

# Magnus Kjaergaard

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

2,549  
citations

218677

26  
h-index

243625

44  
g-index

57  
all docs

57  
docs citations

57  
times ranked

3132  
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimation of Effective Concentrations Enforced by Complex Linker Architectures from Conformational Ensembles. <i>Biochemistry</i> , 2022, 61, 171-182.	2.5	16
2	The optimal docking strength for reversibly tethered kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	18
3	The C-terminal domains of the NMDA receptor: How intrinsically disordered tails affect signalling, plasticity and disease. <i>European Journal of Neuroscience</i> , 2021, 54, 6713-6739.	2.6	31
4	Predicting the effect of disordered linkers on effective concentrations and avidity with the $\alpha$ C calculator. <i>Methods in Enzymology</i> , 2021, 647, 145-171.	1.0	20
5	Nanoscale spatial dependence of avidity in an IgG1 antibody. <i>Scientific Reports</i> , 2021, 11, 12663.	3.3	12
6	The Crystal Structure of the Ca <sup>2+</sup> -ATPase 1 from <i>Listeria monocytogenes</i> reveals a Pump Primed for Dephosphorylation. <i>Journal of Molecular Biology</i> , 2021, 433, 167015.	4.2	5
7	Intrinsic disorder in protein kinase A anchoring proteins signaling complexes. <i>Progress in Molecular Biology and Translational Science</i> , 2021, 183, 271-294.	1.7	2
8	Introducing the special issue on $\alpha$ Proteins and Circuits in Memory. <i>European Journal of Neuroscience</i> , 2021, 54, 6691-6695.	2.6	0
9	Intrinsically disordered linkers control tethered kinases via effective concentration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21413-21419.	7.1	48
10	Identification of on- and off-pathway oligomers in amyloid fibril formation. <i>Chemical Science</i> , 2020, 11, 6236-6247.	7.4	64
11	Measuring Effective Concentrations Enforced by Intrinsically Disordered Linkers. <i>Methods in Molecular Biology</i> , 2020, 2141, 505-518.	0.9	8
12	Coupled Binding and Helix Formation Monitored by Synchrotron-Radiation Circular Dichroism. <i>Biophysical Journal</i> , 2019, 117, 729-742.	0.5	8
13	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
14	Linker Dependence of Avidity in Multivalent Interactions Between Disordered Proteins. <i>Journal of Molecular Biology</i> , 2019, 431, 4784-4795.	4.2	35
15	Structural dynamics of P-type ATPase ion pumps. <i>Biochemical Society Transactions</i> , 2019, 47, 1247-1257.	3.4	53
16	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
17	Oligomer Diversity during the Aggregation of the Repeat Region of Tau. <i>ACS Chemical Neuroscience</i> , 2018, 9, 3060-3071.	3.5	50
18	Dynamics of P-type ATPase Transport Cycle Revealed by Single-Molecule FRET. <i>Biophysical Journal</i> , 2018, 114, 559a.	0.5	2

#	ARTICLE	IF	CITATIONS
19	Functions of intrinsic disorder in transmembrane proteins. Cellular and Molecular Life Sciences, 2017, 74, 3205-3224.	5.4	63
20	Dynamics of P-type ATPase transport revealed by single-molecule FRET. Nature, 2017, 551, 346-351.	27.8	72
21	Engineering a Prototypic P-type ATPase <i>Listeria monocytogenes</i> Ca <sup>2+</sup> -ATPase 1 for Single-Molecule FRET Studies. Bioconjugate Chemistry, 2016, 27, 2176-2187.	3.6	9
22	Single-Molecule Imaging of Individual Amyloid Protein Aggregates in Human Biofluids. ACS Chemical Neuroscience, 2016, 7, 399-406.	3.5	99
23	A mechanistic model of tau amyloid aggregation based on direct observation of oligomers. Nature Communications, 2015, 6, 7025.	12.8	179
24	Can proteins be intrinsically disordered inside a membrane?. Intrinsically Disordered Proteins, 2015, 3, e984570.	1.9	8
25	Helical Propensity in an Intrinsically Disordered Protein Accelerates Ligand Binding. Angewandte Chemie - International Edition, 2014, 53, 1548-1551.	13.8	146
26	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
27	Single-Molecule Measurements of Transient Biomolecular Complexes through Microfluidic Dilution. Analytical Chemistry, 2013, 85, 6855-6859.	6.5	23
28	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
29	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
30	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
31	Temperature-Induced Transitions in Disordered Proteins Probed by NMR Spectroscopy. Methods in Molecular Biology, 2012, 896, 233-247.	0.9	2
32	Analyzing Temperature-Induced Transitions in Disordered Proteins by NMR Spectroscopy and Secondary Chemical Shift Analyses. , 2012, 896, 249-256.		0
33	Disordered proteins studied by chemical shifts. Progress in Nuclear Magnetic Resonance Spectroscopy, 2012, 60, 42-51.	7.5	54
34	The RelA Nuclear Localization Signal Folds upon Binding to Î±BÎ±. Journal of Molecular Biology, 2011, 405, 754-764.	4.2	29
35	The Intracellular Distal Tail of the Na <sup>+</sup> /H <sup>+</sup> Exchanger NHE1 Is Intrinsically Disordered: Implications for NHE1 Trafficking. Biochemistry, 2011, 50, 3469-3480.	2.5	56
36	Random coil chemical shift for intrinsically disordered proteins: effects of temperature and pH. Journal of Biomolecular NMR, 2011, 49, 139-149.	2.8	257

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37	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
38	The interplay between transient $\alpha$ -helix formation and side chain rotamer distributions in disordered proteins probed by methyl chemical shifts. <i>Protein Science</i> , 2011, 20, 2023-2034.	7.6	12
39	Mimicry of the Regulatory Role of Urokinase in Lamellipodia Formation by Introduction of a Non-native Interdomain Disulfide Bond in Its Receptor. <i>Journal of Biological Chemistry</i> , 2011, 286, 43515-43526.	3.4	28
40	Temperature-dependent structural changes in intrinsically disordered proteins: Formation of $\alpha$ -helices or loss of polyproline II?. <i>Protein Science</i> , 2010, 19, 1555-1564.	7.6	200
41	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
42	Rapid mass spectrometric analysis of $>15$ $^{15}\text{N}$ -Leu incorporation fidelity during preparation of specifically labeled NMR samples. <i>Protein Science</i> , 2008, 17, 1636-1639.	7.6	7
43	Structure and ligand interactions of the urokinase receptor (uPAR). <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 5441.	3.0	57
44	Solution structure of recombinant somatomedin B domain from vitronectin produced in <i>Pichia pastoris</i> . <i>Protein Science</i> , 2007, 16, 1934-1945.	7.6	32
45	Thermodynamics Reveal that Helix Four in the NLS of NF- $\kappa$ B p50 Anchors $\beta$ -Sheet, Forming a Very Stable Complex. <i>Journal of Molecular Biology</i> , 2006, 360, 421-434.	4.2	69
46	Structure and Inhibition of the Urokinase-Type Plasminogen Activator Receptor. , 0, , 699-719.		1