, 4433-4448	3
371	Mechanistic insights into TNFR1/MADD death domains in Alzheimer's disease through conformational molecular dynamic analysis. <b>2021</b> , 11, 12256	2
370	Multiscale Models for Fibril Formation: Rare Events Methods, Microkinetic Models, and Population Balances. <b>2021</b> , 11,	1
369	The effects of intramolecular and intermolecular electrostatic repulsions on the stability and aggregation of NISTmAb revealed by HDX-MS, DSC, and nanoDSF. <b>2021</b> , 30, 1686-1700	4
368	Site-Specific Backbone and Side-Chain Contributions to Thermodynamic Stabilizing Forces of the WW Domain. <b>2021</b> , 125, 7108-7116	1
367	Intrinsic basis of thermostability of prolyl oligopeptidase from Pyrococcus furiosus. <b>2021</b> , 11, 11553	O
366	Folding and Intrinsic Disorder of the Receptor Tyrosine Kinase KIT Insert Domain Seen by Conventional Molecular Dynamics Simulations. <b>2021</b> , 22,	3
365	Thoughts on the Protein's Native State. <b>2021</b> , 12, 5963-5966	2
364	Crowding effects on water-mediated hydrophobic interactions. <b>2021</b> , 155, 024903	1
363	A pH-dependent protein stability switch coupled to the perturbed pKa of a single ionizable residue. <b>2021</b> , 274, 106591	1
362	In-capillary (electrophoretic) digestion-reduction-separation: A smart tool for middle-up analysis of mAb. <b>2021</b> , 1648, 462213	2
361	Quantum Convolutional Neural Network on Protein Distance Prediction. 2021,	О
360	Adhesion-mediated mechanosignaling forces mitohormesis. <b>2021</b> , 33, 1322-1341.e13	12

359	Subsecond Time-Resolved Mass Spectrometry in Dynamic Structural Biology. 2021,	3
358	Ensemble epistasis: thermodynamic origins of nonadditivity between mutations. <b>2021</b> , 219,	4
357	The Protein Folding Problem: The Role of Theory. <b>2021</b> , 433, 167126	5
356	Water-mediated interactions destabilize proteins. <b>2021</b> , 30, 2132-2143	4
355	Protein Assembly by Design. <b>2021</b> , 121, 13701-13796	16
354	Identification of Two Early Folding Stage Prion Non-Local Contacts Suggested to Serve as Key Steps in Directing the Final Fold to Be Either Native or Pathogenic. <b>2021</b> , 22,	O
353	Assessment of the resolving power of hydrophobic interaction chromatography for intact protein analysis on non-porous butyl polymethacrylate phases. <b>2021</b> , 1651, 462310	
352	The Promise of Mutation Resistant Drugs for SARS-CoV-2 That Interdict in the Folding of the Spike Protein Receptor Binding Domain. <b>2021</b> , 1, 288-302	O
351	Water Depletion Enhanced by Halogenation of Benzene. <b>2021</b> , 125, 8855-8861	
350	Enzyme Catalysis in Non-Native Environment with Unnatural Selectivity Using Polymeric Nanoreactors.	O
349	Prediction of multiple dry-wet transition pathways with a mesoscale variational approach. <b>2021</b> , 155, 124110	
348	Enzyme Catalysis in Non-Native Environment with Unnatural Selectivity Using Polymeric Nanoreactors. <b>2021</b> ,	1
347	Mechanical couplings of protein backbone and side chains exhibit scale-free network properties and specific hotspots for function. <b>2021</b> , 19, 5309-5320	1
346	Kinematic Reconstruction of Cyclic Peptides and Protein Backbones from Partial Data. <b>2021</b> , 61, 4975-5000	
345	Characterization of Proteinaceous Particles in Monoclonal Antibody Drug Products Using Mass Spectrometry. <b>2021</b> , 110, 3403-3409	0
344	Current trends in protein-surfactant interactions: A review. <b>2021</b> , 341, 117344	4
343	Bionanomaterials based on protein self-assembly: Design and applications in biotechnology. <b>2021</b> , 52, 107835	9
342	Bimolecular quenching of tryptophan fluorescence in a membrane protein: Evolution of local solvation and environment during folding into a bilayer. <b>2021</b> , 260, 119919	2

341	Terahertz spectra and weak intermolecular interactions of nucleosides or nucleoside drugs. <b>2022</b> , 265, 120344	3
340	Characterization of polymers by LenS3 multiangle light scattering. <b>2021</b> , 533-559	
339	Using molecular simulations to investigate how intermolecular interactions dictate liquid structure. <b>2021</b> , 71-91	1
338	Modeling the interaction of SARS-CoV-2 binding to the ACE2 receptor via molecular theory of solvation. <b>2021</b> , 45, 15448-15457	0
337	Structural thermodynamics of a random coil protein in guanidine hydrochloride. <b>2000</b> , 41, 44-49	2
336	Simplified Models for Understanding and Predicting Protein Structure. 57-80	9
335	Fundamental Structures and Behaviors of Proteins. 1-61	3
334	In vitro Protein Refolding. 527-555	1
333	Sequence and Structure of Proteins. 43-86	1
332	A new method for side-chain conformation prediction using a Hopfield network and reproduced rotamers. <b>1996</b> , 17, 1667-1683	5
331	Life at High Temperatures. <b>2006</b> , 167-209	4
330	Gramicidin Channels: Versatile Tools. <b>2007</b> , 33-80	11
329	Computational Determination of the Relative Free Energy of Binding [Application to Alanine Scanning Mutagenesis. <b>2007</b> , 305-339	5
328	Protein Subcellular Location Prediction Based on Pseudo Amino Acid Composition and Immune Genetic Algorithm. <b>2006</b> , 534-542	4
327	Protein Structure Prediction Using Evolutionary Algorithms Hybridized with Backtracking. 2003, 321-328	36
326	Approximate Protein Folding in the HP Side Chain Model on Extended Cubic Lattices (Extended Abstract). <b>1999</b> , 212-223	4
325	Protein Folding. <b>2007</b> , 303-343	6
324	Simulations of Protein Aggregation. <b>2006</b> , 47-77	2

323	De Novo Protein Structure Prediction. <b>2007</b> , 43-63	6
322	The Folding, Stability and Dynamics of T4 Lysozyme: A Perspective Using Nuclear Magnetic Resonance. <b>1993</b> , 258-304	16
321	CGU: An Algorithm for Molecular Structure Prediction. <b>1997</b> , 1-21	11
320	Molecular Basis of Protein Functionality. <b>1996</b> , 27-80	8
319	Membrane Protein Structure and Stability: Implications of the First Crystallographic Analyses. <b>1994</b> , 3-26	8
318	Decoding the Signals of Membrane Protein Sequences. <b>1994</b> , 27-40	6
317	Physical stabilization of proteins in aqueous solution. <b>2002</b> , 13, 61-84	18
316	Enzyme stabilization by directed evolution. <b>2000</b> , 22, 55-76	6
315	High Pressure Effects on Protein Structure. <b>1998</b> , 59-86	4
314	The Role of Interior Side-Chain Packing in Protein Folding and Stability. <b>1994</b> , 549-578	5
313	Protein Folding in the Endoplasmic Reticulum. <b>1993</b> , 125-136	4
312	Molecular Structure Prediction by Global Optimization. <b>1997</b> , 217-234	8
311	Convex Global Underestimation for Molecular Structure Prediction. 2001, 1-18	7
310	Protein Folding: Local Structures, Domains and Assemblies. <b>1991</b> , 137-152	3
309	Theoretical Perspectives on In Vitro and In Vivo Protein Folding. <b>1994</b> , 115-134	13
308	Studies on Hyperstable Proteins: Crystallins from the Eye-Lens and Enzymes from Thermophilic Bacteria. <b>1994</b> , 49-62	3
307	Serine proteinases from cold-adapted organisms. <b>1997</b> , 415, 27-46	10
306	Strategies for Increasing Protein Stability. <b>2020</b> , 2073, 163-181	10

305	Challenges and Issues in the Development of Formulations of Protein Pharmaceuticals. <b>1999</b> , 205-238	1
304	Protein stabilization by the rational design of surface charge-charge interactions. <b>2009</b> , 490, 261-83	27
303	Thermodynamic database for proteins: features and applications. <b>2010</b> , 609, 97-112	16
302	Studying Protein Interior with Fractal Dimension. 2013, 19-84	1
301	Protein Folding Modeling with Neural Cellular Automata Using the Face-Centered Cubic Model. <b>2017</b> , 125-134	1
300	Physics-Based Modeling of Side ChainBide Chain Interactions in the UNRES Force Field. <b>2019</b> , 89-115	2
299	Delta: A Toolset for the Structural Analysis of Biological Sequences on a 3D Triangular Lattice. <b>2007</b> , 518-529	3
298	Folding Protein-Like Structures with Open L-Systems. <b>2007</b> , 1100-1109	2
297	Overcoming the Key Challenges in De Novo Protein Design: Enhancing Computational Efficiency and Incorporating True Backbone Flexibility. <b>2008</b> , 133-183	1
296	Water-Hydrophobic Compound Interactions with the Microbial Cell. <b>2010</b> , 1451-1466	25
296 295	Water-Hydrophobic Compound Interactions with the Microbial Cell. <b>2010</b> , 1451-1466  Interactions of Polarizable Media inWater and the Hydrophobic Interaction. <b>2009</b> , 43-62	25
295	Interactions of Polarizable Media inWater and the Hydrophobic Interaction. <b>2009</b> , 43-62	2
295 294	Interactions of Polarizable Media inWater and the Hydrophobic Interaction. <b>2009</b> , 43-62  Volumetric Properties of Proteins and the Role of Solvent in Conformational Dynamics. <b>2009</b> , 173-186	2
295 294 293	Interactions of Polarizable Media inWater and the Hydrophobic Interaction. 2009, 43-62  Volumetric Properties of Proteins and the Role of Solvent in Conformational Dynamics. 2009, 173-186  Differential Evolution for Protein Structure Prediction Using the HP Model. 2011, 323-333  Psychrophilic enzymes: insights into cold adaptation and catalysis from the first high resolution	2 1 17
295 294 293 292	Interactions of Polarizable Media inWater and the Hydrophobic Interaction. 2009, 43-62  Volumetric Properties of Proteins and the Role of Solvent in Conformational Dynamics. 2009, 173-186  Differential Evolution for Protein Structure Prediction Using the HP Model. 2011, 323-333  Psychrophilic enzymes: insights into cold adaptation and catalysis from the first high resolution crystal structures. 1999, 277-295	2 1 17
295 294 293 292 291	Interactions of Polarizable Media inWater and the Hydrophobic Interaction. 2009, 43-62  Volumetric Properties of Proteins and the Role of Solvent in Conformational Dynamics. 2009, 173-186  Differential Evolution for Protein Structure Prediction Using the HP Model. 2011, 323-333  Psychrophilic enzymes: insights into cold adaptation and catalysis from the first high resolution crystal structures. 1999, 277-295  Environment as Well as Sequence Determines the Secondary Structure of Proteins. 1995, 87-88	2 1 17 1

287	Predictions of Protein Secondary and Tertiary Structure. <b>1994</b> , 203-232	1
286	Urea and Guanidine-HCl Yield Different Unfolding Free Energies for CheY: Which Denaturant Provides the Most Reliable Free Energy Values?. <b>1993</b> , 533-540	2
285	Effects of Mutations on the Performance of Genetic Algorithms Suitable for Protein Folding Simulations. <b>1993</b> , 1283-1286	4
284	From Gas-Phase to Solution. <b>2008</b> , 389-465	2
283	Theoretical and computational advances in protein misfolding. <b>2019</b> , 118, 1-31	1
282	Subunit association and structural analysis of platelet basic protein and related proteins investigated by 1H NMR spectroscopy and circular dichroism <b>1994</b> , 269, 20110-20118	28
281	The effects of deletion of the amino-terminal helix on troponin C function and stability. <b>1994</b> , 269, 9857-9863	26
280	Enthalpy-entropy balance and convergence temperatures in protein unfolding <b>1994</b> , 269, 4047-4049	12
279	Identification of intramolecular interactions in adrenergic receptors <b>1992</b> , 267, 21991-21994	55
278	Thermodynamics of oligosaccharide binding to a monoclonal antibody specific for a Salmonella O-antigen point to hydrophobic interactions in the binding site <b>1992</b> , 267, 8371-8376	87
277	The crystal structure of muscle phosphoglucomutase refined at 2.7-angstrom resolution <b>1992</b> , 267, 6322-6337	65
276	A novel strategy for stabilization of Escherichia coli ribonuclease HI involving a screen for an intragenic suppressor of carboxyl-terminal deletions <b>1994</b> , 269, 26904-26911	34
275	Identification of productive folding intermediates which account for the flow of protein folding pathway <b>1993</b> , 268, 4043-4049	12
274	Determinants of catalytic activity and stability of carbonic anhydrase II as revealed by random mutagenesis <b>1993</b> , 268, 948-954	43
273	The disulfide folding pathway of hirudin elucidated by stop/go folding experiments <b>1993</b> , 268, 20988-20996	96
272	Studies of the association and conformational properties of metal-free insulin in alkaline sodium chloride solutions by one- and two-dimensional 1H NMR <b>1992</b> , 267, 8963-8970	23
271	The folding of hirudin adopts a mechanism of trial and error <b>1992</b> , 267, 3038-3043	35
270	Chapter 6 Thermodynamics of protein folding and stability. <b>1999</b> , 217-270	24

## (2018-2004)

269	Protein Folding, Misfolding, and Aggregation. Formation of Inclusion Bodies and Aggresomes. <b>2004</b> , 69, 971	1
268	Chapter 20:Computer Simulation Studies of Heat Capacity Effects Associated with Hydrophobic Effects. <b>2010</b> , 436-456	6
267	Chapter 21:Partial Molar Heat Capacity Changes of Gases Dissolved in Liquids. <b>2010</b> , 457-471	6
266	Chapter 8:Single Molecule Protein Unfolding Using a Nanopore. <b>2016</b> , 237-269	1
265	The functional impact of Pgm amino acid polymorphism on glycogen content in Drosophila melanogaster. <b>2001</b> , 159, 201-10	29
264	Complex molecular mixtures under cycling gradients as basis for lifell origins.	2
263	Adhesion-mediated mechanosignaling forces mitohormesis.	3
262	Functionalized TiO2 nanotube-based Electrochemical Biosensor for Rapid Detection of SARS-CoV-2.	3
261	Could network structures generated with simple rules imposed on a cubic lattice reproduce the structural descriptors of globular proteins?.	1
260	Protein coevolution and physicochemical adaptation in the APAF-1/apoptosome: structural and functional implications.	1
259	End-to-end differentiable learning of protein structure.	10
258	Microglobule formation and a microscopic order parameter monitoring the phase transition of aqueous poly(N-isopropylacrylamide) solution. <b>2018</b> , 2,	11
257	Numerical study of anomalous diffusion of light in semicrystalline polymer structures. <b>2020</b> , 2,	5
256	The thermal unfolding of hevein, a small disulfide-rich protein. <b>1995</b> , 228, 649-52	11
255	Template-directed protein folding into a metastable state of increased activity. 1995, 232, 528-35	5
254	Denaturation of Globular Proteins in Relation to Their Functional Properties. <b>1996</b> , 181-236	4
253	Why do proteins aggregate? "Intrinsically insoluble proteins" and "dark mediators" revealed by studies on "insoluble proteins" solubilized in pure water. <b>2013</b> , 2, 94	29
252	Myths in Modern Science: The Hydrogen Bond and its Surroundings Part 2. The Hydrophobic-Bond-Myth. <b>2018</b> , 18, 10-20	1

251	Systematic and evolutionary insights derived from mtDNA COI barcode diversity in the Decapoda (Crustacea: Malacostraca). <b>2011</b> , 6, e19449	99
250	3-Deoxyglucosone: a potential glycating agent accountable for structural alteration in H3 histone protein through generation of different AGEs. <b>2015</b> , 10, e0116804	40
249	Engineering Proteins for Thermostability with iRDP Web Server. <b>2015</b> , 10, e0139486	20
248	The Biokinetic Spectrum for Temperature. <b>2016</b> , 11, e0153343	36
247	A case of ezetimibe-effective hypercholesterolemia with a novel heterozygous variant in ABCG5. <b>2020</b> , 67, 1099-1105	2
246	Uncovering dehydration in cytochrome refolding from urea- and guanidine hydrochloride-denatured unfolded state by high pressure spectroscopy. <b>2019</b> , 16, 18-27	3
245	A Simple Principle for Understanding the Combined Cellular Protein Folding and Aggregation. <b>2020</b> , 21, 3-21	4
244	Evaluation of Luciferase Thermal Stability by Arginine Saturation in the Flexible Loops. <b>2020</b> , 17, 30-39	1
243	Rosetta and the Journey to Predict Proteins Structures, 20 Years on. <b>2020</b> , 15, 611-628	5
242	SHEETSPAIR: A Database of Amino Acid Pairs in Protein Sheet Structures. <b>2007</b> , 6, S589-S595	6
241	Protein Folding by Computer: How Far Have We Gone?. <b>2011</b> , 27, 187-194	1
240	Rheological Characterization Bovine Serum Albumin Gels Induced by High Hydrostatic Pressure. <b>2015</b> , 06, 770-779	7
239	Levinthal Paradox Revisited, and Dismissed. <b>2012</b> , 02, 23-32	6
238	MEAN-FIELD THEORY AND COMPUTATION OF ELECTROSTATICS WITH IONIC CONCENTRATION DEPENDENT DIELECTRICS. <b>2016</b> , 14, 249-271	15
237	Attractive SulfurInteraction between Fluorinated Dimethyl Sulfur (FDMS) and Benzene. <b>2007</b> , 28, 959-964	18
236	Stability of buried and networked salt-bridges (BNSB)in thermophilic proteins. <b>2019</b> , 15, 61-67	3
235	Insights from the salt bridge analysis of malate dehydrogenase from H. salinarum and E.coli. <b>2019</b> , 15, 95-103	3
234	Salt-bridges in the microenvironment of stable protein structures. <b>2020</b> , 16, 900-909	1

233	How well do force fields capture the strength of salt bridges in proteins?. 2018, 6, e4967	30
232	Molecular insights into the urea-cholinesulfate interactions in aqueous solution. <b>2021</b> , 23, 25317-25334	Ο
231	On the size, shape and energetics of the hydration shell around alkanes. <b>2021</b> , 23, 24852-24865	0
230	Biomolecular Perturbations in In-Cell Dynamic Nuclear Polarization Experiments. <b>2021</b> , 8, 743829	2
229	A New Strategy for the Preparation of E Isomers of Hydrazones and Anil-Like Compounds: Thermally Stimulated Isomerization of Z Isomers of Anions. <b>2021</b> , 6, 10651-10654	
228	Supramolecular Peptide Nanostructures: Self-assembly and Biomedical Applications. <b>2021</b> , 100082	1
227	Effect of urea on the hydration and aggregation of hydrophobic and amphiphilic solute models: Implications to protein aggregation. <b>2021</b> , 155, 144501	О
226	First-Principles Simulation of Dielectric Function in Biomolecules. <b>2021</b> , 14,	6
225	The impact of calcium phosphate on FITC-BSA loading of sonochemically prepared PLGA nanoparticles for inner ear drug delivery elucidated by two different fluorimetric quantification methods. <b>2021</b> , 79, 105783	
224	Global Minimization and Parameter Estimation in Computational Biology. <b>2001</b> , 153-180	
223	Ribosomes and the Synthesis of Proteins. <b>2001</b> , 1669-1739	
222	Sequence and Structure of Proteins. <b>2001</b> , 43-86	
221	Computer Simulation of Protein Unfolding. <b>2002</b> , 260-268	
220	Pressure-Induced Secondary Structural Changes of Proteins Studied by FTIR Spectroscopy. <b>2002</b> , 101-120	
219	Protein Stability.	
218	Fold Recognition using the OPLS All-Atom Potential and the Surface Generalized Born Solvent Model. <b>2002</b> , 445-476	
217	Protein Structure and Stability: Database-derived Potentials and Prediction.	
216	Protein Design Concepts.	

215	Cell Membranes: Protein Components and Functions. 2002,
214	Drug-Target Binding Forces: Advances in Force Field Approaches. <b>2003</b> , 169-185
213	Protein Adsorption in Relation to Solution Association and Aggregation. 2003,
212	Ocular Delivery and Therapeutics of Proteins and Peptides. <b>2003</b> , 493-514
211	Screening of Enzyme Variants for Thermostability. 2003,
210	On Unfolding Lattice Polygons/Trees and Diameter-4 Trees. <b>2006</b> , 186-195
209	Experimental Studies of Pathways of Protein Folding. 190-205
208	References. <b>2008</b> , 635-661
207	Pressure-Temperature Phase Diagrams of Proteins. 99
206	Engineering Proteins for Stability and Efficient Folding. 1281
206	Engineering Proteins for Stability and Efficient Folding. 1281 o  Multiscale Modeling and Simulation for Fluid Mechanics at the Nanoscale. 2008, 229-290
205	Multiscale Modeling and Simulation for Fluid Mechanics at the Nanoscale. <b>2008</b> , 229-290
205	Multiscale Modeling and Simulation for Fluid Mechanics at the Nanoscale. 2008, 229-290  Predicting Free Energy Changes of Mutations in Proteins. 343
205	Multiscale Modeling and Simulation for Fluid Mechanics at the Nanoscale. 2008, 229-290  Predicting Free Energy Changes of Mutations in Proteins. 343  Folding and Association of Multi-domain and Oligomeric. 32
205 204 203 202	Multiscale Modeling and Simulation for Fluid Mechanics at the Nanoscale. 2008, 229-290  Predicting Free Energy Changes of Mutations in Proteins. 343  Folding and Association of Multi-domain and Oligomeric. 32  Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure. 3
205 204 203 202 201	Multiscale Modeling and Simulation for Fluid Mechanics at the Nanoscale. 2008, 229-290  Predicting Free Energy Changes of Mutations in Proteins. 343  Folding and Association of Multi-domain and Oligomeric. 32  Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure. 3  Thermal Unfolding of Proteins. 70

197	ReceptorLigand Interactions in Biological Systems. 1	1
196	Protein Folding: Energetics.	
195	Proteins: Computational Analysis.	
194	Conformational Equilibrium of the Tetraethylammonium Ion in Alcohols. <b>2009</b> , 58, 471-475	1
193	Logic Programming Techniques in Protein Structure Determination: Methodologies and Results. <b>2009</b> , 560-566	1
192	Protein Folding and Binding: Effective Potentials, Replica Exchange Simulations, and Network Models. <b>2009</b> , 97-121	
191	Low-Resolution Recognition Factors Determine Major Characteristics of the Energy Landscape in Protein Protein Interaction. <b>2009</b> , 21-42	
190	Fine-Tuning Protein Stability. <b>2010</b> , 189-202	
189	Protein Purification. 2012, 35-48	
188	Hydrophobic Enhancement of Dopa-Mediated Adhesion in a Mussel Foot Protein. <b>2014</b> , 43-54	
187	Fundamental Aspects of RNA. <b>2014</b> , 21-36	
186	Predicting the Three-Dimensional Structure of Proteins by Homology-Based Model Building. <b>1991</b> , 137-158	1
185	Physical Approaches to Conformation and Assembly of Biological Macromolecules. <b>1991</b> , 17-28	
184	STOPPED-FLOW CIRCULAR DICHROISM AND 19F NMR AS PROBES FOR THE FOLDING OF RAT INTESTINAL FATTY-ACID BINDING PROTEIN (IFABP)11Supported by NIH research grants DK13332 to C.F. and DK30292 to J.I.G <b>1992</b> , 437-443	
183	Physicochemical Basis of Hydrophobic Interaction Chromatography. <b>1992</b> , 443-480	1
182	Molecular Aspects of Protein Translocation into Chloroplasts. <b>1992</b> , 133-140	
181	Do Well-Populated Intermediates Represent the Pathway of Protein Folding?. <b>1993</b> , 269-273	
180	Protein Stability, Folding and Association. <b>1993</b> , 1-22	

179	Structure, Dynamics and Function of Hydrogen-Bonded Networks in Proteins and Related Systems. <b>1994</b> , 489-508	
178	Conformational Search and Protein Folding. <b>1994</b> , 125-163	Ο
177	Proteins under pressure. <b>1994</b> , 91-104	2
176	Calicheamicin. <b>1994</b> , 130-161	
175	Food enzymes and the new technology. <b>1995</b> , 41-113	1
174	. 1997,	
173	Chapter The secondary structure of proteins. <b>1997</b> , 99-136	
172	Chapter 4 Computational methods relating protein sequence and structure. <b>1997</b> , 165-268	
171	Introduction. <b>1998</b> , 3-14	
170	Bioconversion of Acrylonitrile to Acrylamide Using a Thermostable Nitrile Hydratase. <b>1999</b> , 671-679	
169	Protein Folding and Aggregation: A Revisit of Basic Conception. <b>2015</b> , 63-87	
168	Proteins: Association, Adsorption, and Aggregation. 6258-6281	
167	Introduction to Protein Folding. <b>2016</b> , 5-28	
166	- Molecular Thermodynamic Modeling of Fluctuation Solution Theory Properties. <b>2016</b> , 252-283	
165	Conformational Stability of the NH2-Terminal Propeptide of the Precursor of Pulmonary Surfactant Protein SP-B. <b>2016</b> , 11, e0158430	1
164	Unlocked capacity of proteins to attack membranes characteristic of aggregation: the evil for diseases and aging from Pandoraß box.	2
163	Single-molecule force spectroscopy of protein-membrane interactions.	
162	A shift in aggregation avoidance strategy marks a long-term direction to protein evolution.	1

161	Water and Membranes. 2017, 21-48	
160	End-to-End Differentiable Learning of Protein Structure.	1
159	How well do force fields capture the strength of salt bridges in proteins?.	
158	The solvent-excluded surfaces of water-soluble proteins.	
157	Protein/Emulsifier Interactions. <b>2019</b> , 101-192	1
156	SAXSDom: Modeling multi-domain protein structures using small-angle X-ray scattering data.	
155	Viscoadaptation controls intracellular reaction rates in response to heat and energy availability.	
154	Algorithmic Assessment of Missense Mutation Severity in the Von-Hippel Lindau Protein.	
153	Experimentally-Determined Strengths of Atom-Atom (C, N, O) Interactions Responsible for Protein Self-Assembly in Water: Applications to Folding and Other Protein Processes.	
152	Exploring the evolutionary history of kinetic stability in the alpha-lytic protease family.	
151	De novo mutation in KITLG gene causes a variant of Familial Progressive Hyper- and Hypo-pigmentation (FPHH). <b>2021</b> , e1841	2
150	Transient disorder along pathways to amyloid. <b>2021</b> , 281, 106711	11
149	Interaction of Antifreeze Proteins with Water. <b>2020</b> , 109-127	
148	Stability Studies of Proteinous Compounds. <b>2020</b> , 187-236	
147	The effects of whey protein and oleogel interactions on mechanical properties of oleocolloids and hydro-oleocolloids matrices. <b>2022</b> , 124, 107285	0
146	Membrane Protein Structure and Folding. <b>2020</b> , 159-206	
145	A Custom-Designed Recombinant Multiepitope Protein for Human Cytomegalovirus Diagnosis. <b>2019</b> , 13, 316-328	2
144	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy.	

143	Electrospray-Induced Mass Spectrometry Is Not Suitable for Determination of Peptidic Cu(II) Complexes. <b>2021</b> , 32, 2766-2776	4
142	Evolutionary perspectives on protein structure, stability, and functionality. <b>2002</b> , 82-107	1
141	Protein-Protein Interaction and Macromolecular Visualization. <b>2009</b> , 79-96	
140	On Unfolding 3D Lattice Polygons and 2D Orthogonal Trees. <b>2008</b> , 374-384	1
139	A Robust Class of Stable Proteins in the 2D HPC Model. <b>2008</b> , 180-192	
138	In silico modelling and characterization of eight blast resistance proteins in resistant and susceptible rice cultivars. <b>2020</b> , 18, 75	
137	Algorithmic assessment of missense mutation severity in the Von-Hippel Lindau protein. <b>2020</b> , 15, e0234100	1
136	Electrostatic interactions affecting the active site of class sigma glutathione S-transferase. <b>2000</b> , 347 Pt 1, 193-7	10
135	Modulation of the immune response with T-cell epitopes: the ultimate goal for specific immunotherapy of autoimmune disease. <b>1994</b> , 81, 487-96	21
134	Polymer nano-systems for the encapsulation and delivery of active biomacromolecular therapeutic agents. <b>2021</b> ,	5
133	Tendon Extracellular Matrix Assembly, Maintenance and Dysregulation Throughout Life. <b>2021</b> , 1348, 45-103	4
132	Metal Ion Binding Induces Local Protein Unfolding and Destabilizes Human Carbonic Anhydrase II <b>2022</b> ,	O
131	Using all-atom simulations in explicit solvent to study aggregation of amphipathic peptides into amyloid-like fibrils. <b>2022</b> , 347, 118283	2
130	Untangling the complexity of membrane protein folding <b>2022</b> , 72, 237-247	1
129	Seeking Solvation: Exploring the Role of Protein Hydration in Silk Gelation 2022, 27,	1
128	Critical Role of E1623 Residue in S3-S4 Loop of Nav1.1 Channel and Correlation Between Nature of Substitution and Functional Alteration <b>2021</b> , 14, 797628	O
127	Influence of Long-Range Forces on the Transition States and Dynamics of NaCl Ion-Pair Dissociation in Water <b>2022</b> ,	1
126	Decay Processes in Cationic Alkali Metals in Microsolvated Clusters: A Complex Absorbing Potential Based Equation-of-Motion Coupled Cluster Investigation <b>2022</b> ,	O

125	Application of circular dichroism spectroscopy in studying protein folding, stability, and interaction. <b>2022</b> , 213-224	О
124	The stability and dynamics of computationally designed proteins 2022, 35,	2
123	Identifying nonadditive contributions to the hydrophobicity of chemically heterogeneous surfaces via dual-loop active learning <b>2022</b> , 156, 024701	2
122	How sticky are our proteins? Quantifying hydrophobicity of the human proteome.	1
121	From Protein Design to the Energy Landscape of a Cold Unfolding Protein 2022,	O
120	Molecular interactions of esculin with bovine serum albumin and recognition of binding sites with spectroscopy and molecular docking <b>2022</b> , 1-15	2
119	Modulation of an n->∄ interaction with ⊞luoro groups. <b>2010</b> , 2010, 251-262	10
118	Investigations on the role of cation-linteractions in active centers of superoxide dismutase. <b>2022</b> , 13-13	O
117	Investigating binding dynamics of trans resveratrol to HSA for an efficient displacement of aflatoxin B using spectroscopy and molecular simulation <b>2022</b> , 12, 2400	1
116	Neural-augmented two-stage Monte Carlo tree search with over-sampling for protein folding in HP Model. <b>2022</b> , 17, 685-694	
115	Molten globule-like transition state of protein barnase measured with calorimetric force spectroscopy <b>2022</b> , 119, e2112382119	1
114	Protein Folding Interdiction Strategy for Therapeutic Drug Development in Viral Diseases: Ebola VP40 and Influenza A M1 <b>2022</b> , 23,	1
113	On the Number of Saturated and Optimal Extended 2-Regular Simple Stacks in the Nussinov-Jacobson Energy Model <b>2022</b> ,	O
112	Macromolecular Crowding Is More than Hard-Core Repulsions 2022,	4
111	Conformer-Specific Spectroscopy and IR-Induced Isomerization of a Model Peptide: Ac-Phe-NHMe <b>2022</b> ,	1
110	REMOVED: Water Structure, Properties and Some Applications [A review. <b>2022</b> , 6, 100053	4
109	Heterogeneity in Protein Folding and Unfolding Reactions 2022,	1
108	Calcium-induced environmental adaptability of the blood protein vitronectin.	

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107	The Statistical Trends of Protein Evolution: A Lesson from AlphaFold Database.	
106	Rational Protein Engineering of Bacterial N-demethylases to Create Biocatalysts for the Production of Methylxanthines.	O
105	Dissecting the stability determinants of a challenging de novo protein fold using massively parallel design and experimentation.	О
104	Role of Branched-chain Amino Acid Metabolism in Tumor Development and Progression <b>2021</b> , 26, 237-243	1
103	Systematic study of cooperative interplay between single-electron pnicogen bond and halogen bond in X3CIIPH2YIIClY (X=H, CH3; Y=CN, NC) complexes in two different minima configuration.	О
102	Could network structures generated with simple rules imposed on a cubic lattice reproduce the structural descriptors of globular proteins?. <b>2021</b> , 10,	
101	Entropy in the Molecular Recognition of Membrane Protein-Lipid Interactions <b>2021</b> , 12, 12218-12224	3
100	Molecular Structure Determination: Convex Global Underestimation. <b>2001</b> , 1511-1515	
99	Simulations of Protein Aggregation. <b>2006</b> , 47-77	
98	De Novo Protein DesignUsing Rigid Templates. <b>2008</b> , 643-648	
97	Molecular Structure Determination: Convex Global Underestimation. 2008, 2311-2316	
96	Data_Sheet_1.PDF. <b>2019</b> ,	
95	Data_Sheet_1.PDF. <b>2019</b> ,	

Turning Failures into Applications: The Problem of Protein & Prediction.. 2022, 2449, 169-185

Unravelling the molecular interaction of diselenodipropionic acid (DSePA) with human serum

Proton-enabled biomimetic stabilization of small-molecule organic cathode in aqueous zinc-ion

Contribution of hydrophobic interactions to protein mechanical stability.. 2022, 20, 1946-1956

Capturing protein denaturation using electrical Impedance technique. 2022, 119301

124

94

93

92

91

90

albumin (HSA).

batteries.

89	Non-glycosylated SARS-CoV-2 RBD elicited a robust neutralizing antibody response in mice <b>2022</b> , 506, 113279	0
88	Roles of interfacial water states on advanced biomedical material design <b>2022</b> , 186, 114310	1
87	Statistical and energetic analysis of hydrogen bonds in short and long peptide nanotapes/nanofibers using molecular dynamics simulations. <b>2022</b> , 359, 119308	Ο
86	Benchmarking Adaptive Steered Molecular Dynamics (ASMD) on CHARMM Force Fields 2022,	Ο
85	Principles and practical applications of structure-based vaccine design. <b>2022</b> , 77, 102209	1
84	Minimal Increments of Hydrophobic Collapse within the N-Terminus of the Neuropeptide Galanin.  Biochemistry,  3.2	O
83	Non-equilibrium protein folding and activation by ATP-driven chaperones.	1
82	General Principles Underpinning Amyloid Structure. 2022, 16,	5
81	How do plants feel the heat and survive?. 2022,	2
80	Early selection of the amino acid alphabet was adaptively shaped by biophysical constraints of foldability.	
79	Specific protein-urea interactions. 2022,	
78	Structural Design and Assessing of Recombinantly Expressed African Swine Fever Virus p72 Trimer in Saccharomyces cerevisiae. 13,	O
77	Entropies Derived from the Packing Geometries within a Single Protein Structure. 2022, 7, 20719-20730	
76	Non-Equilibrium Protein Folding and Activation by ATP-Driven Chaperones. <b>2022</b> , 12, 832	Ο
75	Sequence dependent folding motifs of the secondary structures of Gly-Pro and Pro-Gly containing oligopeptides.	1
74	Genetic diversity of the LILRB1 and LILRB2 coding regions in an admixed Brazilian population sample.	1
73	Accurate protein stability predictions from homology models.	0
72	Core packing of well-defined X-ray and NMR structures is the same. <b>2022</b> , 31,	

71	How Good Is the Density-Corrected SCAN Functional for Neutral and Ionic Aqueous Systems, and What Is So Right about the Hartreeflock Density?.	2
70	Structure and Orientation of Water and Choline Chloride Molecules Around a Methane Hydrophobe: A Computer Simulation Study.	
69	En Route to Stabilized Compact Conformations of Single-Chain Polymeric Nanoparticles in Complex Media.	0
68	A novel TYMP mutation in a family with MNGIE syndrome: Molecular docking, dynamic simulation and computational investigations.	
67	Protein aggregation rate depends on mechanical stability of fibrillar structure .	1
66	Interdiction in the Early Folding of the p53 DNA-Binding Domain Leads to Its Amyloid-Like Misfolding. <b>2022</b> , 27, 4810	
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64	Microhydration of Phenyl Formate: Gas-Phase Laser Spectroscopy, Microwave Spectroscopy, and Quantum Chemistry Calculations.	1
63	Modeling protein structure as a stable static equilibrium. <b>2022</b> , 106,	
62	Influence of cationInteractions to the structural stability of phycocyanin proteins: A computational study. <b>2022</b> , 100, 107752	
61	The neuropeptide galanin adopts an irregular secondary structure. <b>2022</b> , 626, 121-128	
60	Calcium-induced environmental adaptability of the blood protein vitronectin. 2022,	O
59	Structural organization of peptides. <b>2023</b> , 1-33	О
58	How Did Life Emerge in Chemically Complex Messy Environments?. <b>2022</b> , 12, 1319	O
57	Symmetrization in the Calculation Pipeline of Gauss Function-Based Modeling of Hydrophobicity in Protein Structures. <b>2022</b> , 14, 1876	1
56	The Statistical Trends of Protein Evolution: A Lesson from AlphaFold Database.	O
55	Development of Alternating Copolymerization of Peptides and Exploration of the Function of Alternating Sequences. <b>2022</b> , 80, 941-951	О
54	Dissecting the stability determinants of a challenging de novo protein fold using massively parallel design and experimentation. <b>2022</b> , 119,	О

53	Contribution of phosphorylation modification by sodium tripolyphosphate to the properties of surimi-crabmeat mixed gels. <b>2022</b> , 169, 114052	0
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50	Introducing or removing heparan sulfate binding sites does not alter brain uptake of the blood-brain barrier shuttle scFv8D3.	О
49	Logistic Regression-Guided Identification of Cofactor Specificity-Contributing Residues in Enzyme with Sequence Datasets Partitioned by Catalytic Properties.	0
48	Organic solvents aggregating and shaping structural folding of protein, a case study of the protease enzyme. <b>2022</b> , 291, 106909	1
47	Difference in the hydration state of water at the hydrophobic interface of structural isomers of propanol investigated by U.V visible absorption and Raman spectroscopic study. <b>2022</b> , 368, 120530	O
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38	An efficient method to predict protein thermostability in alanine mutation. <b>2022</b> , 24, 29629-29639	O
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36	Effect of Structural and Optical Isomerism of Aliphatic Dipeptides on the Enthalpic Characteristics of Interaction with Xylitol in Water. <b>2022</b> , 96, 2687-2691	О

35	Introducing or removing heparan sulfate binding sites does not alter brain uptake of the bloodBrain barrier shuttle scFv8D3. <b>2022</b> , 12,	O
34	Atomic-Level Thermodynamics Analysis of the Binding Free Energy of SARS-CoV -2 Neutralizing Antibodies.	O
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