

Birthe B Kragelund

List of Publications by Year in descending order

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150
papers

7,082
citations

53660

45
h-index

74018

75
g-index

165
all docs

165
docs citations

165
times ranked

8185
citing authors

#	ARTICLE	IF	CITATIONS
1	The denatured state of HIV-1 protease under native conditions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 96-109.	1.5	1
2	Structure, dynamics, and stability of the globular domain of human linker histone H1.0 and the role of positive charges. <i>Protein Science</i> , 2022, 31, 918-932.	3.1	7
3	The highly disordered protein prothymosin alpha as a novel neuroprotector of the brain. <i>Biophysical Journal</i> , 2022, 121, 58a.	0.2	0
4	Insight into calcium-binding motifs of intrinsically disordered proteins. <i>Biophysical Journal</i> , 2022, 121, 300a.	0.2	0
5	$\hat{\pm}$ -hub coregulator structure and flexibility determine transcription factor binding and selection in regulatory interactomes. <i>Journal of Biological Chemistry</i> , 2022, 298, 101963.	1.6	5
6	Disorder in a two-domain neuronal Ca ²⁺ -binding protein regulates domain stability and dynamics using ligand mimicry. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 2263-2278.	2.4	4
7	Connecting the $\hat{\pm}$ -hubs: same fold, disordered ligands, new functions. <i>Cell Communication and Signaling</i> , 2021, 19, 2.	2.7	9
8	$\hat{\pm}$ -Hub domains and intrinsically disordered proteins: A decisive combo. <i>Journal of Biological Chemistry</i> , 2021, 296, 100226.	1.6	16
9	Evolution of A bHLH Interaction Motif. <i>International Journal of Molecular Sciences</i> , 2021, 22, 447.	1.8	5
10	Dynamic Na ⁺ /H ⁺ exchanger 1 (NHE1) $\hat{\pm}$ calmodulin complexes of varying stoichiometry and structure regulate Ca ²⁺ -dependent NHE1 activation. <i>ELife</i> , 2021, 10, .	2.8	11
11	Binding Sites for Oligosaccharide Repeats from Lactic Acid Bacteria Exopolysaccharides on Bovine β -Lactoglobulin Identified by NMR Spectroscopy. <i>ACS Omega</i> , 2021, 6, 9039-9052.	1.6	7
12	Refinement of $\hat{\pm}$ -Synuclein Ensembles Against SAXS Data: Comparison of Force Fields and Methods. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 654333.	1.6	51
13	Ubiquitin Interacting Motifs: Duality Between Structured and Disordered Motifs. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 676235.	1.6	6
14	Order and disorder $\hat{\pm}$ An integrative structure of the full-length human growth hormone receptor. <i>Science Advances</i> , 2021, 7, .	4.7	25
15	On the specificity of protein $\hat{\pm}$ protein interactions in the context of disorder. <i>Biochemical Journal</i> , 2021, 478, 2035-2050.	1.7	41
16	The disordered PCI $\hat{\pm}$ binding human proteins CSNAP and DSS1 have diverged in structure and function. <i>Protein Science</i> , 2021, 30, 2069-2082.	3.1	8
17	Insight into Calcium-Binding Motifs of Intrinsically Disordered Proteins. <i>Biomolecules</i> , 2021, 11, 1173.	1.8	16
18	On the Potential of Machine Learning to Examine the Relationship Between Sequence, Structure, Dynamics and Function of Intrinsically Disordered Proteins. <i>Journal of Molecular Biology</i> , 2021, 433, 167196.	2.0	51

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19	Quantification of Conformational Entropy Unravels Effect of Disordered Flanking Region in Coupled Folding and Binding. <i>Journal of the American Chemical Society</i> , 2021, 143, 14540-14550.	6.6	22
20	Flanking Disorder of the Folded α -Hub Domain from Radical Induced Cell Death1 Affects Transcription Factor Binding by Ensemble Redistribution. <i>Journal of Molecular Biology</i> , 2021, 433, 167320.	2.0	17
21	IDDomainSpotter: Compositional bias reveals domains in long disordered protein regions—Insights from transcription factors. <i>Protein Science</i> , 2020, 29, 169-183.	3.1	14
22	Polyelectrolyte interactions enable rapid association and dissociation in high-affinity disordered protein complexes. <i>Nature Communications</i> , 2020, 11, 5736.	5.8	74
23	Effects of Ligand Binding on the Energy Landscape of Acyl-CoA-Binding Protein. <i>Biophysical Journal</i> , 2020, 119, 1821-1832.	0.2	15
24	Orchestration of signaling by structural disorder in class 1 cytokine receptors. <i>Cell Communication and Signaling</i> , 2020, 18, 132.	2.7	20
25	The Non-Fibrillating N-Terminal of α -Synuclein Binds and Co-Fibrillates with Heparin. <i>Biomolecules</i> , 2020, 10, 1192.	1.8	6
26	The intracellular lipid-binding domain of human Na ⁺ /H ⁺ exchanger 1 forms a lipid-protein co-structure essential for activity. <i>Communications Biology</i> , 2020, 3, 731.	2.0	11
27	Interactions by Disorder – A Matter of Context. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 110.	1.6	124
28	Yeast recombinant production of intact human membrane proteins with long intrinsically disordered intracellular regions for structural studies. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183272.	1.4	6
29	Mutations in a Single Signaling Pathway Allow Cell Growth in Heavy Water. <i>ACS Synthetic Biology</i> , 2020, 9, 733-748.	1.9	14
30	Efficient refolding and reconstitution of tissue factor into nanodiscs facilitates structural investigation of a multicomponent system on a lipid bilayer. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183214.	1.4	3
31	Peptides containing the PCNA interacting motif APIM bind to the β -clamp and inhibit bacterial growth and mutagenesis. <i>Nucleic Acids Research</i> , 2020, 48, 5540-5554.	6.5	20
32	Avidity within the N-terminal anchor drives α -synuclein membrane interaction and insertion. <i>FASEB Journal</i> , 2020, 34, 7462-7482.	0.2	28
33	Specificity of MYB interactions relies on motifs in ordered and disordered contexts. <i>Nucleic Acids Research</i> , 2019, 47, 9592-9608.	6.5	30
34	Molecular basis for the binding and selective dephosphorylation of Na ⁺ /H ⁺ exchanger 1 by calcineurin. <i>Nature Communications</i> , 2019, 10, 3489.	5.8	36
35	Transmembrane Protein Aptamer Induces Cooperative Signaling by the EPO Receptor and the Cytokine Receptor β -Common Subunit. <i>iScience</i> , 2019, 17, 167-181.	1.9	15
36	R2R3 MYB Transcription Factors – Functions outside the DNA-Binding Domain. <i>Trends in Plant Science</i> , 2019, 24, 934-946.	4.3	109

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37	Random coil chemical shifts for serine, threonine and tyrosine phosphorylation over a broad pH range. <i>Journal of Biomolecular NMR</i> , 2019, 73, 713-725.	1.6	24
38	The PCNA interaction motifs revisited: thinking outside the PIP-box. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 4923-4943.	2.4	77
39	Dynamical Oligomerisation of Histidine Rich Intrinsically Disordered Proteins Is Regulated through Zinc-Histidine Interactions. <i>Biomolecules</i> , 2019, 9, 168.	1.8	22
40	Alginate Trisaccharide Binding Sites on the Surface of β -Lactoglobulin Identified by NMR Spectroscopy: Implications for Molecular Network Formation. <i>ACS Omega</i> , 2019, 4, 6165-6174.	1.6	11
41	Distinct β -Synuclein:Lipid Co-Structure Complexes Affect Amyloid Nucleation through Fibril Mimetic Behavior. <i>Biochemistry</i> , 2019, 58, 5052-5065.	1.2	12
42	Evolutionary conservation of the intrinsic disorder-based Radical-Induced Cell Death1 hub interactome. <i>Scientific Reports</i> , 2019, 9, 18927.	1.6	19
43	The transmembrane autophagy cargo receptors AT11 and AT12 interact with ATC8 through intrinsically disordered regions with distinct biophysical properties. <i>Biochemical Journal</i> , 2019, 476, 449-465.	1.7	24
44	Extreme disorder in an ultrahigh-affinity protein complex. <i>Nature</i> , 2018, 555, 61-66.	13.7	538
45	Structure of Radical-Induced Cell Death1 Hub Domain Reveals a Common β -Scaffold for Disorder in Transcriptional Networks. <i>Structure</i> , 2018, 26, 734-746.e7.	1.6	28
46	Role of protein dynamics in transmembrane receptor signalling. <i>Current Opinion in Structural Biology</i> , 2018, 48, 74-82.	2.6	26
47	The Complex Conformational Dynamics of Neuronal Calcium Sensor-1: A Single Molecule Perspective. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 468.	1.4	13
48	Expanded Interactome of the Intrinsically Disordered Protein Dss1. <i>Cell Reports</i> , 2018, 25, 862-870.	2.9	14
49	Characterization of Dynamic IDP Complexes by NMR Spectroscopy. <i>Methods in Enzymology</i> , 2018, 611, 193-226.	0.4	29
50	Cytokine Receptors. <i>Endocrinology</i> , 2018, , 157-185.	0.1	6
51	A disordered acidic domain in GPIHBP1 harboring a sulfated tyrosine regulates lipoprotein lipase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6020-E6029.	3.3	51
52	Cold Denaturation of the HIV-1 Protease Monomer. <i>Biochemistry</i> , 2017, 56, 1029-1032.	1.2	7
53	A phosphorylation-motif for tuneable helix stabilisation in intrinsically disordered proteins â€“ Lessons from the sodium proton exchanger 1 (NHE1). <i>Cellular Signalling</i> , 2017, 37, 40-51.	1.7	34
54	Functions of intrinsic disorder in transmembrane proteins. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3205-3224.	2.4	63

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55	(S)Pinning down protein interactions by NMR. <i>Protein Science</i> , 2017, 26, 436-451.	3.1	58
56	An Efficient Method for Estimating the Hydrodynamic Radius of Disordered Protein Conformations. <i>Biophysical Journal</i> , 2017, 113, 550-557.	0.2	110
57	Behaviour of intrinsically disordered proteins in protein-protein complexes with an emphasis on fuzziness. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3175-3183.	2.4	104
58	Eukaryotic transcription factors: paradigms of protein intrinsic disorder. <i>Biochemical Journal</i> , 2017, 474, 2509-2532.	1.7	108
59	Structures and Short Linear Motif of Disordered Transcription Factor Regions Provide Clues to the Interactome of the Cellular Hub Protein Radical-induced Cell Death1. <i>Journal of Biological Chemistry</i> , 2017, 292, 512-527.	1.6	55
60	Deoxynucleoside Salvage in Fission Yeast Allows Rescue of Ribonucleotide Reductase Deficiency but Not Spd1-Mediated Inhibition of Replication. <i>Genes</i> , 2017, 8, 128.	1.0	5
61	Single methyl groups can act as toggle switches to specify transmembrane Protein-protein interactions. <i>ELife</i> , 2017, 6, .	2.8	14
62	Cytokine Receptors. <i>Endocrinology</i> , 2017, , 1-29.	0.1	1
63	The Ku70 80 ring in Non-Homologous End-Joining easy to slip on hard to remove. <i>Frontiers in Bioscience - Landmark</i> , 2016, 21, 514-527.	3.0	32
64	Prolactin Signaling Stimulates Invasion via Na ⁺ /H ⁺ Exchanger NHE1 in T47D Human Breast Cancer Cells. <i>Molecular Endocrinology</i> , 2016, 30, 693-708.	3.7	23
65	A combined computational and structural model of the full-length human prolactin receptor. <i>Nature Communications</i> , 2016, 7, 11578.	5.8	52
66	DSS1/Sem1, a Multifunctional and Intrinsically Disordered Protein. <i>Trends in Biochemical Sciences</i> , 2016, 41, 446-459.	3.7	42
67	Understanding single-pass transmembrane receptor signaling from a structural viewpoint” what are we missing?. <i>FEBS Journal</i> , 2016, 283, 4424-4451.	2.2	49
68	The human Na ⁺ /H ⁺ exchanger 1 is a membrane scaffold protein for extracellular signal-regulated kinase 2. <i>BMC Biology</i> , 2016, 14, 31.	1.7	45
69	An efficient arabinoxylan-debranching β -1-arabinofuranosidase of family GH62 from <i>Aspergillus nidulans</i> contains a secondary carbohydrate binding site. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 6265-6277.	1.7	23
70	Cytokine Receptors. <i>Endocrinology</i> , 2016, , 1-29.	0.1	4
71	A de Novo-Designed Monomeric, Compact Three-Helix Bundle Protein on a Carbohydrate Template. <i>ChemBioChem</i> , 2015, 16, 1905-1918.	1.3	2
72	Globular and disordered”the non-identical twins in protein-protein interactions. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 40.	1.6	36

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73	Functional Characterization of a Conserved Archaeal Viral Operon Revealing Single-Stranded DNA Binding, Annealing and Nuclease Activities. <i>Journal of Molecular Biology</i> , 2015, 427, 2179-2191.	2.0	32
74	Intrinsically disordered cytoplasmic domains of two cytokine receptors mediate conserved interactions with membranes. <i>Biochemical Journal</i> , 2015, 468, 495-506.	1.7	68
75	Residue 146 regulates prolactin receptor folding, basal activity and ligand-responsiveness: Potential implications in breast tumorigenesis. <i>Molecular and Cellular Endocrinology</i> , 2015, 401, 173-188.	1.6	14
76	Protein intrinsic disorder in <i>Arabidopsis</i> NAC transcription factors: transcriptional activation by ANAC013 and ANAC046 and their interactions with RCD1. <i>Biochemical Journal</i> , 2015, 465, 281-294.	1.7	48
77	Single-Molecule Folding Mechanisms of the apo- and Mg ²⁺ -Bound States of Human Neuronal Calcium Sensor-1. <i>Biophysical Journal</i> , 2015, 109, 113-123.	0.2	16
78	A Residue Quartet in the Extracellular Domain of the Prolactin Receptor Selectively Controls Mitogen-activated Protein Kinase Signaling. <i>Journal of Biological Chemistry</i> , 2015, 290, 11890-11904.	1.6	4
79	Exploiting Hydrophobicity for Efficient Production of Transmembrane Helices for Structure Determination by NMR Spectroscopy. <i>Analytical Chemistry</i> , 2015, 87, 9126-9131.	3.2	11
80	A Two-step Protein Quality Control Pathway for a Misfolded DJ-1 Variant in Fission Yeast. <i>Journal of Biological Chemistry</i> , 2015, 290, 21141-21153.	1.6	22
81	Single Site Suppressors of a Fission Yeast Temperature-Sensitive Mutant in <i>cdc48</i> Identified by Whole Genome Sequencing. <i>PLoS ONE</i> , 2015, 10, e0117779.	1.1	8
82	Dss1 Is a 26S Proteasome Ubiquitin Receptor. <i>Molecular Cell</i> , 2014, 56, 453-461.	4.5	81
83	Spd2 assists Spd1 in modulation of RNR architecture but does not regulate deoxynucleotide pools. <i>Journal of Cell Science</i> , 2014, 127, 2460-70.	1.2	11
84	Structural Dynamics and Regulation of the Mammalian SLC9A Family of Na ⁺ /H ⁺ Exchangers. <i>Current Topics in Membranes</i> , 2014, 73, 69-148.	0.5	71
85	Direct single-molecule observation of calcium-dependent misfolding in human neuronal calcium sensor-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13069-13074.	3.3	45
86	Who climbs the tryptophan ladder? On the structure and function of the WSXWS motif in cytokine receptors and thrombospondin repeats. <i>Cytokine and Growth Factor Reviews</i> , 2014, 25, 337-341.	3.2	31
87	C-Terminal ERK D- (and F-Like) Domains Link the Na ⁺ /H ⁺ Exchanger NHE1 to ERK2 Phosphorylation and Regulation via Scaffolding. <i>Biophysical Journal</i> , 2014, 106, 426a.	0.2	0
88	The Structure and Oligomericity of the Transmembrane Domain of Cytokine Receptors is Modulated by the Protein/Lipid Ratio. <i>Biophysical Journal</i> , 2014, 106, 21a.	0.2	0
89	Exploring the Minimally Frustrated Energy Landscape of Unfolded ACBP. <i>Journal of Molecular Biology</i> , 2014, 426, 722-734.	2.0	17
90	Single-Molecule Folding Mechanism of an EF-Hand Neuronal Calcium Sensor. <i>Structure</i> , 2013, 21, 1812-1821.	1.6	27

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91	Strains of the soil fungus <i>Mortierella</i> show different degradation potentials for the phenylurea herbicide diuron. <i>Biodegradation</i> , 2013, 24, 765-774.	1.5	79
92	Solution properties of the archaeal CRISPR DNA repeat-binding homeodomain protein Cbp2. <i>Nucleic Acids Research</i> , 2013, 41, 3424-3435.	6.5	10
93	Gentamicin Binds to the Megalin Receptor as a Competitive Inhibitor Using the Common Ligand Binding Motif of Complement Type Repeats. <i>Journal of Biological Chemistry</i> , 2013, 288, 4424-4435.	1.6	47
94	New horizons for lipoprotein receptors: communication by β -propellers. <i>Journal of Lipid Research</i> , 2013, 54, 2763-2774.	2.0	13
95	The Transcriptional Repressor Domain of Gli3 Is Intrinsically Disordered. <i>PLoS ONE</i> , 2013, 8, e76972.	1.1	5
96	Direct interaction with the Na ⁺ /H ⁺ exchanger NHE1 regulates ERK1/2 activity. <i>FASEB Journal</i> , 2013, 27, 730.1.	0.2	1
97	β -Microseminoprotein Endows Post Coital Seminal Plasma with Potent Candidacidal Activity by a Calcium- and pH-Dependent Mechanism. <i>PLoS Pathogens</i> , 2012, 8, e1002625.	2.1	24
98	Structure and Dynamic Properties of Membrane Proteins using NMR. , 2012, 2, 1491-1539.		5
99	A Highly Compliant Protein Native State with a Spontaneous-like Mechanical Unfolding Pathway. <i>Journal of the American Chemical Society</i> , 2012, 134, 17068-17075.	6.6	29
100	The C-Terminal Tail of Human Neuronal Calcium Sensor 1 Regulates the Conformational Stability of the Ca ²⁺ -Activated State. <i>Journal of Molecular Biology</i> , 2012, 417, 51-64.	2.0	31
101	Temperature-Induced Transitions in Disordered Proteins Probed by NMR Spectroscopy. <i>Methods in Molecular Biology</i> , 2012, 896, 233-247.	0.4	2
102	Order by disorder in plant signaling. <i>Trends in Plant Science</i> , 2012, 17, 625-632.	4.3	65
103	Analyzing Temperature-Induced Transitions in Disordered Proteins by NMR Spectroscopy and Secondary Chemical Shift Analyses. , 2012, 896, 249-256.		0
104	The WSXWS Motif in Cytokine Receptors Is a Molecular Switch Involved in Receptor Activation: Insight from Structures of the Prolactin Receptor. <i>Structure</i> , 2012, 20, 270-282.	1.6	73
105	Senescence-associated Barley NAC (NAM, ATAF1,2, CUC) Transcription Factor Interacts with Radical-induced Cell Death 1 through a Disordered Regulatory Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 35418-35429.	1.6	84
106	Streptococcal pyogenic exotoxin B (SpeB) boosts the contact system via binding of α -1 antitrypsin. <i>Biochemical Journal</i> , 2011, 434, 123-132.	1.7	7
107	The Intracellular Distal Tail of the Na ⁺ /H ⁺ Exchanger NHE1 Is Intrinsically Disordered: Implications for NHE1 Trafficking. <i>Biochemistry</i> , 2011, 50, 3469-3480.	1.2	56
108	Development of prolactin receptor antagonists with reduced pH dependence of receptor binding. <i>Journal of Molecular Recognition</i> , 2011, 24, 533-547.	1.1	6

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109	Protein stability, flexibility and function. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 969-976.	1.1	178
110	Temperature-dependent structural changes in intrinsically disordered proteins: Formation of α -helices or loss of polyproline II?. <i>Protein Science</i> , 2010, 19, 1555-1564.	3.1	200
111	Regulation of ribonucleotide reductase by Spd1 involves multiple mechanisms. <i>Genes and Development</i> , 2010, 24, 1145-1159.	2.7	41
112	Crystal Structure of an Affinity-matured Prolactin Complexed to Its Dimerized Receptor Reveals the Topology of Hormone Binding Site 2. <i>Journal of Biological Chemistry</i> , 2010, 285, 8422-8433.	1.6	59
113	Functional aspects of protein flexibility. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 2231-2247.	2.4	207
114	Metabolites of the phenylurea herbicides chlorotoluron, diuron, isoproturon and linuron produced by the soil fungus <i>Mortierella</i> sp.. <i>Environmental Pollution</i> , 2009, 157, 2806-2812.	3.7	72
115	Structure of the Mature Streptococcal Cysteine Protease Exotoxin mSpeB in Its Active Dimeric Form. <i>Journal of Molecular Biology</i> , 2009, 393, 693-703.	2.0	15
116	Phosphate Selective Uranyl Photoaffinity Cleavage of Proteins. Determination of Phosphorylation Sites. <i>ChemBioChem</i> , 2008, 9, 2377-2381.	1.3	11
117	The Intrinsically Disordered RNR Inhibitor Sml1 Is a Dynamic Dimer. <i>Biochemistry</i> , 2008, 47, 13428-13437.	1.2	53
118	Mechanism of the Ca ²⁺ -induced Enhancement of the Intrinsic Factor VIIa Activity. <i>Journal of Biological Chemistry</i> , 2008, 283, 25863-25870.	1.6	11
119	Acyl-CoA-binding protein (ACBP) localizes to the endoplasmic reticulum and Golgi in a ligand-dependent manner in mammalian cells. <i>Biochemical Journal</i> , 2008, 410, 463-472.	1.7	30
120	Structural and Thermodynamic Bases for the Design of Pure Prolactin Receptor Antagonists. <i>Journal of Biological Chemistry</i> , 2007, 282, 33118-33131.	1.6	66
121	Engineering the substrate and inhibitor specificities of human coagulation Factor VIIa. <i>Biochemical Journal</i> , 2007, 405, 429-438.	1.7	23
122	A loop of coagulation factor VIIa influencing macromolecular substrate specificity. <i>FEBS Letters</i> , 2007, 581, 71-76.	1.3	4
123	Structure-activity study of the antibacterial peptide fallaxin. <i>Protein Science</i> , 2007, 16, 1969-1976.	3.1	38
124	Acyl-CoA binding proteins; structural and functional conservation over 2000 MYA. <i>Molecular and Cellular Biochemistry</i> , 2007, 299, 55-65.	1.4	84
125	Binding Site Structure of One LRP-RAP Complex: Implications for a Common Ligand-Receptor Binding Motif. <i>Journal of Molecular Biology</i> , 2006, 362, 700-716.	2.0	62
126	Structure of the human beta-ketoacyl [ACP] synthase from the mitochondrial type II fatty acid synthase. <i>Protein Science</i> , 2006, 16, 261-272.	3.1	56

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127	Different secondary structure elements as scaffolds for protein folding transition states of two homologous four-helix bundles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 80-90.	1.5	51
128	Hydroxylation of the Herbicide Isoproturon by Fungi Isolated from Agricultural Soil. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7927-7932.	1.4	46
129	Reversible Dimerization of Acid-Denatured ACBP Controlled by Helix A4. <i>Biochemistry</i> , 2005, 44, 1375-1384.	1.2	17
130	Solution Structure of Human Prolactin. <i>Journal of Molecular Biology</i> , 2005, 351, 810-823.	2.0	105
131	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, 602-616.	3.1	207
132	Structure and Biochemical Function of a Prototypical Arabidopsis U-box Domain. <i>Journal of Biological Chemistry</i> , 2004, 279, 40053-40061.	1.6	85
133	Early kinetic intermediate in the folding of acyl-CoA binding protein detected by fluorescence labeling and ultrarapid mixing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9807-9812.	3.3	95
134	Fluorescently labelled bovine acyl-CoA-binding protein acting as an acyl-CoA sensor: interaction with CoA and acyl-CoA esters and its use in measuring free acyl-CoA esters and non-esterified fatty acids. <i>Biochemical Journal</i> , 2002, 365, 165-172.	1.7	22
135	Transient Intermediary States with High and Low Folding Probabilities in the Apparent Two-state Folding Equilibrium of ACBP at Low pH. <i>Journal of Molecular Biology</i> , 2002, 318, 805-814.	2.0	34
136	Transient Structure Formation in Unfolded Acyl-coenzyme A-binding Protein Observed by Site-directed Spin Labelling. <i>Journal of Molecular Biology</i> , 2002, 324, 349-357.	2.0	85
137	¹ H, ¹³ C, and ¹⁵ N assignments of un-myristoylated Ca ²⁺ -frequentin, a synaptic efficacy modulator. <i>Journal of Biomolecular NMR</i> , 2000, 16, 85-86.	1.6	7
138	Formation of hydrogen bonds precedes the rate-limiting formation of persistent structure in the folding of ACBP. <i>Journal of Molecular Biology</i> , 2000, 301, 1307-1314.	2.0	31
139	The formation of a native-like structure containing eight conserved hydrophobic residues is rate limiting in two-state protein folding of ACBP. <i>Nature Structural Biology</i> , 1999, 6, 594-601.	9.7	128
140	Acyl-coenzyme A binding protein (ACBP). <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 1999, 1441, 150-161.	1.2	95
141	Conserved Residues and Their Role in the Structure, Function, and Stability of Acyl-Coenzyme A Binding Protein. <i>Biochemistry</i> , 1999, 38, 2386-2394.	1.2	82
142	Mapping the lifetimes of local opening events in a native state protein. <i>Protein Science</i> , 1998, 7, 2237-2248.	3.1	25
143	Hydrophobic Core Substitutions in Calbindin D9k: Effects on Ca ²⁺ -Binding and Dissociation. <i>Biochemistry</i> , 1998, 37, 8926-8937.	1.2	39
144	Barley lipid-transfer protein complexed with palmitoyl CoA: the structure reveals a hydrophobic binding site that can expand to fit both large and small lipid-like ligands. <i>Structure</i> , 1997, 5, 291-306.	1.6	134

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145	Thermodynamics of Ligand Binding to Acyl-Coenzyme A Binding Protein Studied by Titration Calorimetry. <i>Biochemistry</i> , 1996, 35, 14118-14126.	1.2	140
146	Fast and One-step Folding of Closely and Distantly Related Homologous Proteins of a Four-helix Bundle Family. <i>Journal of Molecular Biology</i> , 1996, 256, 187-200.	2.0	107
147	Probing the Nature of Noncovalent Interactions by Mass Spectrometry. A Study of Protein ¹³ C CoA Ligand Binding and Assembly. <i>Journal of the American Chemical Society</i> , 1996, 118, 8646-8653.	6.6	304
148	Folding of a four-helix bundle: studies of acyl-coenzyme A binding protein. <i>Biochemistry</i> , 1995, 34, 7217-7224.	1.2	169
149	Local Perturbations by Ligand Binding of Hydrogen Deuterium Exchange Kinetics in a Four-helix Bundle Protein, Acyl Coenzyme A Binding Protein (ACBP). <i>Journal of Molecular Biology</i> , 1995, 250, 695-706.	2.0	47
150	Three-dimensional Structure of the Complex between Acyl-Coenzyme A Binding Protein and Palmitoyl-Coenzyme A. <i>Journal of Molecular Biology</i> , 1993, 230, 1260-1277.	2.0	164