Magnus Kjaergaard

List of Publications by Year
in descending order

46 papers	2,549 citations	218381 26 h-index	243296 44 g-index
57 all docs	57 docs citations	57 times ranked	3132 citing authors

#	Article	IF	Citations
1	Random coil chemical shift for intrinsically disordered proteins: effects of temperature and pH. Journal of Biomolecular NMR, 2011, 49, 139-149.	1.6	257
2	Sequence correction of random coil chemical shifts: correlation between neighbor correction factors and changes in the Ramachandran distribution. Journal of Biomolecular NMR, 2011, 50, 157-165.	1.6	237
3	Temperatureâ€dependent structural changes in intrinsically disordered proteins: Formation of Î±â€'helices or loss of polyproline II?. Protein Science, 2010, 19, 1555-1564.	3.1	200
4	A mechanistic model of tau amyloid aggregation based on direct observation of oligomers. Nature Communications, 2015, 6, 7025.	5.8	179
5	Conformational selection in the molten globule state of the nuclear coactivator binding domain of CBP. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12535-12540.	3.3	152
6	Helical Propensity in an Intrinsically Disordered Protein Accelerates Ligand Binding. Angewandte Chemie - International Edition, 2014, 53, 1548-1551.	7.2	146
7	Effective concentrations enforced by intrinsically disordered linkers are governed by polymer physics. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23124-23131.	3.3	122
8	Single-Molecule Imaging of Individual Amyloid Protein Aggregates in Human Biofluids. ACS Chemical Neuroscience, 2016, 7, 399-406.	1.7	99
9	Hsp70 Inhibits the Nucleation and Elongation of Tau and Sequesters Tau Aggregates with High Affinity. ACS Chemical Biology, 2018, 13, 636-646.	1.6	96
10	Dynamics of P-type ATPase transport revealed by single-molecule FRET. Nature, 2017, 551, 346-351.	13.7	72
11	Thermodynamics Reveal that Helix Four in the NLS of NF-ÎºB p65 Anchors IÎºBÎ±, Forming a Very Stable Complex. Journal of Molecular Biology, 2006, 360, 421-434.	2.0	69
12	Identification of on- and off-pathway oligomers in amyloid fibril formation. Chemical Science, 2020, 11, 6236-6247.	3.7	64
13	Functions of intrinsic disorder in transmembrane proteins. Cellular and Molecular Life Sciences, 2017, 74, 3205-3224.	2.4	63
14	Structure and ligand interactions of the urokinase receptor (uPAR). Frontiers in Bioscience - Landmark, 2008, Volume, 5441.	3.0	57
15	The Intracellular Distal Tail of the Na⁺/H⁺Exchanger NHE1 Is Intrinsically Disordered: Implications for NHE1 Trafficking. Biochemistry, 2011, 50, 3469-3480.	1.2	56
16	Disordered proteins studied by chemical shifts. Progress in Nuclear Magnetic Resonance Spectroscopy, 2012, 60, 42-51.	3.9	54
17	Structural dynamics of P-type ATPase ion pumps. Biochemical Society Transactions, 2019, 47, 1247-1257.	1.6	53
18	Oligomer Diversity during the Aggregation of the Repeat Region of Tau. ACS Chemical Neuroscience, 2018, 9, 3060-3071.	1.7	50

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19	Intrinsically disordered linkers control tethered kinases via effective concentration. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21413-21419.	3.3	48
20	Modulation of the Intrinsic Helix Propensity of an Intrinsically Disordered Protein Reveals Long-Range Helixâ€"Helix Interactions. Journal of the American Chemical Society, 2013, 135, 10155-10163.	6.6	44
21	A Flexible Multidomain Structure Drives the Function of the Urokinase-type Plasminogen Activator Receptor (uPAR)*. Journal of Biological Chemistry, 2012, 287, 34304-34315.	1.6	43
22	A Folded Excited State of Ligand-Free Nuclear Coactivator Binding Domain (NCBD) Underlies Plasticity in Ligand Recognition. Biochemistry, 2013, 52, 1686-1693.	1.2	39
23	Linker Dependence of Avidity in Multivalent Interactions Between Disordered Proteins. Journal of Molecular Biology, 2019, 431, 4784-4795.	2.0	35
24	Solution structure of recombinant somatomedin B domain from vitronectin produced in <i>Pichia pastoris</i>. Protein Science, 2007, 16, 1934-1945.	3.1	32
25	The Câ€•terminal domains of the NMDA receptor: How intrinsically disordered tails affect signalling, plasticity and disease. European Journal of Neuroscience, 2021, 54, 6713-6739.	1.2	31
26	The RelA Nuclear Localization Signal Folds upon Binding to IÎºBÎ±. Journal of Molecular Biology, 2011, 405, 754-764.	2.0	29
27	Mimicry of the Regulatory Role of Urokinase in Lamellipodia Formation by Introduction of a Non-native Interdomain Disulfide Bond in Its Receptor. Journal of Biological Chemistry, 2011, 286, 43515-43526.	1.6	28
28	Single-Molecule Measurements of Transient Biomolecular Complexes through Microfluidic Dilution. Analytical Chemistry, 2013, 85, 6855-6859.	3.2	23
29	Is a Malleable Protein Necessarily Highly Dynamic? The Hydrophobic Core of the Nuclear Coactivator Binding Domain Is Well Ordered. Biophysical Journal, 2012, 102, 1627-1635.	0.2	22
30	Predicting the effect of disordered linkers on effective concentrations and avidity with the â€œC calculatorâ€• app. Methods in Enzymology, 2021, 647, 145-171.	0.4	20
31	The optimal docking strength for reversibly tethered kinases. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	18
32	Estimation of Effective Concentrations Enforced by Complex Linker Architectures from Conformational Ensembles. Biochemistry, 2022, 61, 171-182.	1.2	16
33	The interplay between transient Î±â€•helix formation and side chain rotamer distributions in disordered proteins probed by methyl chemical shifts. Protein Science, 2011, 20, 2023-2034.	3.1	12
34	Nanoscale spatial dependence of avidity in an IgG1 antibody. Scientific Reports, 2021, 11, 12663.	1.6	12
35	Engineering a Prototypic P-type ATPase <i>Listeria monocytogenes</i> Ca²⁺-ATPase 1 for Single-Molecule FRET Studies. Bioconjugate Chemistry, 2016, 27, 2176-2187.	1.8	9
36	Can proteins be intrinsically disordered inside a membrane?. Intrinsically Disordered Proteins, 2015, 3, e984570.	1.9	8

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37	Coupled Binding and Helix Formation Monitored by Synchrotron-Radiation Circular Dichroism. Biophysical Journal, 2019, 117, 729-742.	0.2	8
38	Measuring Effective Concentrations Enforced by Intrinsically Disordered Linkers. Methods in Molecular Biology, 2020, 2141, 505-518.	0.4	8
39	Rapid mass spectrometric analysis of ¹⁵Nâ€Łeu incorporation fidelity during preparation of specifically labeled NMR samples. Protein Science, 2008, 17, 1636-1639.	3.1	7
40	The Crystal Structure of the Ca2+-ATPase 1 from Listeria monocytogenes reveals a Pump Primed for Dephosphorylation. Journal of Molecular Biology, 2021, 433, 167015.	2.0	5
41	Temperature-Induced Transitions in Disordered Proteins Probed by NMR Spectroscopy. Methods in Molecular Biology, 2012, 896, 233-247.	0.4	2
42	Dynamics of P-type ATPase Transport Cycle Revealed by Single-Molecule FRET. Biophysical Journal, 2018, 114, 559a.	0.2	2
43	Intrinsic disorder in protein kinase A anchoring proteins signaling complexes. Progress in Molecular Biology and Translational Science, 2021, 183, 271-294.	0.9	2
44	Structure and Inhibition of the Urokinase-Type Plasminogen Activator Receptor. , 0, , 699-719.		1
45	Analyzing Temperature-Induced Transitions in Disordered Proteins by NMR Spectroscopy and Secondary Chemical Shift Analyses. , 2012, 896, 249-256.		0
46	Introducing the special issue on â€œProteins and Circuits in Memoryâ€• European Journal of Neuroscience, 2021, 54, 6691-6695.	1.2	0