

Kaare Teilum

List of Publications by Year in descending order

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69
papers

3,552
citations

147801

31
h-index

144013

57
g-index

83
all docs

83
docs citations

83
times ranked

4592
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	7.6	207
2	Functional aspects of protein flexibility. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 2231-2247.	5.4	207
3	Protein stability, flexibility and function. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 969-976.	2.3	178
4	Fractional ¹³ C enrichment of isolated carbons using [1- ¹³ C]- or [2- ¹³ C]-glucose facilitates the accurate measurement of dynamics at backbone C α and side-chain methyl positions in proteins. <i>Journal of Biomolecular NMR</i> , 2007, 38, 199-212.	2.8	160
5	Determination of an Ensemble of Structures Representing the Denatured State of the Bovine Acyl-Coenzyme A Binding Protein. <i>Journal of the American Chemical Society</i> , 2004, 126, 3291-3299.	13.7	155
6	Conformational selection in the molten globule state of the nuclear coactivator binding domain of CBP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12535-12540.	7.1	152
7	Arabidopsis ATP A2 peroxidase. Expression and high-resolution structure of a plant peroxidase with implications for lignification. <i>Plant Molecular Biology</i> , 2000, 44, 231-243.	3.9	149
8	Helical Propensity in an Intrinsically Disordered Protein Accelerates Ligand Binding. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1548-1551.	13.8	146
9	Structure of soybean seed coat peroxidase: A plant peroxidase with unusual stability and haem-apoprotein interactions. <i>Protein Science</i> , 2001, 10, 108-115.	7.6	122
10	Solution Structure of Human Prolactin. <i>Journal of Molecular Biology</i> , 2005, 351, 810-823.	4.2	105
11	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.	5.4	104
12	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.	7.1	95
13	Remeasuring HEWL pK _a values by NMR spectroscopy: Methods, analysis, accuracy, and implications for theoretical pK _a calculations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 685-702.	2.6	89
14	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.	4.2	85
15	Protein Dielectric Constants Determined from NMR Chemical Shift Perturbations. <i>Journal of the American Chemical Society</i> , 2013, 135, 16968-16976.	13.7	82
16	Biosynthetic ¹³ C Labeling of Aromatic Side Chains in Proteins for NMR Relaxation Measurements. <i>Journal of the American Chemical Society</i> , 2006, 128, 2506-2507.	13.7	76
17	Transient structural distortion of metal-free Cu/Zn superoxide dismutase triggers aberrant oligomerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18273-18278.	7.1	74
18	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.	3.3	73

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19	Rapid Formation of a Preoligomeric Peptideâ€“Metalâ€“Peptide Complex Following Copper(II) Binding to Amyloid Î²â€“Peptides. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 2532-2535.	13.8	69
20	Amyloid-Î² and Î±-Synuclein Decrease the Level of Metal-Catalyzed Reactive Oxygen Species by Radical Scavenging and Redox Silencing. <i>Journal of the American Chemical Society</i> , 2016, 138, 3966-3969.	13.7	69
21	(S)Pinning down protein interactions by NMR. <i>Protein Science</i> , 2017, 26, 436-451.	7.6	58
22	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.	2.6	51
23	Binding Revisitedâ€“Avidity in Cellular Function and Signaling. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 615565.	3.5	47
24	relax: the analysis of biomolecular kinetics and thermodynamics using NMR relaxation dispersion data. <i>Bioinformatics</i> , 2014, 30, 2219-2220.	4.1	45
25	The Human Selenoprotein VCP-interacting Membrane Protein (VIMP) Is Non-globular and Harbors a Reductase Function in an Intrinsically Disordered Region. <i>Journal of Biological Chemistry</i> , 2012, 287, 26388-26399.	3.4	41
26	On the specificity of proteinâ€“protein interactions in the context of disorder. <i>Biochemical Journal</i> , 2021, 478, 2035-2050.	3.7	41
27	A Folded Excited State of Ligand-Free Nuclear Coactivator Binding Domain (NCBD) Underlies Plasticity in Ligand Recognition. <i>Biochemistry</i> , 2013, 52, 1686-1693.	2.5	39
28	The pK_a Value and Accessibility of Cysteine Residues Are Key Determinants for Protein Substrate Discrimination by Glutaredoxin. <i>Biochemistry</i> , 2014, 53, 2533-2540.	2.5	38
29	Globular and disorderedâ€“the non-identical twins in protein-protein interactions. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 40.	3.5	36
30	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.	4.2	34
31	Protein Interacting with C-kinase 1 (PICK1) Binding Promiscuity Relies on Unconventional PSD-95/Discs-Large/ZO-1 Homology (PDZ) Binding Modes for Nonclass II PDZ Ligands. <i>Journal of Biological Chemistry</i> , 2014, 289, 25327-25340.	3.4	34
32	Structure of Dimeric and Tetrameric Complexes of the BAR Domain Protein PICK1 Determined by Small-Angle X-Ray Scattering. <i>Structure</i> , 2015, 23, 1258-1270.	3.3	34
33	A Soluble, Folded Protein without Charged Amino Acid Residues. <i>Biochemistry</i> , 2016, 55, 3949-3956.	2.5	34
34	Non-uniform sampling of NMR relaxation data. <i>Journal of Biomolecular NMR</i> , 2016, 64, 165-173.	2.8	33
35	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.	4.2	31
36	The Capsid Domain of Arc Changes Its Oligomerization Propensity through Direct Interaction with the NMDA Receptor. <i>Structure</i> , 2019, 27, 1071-1081.e5.	3.3	31

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37	Solution Structures of Human and Porcine Î²-Microseminoprotein. <i>Journal of Molecular Biology</i> , 2006, 362, 502-515.	4.2	27
38	Structure of the competence pilus major pilin ComGC in <i>Streptococcus pneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 14134-14146.	3.4	27
39	Aggregation-Prone Amyloid-Î²...Cu ^{II} Species Formed on the Millisecond Timescale under Mildly Acidic Conditions. <i>ChemBioChem</i> , 2015, 16, 1293-1297.	2.6	26
40	The three-dimensional structure of an H-superfamily conotoxin reveals a granulin fold arising from a common ICK cysteine framework. <i>Journal of Biological Chemistry</i> , 2019, 294, 8745-8759.	3.4	26
41	Molecular dynamics ensemble refinement of the heterogeneous native state of NCBD using chemical shifts and NOEs. <i>PeerJ</i> , 2018, 6, e5125.	2.0	25
42	Off-resonance rotating-frame relaxation dispersion experiment for ¹³ C in aromatic side chains using L-optimized TROSY-selection. <i>Journal of Biomolecular NMR</i> , 2014, 59, 23-29.	2.8	24
43	Fitting Side-Chain NMR Relaxation Data Using Molecular Simulations. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 5262-5275.	5.3	23
44	The inverted chevron plot measured by NMR relaxation reveals a native-like unfolding intermediate in acyl-CoA binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6877-6882.	7.1	22
45	Is a Malleable Protein Necessarily Highly Dynamic? The Hydrophobic Core of the Nuclear Coactivator Binding Domain Is Well Ordered. <i>Biophysical Journal</i> , 2012, 102, 1627-1635.	0.5	22
46	Global analysis of protein stability by temperature and chemical denaturation. <i>Analytical Biochemistry</i> , 2020, 605, 113863.	2.4	20
47	A high-affinity, bivalent PDZ domain inhibitor complexes PICK1 to alleviate neuropathic pain. <i>EMBO Molecular Medicine</i> , 2020, 12, e11248.	6.9	20
48	Disulfide Bond Formation and Folding of Plant Peroxidases Expressed as Inclusion Body Protein in <i>Escherichia coli</i> Thioredoxin Reductase Negative Strains. <i>Protein Expression and Purification</i> , 1999, 15, 77-82.	1.3	17
49	The Pathogenic A2V Mutant Exhibits Distinct Aggregation Kinetics, Metal Site Structure, and Metal Exchange of the Cu ²⁺ -AÎ² Complex. <i>Chemistry - A European Journal</i> , 2017, 23, 13591-13595.	3.3	17
50	Millisecond Dynamics in Glutaredoxin during Catalytic Turnover Is Dependent on Substrate Binding and Absent in the Resting States. <i>Journal of the American Chemical Society</i> , 2011, 133, 3034-3042.	13.7	16
51	NCAM2 Fibronectin type-III domains form a rigid structure that binds and activates the Fibroblast Growth Factor Receptor. <i>Scientific Reports</i> , 2018, 8, 8957.	3.3	16
52	Charge Interactions in a Highly Charge-Depleted Protein. <i>Journal of the American Chemical Society</i> , 2021, 143, 2500-2508.	13.7	15
53	Direct assessment of substrate binding to the Neurotransmitter:Sodium Symporter LeuT by solid state NMR. <i>ELife</i> , 2017, 6, .	6.0	15
54	Mechanisms of PDZ domain scaffold assembly illuminated by use of supported cell membrane sheets. <i>ELife</i> , 2019, 8, .	6.0	15

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55	Disease-linked mutations cause exposure of a protein quality control degron. <i>Structure</i> , 2022, 30, 1245-1253.e5.	3.3	14
56	Purification, crystallization and preliminary X-ray diffraction analysis of the carbohydrate-binding domain of flocculin, a cell-adhesion molecule from <i>Saccharomyces carlsbergensis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2135-2137.	2.5	13
57	Linking thermodynamics and measurements of protein stability. <i>Protein Engineering, Design and Selection</i> , 2021, 34, .	2.1	13
58	Synergistic stabilization of a double mutant in chymotrypsin inhibitor 2 from a library screen in <i>E. coli</i> . <i>Communications Biology</i> , 2021, 4, 980.	4.4	13
59	A dual-reporter system for investigating and optimizing protein translation and folding in <i>E. coli</i> . <i>Nature Communications</i> , 2021, 12, 6093.	12.8	12
60	Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry. <i>Jacs Au</i> , 2021, 1, 2385-2393.	7.9	12
61	The extraordinary thermal stability of EstA from <i>S. islandicus</i> is independent of post translational modifications. <i>Protein Science</i> , 2017, 26, 1819-1827.	7.6	8
62	Software for reconstruction of nonuniformly sampled NMR data. <i>Magnetic Resonance in Chemistry</i> , 2021, 59, 315-323.	1.9	6
63	Ubiquitin Interacting Motifs: Duality Between Structured and Disordered Motifs. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 676235.	3.5	6
64	Double Mutant of Chymotrypsin Inhibitor 2 Stabilized through Increased Conformational Entropy. <i>Biochemistry</i> , 2022, 61, 160-170.	2.5	6
65	Bidirectional protein-protein interactions control liquid-liquid phase separation of PSD-95 and its interaction partners. <i>IScience</i> , 2022, 25, 103808.	4.1	6
66	Conformational heterogeneity of Savinase from NMR, HDX-MS and X-ray diffraction analysis. <i>PeerJ</i> , 2020, 8, e9408.	2.0	2
67	Towards Improved Biophysical Calculations to Identify Disease-Causing Mutations. <i>Biophysical Journal</i> , 2018, 114, 199a.	0.5	0
68	Transient Structural Distortion and Oligomerization of the Capsid Forming Protein Arc is Attenuated by Ligand Binding. <i>Biophysical Journal</i> , 2019, 116, 48a.	0.5	0
69	The Determinants for Ligand Binding of the Domesticated Retroviral Protein Arc. <i>Biophysical Journal</i> , 2020, 118, 195a.	0.5	0