

Pernilla Wittung-stafshede

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

245 papers	10,235 citations	50 h-index	90 g-index
282 ext. papers	11,663 ext. citations	6 avg, IF	6.34 L-index

#	Paper	IF	Citations
245	Orientation of β -Synuclein at Negatively Charged Lipid Vesicles: Linear Dichroism Reveals Time-Dependent Changes in Helix Binding Mode. <i>Journal of the American Chemical Society</i> , 2021 , 143, 18899-18906	16.4	3
244	The copper chaperone CCS facilitates copper binding to MEK1/2 to promote kinase activation. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101314	5.4	2
243	Effects of the Toxic Metals Arsenite and Cadmium on β -Synuclein Aggregation In Vitro and in Cells. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
242	ATP7A-Regulated Enzyme Metalation and Trafficking in the Menkes Disease Puzzle. <i>Biomedicines</i> , 2021 , 9,	4.8	6
241	The Zero-Order Loop in Apoazurin Modulates Folding Mechanism In Silico. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 3501-3509	3.4	2
240	Response to crowded conditions reveals compact nucleus for amyloid formation of folded protein. <i>QRB Discovery</i> , 2021 , 2,	2.7	1
239	Macromolecular crowding modulates β -Synuclein amyloid fiber growth. <i>Biophysical Journal</i> , 2021 , 120, 3374-3381	2.9	9
238	Another pearl in the "copper-transport" necklace. <i>Biophysical Journal</i> , 2021 , 120, 4305-4306	2.9	
237	C-terminal truncation of β -Synuclein alters DNA structure from extension to compaction. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 568, 43-47	3.4	1
236	Impact of crowded environments on binding between protein and single-stranded DNA. <i>Scientific Reports</i> , 2021 , 11, 17682	4.9	1
235	Gut power: Modulation of human amyloid formation by amyloidogenic proteins in the gastrointestinal tract. <i>Current Opinion in Structural Biology</i> , 2021 , 72, 33-38	8.1	1
234	Crosstalk Between Alpha-Synuclein and Other Human and Non-Human Amyloidogenic Proteins: Consequences for Amyloid Formation in Parkinson's Disease. <i>Journal of Parkinson's Disease</i> , 2020 , 10, 819-830	5.3	4
233	The Caenorhabditis elegans homolog of human copper chaperone Atox1, CUC-1, aids in distal tip cell migration. <i>BioMetals</i> , 2020 , 33, 147-157	3.4	0
232	Single-vesicle imaging reveals lipid-selective and stepwise membrane disruption by monomeric β -Synuclein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 14178-14186	11.5	20
231	Differential effects of Cu and Fe ions on in vitro amyloid formation of biologically-relevant β -Synuclein variants. <i>BioMetals</i> , 2020 , 33, 97-106	3.4	5
230	Single-cell tracking demonstrates copper chaperone Atox1 to be required for breast cancer cell migration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 2014-2019	11.5	28
229	Female Faculty: Why So Few and Why Care?. <i>Chemistry - A European Journal</i> , 2020 , 26, 8319-8323	4.8	10

228	A gut bacterial amyloid promotes β -synuclein aggregation and motor impairment in mice. <i>ELife</i> , 2020 , 9,	8.9	117
227	Mirror-Image 5S Ribonucleoprotein Complexes. <i>Angewandte Chemie</i> , 2020 , 132, 3753-3760	3.6	0
226	Correlation between Cellular Uptake and Cytotoxicity of Fragmented β -Synuclein Amyloid Fibrils Suggests Intracellular Basis for Toxicity. <i>ACS Chemical Neuroscience</i> , 2020 , 11, 233-241	5.7	14
225	Mirror-Image 5S Ribonucleoprotein Complexes. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 3724-3731	16.4	10
224	Evaluation of copper chaperone ATOX1 as prognostic biomarker in breast cancer. <i>Breast Cancer</i> , 2020 , 27, 505-509	3.4	11
223	Amyloid formation of fish β -parvalbumin involves primary nucleation triggered by disulfide-bridged protein dimers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 27997-28004	11.5	4
222	My journey in academia: things not on the CV. <i>Pure and Applied Chemistry</i> , 2020 , 92, 789-796	2.1	
221	Synaptic vesicle mimics affect the aggregation of wild-type and A53T β -synuclein variants differently albeit similar membrane affinity. <i>Protein Engineering, Design and Selection</i> , 2019 , 32, 59-66	1.9	5
220	Crowding-Induced Elongated Conformation of Urea-Unfolded Apoazurin: Investigating the Role of Crowder Shape in Silico. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 3607-3617	3.4	16
219	Copper relay path through the N-terminus of Wilson disease protein, ATP7B. <i>Metallomics</i> , 2019 , 11, 1472-1480	4.5	11
218	Wilson disease missense mutations in ATP7B affect metal-binding domain structural dynamics. <i>BioMetals</i> , 2019 , 32, 875-885	3.4	5
217	Interaction between Copper Chaperone Atox1 and Parkinson's Disease Protein β -Synuclein Includes Metal-Binding Sites and Occurs in Living Cells. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 4659-4668	5.7	10
216	Membrane-Protein-Hydration Interaction of β -Synuclein with Anionic Vesicles Probed via Angle-Resolved Second-Harmonic Scattering. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 1044-1049	3.4	8
215	Folding of copper proteins: role of the metal?. <i>Quarterly Reviews of Biophysics</i> , 2018 , 51, e4	7	15
214	Abundant fish protein inhibits β -synuclein amyloid formation. <i>Scientific Reports</i> , 2018 , 8, 5465	4.9	17
213	Fucosylated Molecules Competitively Interfere with Cholera Toxin Binding to Host Cells. <i>ACS Infectious Diseases</i> , 2018 , 4, 758-770	5.5	28
212	Synergistic Effects of Copper Sites on Apparent Stability of Multicopper Oxidase, Fet3p. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	3
211	Alpha-Synuclein Modulates the Physical Properties of DNA. <i>Chemistry - A European Journal</i> , 2018 , 24, 15685-15690	4.8	19

210	In Vitro Analysis of β -Synuclein Amyloid Formation and Cross-Reactivity. <i>Methods in Molecular Biology</i> , 2018 , 1779, 73-83	1.4	2
209	Copper chaperone blocks amyloid formation via ternary complex. <i>Quarterly Reviews of Biophysics</i> , 2018 , 51, e6	7	7
208	3D-Models of Insulin-Producing β -Cells: from Primary Islet Cells to Stem Cell-Derived Islets. <i>Stem Cell Reviews and Reports</i> , 2018 , 14, 177-188	6.4	10
207	Copper Chaperone Atox1 Interacts with Cell Cycle Proteins. <i>Computational and Structural Biotechnology Journal</i> , 2018 , 16, 443-449	6.8	9
206	Copper distribution in breast cancer cells detected by time-of-flight secondary ion mass spectrometry with delayed extraction methodology. <i>Biointerphases</i> , 2018 , 13, 06E412	1.8	6
205	Geometrical Description of Protein Structural Motifs. <i>Journal of Physical Chemistry B</i> , 2018 , 122, 11289-11294	12.94	4
204	A Luminal Loop of Wilson Disease Protein Binds Copper and Is Required for Protein Activity. <i>Biophysical Journal</i> , 2018 , 115, 1007-1018	2.9	2
203	Unraveling amyloid formation paths of Parkinson's disease protein β -Synuclein triggered by anionic vesicles. <i>Quarterly Reviews of Biophysics</i> , 2017 , 50, e3	7	19
202	Defining the human copper proteome and analysis of its expression variation in cancers. <i>Metallomics</i> , 2017 , 9, 112-123	4.5	62
201	Copper chaperone Atox1 plays role in breast cancer cell migration. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 483, 301-304	3.4	34
200	Extracellular vesicles from human pancreatic islets suppress human islet amyloid polypeptide amyloid formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 11127-11132	11.5	18
199	Copper chaperone ATOX1 regulates pluripotency factor OCT4 in preimplantation mouse embryos. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 491, 147-153	3.4	5
198	The six metal binding domains in human copper transporter, ATP7B: molecular biophysics and disease-causing mutations. <i>BioMetals</i> , 2017 , 30, 823-840	3.4	16
197	Probing functional roles of Wilson disease protein (ATP7B) copper-binding domains in yeast. <i>Metallomics</i> , 2017 , 9, 981-988	4.5	10
196	Disease-causing point-mutations in metal-binding domains of Wilson disease protein decrease stability and increase structural dynamics. <i>BioMetals</i> , 2017 , 30, 27-35	3.4	13
195	Roles of Copper-Binding Proteins in Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	32
194	Second harmonic generation for collagen I characterization in rectal cancer patients with and without preoperative radiotherapy. <i>Journal of Biomedical Optics</i> , 2017 , 22, 1-6	3.5	6
193	Effects of small-molecule amyloid modulators on a Drosophila model of Parkinson's disease. <i>PLoS ONE</i> , 2017 , 12, e0184117	3.7	10

192	A stretched conformation of DNA with a biological role?. <i>Quarterly Reviews of Biophysics</i> , 2017 , 50, e11	7	15
191	A Copper Story: From Protein Folding and Metal Transport to Cancer. <i>Israel Journal of Chemistry</i> , 2016 , 56, 671-681	3.4	5
190	Cross-talk between amyloidogenic proteins in type-2 diabetes and Parkinson's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 12473-12477	11.5	80
189	Extended functional repertoire for human copper chaperones. <i>Biomolecular Concepts</i> , 2016 , 7, 29-39	3.7	27
188	Copper binding triggers compaction in N-terminal tail of human copper pump ATP7B. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 470, 663-669	3.4	13
187	The C-Terminus of Human Copper Importer Ctr1 Acts as a Binding Site and Transfers Copper to Atox1. <i>Biophysical Journal</i> , 2016 , 110, 95-102	2.9	30
186	Gut Microbiota Regulate Motor Deficits and Neuroinflammation in a Model of Parkinson's Disease. <i>Cell</i> , 2016 , 167, 1469-1480.e12	56.2	1558
185	Attenuating <i>Listeria monocytogenes</i> Virulence by Targeting the Regulatory Protein PrfA. <i>Cell Chemical Biology</i> , 2016 , 23, 404-14	8.2	20
184	Insulin-degrading enzyme is activated by the C-terminus of β -synuclein. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 466, 192-5	3.4	18
183	Unresolved questions in human copper pump mechanisms. <i>Quarterly Reviews of Biophysics</i> , 2015 , 48, 471-8	7	13
182	Insulin-degrading enzyme prevents β -synuclein fibril formation in a nonproteolytical manner. <i>Scientific Reports</i> , 2015 , 5, 12531	4.9	59
181	Single injection of small-molecule amyloid accelerator results in cell death of nigral dopamine neurons in mice. <i>Npj Parkinson's Disease</i> , 2015 , 1, 15024	9.7	7
180	Identification of New Potential Interaction Partners for Human Cytoplasmic Copper Chaperone Atox1: Roles in Gene Regulation?. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 16728-39	6.3	20
179	Bacterial Chaperones CsgE and CsgC Differentially Modulate Human β -Synuclein Amyloid Formation via Transient Contacts. <i>PLoS ONE</i> , 2015 , 10, e0140194	3.7	47
178	Enthalpy-entropy compensation at play in human copper ion transfer. <i>Scientific Reports</i> , 2015 , 5, 10518	4.9	15
177	Direct Correlation Between Ligand-Induced β -Synuclein Oligomers and Amyloid-like Fibril Growth. <i>Scientific Reports</i> , 2015 , 5, 10422	4.9	27
176	Synthesis of Multiring Fused 2-Pyridones via a Nitrene Insertion Reaction: Fluorescent Modulators of β -Synuclein Amyloid Formation. <i>Organic Letters</i> , 2015 , 17, 6194-7	6.2	13
175	Human cytoplasmic copper chaperones Atox1 and CCS exchange copper ions in vitro. <i>BioMetals</i> , 2015 , 28, 577-85	3.4	19

174	The bacterial curli system possesses a potent and selective inhibitor of amyloid formation. <i>Molecular Cell</i> , 2015 , 57, 445-55	17.6	137
173	Human Copper Chaperone Atox1 Translocates to the Nucleus but does not Bind DNA In Vitro. <i>Protein and Peptide Letters</i> , 2015 , 22, 532-8	1.9	17
172	Synthetic crowding agent dextran causes excluded volume interactions exclusively to tracer protein apoazurin. <i>FEBS Letters</i> , 2014 , 588, 811-4	3.8	24
171	T versus D in the MTCXXC motif of copper transport proteins plays a role in directional metal transport. <i>Journal of Biological Inorganic Chemistry</i> , 2014 , 19, 1037-47	3.7	14
170	Folding of an unfolded protein by macromolecular crowding in vitro. <i>Biochemistry</i> , 2014 , 53, 2271-7	3.2	46
169	Macromolecular crowding effects on two homologs of ribosomal protein s16: protein-dependent structural changes and local interactions. <i>Biophysical Journal</i> , 2014 , 107, 401-410	2.9	10
168	Interaction between the anticancer drug Cisplatin and the copper chaperone Atox1 in human melanoma cells. <i>Protein and Peptide Letters</i> , 2014 , 21, 63-8	1.9	16
167	Effects of macromolecular crowding agents on protein folding in vitro and in silico. <i>Biophysical Reviews</i> , 2013 , 5, 137-145	3.7	55
166	Modulation of curli assembly and pellicle biofilm formation by chemical and protein chaperones. <i>Chemistry and Biology</i> , 2013 , 20, 1245-54		56
165	Modulation of β -synuclein fibrillization by ring-fused 2-pyridones: templation and inhibition involve oligomers with different structure. <i>Archives of Biochemistry and Biophysics</i> , 2013 , 532, 84-90	4.1	25
164	Direct observation of protein unfolded state compaction in the presence of macromolecular crowding. <i>Biophysical Journal</i> , 2013 , 104, 694-704	2.9	53
163	Quantification of excluded volume effects on the folding landscape of <i>Pseudomonas aeruginosa</i> apoazurin in vitro. <i>Biophysical Journal</i> , 2013 , 105, 1689-99	2.9	41
162	Small pH and salt variations radically alter the thermal stability of metal-binding domains in the copper transporter, Wilson disease protein. <i>Journal of Physical Chemistry B</i> , 2013 , 117, 13038-50	3.4	14
161	Determinants for simultaneous binding of copper and platinum to human chaperone Atox1: hitchhiking not hijacking. <i>PLoS ONE</i> , 2013 , 8, e70473	3.7	37
160	Reaction of platinum anticancer drugs and drug derivatives with a copper transporting protein, Atox1. <i>Biochemical Pharmacology</i> , 2012 , 83, 874-81	6	28
159	Effects of macromolecular crowding on burst phase kinetics of cytochrome c folding. <i>Biochemistry</i> , 2012 , 51, 9836-45	3.2	40
158	Similar but different: thermodynamic and structural characterization of a pair of enantiomers binding to acetylcholinesterase. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 12716-20	16.4	15
157	Mechanisms of protein oligomerization: inhibitor of functional amyloids templates β -synuclein fibrillation. <i>Journal of the American Chemical Society</i> , 2012 , 134, 3439-44	16.4	87

156	Role of metal in folding and stability of copper proteins in vitro. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012 , 1823, 1594-603	4.9	64
155	In vitro thermodynamic dissection of human copper transfer from chaperone to target protein. <i>PLoS ONE</i> , 2012 , 7, e36102	3.7	23
154	Discovery of ligands for ADP-ribosyltransferases via docking-based virtual screening. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 7706-18	8.3	35
153	Interactions between DNA, transcriptional regulator Dreb2a and the Med25 mediator subunit from <i>Arabidopsis thaliana</i> involve conformational changes. <i>Nucleic Acids Research</i> , 2012 , 40, 5938-50	20.1	22
152	Protein folding inside the cell. <i>Biophysical Journal</i> , 2011 , 101, 265-6	2.9	7
151	Macromolecular crowding extended to a heptameric system: the Co-chaperonin protein 10. <i>Biochemistry</i> , 2011 , 50, 3034-44	3.2	22
150	Macromolecular crowding tunes folding landscape of parallel α -protein, apoflavodoxin. <i>Journal of the American Chemical Society</i> , 2011 , 133, 646-8	16.4	38
149	Comparison of chemical and thermal protein denaturation by combination of computational and experimental approaches. II. <i>Journal of Chemical Physics</i> , 2011 , 135, 175102	3.9	24
148	Cisplatin binds human copper chaperone Atox1 and promotes unfolding in vitro. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 6951-6	11.5	85
147	Experimental evolution of adenylate kinase reveals contrasting strategies toward protein thermostability. <i>Biophysical Journal</i> , 2010 , 99, 887-96	2.9	21
146	Interdomain interactions modulate collective dynamics of the metal-binding domains in the Wilson disease protein. <i>Journal of Physical Chemistry B</i> , 2010 , 114, 1836-48	3.4	18
145	Factors defining effects of macromolecular crowding on protein stability: an in vitro/in silico case study using cytochrome c. <i>Biochemistry</i> , 2010 , 49, 6519-30	3.2	116
144	Copper-transfer mechanism from the human chaperone Atox1 to a metal-binding domain of Wilson disease protein. <i>Journal of Physical Chemistry B</i> , 2010 , 114, 3698-706	3.4	42
143	Residue-specific analysis of frustration in the folding landscape of repeat beta/alpha protein apoflavodoxin. <i>Journal of Molecular Biology</i> , 2010 , 396, 75-89	6.5	11
142	Non-linear effects of macromolecular crowding on enzymatic activity of multi-copper oxidase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010 , 1804, 740-4	4	54
141	Metal Ions, Protein Folding, and Conformational States 2010 , 3-11		1
140	Stability and Folding of Copper-Binding Proteins 2010 , 61-80		1
139	Med8, Med18, and Med20 subunits of the Mediator head domain are interdependent upon each other for folding and complex formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 20728-33	11.5	6

138	Folding, stability and shape of proteins in crowded environments: experimental and computational approaches. <i>International Journal of Molecular Sciences</i> , 2009 , 10, 572-88	6.3	57
137	Pseudosymmetry, high copy number and twinning complicate the structure determination of <i>Desulfovibrio desulfuricans</i> (ATCC 29577) flavodoxin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 523-34		7
136	Lysine-60 in copper chaperone Atox1 plays an essential role in adduct formation with a target Wilson disease domain. <i>Journal of the American Chemical Society</i> , 2009 , 131, 16371-3	16.4	38
135	Conformational dynamics of metal-binding domains in Wilson disease protein: molecular insights into selective copper transfer. <i>Biochemistry</i> , 2009 , 48, 5849-63	3.2	21
134	Tuning of copper-loop flexibility in <i>Bacillus subtilis</i> CopZ copper chaperone: role of conserved residues. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 1919-32	3.4	12
133	Differential roles of Met10, Thr11, and Lys60 in structural dynamics of human copper chaperone Atox1. <i>Biochemistry</i> , 2009 , 48, 960-72	3.2	17
132	Predicting protein folding cores by empirical potential functions. <i>Archives of Biochemistry and Biophysics</i> , 2009 , 483, 16-22	4.1	4
131	Macromolecular crowding modulates folding mechanism of alpha/beta protein apoflavodoxin. <i>Biophysical Journal</i> , 2009 , 96, 671-80	2.9	69
130	Direct optical detection of aptamer conformational changes induced by target molecules. <i>Analytical Chemistry</i> , 2009 , 81, 10002-6	7.8	78
129	Gold nanoparticles can induce the formation of protein-based aggregates at physiological pH. <i>Nano Letters</i> , 2009 , 9, 666-71	11.5	317
128	Mapping the domain structure of the influenza A virus polymerase acidic protein (PA) and its interaction with the basic protein 1 (PB1) subunit. <i>Virology</i> , 2008 , 379, 135-42	3.6	32
127	Role of copper in thermal stability of human ceruloplasmin. <i>Biophysical Journal</i> , 2008 , 94, 1384-91	2.9	37
126	Location and flexibility of the unique C-terminal tail of Aquifex aeolicus co-chaperonin protein 10 as derived by cryo-electron microscopy and biophysical techniques. <i>Journal of Molecular Biology</i> , 2008 , 381, 707-17	6.5	13
125	Stability and ATP binding of the nucleotide-binding domain of the Wilson disease protein: effect of the common H1069Q mutation. <i>Journal of Molecular Biology</i> , 2008 , 383, 1097-111	6.5	27
124	Role of cations in stability of acidic protein <i>Desulfovibrio desulfuricans</i> apoflavodoxin. <i>Archives of Biochemistry and Biophysics</i> , 2008 , 474, 128-35	4.1	18
123	Effect of Hofmeister ions on protein thermal stability: roles of ion hydration and peptide groups?. <i>Archives of Biochemistry and Biophysics</i> , 2008 , 479, 69-73	4.1	80
122	Structure and dynamics of Cu(I) binding in copper chaperones Atox1 and CopZ: a computer simulation study. <i>Journal of Physical Chemistry B</i> , 2008 , 112, 4583-93	3.4	26
121	Conserved residues modulate copper release in human copper chaperone Atox1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 11158-63	11.5	40

120	In vitro unfolding of yeast multicopper oxidase Fet3p variants reveals unique role of each metal site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 19258-63	11.5	26
119	Response to Harve et al: Effects on protein folding speed and shape despite possible size changes in Ficoll 70. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, E120-E120	11.5	78
118	Crowded, cell-like environment induces shape changes in aspherical protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 11754-9	11.5	173
117	An adaptive mutation in adenylate kinase that increases organismal fitness is linked to stability-activity trade-offs. <i>Protein Engineering, Design and Selection</i> , 2008 , 21, 19-27	1.9	26
116	Discrete roles of copper ions in chemical unfolding of human ceruloplasmin. <i>Biochemistry</i> , 2007 , 46, 9638-44	9.44	26
115	Molecular crowding enhances native structure and stability of alpha/beta protein flavodoxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 18976-81	11.5	212
114	Impact of cofactor on stability of bacterial (CopZ) and human (Atox1) copper chaperones. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007 , 1774, 1316-22	4	26
113	Thermodynamic stability and folding of proteins from hyperthermophilic organisms. <i>FEBS Journal</i> , 2007 , 274, 4023-33	5.7	85
112	Establishing the entatic state in folding metallated Pseudomonas aeruginosa azurin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3159-64	11.5	25
111	Folding and assembly of co-chaperonin heptamer probed by forster resonance energy transfer. <i>Archives of Biochemistry and Biophysics</i> , 2007 , 464, 306-13	4.1	3
110	Role of copper in folding and stability of cupredoxin-like copper-carrier protein CopC. <i>Archives of Biochemistry and Biophysics</i> , 2007 , 467, 58-66	4.1	12
109	Macromolecular crowding increases structural content of folded proteins. <i>FEBS Letters</i> , 2007 , 581, 5065-68	3.98	95
108	Correlation between protein stability cores and protein folding kinetics: a case study on Pseudomonas aeruginosa apo-azurin. <i>Structure</i> , 2006 , 14, 1401-10	5.2	10
107	On the precision of experimentally determined protein folding rates and phi-values. <i>Protein Science</i> , 2006 , 15, 553-63	6.3	39
106	Differential effects of alcohols on conformational switchovers in alpha-helical and beta-sheet protein models. <i>Biochemistry</i> , 2006 , 45, 7740-9	3.2	55
105	Phi-value analysis of apo-azurin folding: comparison between experiment and theory. <i>Biochemistry</i> , 2006 , 45, 6458-66	3.2	21
104	Folding of Desulfovibrio desulfuricans flavodoxin is accelerated by cofactor fly-casting. <i>Archives of Biochemistry and Biophysics</i> , 2006 , 451, 51-8	4.1	20
103	Folding and assembly pathways of co-chaperonin proteins 10: Origin of bacterial thermostability. <i>Archives of Biochemistry and Biophysics</i> , 2006 , 456, 8-18	4.1	16

102	Kinetic folding and assembly mechanisms differ for two homologous heptamers. <i>Journal of Molecular Biology</i> , 2006 , 363, 729-42	6.5	18
101	Solvation of the folding-transition state in <i>Pseudomonas aeruginosa</i> azurin is modulated by metal: Solvation of azurin's folding nucleus. <i>Protein Science</i> , 2006 , 15, 843-52	6.3	13
100	Unfolding of heptameric co-chaperonin protein follows "fly casting" mechanism: observation of transient nonnative heptamer. <i>Journal of the American Chemical Society</i> , 2005 , 127, 16402-3	16.4	24
99	Role of the unique peptide tail in hyperthermostable Aquifex aeolicus cochaperonin protein 10. <i>Biochemistry</i> , 2005 , 44, 14385-95	3.2	10
98	Snapshots of a dynamic folding nucleus in zinc-substituted <i>Pseudomonas aeruginosa</i> azurin. <i>Biochemistry</i> , 2005 , 44, 10054-62	3.2	31
97	Effect of inorganic phosphate on FMN binding and loop flexibility in <i>Desulfovibrio desulfuricans</i> apo-flavodoxin. <i>Journal of Molecular Biology</i> , 2005 , 349, 87-97	6.5	23
96	Unique complex between bacterial azurin and tumor-suppressor protein p53. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 332, 965-8	3.4	49
95	Interface mutation in heptameric co-chaperonin protein 10 destabilizes subunits but not interfaces. <i>Archives of Biochemistry and Biophysics</i> , 2005 , 439, 175-83	4.1	5
94	Protein folding: defining a "standard" set of experimental conditions and a preliminary kinetic data set of two-state proteins. <i>Protein Science</i> , 2005 , 14, 602-16	6.3	181
93	Dissecting homo-heptamer thermodynamics by isothermal titration calorimetry: entropy-driven assembly of co-chaperonin protein 10. <i>Biophysical Journal</i> , 2005 , 89, 3332-6	2.9	49
92	FMN binding and unfolding of <i>Desulfovibrio desulfuricans</i> flavodoxin: "hidden" intermediates at low denaturant concentrations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005 , 1747, 239-40	4.0	17
91	The experimental folding landscape of monomeric lactose repressor, a large two-domain protein, involves two kinetic intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 14563-8	11.5	25
90	Characterization of the folding landscape of monomeric lactose repressor: quantitative comparison of theory and experiment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 14569-74	11.5	45
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