Pernilla Wittung-stafshede

List of Publications by Year
in descending order

267	12,817	30070 54	32842 100
papers	citations	h-index	g-index

282	282	282	13748
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Gut Microbiota Regulate Motor Deficits and Neuroinflammation in a Model of Parkinsonâ€™s Disease. Cell, 2016, 167, 1469-1480.e12.	28.9	2,399
2	DNA-like double helix formed by peptide nucleic acid. Nature, 1994, 368, 561-563.	27.8	491
3	Gold Nanoparticles Can Induce the Formation of Protein-based Aggregates at Physiological pH. Nano Letters, 2009, 9, 666-671.	9.1	352
4	Ionic Effects on the Stability and Conformation of Peptide Nucleic Acid Complexes. Journal of the American Chemical Society, 1996, 118, 5544-5552.	13.7	271
5	A gut bacterial amyloid promotes Î±-synuclein aggregation and motor impairment in mice. ELife, 2020, 9, .	6.0	251
6	Molecular crowding enhances native structure and stability of Î±/Î² protein flavodoxin. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18976-18981.	7.1	245
7	Protein folding: Defining a â€œstandardâ€•set of experimental conditions and a preliminary kinetic data set of two-state proteins. Protein Science, 2005, 14, 602-616.	7.6	207
8	Crowded, cell-like environment induces shape changes in aspherical protein. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11754-11759.	7.1	194
9	The Bacterial Curli System Possesses a Potent and Selective Inhibitor of Amyloid Formation. Molecular Cell, 2015, 57, 445-455.	9.7	176
10	Defining the human copper proteome and analysis of its expression variation in cancers. Metallomics, 2017, 9, 112-123.	2.4	168
11	Role of Cofactors in Protein Folding. Accounts of Chemical Research, 2002, 35, 201-208.	15.6	167
12	Effects of folding on metalloprotein active sites. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 4246-4249.	7.1	153
13	Factors Defining Effects of Macromolecular Crowding on Protein Stability: An in Vitro/in Silico Case Study Using Cytochrome c. Biochemistry, 2010, 49, 6519-6530.	2.5	137
14	Structure-Activity Studies of the Binding of Modified Peptide Nucleic Acids (PNAs) to DNA. Journal of the American Chemical Society, 1994, 116, 7964-7970.	13.7	135
15	Cross-talk between amyloidogenic proteins in type-2 diabetes and Parkinsonâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12473-12477.	7.1	129
16	Phospholipid membrane permeability of peptide nucleic acid. FEBS Letters, 1995, 365, 27-29.	2.8	124
17	Protein Folding Triggered by Electron Transfer. Accounts of Chemical Research, 1998, 31, 755-763.	15.6	119
18	Cytochrome b562 folding triggered by electron transfer: Approaching the speed limit for formation of a four-helix-bundle protein. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 6587-6590.	7.1	117

#	Article	IF	Citations
19	Direct Observation of Strand Invasion by Peptide Nucleic Acid (PNA) into Double-Stranded DNA. Journal of the American Chemical Society, 1996, 118, 7049-7054.	13.7	113
20	Macromolecular crowding increases structural content of folded proteins. FEBS Letters, 2007, 581, 5065-5069.	2.8	111
21	The J-Domain of Hsp40 Couples ATP Hydrolysis to Substrate Capture in Hsp70â€. Biochemistry, 2003, 42, 4937-4944.	2.5	105
22	Mechanisms of Protein Oligomerization: Inhibitor of Functional Amyloids Templates Î±-Synuclein Fibrillation. Journal of the American Chemical Society, 2012, 134, 3439-3444.	13.7	101
23	Peptide Nucleic Acids with a Conformationally Constrained Chiral Cyclohexylâ€Derived Backbone. Chemistry - A European Journal, 1997, 3, 912-919.	3.3	97
24	Role of cofactors in metalloprotein folding. Quarterly Reviews of Biophysics, 2004, 37, 285-314.	5.7	94
25	Effect of Hofmeister ions on protein thermal stability: Roles of ion hydration and peptide groups?. Archives of Biochemistry and Biophysics, 2008, 479, 69-73.	3.0	94
26	Cisplatin binds human copper chaperone Atox1 and promotes unfolding in vitro. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6951-6956.	7.1	94
27	Thermodynamic stability and folding of proteins from hyperthermophilic organisms. FEBS Journal, 2007, 274, 4023-4033.	4.7	92
28	Induced Chirality in PNA-PNA Duplexes. Journal of the American Chemical Society, 1995, 117, 10167-10173.	13.7	91
29	Direct Optical Detection of Aptamer Conformational Changes Induced by Target Molecules. Analytical Chemistry, 2009, 81, 10002-10006.	6.5	89
30	Extended DNA-Recognition Repertoire of Peptide Nucleic Acid (PNA):Â PNAâ^'dsDNA Triplex Formed with Cytosine-Rich Homopyrimidine PNA. Biochemistry, 1997, 36, 7973-7979.	2.5	88
31	Insulin-degrading enzyme prevents Î±-synuclein fibril formation in a nonproteolytical manner. Scientific Reports, 2015, 5, 12531.	3.3	88
32	Reduction potentials of blue and purple copper proteins in their unfolded states: a closer look at rack-induced coordination. Journal of Biological Inorganic Chemistry, 1998, 3, 367-370.	2.6	83
33	The effect of the metal ion on the folding energetics of azurin: a comparison of the native, zinc and apoprotein. BBA - Proteins and Proteomics, 1997, 1342, 19-27.	2.1	79
34	Single-cell tracking demonstrates copper chaperone Atox1 to be required for breast cancer cell migration. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2014-2019.	7.1	78
35	Interactions of DNA binding ligands with PNA-DNA hybrids. Nucleic Acids Research, 1994, 22, 5371-5377.	14.5	77
36	Macromolecular Crowding Modulates Folding Mechanism of Î±/Î² Protein Apoflavodoxin. Biophysical Journal, 2009, 96, 671-680.	0.5	77

#	Article	IF	Citations
37	Role of metal in folding and stability of copper proteins in vitro. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 1594-1603.	4.1	76
38	The CuA center of cytochrome-c oxidase: electronic structure and spectra of models compared to the properties of CuA domains.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 7167-7171.	7.1	74
39	Modulation of Curli Assembly and Pellicle Biofilm Formation by Chemical and Protein Chaperones. Chemistry and Biology, 2013, 20, 1245-1254.	6.0	72
40	The effect of redox state on the folding free energy of azurin. Journal of Biological Inorganic Chemistry, 1997, 2, 368-371.	2.6	69
41	Effects of macromolecular crowding agents on protein folding in vitro and in silico. Biophysical Reviews, 2013, 5, 137-145.	3.2	69
42	Far-UV Time-Resolved Circular Dichroism Detection of Electron-Transfer-Triggered CytochromecFolding. Journal of the American Chemical Society, 1999, 121, 3811-3817.	13.7	68
43	Roles of Copper-Binding Proteins in Breast Cancer. International Journal of Molecular Sciences, 2017, 18, 871.	4.1	68
44	A Hyperthermophilic Plant-Type [2Fe-2S] Ferredoxin from Aquifex aeolicus Is Stabilized by a Disulfide Bond. Biochemistry, 2002, 41, 3096-3108.	2.5	67
45	Role of Cofactors in Folding of the Blue-Copper Protein Azurin. Inorganic Chemistry, 2004, 43, 7926-7933.	4.0	66
46	Folding, Stability and Shape of Proteins in Crowded Environments: Experimental and Computational Approaches. International Journal of Molecular Sciences, 2009, 10, 572-588.	4.1	65
47	Copper Binding before Polypeptide Folding Speeds Up Formation of Active (Holo)Pseudomonas aeruginosaAzurinâ€. Biochemistry, 2001, 40, 13728-13733.	2.5	64
48	Differential Effects of Alcohols on Conformational Switchovers in Î±-Helical and Î²-Sheet Protein Modelsâ€. Biochemistry, 2006, 45, 7740-7749.	2.5	64
49	Biological Relevance of Metal Binding before Protein Folding. Journal of the American Chemical Society, 2001, 123, 10135-10136.	13.7	61
50	Non-linear effects of macromolecular crowding on enzymatic activity of multi-copper oxidase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 740-744.	2.3	60
51	Bacterial Chaperones CsgE and CsgC Differentially Modulate Human Î±-Synuclein Amyloid Formation via Transient Contacts. PLoS ONE, 2015, 10, e0140194.	2.5	57
52	Quantification of Excluded Volume Effects on the Folding Landscape of Pseudomonas aeruginosa Apoazurin InÂVitro. Biophysical Journal, 2013, 105, 1689-1699.	0.5	56
53	Unique complex between bacterial azurin and tumor-suppressor protein p53. Biochemical and Biophysical Research Communications, 2005, 332, 965-968.	2.1	55
54	Direct Observation of Protein Unfolded State Compaction in the Presence of Macromolecular Crowding. Biophysical Journal, 2013, 104, 694-704.	0.5	55

#	Article	IF	Citations
55	Folding of an Unfolded Protein by Macromolecular Crowding in Vitro. Biochemistry, 2014, 53, 2271-2277.	2.5	53
56	Dissecting Homo-Heptamer Thermodynamics by Isothermal Titration Calorimetry: Entropy-Driven Assembly of Co-Chaperonin Protein 10. Biophysical Journal, 2005, 89, 3332-3336.	0.5	51
57	Characterization of the folding landscape of monomeric lactose repressor: Quantitative comparison of theory and experiment. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14569-14574.	7.1	49
58	The C-Terminus of Human Copper Importer Ctr1 Acts as a Binding Site and Transfers Copper to Atox1. Biophysical Journal, 2016, 110, 95-102.	0.5	49
59	Single-vesicle imaging reveals lipid-selective and stepwise membrane disruption by monomeric Î±-synuclein. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14178-14186.	7.1	49
60	Rapid Formation of a Four-Helix Bundle. Cytochromeb562Folding Triggered by Electron Transfer. Journal of the American Chemical Society, 1997, 119, 9562-9563.	13.7	48
61	Copper Stabilizes Azurin by Decreasing the Unfolding Rate. Archives of Biochemistry and Biophysics, 2001, 390, 146-148.	3.0	48
62	Macromolecular Crowding Tunes Folding Landscape of Parallel Î±/Î² Protein, Apoflavodoxin. Journal of the American Chemical Society, 2011, 133, 646-648.	13.7	48
63	Copper chaperone Atox1 plays role in breast cancer cell migration. Biochemical and Biophysical Research Communications, 2017, 483, 301-304.	2.1	46
64	Copper-Triggered Î²-Hairpin Formation:Â Initiation Site for Azurin Folding?. Journal of the American Chemical Society, 2000, 122, 6337-6338.	13.7	45
65	Reversible denaturation of oligomeric human chaperonin 10: Denatured state depends on chemical denaturant. Protein Science, 2000, 9, 2109-2117.	7.6	44
66	Copper-Transfer Mechanism from the Human Chaperone Atox1 to a Metal-Binding Domain of Wilson Disease Protein. Journal of Physical Chemistry B, 2010, 114, 3698-3706.	2.6	44
67	Conserved residues modulate copper release in human copper chaperone Atox1. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11158-11163.	7.1	43
68	Effects of Macromolecular Crowding on Burst Phase Kinetics of Cytochrome c Folding. Biochemistry, 2012, 51, 9836-9845.	2.5	43
69	Folding of Deoxymyoglobin Triggered by Electron Transfer. Journal of Physical Chemistry A, 1998, 102, 5599-5601.	2.5	42
70	Role of structural determinants in folding of the sandwich-like protein Pseudomonas aeruginosa azurin. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3984-3987.	7.1	42
71	Role of Copper in Thermal Stability of Human Ceruloplasmin. Biophysical Journal, 2008, 94, 1384-1391.	0.5	42
72	Fucosylated Molecules Competitively Interfere with Cholera Toxin Binding to Host Cells. ACS Infectious Diseases, 2018, 4, 758-770.	3.8	42

#	Article	IF	Citations
73	On the precision of experimentally determined protein folding rates and Â-values. Protein Science, 2006, 15, 553-563.	7.6	41
74	An Isc-Type Extremely Thermostable [2Feâ˜2S] Ferredoxin from Aquifex aeolicus. Biochemical, Spectroscopic, and Unfolding Studies. Biochemistry, 2003, 42, 1354-1364.	2.5	40
75	Lysine-60 in Copper Chaperone Atox1 Plays an Essential Role in Adduct Formation with a Target Wilson Disease Domain. Journal of the American Chemical Society, 2009, 131, 16371-16373.	13.7	40
76	Determinants for Simultaneous Binding of Copper and Platinum to Human Chaperone Atox1: Hitchhiking not Hijacking. PLoS ONE, 2013, 8, e70473.	2.5	40
77	Stability and folding of the ferredoxin from the hyperthermophilic archaeon Acidianus ambivalens. Journal of Inorganic Biochemistry, 2000, 78, 35-41.	3.5	38
78	Presence of the cofactor speeds up folding ofDesulfovibrio desulfuricansflavodoxin. Protein Science, 2002, 11, 1129-1135.	7.6	38
79	ATP7A-Regulated Enzyme Metalation and Trafficking in the Menkes Disease Puzzle. Biomedicines, 2021, 9, 391.	3.2	38
80	Evidence for Elongation of the Helical Pitch of the RecA Filament Upon ATP and ADP Binding Using Small-Angle Neutron Scattering. FEBS Journal, 1995, 233, 579-583.	0.2	37
81	Heme orientation affects holo-myoglobin folding and unfolding kinetics1. FEBS Letters, 2000, 470, 203-206.	2.8	37
82	Discovery of Ligands for ADP-Ribosyltransferases via Docking-Based Virtual Screening. Journal of Medicinal Chemistry, 2012, 55, 7706-7718.	6.4	37
83	Probing copper ligands in denatured Pseudomonas aeruginosa azurin: unfolding His117Gly and His46Gly mutants. Journal of Biological Inorganic Chemistry, 2001, 6, 182-188.	2.6	36
84	The Largest Protein Observed To Fold by Two-State Kinetic Mechanism Does Not Obey Contact-Order Correlation. Journal of the American Chemical Society, 2003, 125, 9606-9607.	13.7	36
85	Effect of Redox State on the Folding Free Energy of a Thermostable Electron-Transfer Metalloprotein:Â The CuADomain of Cytochrome Oxidase fromThermus thermophilusâ€. Biochemistry, 1998, 37, 3172-3177.	2.5	35
86	X-ray absorption spectroscopy of folded and unfolded copper(I) azurin. Inorganica Chimica Acta, 2000, 297, 278-282.	2.4	35
87	Detection of point mutations in DNA by PNA-based quartz-crystal biosensor. Colloids and Surfaces A: Physicochemical and Engineering Aspects, 2000, 174, 269-273.	4.7	35
88	Methionine-121 coordination determines metal specificity in unfolded Pseudomonas aeruginosa azurin. Journal of Biological Inorganic Chemistry, 2004, 9, 281-288.	2.6	35
89	Snapshots of a Dynamic Folding Nucleus in Zinc-Substituted Pseudomonas aeruginosa Azurin. Biochemistry, 2005, 44, 10054-10062.	2.5	35
90	Attenuating Listeria monocytogenes Virulence by Targeting the Regulatory Protein PrfA. Cell Chemical Biology, 2016, 23, 404-414.	5.2	35

#	Article	IF	Citations
91	Observation of a PNAâ˜PNAâ˜PNA Triplex. Journal of the American Chemical Society, 1997, 119, 3189-3190.	13.7	34
92	Mapping the domain structure of the influenza A virus polymerase acidic protein (PA) and its interaction with the basic protein 1 (PB1) subunit. Virology, 2008, 379, 135-142.	2.4	34
93	Equilibrium Unfolding of Dimeric Desulfoferrodoxin Involves a Monomeric Intermediate:â€‰ Iron Cofactors Dissociate after Polypeptide Unfolding. Biochemistry, 2001, 40, 4940-4948.	2.5	33
94	Extended functional repertoire for human copper chaperones. Biomolecular Concepts, 2016, 7, 29-39.	2.2	33
95	Glycosaminoglycans in human retinoblastoma cells: heparan sulfate, a modulator of the pigment epithelium-derived factor-receptor interactions. BMC Biochemistry, 2003, 4, 1.	4.4	32
96	An adaptive mutation in adenylate kinase that increases organismal fitness is linked to stability-activity trade-offs. Protein Engineering, Design and Selection, 2007, 21, 19-27.	2.1	32
97	In vitro unfolding of yeast multicopper oxidase Fet3p variants reveals unique role of each metal site. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19258-19263.	7.1	32
98	Synthetic crowding agent dextran causes excluded volume interactions exclusively to tracer protein apoazurin. FEBS Letters, 2014, 588, 811-814.	2.8	32
99	Extracellular vesicles from human pancreatic islets suppress human islet amyloid polypeptide amyloid formation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11127-11132.	7.1	31
100	High stability of a ferredoxin from the hyperthermophilic archaeonA. ambivalens: Involvement of electrostatic interactions and cofactors. Protein Science, 2001, 10, 1539-1548.	7.6	30
101	Studies of Pseudomonas aeruginosa Azurin Mutants: Cavities in Î²-Barrel Do Not Affect Refolding Speed. Biophysical Journal, 2002, 82, 2645-2651.	0.5	30
102	Structure and Dynamics of Cu(I) Binding in Copper Chaperones Atox1 and CopZ:â€‰ A Computer Simulation Study. Journal of Physical Chemistry B, 2008, 112, 4583-4593.	2.6	30
103	Macromolecular Crowding Extended to a Heptameric System: The Co-chaperonin Protein 10. Biochemistry, 2011, 50, 3034-3044.	2.5	29
104	Reaction of platinum anticancer drugs and drug derivatives with a copper transporting protein, Atox1. Biochemical Pharmacology, 2012, 83, 874-881.	4.4	29
105	Direct Correlation Between Ligand-Induced Î±-Synuclein Oligomers and Amyloid-like Fibril Growth. Scientific Reports, 2015, 5, 10422.	3.3	29
106	Human cytoplasmic copper chaperones Atox1 and CCS exchange copper ions in vitro. BioMetals, 2015, 28, 577-585.	4.1	29
107	The six metal binding domains in human copper transporter, ATP7B: molecular biophysics and disease-causing mutations. BioMetals, 2017, 30, 823-840.	4.1	29
108	Abundant fish protein inhibits Î±-synuclein amyloid formation. Scientific Reports, 2018, 8, 5465.	3.3	29

#	Article	IF	Citations
109	Alphaâ€Synuclein Modulates the Physical Properties of DNA. Chemistry - A European Journal, 2018, 24, 15685-15690.	3.3	29
110	Hybridization of 2'-ribose modified mixed-sequence oligonucleotides: thermodynamic and kinetic studies. Nucleic Acids Research, 2001, 29, 2163-2170.	14.5	28
111	Can Cofactor-Binding Sites in Proteins Be Flexible?Desulfovibrio desulfuricansFlavodoxin Binds FMN Dimerâ€. Biochemistry, 2003, 42, 13074-13080.	2.5	28
112	Impact of cofactor on stability of bacterial (CopZ) and human (Atox1) copper chaperones. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2007, 1774, 1316-1322.	2.3	28
113	Stability and ATP Binding of the Nucleotide-binding Domain of the Wilson Disease Protein: Effect of the Common H1069Q Mutation. Journal of Molecular Biology, 2008, 383, 1097-1111.	4.2	28
114	Macromolecular crowding modulates Î±-synuclein amyloid fiber growth. Biophysical Journal, 2021, 120, 3374-3381.	0.5	28
115	Triplet-state quenching in complexes between Zn-cytochrome c and cytochrome oxidase or its CuA domain. Biophysical Chemistry, 1995, 54, 191-197.	2.8	27
116	Approaching the speed limit for Greek Key Î²-barrel formation: transition-state movement tunes folding rate of zinc-substituted azurin. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1651, 1-4.	2.3	27
117	The experimental folding landscape of monomeric lactose repressor, a large two-domain protein, involves two kinetic intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14563-14568.	7.1	27
118	Interactions between DNA, transcriptional regulator Dreb2a and the Med25 mediator subunit from Arabidopsis thaliana involve conformational changes. Nucleic Acids Research, 2012, 40, 5938-5950.	14.5	27
119	Insulin-degrading enzyme is activated by the C-terminus of Î±-synuclein. Biochemical and Biophysical Research Communications, 2015, 466, 192-195.	2.1	27
120	Evaluation of copper chaperone ATOX1 as prognostic biomarker in breast cancer. Breast Cancer, 2020, 27, 505-509.	2.9	27
121	The cupredoxin fold is found in the soluble CuAand CyoA domains of two terminal oxidases. FEBS Letters, 1994, 349, 286-288.	2.8	26
122	PNA-Peptide Chimerae. Tetrahedron Letters, 1995, 36, 6933-6936.	1.4	26
123	Ït-Value Analysis of Apo-Azurin Folding:â€‰ Comparison between Experiment and Theory. Biochemistry, 2006, 45, 6458-6466.	2.5	26
124	Establishing the entatic state in folding metallated Pseudomonas aeruginosa azurin. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3159-3164.	7.1	26
125	Discrete Roles of Copper Ions in Chemical Unfolding of Human Ceruloplasmin. Biochemistry, 2007, 46, 9638-9644.	2.5	26
126	Conformational Dynamics of Metal-Binding Domains in Wilson Disease Protein: Molecular Insights into Selective Copper Transfer. Biochemistry, 2009, 48, 5849-5863.	2.5	26

#	Article	IF	Citations
127	Experimental Evolution of Adenylate Kinase Reveals Contrasting Strategies toward Protein Thermostability. Biophysical Journal, 2010, 99, 887-896.	0.5	26
128	Comparison of chemical and thermal protein denaturation by combination of computational and experimental approaches. II. Journal of Chemical Physics, 2011, 135, 175102.	3.0	26
129	In Vitro Thermodynamic Dissection of Human Copper Transfer from Chaperone to Target Protein. PLoS ONE, 2012, 7, e36102.	2.5	26
130	Modulation of Î±-synuclein fibrillization by ring-fused 2-pyridones: Templation and inhibition involve oligomers with different structure. Archives of Biochemistry and Biophysics, 2013, 532, 84-90.	3.0	26
131	Identification of New Potential Interaction Partners for Human Cytoplasmic Copper Chaperone Atox1: Roles in Gene Regulation?. International Journal of Molecular Sciences, 2015, 16, 16728-16739.	4.1	26
132	Correlation between Cellular Uptake and Cytotoxicity of Fragmented Î±-Synuclein Amyloid Fibrils Suggests Intracellular Basis for Toxicity. ACS Chemical Neuroscience, 2020, 11, 233-241.	3.5	26
133	Thermal Unfolding of Apo and Holo Desulfovibrio desulfuricans Flavodoxin:â€‰ Cofactor Stabilizes Folded and Intermediate States. Biochemistry, 2004, 43, 12855-12864.	2.5	25
134	Crowding-Induced Elongated Conformation of Urea-Unfolded Apoazurin: Investigating the Role of Crowder Shape in Silico. Journal of Physical Chemistry B, 2019, 123, 3607-3617.	2.6	25
135	No cofactor effect on equilibrium unfolding of Desulfovibrio desulfuricans flavodoxin. BBA - Proteins and Proteomics, 2000, 1479, 214-224.	2.1	24
136	Unfolding of Heptameric Co-chaperonin Protein Follows â€œFly Castingâ€•Mechanism:Â Observation of Transient Nonnative Heptamer. Journal of the American Chemical Society, 2005, 127, 16402-16403.	13.7	24
137	Effect of Inorganic Phosphate on FMN Binding and Loop Flexibility in Desulfovibrio desulfuricans Apo-flavodoxin. Journal of Molecular Biology, 2005, 349, 87-97.	4.2	24
138	Formation of a linear [3Fe-4S] cluster in a seven-iron ferredoxin triggered by polypeptide unfolding. Journal of Biological Inorganic Chemistry, 2002, 7, 357-362.	2.6	23
139	Folding of copper proteins: role of the metal?. Quarterly Reviews of Biophysics, 2018, 51, e4.	5.7	23
140	Human Copper Chaperone Atox1 Translocates to the Nucleus but does not Bind DNA In Vitro. Protein and Peptide Letters, 2015, 22, 532-538.	0.9	23
141	Effects of protein folding on metalloprotein redox-active sites: electron-transfer properties of blue and purple copper proteins. Coordination Chemistry Reviews, 1999, 185-186, 127-140.	18.8	22
142	Electron-transfer studies with the CuA domain of Thermus thermophilus cytochrome ba3. Inorganica Chimica Acta, 1996, 243, 141-145.	2.4	21
143	A stable, molten-globule-like cytochrome c. BBA - Proteins and Proteomics, 1998, 1382, 324-332.	2.1	21
144	Folding of Desulfovibrio desulfuricans flavodoxin is accelerated by cofactor fly-casting. Archives of Biochemistry and Biophysics, 2006, 451, 51-58.	3.0	21

#	Article	IF	Citations
145	Interdomain Interactions Modulate Collective Dynamics of the Metal-Binding Domains in the Wilson Disease Protein. Journal of Physical Chemistry B, 2010, 114, 1836-1848.	2.6	21
146	Unraveling amyloid formation paths of Parkinson's disease protein Î±-synuclein triggered by anionic vesicles. Quarterly Reviews of Biophysics, 2017, 50, e3.	5.7	21
147	The copper chaperone CCS facilitates copper binding to MEK1/2 to promote kinase activation. Journal of Biological Chemistry, 2021, 297, 101314.	3.4	21
148	Probing the interface in a human co-chaperonin heptamer: residues disrupting oligomeric unfolded state identified. BMC Biochemistry, 2003, 4, 14.	4.4	20
149	Interaction between Copper Chaperone Atox1 and Parkinsonâ€™s Disease Protein Î±-Synuclein Includes Metal-Binding Sites and Occurs in Living Cells. ACS Chemical Neuroscience, 2019, 10, 4659-4668.	3.5	20
150	Mirrorâ€image 5S Ribonucleoprotein Complexes. Angewandte Chemie - International Edition, 2020, 59, 3724-3731.	13.8	20
151	Cytochrome c 553 , a small heme protein that lacks misligation in its unfolded state, folds with rapid two-state kinetics 1 1Edited by C. R. Matthews. Journal of Molecular Biology, 2000, 301, 769-773.	4.2	19
152	Slow unfolding explains high stability of thermostable ferredoxins: common mechanism governing thermostability?. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1700, 1-4.	2.3	19
153	Kinetic Folding and Assembly Mechanisms Differ for Two Homologous Heptamers. Journal of Molecular Biology, 2006, 363, 729-742.	4.2	19
154	Interaction between the Anticancer Drug Cisplatin and the Copper Chaperone Atox1 in Human Melanoma Cells. Protein and Peptide Letters, 2013, 21, 63-68.	0.9	19
155	Copper Chaperone Atox1 Interacts with Cell Cycle Proteins. Computational and Structural Biotechnology Journal, 2018, 16, 443-449.	4.1	19
156	Copper relay path through the N-terminus of Wilson disease protein, ATP7B. Metallomics, 2019, 11, 1472-1480.	2.4	19
157	High-potential states of blue and purple copper proteins. BBA - Proteins and Proteomics, 1998, 1388, 437-443.	2.1	18
158	High thermal and chemical stability of Thermus thermophilus seven-iron ferredoxin. FEBS Journal, 2003, 270, 4736-4743.	0.2	18
159	FMN binding and unfolding of Desulfovibrio desulfuricans flavodoxin: â€œhiddenâ€•intermediates at low denaturant concentrations. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1747, 239-250.	2.3	18
160	Role of cations in stability of acidic protein Desulfovibrio desulfuricans apoflavodoxin. Archives of Biochemistry and Biophysics, 2008, 474, 128-135.	3.0	18
161	Similar but Different: Thermodynamic and Structural Characterization of a Pair of Enantiomers Binding to Acetylcholinesterase. Angewandte Chemie - International Edition, 2012, 51, 12716-12720.	13.8	18
162	Enthalpy-entropy compensation at play in human copper ion transfer. Scientific Reports, 2015, 5, 10518.	3.3	18

#	Article	IF	Citations
163	Synthesis of Multiring Fused 2-Pyridones via a Nitrene Insertion Reaction: Fluorescent Modulators of Î±-Synuclein Amyloid Formation. Organic Letters, 2015, 17, 6194-6197.	4.6	18
164	Female Faculty: Why So Few and Why Care?. Chemistry - A European Journal, 2020, 26, 8319-8323.	3.3	18
165	Absorption flattening in the optical spectra of liposome-entrapped substances. FEBS Letters, 1994, 352, 37-40.	2.8	17
166	Effect of redox state on unfolding energetics of heme proteins. BBA - Proteins and Proteomics, 1999, 1432, 401-405.	2.1	17
167	In VitroMembrane Penetration of Modified Peptide Nucleic Acid (PNA). Journal of Biomolecular Structure and Dynamics, 1999, 17, 33-40.	3.5	17
168	Role of copper in folding and stability of cupredoxin-like copper-carrier protein CopC. Archives of Biochemistry and Biophysics, 2007, 467, 58-66.	3.0	17
169	Differential Roles of Met10, Thr11, and Lys60 in Structural Dynamics of Human Copper Chaperone Atox1. Biochemistry, 2009, 48, 960-972.	2.5	17
170	Macromolecular Crowding Effects on Two Homologs of Ribosomal Protein S16: Protein-Dependent Structural Changes and Local Interactions. Biophysical Journal, 2014, 107, 401-410.	0.5	17
171	A stretched conformation of DNA with a biological role?. Quarterly Reviews of Biophysics, 2017, 50, e11.	5.7	17
172	Secondary Structure of RecA in Solution. The Effects of Cofactor, DNA and Ionic Conditions. FEBS Journal, 1995, 228, 149-154.	0.2	17
173	Second-Site RecAâ˜DNA Interactions:Â Lack of Identical Recognition. Biochemistry, 1996, 35, 15349-15355.	2.5	16
174	Equilibrium unfolding of a small lowâ€potential cytochrome, cytochrome c₅₅₃ from Desulfovibrio vulgaris. Protein Science, 1999, 8, 1523-1529.	7.6	16
175	Low stability for monomeric human chaperonin protein 10: interprotein interactions contribute majority of oligomer stability. Archives of Biochemistry and Biophysics, 2002, 405, 280-282.	3.0	16
176	Folding and assembly pathways of co-chaperonin proteins 10: Origin of bacterial thermostability. Archives of Biochemistry and Biophysics, 2006, 456, 8-18.	3.0	16
177	Copper binding triggers compaction in N-terminal tail of human copper pump ATP7B. Biochemical and Biophysical Research Communications, 2016, 470, 663-669.	2.1	16
178	Redox-Dependent Copper Ion Modulation of Amyloid-Î² (1-42) Aggregation In Vitro. Biomolecules, 2020, 10, 924.	4.0	16
179	Crosstalk Between Alpha-Synuclein and Other Human and Non-Human Amyloidogenic Proteins: Consequences for Amyloid Formation in Parkinsonâ€™s Disease. Journal of Parkinson's Disease, 2020, 10, 819-830.	2.8	16
180	Small pH and Salt Variations Radically Alter the Thermal Stability of Metal-Binding Domains in the Copper Transporter, Wilson Disease Protein. Journal of Physical Chemistry B, 2013, 117, 13038-13050.	2.6	15

#	Article	IF	Citations
181	T versus D in the MTCXXC motif of copper transport proteins plays a role in directional metal transport. Journal of Biological Inorganic Chemistry, 2014, 19, 1037-1047.	2.6	15
182	3D-Models of Insulin-Producing Î²-Cells: from Primary Islet Cells to Stem Cell-Derived Islets. Stem Cell Reviews and Reports, 2018, 14, 177-188.	5.6	15
183	Amyloid formation of fish Î²-parvalbumin involves primary nucleation triggered by disulfide-bridged protein dimers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27997-28004.	7.1	15
184	Monomer topology defines folding speed of heptamer. Protein Science, 2004, 13, 1317-1321.	7.6	14
185	Solvation of the folding-transition state in Pseudomonas aeruginosa azurin is modulated by metal: Solvation of azurin's folding nucleus. Protein Science, 2006, 15, 843-852.	7.6	14
186	Unresolved questions in human copper pump mechanisms. Quarterly Reviews of Biophysics, 2015, 48, 471-478.	5.7	14
187	Redox-linked conformational changes in cytochromecoxidase. FEBS Letters, 1996, 388, 47-49.	2.8	13
188	A ferredoxin from the thermohalophilic bacterium Rhodothermus marinus. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2002, 1601, 1-8.	2.3	13
189	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. Journal of Molecular Biology, 2008, 381, 707-717.	4.2	13
190	Residue-Specific Analysis of Frustration in the Folding Landscape of Repeat Î²/Î± Protein Apoflavodoxin. Journal of Molecular Biology, 2010, 396, 75-89.	4.2	13
191	Disease-causing point-mutations in metal-binding domains of Wilson disease protein decrease stability and increase structural dynamics. BioMetals, 2017, 30, 27-35.	4.1	13
192	How Do Cofactors Modulate Protein Folding?. Protein and Peptide Letters, 2005, 12, 165-170.	0.9	13
193	Effects of the Toxic Metals Arsenite and Cadmium on Î±-Synuclein Aggregation In Vitro and in Cells. International Journal of Molecular Sciences, 2021, 22, 11455.	4.1	13
194	Formation of linear three-iron clusters in Aquifex aeolicus two-iron ferredoxins: effect of protein-unfolding speed. Archives of Biochemistry and Biophysics, 2004, 427, 154-163.	3.0	12
195	Correlation between Protein Stability Cores and Protein Folding Kinetics: A Case Study on Pseudomonas aeruginosa Apo-Azurin. Structure, 2006, 14, 1401-1410.	3.3	12
196	Tuning of Copper-Loop Flexibility in Bacillus subtilis CopZ Copper Chaperone: Role of Conserved Residues. Journal of Physical Chemistry B, 2009, 113, 1919-1932.	2.6	12
197	Probing functional roles of Wilson disease protein (ATP7B) copper-binding domains in yeast. Metallomics, 2017, 9, 981-988.	2.4	12
198	Base Orientation of Second DNA in RecAÂ·DNA Filaments. Journal of Biological Chemistry, 1998, 273, 15682-15686.	3.4	11

#	Article	IF	Citations
199	Characterization of Surface Antigen from Lyme Disease Spirochete Borrelia burgdorferi. Biochemical and Biophysical Research Communications, 2001, 289, 389-394.	2.1	11
200	Exceptional stability of a [2Feâ€“2S] ferredoxin from hyperthermophilic bacterium Aquifex aeolicus. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2002, 1599, 82-89.	2.3	11
201	Copper distribution in breast cancer cells detected by time-of-flight secondary ion mass spectrometry with delayed extraction methodology. Biointerphases, 2018, 13, 06E412.	1.6	11
202	Differential effects of Cu2+ and Fe3+ ions on in vitro amyloid formation of biologically-relevant Î±-synuclein variants. BioMetals, 2020, 33, 97-106.	4.1	11
203	Effects of small-molecule amyloid modulators on a Drosophila model of Parkinsonâ€™s disease. PLoS ONE, 2017, 12, e0184117.	2.5	11
204	Role of the Unique Peptide Tail in HyperthermostableAquifex aeolicusCochaperonin Protein 10â€. Biochemistry, 2005, 44, 14385-14395.	2.5	10
205	Copper chaperone blocks amyloid formation via ternary complex. Quarterly Reviews of Biophysics, 2018, 51, e6.	5.7	10
206	Membraneâ€“Proteinâ€“Hydration Interaction of Î±-Synuclein with Anionic Vesicles Probed via Angle-Resolved Second-Harmonic Scattering. Journal of Physical Chemistry B, 2019, 123, 1044-1049.	2.6	10
207	Fluorescence-detected interactions of oligonucleotides in RecA complexes. FEBS Letters, 1995, 368, 64-68.	2.8	9
208	Single injection of small-molecule amyloid accelerator results in cell death of nigral dopamine neurons in mice. Npj Parkinson's Disease, 2015, 1, 15024.	5.3	9
209	Buried water molecules contribute to cytochrome f stability. Archives of Biochemistry and Biophysics, 2002, 404, 335-337.	3.0	8
210	First characterization of co-chaperonin protein 10 from hyper-thermophilic Aquifex aeolicus. Biochemical and Biophysical Research Communications, 2004, 317, 176-180.	2.1	8
211	Geometrical Description of Protein Structural Motifs. Journal of Physical Chemistry B, 2018, 122, 11289-11294.	2.6	8
212	Wilson disease missense mutations in ATP7B affect metal-binding domain structural dynamics. BioMetals, 2019, 32, 875-885.	4.1	8
213	Second harmonic generation for collagen I characterization in rectal cancer patients with and without preoperative radiotherapy. Journal of Biomedical Optics, 2017, 22, 1.	2.6	8
214	Orientation of Î±-Synuclein at Negatively Charged Lipid Vesicles: Linear Dichroism Reveals Time-Dependent Changes in Helix Binding Mode. Journal of the American Chemical Society, 2021, 143, 18899-18906.	13.7	8
215	Crossroads between copper ions and amyloid formation in Parkinsonâ€™s disease. Essays in Biochemistry, 0, , .	4.7	8
216	Med8, Med18, and Med20 subunits of the Mediator head domain are interdependent upon each other for folding and complex formation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20728-20733.	7.1	7

#	Article	IF	Citations
217	Pseudosymmetry, high copy number and twinning complicate the structure determination ofDesulfovibrio desulfuricans(ATCC 29577) flavodoxin. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 523-534.	2.5	7
218	Protein Folding Inside the Cell. Biophysical Journal, 2011, 101, 265-266.	0.5	7
219	Gut power: Modulation of human amyloid formation by amyloidogenic proteins in the gastrointestinal tract. Current Opinion in Structural Biology, 2022, 72, 33-38.	5.7	7
220	The L2 loop peptide of RecA stiffens and restricts base motions of single-stranded DNA similar to the intact protein1. FEBS Letters, 1999, 446, 30-34.	2.8	6
221	Novel “Three-in-one” Peptide Device for Genetic Drug Delivery. Protein and Peptide Letters, 2003, 10, 1-7.	0.9	6
222	Interface mutation in heptameric co-chaperonin protein 10 destabilizes subunits but not interfaces. Archives of Biochemistry and Biophysics, 2005, 439, 175-183.	3.0	6
223	A Copper Story: From Protein Folding and Metal Transport to Cancer. Israel Journal of Chemistry, 2016, 56, 671-681.	2.3	6
224	Copper chaperone ATOX1 regulates pluripotency factor OCT4 in preimplantation mouse embryos. Biochemical and Biophysical Research Communications, 2017, 491, 147-153.	2.1	6
225	Synaptic vesicle mimics affect the aggregation of wild-type and A53T Î±-synuclein variants differently albeit similar membrane affinity. Protein Engineering, Design and Selection, 2019, 32, 59-66.	2.1	6
226	C-terminal truncation of <mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.svg"><mml:mrow><mml:mi>Î±</mml:mi></mml:mrow></mml:math>-synuclein alters DNA structure from extension to compaction. Biochemical and Biophysical Research Communications, 2021, 568, 43-47.	2.1	6
227	Impact of crowded environments on binding between protein and single-stranded DNA. Scientific Reports, 2021, 11, 17682.	3.3	6
228	Spectroscopic Observation of Renaturation Between Polynucleotides Interacting with RecA in the Presence of ATP Hydrolysis. FEBS Journal, 1994, 224, 39-45.	0.2	5
229	If space is provided, bulky modification on the rim of Azurin's Î²-barrel results in folded protein. FEBS Letters, 2002, 531, 209-214.	2.8	5
230	Unfolding the unique c-type heme protein, Chlamydomonas reinhardtii cytochrome f. BBA - Proteins and Proteomics, 2002, 1596, 163-171.	2.1	5
231	In Vitro Analysis of Î±-Synuclein Amyloid Formation and Cross-Reactivity. Methods in Molecular Biology, 2018, 1779, 73-83.	0.9	5
232	Predicting protein folding cores by empirical potential functions. Archives of Biochemistry and Biophysics, 2009, 483, 16-22.	3.0	4
233	Folding and assembly of co-chaperonin heptamer probed by forster resonance energy transfer. Archives of Biochemistry and Biophysics, 2007, 464, 306-313.	3.0	3
234	A Luminal Loop of Wilson Disease Protein Binds Copper and Is Required for Protein Activity. Biophysical Journal, 2018, 115, 1007-1018.	0.5	3

#	Article	IF	Citations
235	Synergistic Effects of Copper Sites on Apparent Stability of Multicopper Oxidase, Fet3p. International Journal of Molecular Sciences, 2018, 19, 269.	4.1	3
236	The Caenorhabditis elegans homolog of human copper chaperone Atox1, CUC-1, aids in distal tip cell migration. BioMetals, 2020, 33, 147-157.	4.1	3
237	The Zero-Order Loop in Apoazurin Modulates Folding Mechanism In Silico. Journal of Physical Chemistry B, 2021, 125, 3501-3509.	2.6	3
238	Frustration Dynamics and Electron-Transfer Reorganization Energies in Wild-Type and Mutant Azurins. Journal of the American Chemical Society, 2022, 144, 4178-4185.	13.7	3
239	Stability Determines Formation Rate of Four-Helix-Bundle Protein. Archives of Biochemistry and Biophysics, 2000, 378, 190-191.	3.0	2
240	The Rate of Formation of Cytochrome c553 Is Not Dependent on the Nature of the Unfolded State. Archives of Biochemistry and Biophysics, 2001, 389, 150-152.	3.0	1
241	Residue Specific Analysis of Frustration in Folding Landscape of Repeat Alpha/Beta Protein Apoflavodoxin. Biophysical Journal, 2010, 98, 200a.	0.5	1
242	In Vitro effects of Macromolecular Crowding on Protein Stability, Structure and Folding. Biophysical Journal, 2013, 104, 576a.	0.5	1
243	Mirrorâ€Image 5S Ribonucleoprotein Complexes. Angewandte Chemie, 2020, 132, 3753-3760.	2.0	1
244	Response to crowded conditions reveals compact nucleus for amyloid formation of folded protein. QRB Discovery, 2021, 2, .	1.6	1
245	A large â€˜discoveryâ€™ experiment: Gender Initiative for Excellence (Genie) at Chalmers University of Technology. QRB Discovery, 2021, 2, .	1.6	1
246	Metal Ions, Protein Folding, and Conformational States. , 2010, , 3-11.		1
247	Stability and Folding of Copper-Binding Proteins. , 2010, , 61-80.		1
248	Evaluation of ATOX1 as a Potential Predictive Biomarker for Tetrathiomolybdate Treatment of Breast Cancer Patients with High Risk of Recurrence. Biomedicines, 2021, 9, 1887.	3.2	1
249	Formation of linear three-iron clusters in Aquifex aeolicus two-iron ferredoxins: effect of protein-unfolding speed. Archives of Biochemistry and Biophysics, 2004, 427, 154-154.	3.0	0
250	Response to Harve et al : Effects on protein folding speed and shape despite possible size changes in Ficoll 70. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, .	7.1	0
251	Crowded, Cell-like Environment Induces Shape Changes In Aspherical Protein. Biophysical Journal, 2009, 96, 568a.	0.5	0
252	Protein Structure, Stability and Folding in the Cell - in vitro Biophysical Approaches. Biophysical Journal, 2010, 98, 5a.	0.5	0

#	Article	IF	Citations
253	In Vitro Interactions Between Model Proteins and Amyloid Inhibitors. Biophysical Journal, 2011, 100, 400a.	0.5	0
254	Factors Defining Effects of Macromolecular Crowding on Protein Stability: an in vitro/in Silico Case Study using Cytochrome C. Biophysical Journal, 2011, 100, 396a.	0.5	0
255	Effects of Macromolecular Crowding on Oligomeric Protein Unfolding: Case Study with Human Co-Chaperonin Protein 10 (cpn10). Biophysical Journal, 2011, 100, 213a.	0.5	0
256	Comparison of Chemical and Thermal Protein Denaturation by Combination of Computational and Experimental Approaches. Biophysical Journal, 2012, 102, 457a-458a.	0.5	0
257	Effects of Macromolecular Crowding on Protein Biophysics. Biophysical Journal, 2012, 102, 475a.	0.5	0
258	Tuning of Alpha-Synuclein Aggregation by Small Molecules and Bacterial Proteins. Biophysical Journal, 2015, 108, 522a.	0.5	0
259	Protein Interactions that Enable Safe and Efficient Copper Ion Transport in the Human Cytoplasm. Biophysical Journal, 2016, 110, 179a.	0.5	0
260	Cross-Reactivity of Alpha-Synuclein with Other Cellular Components Can Dramatically Modulate Amyloid Formation. Biophysical Journal, 2017, 112, 365a.	0.5	0
261	The Role of Lipid Chemistry in Alpha-Synuclein Membrane Binding and Aggregation. Biophysical Journal, 2018, 114, 277a.	0.5	0
262	Interaction of the Copper Chaperone Atox1 with Alpha-Synuclein. Biophysical Journal, 2018, 114, 77a.	0.5	0
263	Exosomes from Human Pancreatic Islets Suppress IAPP Amyloid Formation. Biophysical Journal, 2018, 114, 78a.	0.5	0
264	Alpha-Synuclein Binds to DNA and Modulates its Physical Properties. Biophysical Journal, 2019, 116, 506a.	0.5	0
265	My journey in academia: things not on the CV. Pure and Applied Chemistry, 2020, 92, 789-796.	1.9	0
266	Another pearl in the â€œcopper-transportâ€•necklace. Biophysical Journal, 2021, 120, 4305-4306.	0.5	0
267	Structural and Molecular Determinants of CCS-Mediated Copper Activation of MEK1/2. SSRN Electronic Journal, 0, , .	0.4	0