

Magnus Kjaergaard

List of Publications by Year in descending order

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46
papers

2,549
citations

218381

26
h-index

243296

44
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all docs

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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.	1.2	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, .	3.3	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.	1.2	31
4	Predicting the effect of disordered linkers on effective concentrations and avidity with the α C calculator. <i>Methods in Enzymology</i> , 2021, 647, 145-171.	0.4	20
5	Nanoscale spatial dependence of avidity in an IgG1 antibody. <i>Scientific Reports</i> , 2021, 11, 12663.	1.6	12
6	The Crystal Structure of the Ca ²⁺ -ATPase 1 from <i>Listeria monocytogenes</i> reveals a Pump Primed for Dephosphorylation. <i>Journal of Molecular Biology</i> , 2021, 433, 167015.	2.0	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.	0.9	2
8	Introducing the special issue on α Proteins and Circuits in Memory. <i>European Journal of Neuroscience</i> , 2021, 54, 6691-6695.	1.2	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.	3.3	48
10	Identification of on- and off-pathway oligomers in amyloid fibril formation. <i>Chemical Science</i> , 2020, 11, 6236-6247.	3.7	64
11	Measuring Effective Concentrations Enforced by Intrinsically Disordered Linkers. <i>Methods in Molecular Biology</i> , 2020, 2141, 505-518.	0.4	8
12	Coupled Binding and Helix Formation Monitored by Synchrotron-Radiation Circular Dichroism. <i>Biophysical Journal</i> , 2019, 117, 729-742.	0.2	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.	3.3	122
14	Linker Dependence of Avidity in Multivalent Interactions Between Disordered Proteins. <i>Journal of Molecular Biology</i> , 2019, 431, 4784-4795.	2.0	35
15	Structural dynamics of P-type ATPase ion pumps. <i>Biochemical Society Transactions</i> , 2019, 47, 1247-1257.	1.6	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.	1.6	96
17	Oligomer Diversity during the Aggregation of the Repeat Region of Tau. <i>ACS Chemical Neuroscience</i> , 2018, 9, 3060-3071.	1.7	50
18	Dynamics of P-type ATPase Transport Cycle Revealed by Single-Molecule FRET. <i>Biophysical Journal</i> , 2018, 114, 559a.	0.2	2

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19	Functions of intrinsic disorder in transmembrane proteins. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3205-3224.	2.4	63
20	Dynamics of P-type ATPase transport revealed by single-molecule FRET. <i>Nature</i> , 2017, 551, 346-351.	13.7	72
21	Engineering a Prototypic P-type ATPase <i>Listeria monocytogenes</i> Ca ²⁺ -ATPase 1 for Single-Molecule FRET Studies. <i>Bioconjugate Chemistry</i> , 2016, 27, 2176-2187.	1.8	9
22	Single-Molecule Imaging of Individual Amyloid Protein Aggregates in Human Biofluids. <i>ACS Chemical Neuroscience</i> , 2016, 7, 399-406.	1.7	99
23	A mechanistic model of tau amyloid aggregation based on direct observation of oligomers. <i>Nature Communications</i> , 2015, 6, 7025.	5.8	179
24	Can proteins be intrinsically disordered inside a membrane?. <i>Intrinsically Disordered Proteins</i> , 2015, 3, e984570.	1.9	8
25	Helical Propensity in an Intrinsically Disordered Protein Accelerates Ligand Binding. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1548-1551.	7.2	146
26	Modulation of the Intrinsic Helix Propensity of an Intrinsically Disordered Protein Reveals Long-Range Helix-Helix Interactions. <i>Journal of the American Chemical Society</i> , 2013, 135, 10155-10163.	6.6	44
27	Single-Molecule Measurements of Transient Biomolecular Complexes through Microfluidic Dilution. <i>Analytical Chemistry</i> , 2013, 85, 6855-6859.	3.2	23
28	A Folded Excited State of Ligand-Free Nuclear Coactivator Binding Domain (NCBD) Underlies Plasticity in Ligand Recognition. <i>Biochemistry</i> , 2013, 52, 1686-1693.	1.2	39
29	A Flexible Multidomain Structure Drives the Function of the Urokinase-type Plasminogen Activator Receptor (uPAR)*. <i>Journal of Biological Chemistry</i> , 2012, 287, 34304-34315.	1.6	43
30	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.	0.2	22
31	Temperature-Induced Transitions in Disordered Proteins Probed by NMR Spectroscopy. <i>Methods in Molecular Biology</i> , 2012, 896, 233-247.	0.4	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. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2012, 60, 42-51.	3.9	54
34	The RelA Nuclear Localization Signal Folds upon Binding to Î±BÎ±. <i>Journal of Molecular Biology</i> , 2011, 405, 754-764.	2.0	29
35	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
36	Random coil chemical shift for intrinsically disordered proteins: effects of temperature and pH. <i>Journal of Biomolecular NMR</i> , 2011, 49, 139-149.	1.6	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.	1.6	237
38	The interplay between transient α -helix formation and side chain rotamer distributions in disordered proteins probed by methyl chemical shifts. <i>Protein Science</i> , 2011, 20, 2023-2034.	3.1	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.	1.6	28
40	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
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.	3.3	152
42	Rapid mass spectrometric analysis of >15 ^{15}N -Leu incorporation fidelity during preparation of specifically labeled NMR samples. <i>Protein Science</i> , 2008, 17, 1636-1639.	3.1	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.	3.1	32
45	Thermodynamics Reveal that Helix Four in the NLS of NF- κ B p50 Anchors β -Sheet, Forming a Very Stable Complex. <i>Journal of Molecular Biology</i> , 2006, 360, 421-434.	2.0	69
46	Structure and Inhibition of the Urokinase-Type Plasminogen Activator Receptor. , 0, , 699-719.		1