

Magnus Kjaergaard

List of Publications by Year in descending order

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46
papers

2,549
citations

218677

26
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243625

44
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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. <i>Journal of Biomolecular NMR</i> , 2011, 49, 139-149.	2.8	257
2	Sequence correction of random coil chemical shifts: correlation between neighbor correction factors and changes in the Ramachandran distribution. <i>Journal of Biomolecular NMR</i> , 2011, 50, 157-165.	2.8	237
3	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.	7.6	200
4	A mechanistic model of tau amyloid aggregation based on direct observation of oligomers. <i>Nature Communications</i> , 2015, 6, 7025.	12.8	179
5	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
6	Helical Propensity in an Intrinsically Disordered Protein Accelerates Ligand Binding. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1548-1551.	13.8	146
7	Effective concentrations enforced by intrinsically disordered linkers are governed by polymer physics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23124-23131.	7.1	122
8	Single-Molecule Imaging of Individual Amyloid Protein Aggregates in Human Biofluids. <i>ACS Chemical Neuroscience</i> , 2016, 7, 399-406.	3.5	99
9	Hsp70 Inhibits the Nucleation and Elongation of Tau and Sequesters Tau Aggregates with High Affinity. <i>ACS Chemical Biology</i> , 2018, 13, 636-646.	3.4	96
10	Dynamics of P-type ATPase transport revealed by single-molecule FRET. <i>Nature</i> , 2017, 551, 346-351.	27.8	72
11	Thermodynamics Reveal that Helix Four in the NLS of NF- κ B p65 Anchors κ B β , Forming a Very Stable Complex. <i>Journal of Molecular Biology</i> , 2006, 360, 421-434.	4.2	69
12	Identification of on- and off-pathway oligomers in amyloid fibril formation. <i>Chemical Science</i> , 2020, 11, 6236-6247.	7.4	64
13	Functions of intrinsic disorder in transmembrane proteins. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3205-3224.	5.4	63
14	Structure and ligand interactions of the urokinase receptor (uPAR). <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 5441.	3.0	57
15	The Intracellular Distal Tail of the Na ⁺ /H ⁺ Exchanger NHE1 Is Intrinsically Disordered: Implications for NHE1 Trafficking. <i>Biochemistry</i> , 2011, 50, 3469-3480.	2.5	56
16	Disordered proteins studied by chemical shifts. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2012, 60, 42-51.	7.5	54
17	Structural dynamics of P-type ATPase ion pumps. <i>Biochemical Society Transactions</i> , 2019, 47, 1247-1257.	3.4	53
18	Oligomer Diversity during the Aggregation of the Repeat Region of Tau. <i>ACS Chemical Neuroscience</i> , 2018, 9, 3060-3071.	3.5	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.	7.1	48
20	Modulation of the Intrinsic Helix Propensity of an Intrinsically Disordered Protein Reveals Long-Range Helix-Helix Interactions. Journal of the American Chemical Society, 2013, 135, 10155-10163.	13.7	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.	3.4	43
22	A Folded Excited State of Ligand-Free Nuclear Coactivator Binding Domain (NCBD) Underlies Plasticity in Ligand Recognition. Biochemistry, 2013, 52, 1686-1693.	2.5	39
23	Linker Dependence of Avidity in Multivalent Interactions Between Disordered Proteins. Journal of Molecular Biology, 2019, 431, 4784-4795.	4.2	35
24	Solution structure of recombinant somatomedin B domain from vitronectin produced in <i>Pichia pastoris</i> . Protein Science, 2007, 16, 1934-1945.	7.6	32
25	The C-terminal domains of the NMDA receptor: How intrinsically disordered tails affect signalling, plasticity and disease. European Journal of Neuroscience, 2021, 54, 6713-6739.	2.6	31
26	The RelA Nuclear Localization Signal Folds upon Binding to I κ B β . Journal of Molecular Biology, 2011, 405, 754-764.	4.2	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.	3.4	28
28	Single-Molecule Measurements of Transient Biomolecular Complexes through Microfluidic Dilution. Analytical Chemistry, 2013, 85, 6855-6859.	6.5	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.	0.5	22
30	Predicting the effect of disordered linkers on effective concentrations and avidity with the α Ca calculator app. Methods in Enzymology, 2021, 647, 145-171.	1.0	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, .	7.1	18
32	Estimation of Effective Concentrations Enforced by Complex Linker Architectures from Conformational Ensembles. Biochemistry, 2022, 61, 171-182.	2.5	16
33	The interplay between transient α -helix formation and side chain rotamer distributions in disordered proteins probed by methyl chemical shifts. Protein Science, 2011, 20, 2023-2034.	7.6	12
34	Nanoscale spatial dependence of avidity in an IgG1 antibody. Scientific Reports, 2021, 11, 12663.	3.3	12
35	Engineering a Prototypic P-type ATPase <i>Listeria monocytogenes</i> Ca ²⁺ -ATPase 1 for Single-Molecule FRET Studies. Bioconjugate Chemistry, 2016, 27, 2176-2187.	3.6	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.	0.5	8
38	Measuring Effective Concentrations Enforced by Intrinsically Disordered Linkers. Methods in Molecular Biology, 2020, 2141, 505-518.	0.9	8
39	Rapid mass spectrometric analysis of ¹⁵ N- ¹⁵ Leu incorporation fidelity during preparation of specifically labeled NMR samples. Protein Science, 2008, 17, 1636-1639.	7.6	7
40	The Crystal Structure of the Ca ²⁺ -ATPase 1 from <i>Listeria monocytogenes</i> reveals a Pump Primed for Dephosphorylation. Journal of Molecular Biology, 2021, 433, 167015.	4.2	5
41	Temperature-Induced Transitions in Disordered Proteins Probed by NMR Spectroscopy. Methods in Molecular Biology, 2012, 896, 233-247.	0.9	2
42	Dynamics of P-type ATPase Transport Cycle Revealed by Single-Molecule FRET. Biophysical Journal, 2018, 114, 559a.	0.5	2
43	Intrinsic disorder in protein kinase A anchoring proteins signaling complexes. Progress in Molecular Biology and Translational Science, 2021, 183, 271-294.	1.7	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 "Proteins and Circuits in Memory". European Journal of Neuroscience, 2021, 54, 6691-6695.	2.6	0