

Malene Ringkj bing Jensen

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

5,926
citations

81900

39
h-index

76900

74
g-index

90
all docs

90
docs citations

90
times ranked

5377
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Flexible-meccano</i> : a tool for the generation of explicit ensemble descriptions of intrinsically disordered proteins and their associated experimental observables. <i>Bioinformatics</i> , 2012, 28, 1463-1470.	4.1	324
2	Targeting the disordered C terminus of PTP1B with an allosteric inhibitor. <i>Nature Chemical Biology</i> , 2014, 10, 558-566.	8.0	294
3	NMR Characterization of Long-Range Order in Intrinsically Disordered Proteins. <i>Journal of the American Chemical Society</i> , 2010, 132, 8407-8418.	13.7	276
4	Plasticity of an Ultrafast Interaction between Nucleoporins and Nuclear Transport Receptors. <i>Cell</i> , 2015, 163, 734-745.	28.9	255
5	Exploring Free-Energy Landscapes of Intrinsically Disordered Proteins at Atomic Resolution Using NMR Spectroscopy. <i>Chemical Reviews</i> , 2014, 114, 6632-6660.	47.7	252
6	Describing intrinsically disordered proteins at atomic resolution by NMR. <i>Current Opinion in Structural Biology</i> , 2013, 23, 426-435.	5.7	193
7	Quantitative Description of Backbone Conformational Sampling of Unfolded Proteins at Amino Acid Resolution from NMR Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2009, 131, 17908-17918.	13.7	187
8	Intrinsic disorder in measles virus nucleocapsids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9839-9844.	7.1	179
9	Predictive Atomic Resolution Descriptions of Intrinsically Disordered hTau40 and α -Synuclein in Solution from NMR and Small Angle Scattering. <i>Structure</i> , 2014, 22, 238-249.	3.3	171
10	Defining Conformational Ensembles of Intrinsically Disordered and Partially Folded Proteins Directly from Chemical Shifts. <i>Journal of the American Chemical Society</i> , 2010, 132, 1270-1272.	13.7	165
11	A thermodynamic switch modulates abscisic acid receptor sensitivity. <i>EMBO Journal</i> , 2011, 30, 4171-4184.	7.8	161
12	Quantitative Determination of the Conformational Properties of Partially Folded and Intrinsically Disordered Proteins Using NMR Dipolar Couplings. <i>Structure</i> , 2009, 17, 1169-1185.	3.3	160
13	Measles virus nucleocapsid and phosphoproteins form liquid-like phase-separated compartments that promote nucleocapsid assembly. <i>Science Advances</i> , 2020, 6, eaaz7095.	10.3	148
14	Visualizing the Molecular Recognition Trajectory of an Intrinsically Disordered Protein Using Multinuclear Relaxation Dispersion NMR. <i>Journal of the American Chemical Society</i> , 2015, 137, 1220-1229.	13.7	128
15	Quantitative Conformational Analysis of Partially Folded Proteins from Residual Dipolar Couplings: Application to the Molecular Recognition Element of Sendai Virus Nucleoprotein. <i>Journal of the American Chemical Society</i> , 2008, 130, 8055-8061.	13.7	127
16	Structure of Nipah virus unassembled nucleoprotein in complex with its viral chaperone. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 754-759.	8.2	119
17	Binding Mechanisms of Intrinsically Disordered Proteins: Theory, Simulation, and Experiment. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 52.	3.5	118
18	Mapping the Potential Energy Landscape of Intrinsically Disordered Proteins at Amino Acid Resolution. <i>Journal of the American Chemical Society</i> , 2012, 134, 15138-15148.	13.7	113

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19	Structure of the Vesicular Stomatitis Virus N0-P Complex. <i>PLoS Pathogens</i> , 2011, 7, e1002248.	4.7	111
20	Structural characterization of α -synuclein in an aggregation prone state. <i>Protein Science</i> , 2009, 18, 1840-1846.	7.6	97
21	Towards a robust description of intrinsic protein disorder using nuclear magnetic resonance spectroscopy. <i>Molecular BioSystems</i> , 2012, 8, 58-68.	2.9	95
22	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	14.5	95
23	Identification of Dynamic Modes in an Intrinsically Disordered Protein Using Temperature-Dependent NMR Relaxation. <i>Journal of the American Chemical Society</i> , 2016, 138, 6240-6251.	13.7	90
24	Solution structure of the C-terminal X domain of the measles virus phosphoprotein and interaction with the intrinsically disordered C-terminal domain of the nucleoprotein. <i>Journal of Molecular Recognition</i> , 2010, 23, 435-447.	2.1	81
25	Elucidating binding mechanisms and dynamics of intrinsically disordered protein complexes using NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 2019, 54, 10-18.	5.7	78
26	Conformational Propensities of Intrinsically Disordered Proteins from NMR Chemical Shifts. <i>ChemPhysChem</i> , 2013, 14, 3034-3045.	2.1	69
27	Atomic Resolution Description of the Interaction between the Nucleoprotein and Phosphoprotein of Hendra Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003631.	4.7	68
28	Characterization of intrinsically disordered proteins and their dynamic complexes: From in vitro to cell-like environments. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2018, 109, 79-100.	7.5	67
29	Structure of the Tetramerization Domain of Measles Virus Phosphoprotein. <i>Journal of Virology</i> , 2013, 87, 7166-7169.	3.4	66
30	Characterization of the Interactions between the Nucleoprotein and the Phosphoprotein of Henipavirus. <i>Journal of Biological Chemistry</i> , 2011, 286, 13583-13602.	3.4	65
31	Structure and dynamics of the MKK7/JNK signaling complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3409-3414.	7.1	64
32	Deciphering the Dynamic Interaction Profile of an Intrinsically Disordered Protein by NMR Exchange Spectroscopy. <i>Journal of the American Chemical Society</i> , 2018, 140, 1148-1158.	13.7	64
33	Self-association of a highly charged arginine-rich cell-penetrating peptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11428-11433.	7.1	63
34	Small-Angle X-Ray Scattering- and Nuclear Magnetic Resonance-Derived Conformational Ensemble of the Highly Flexible Antitoxin PaaA2. <i>Structure</i> , 2014, 22, 854-865.	3.3	61
35	A Unified Description of Intrinsically Disordered Protein Dynamics under Physiological Conditions Using NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2019, 141, 17817-17829.	13.7	55
36	NMR Provides Unique Insight into the Functional Dynamics and Interactions of Intrinsically Disordered Proteins. <i>Chemical Reviews</i> , 2022, 122, 9331-9356.	47.7	51

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37	The intrinsically disordered SARS-CoV-2 nucleoprotein in dynamic complex with its viral partner nsp3a. <i>Science Advances</i> , 2022, 8, eabm4034.	10.3	50
38	The N ⁰ binding region of the vesicular stomatitis virus phosphoprotein is globally disordered but contains transient β -helices. <i>Protein Science</i> , 2011, 20, 542-556.	7.6	49
39	Large-Scale Conformational Dynamics Control H5N1 Influenza Polymerase PB2 Binding to Importin β . <i>Journal of the American Chemical Society</i> , 2015, 137, 15122-15134.	13.7	49
40	An ultraweak interaction in the intrinsically disordered replication machinery is essential for measles virus function. <i>Science Advances</i> , 2018, 4, eaat7778.	10.3	49
41	Accurate characterization of weak macromolecular interactions by titration of NMR residual dipolar couplings: application to the CD2AP SH3-C:ubiquitin complex. <i>Nucleic Acids Research</i> , 2009, 37, e70-e70.	14.5	46
42	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.	13.7	44
43	Molecular basis of host-adaptation interactions between influenza virus polymerase PB2 subunit and ANP32A. <i>Nature Communications</i> , 2020, 11, 3656.	12.8	43
44	Specific and Nonspecific Interactions in Ultraweak Protein-Protein Associations Revealed by Solvent Paramagnetic Relaxation Enhancements. <i>Journal of the American Chemical Society</i> , 2014, 136, 10277-10286.	13.7	41
45	Self-Assembly of Measles Virus Nucleocapsid-Like Particles: Kinetics and RNA Sequence Dependence. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 9356-9360.	13.8	41
46	Sequence-Specific Mapping of the Interaction between Urea and Unfolded Ubiquitin from Ensemble Analysis of NMR and Small Angle Scattering Data. <i>Journal of the American Chemical Society</i> , 2012, 134, 4429-4436.	13.7	38
47	Pilotin secretin recognition in the type II secretion system of <i>Klebsiella oxytoca</i> . <i>Molecular Microbiology</i> , 2011, 82, 1422-1432.	2.5	37
48	Ensemble Structure of the Modular and Flexible Full-Length Vesicular Stomatitis Virus Phosphoprotein. <i>Journal of Molecular Biology</i> , 2012, 423, 182-197.	4.2	37
49	Probing electric fields in proteins in solution by NMR spectroscopy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 333-343.	2.6	36
50	Quantitative Model-free Analysis of Urea Binding to Unfolded Ubiquitin Using a Combination of Small Angle X-ray and Neutron Scattering. <i>Journal of the American Chemical Society</i> , 2009, 131, 8769-8771.	13.7	36
51	Structure, dynamics and phase separation of measles virus RNA replication machinery. <i>Current Opinion in Virology</i> , 2020, 41, 59-67.	5.4	36
52	Assembly and cryo-EM structures of RNA-specific measles virus nucleocapsids provide mechanistic insight into paramyxoviral replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4256-4264.	7.1	35
53	On the Origin of NMR Dipolar Waves in Transient Helical Elements of Partially Folded Proteins. <i>Journal of the American Chemical Society</i> , 2008, 130, 11266-11267.	13.7	33
54	Multi-timescale Conformational Dynamics of the SH3 Domain of CD2-Associated Protein using NMR Spectroscopy and Accelerated Molecular Dynamics. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 6103-6106.	13.8	33

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55	Structural and Biophysical Characterization of Murine Rif1 C Terminus Reveals High Specificity for DNA Cruciform Structures. <i>Journal of Biological Chemistry</i> , 2014, 289, 13903-13911.	3.4	32
56	Insights into the Structure and Dynamics of Measles Virus Nucleocapsids by 1H-detected Solid-state NMR. <i>Biophysical Journal</i> , 2014, 107, 941-946.	0.5	30
57	Quantitative Description of Intrinsically Disordered Proteins Using Single-Molecule FRET, NMR, and SAXS. <i>Journal of the American Chemical Society</i> , 2021, 143, 20109-20121.	13.7	29
58	Structural Description of the Nipah Virus Phosphoprotein and Its Interaction with STAT1. <i>Biophysical Journal</i> , 2020, 118, 2470-2488.	0.5	28
59	Testing the validity of ensemble descriptions of intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1557-8.	7.1	27
60	Binding ability of a HHP-tagged protein towards Ni ²⁺ studied by paramagnetic NMR relaxation: The possibility of obtaining long-range structure information. <i>Journal of Biomolecular NMR</i> , 2004, 29, 175-185.	2.8	26
61	Visualizing protein breathing motions associated with aromatic ring flipping. <i>Nature</i> , 2022, 602, 695-700.	27.8	26
62	Structural Disorder within Sendai Virus Nucleoprotein and Phosphoprotein: Insight into the Structural Basis of Molecular Recognition. <i>Protein and Peptide Letters</i> , 2010, 17, 952-960.	0.9	25
63	Intrinsically disordered proteins implicated in paramyxoviral replication machinery. <i>Current Opinion in Virology</i> , 2014, 5, 72-81.	5.4	23
64	Investigating the Role of Large-Scale Domain Dynamics in Protein-Protein Interactions. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 54.	3.5	23
65	A General Method for Determining the Electron Self-Exchange Rates of Blue Copper Proteins by Longitudinal NMR Relaxation. <i>Journal of the American Chemical Society</i> , 2002, 124, 4093-4096.	13.7	22
66	Disentangling the Coil: Modulation of Conformational and Dynamic Properties by Site-Directed Mutation in the Non-Native State of Hen Egg White Lysozyme. <i>Biochemistry</i> , 2012, 51, 3361-3372.	2.5	22
67	Direct Prediction of NMR Residual Dipolar Couplings from the Primary Sequence of Unfolded Proteins. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 687-690.	13.8	19
68	Exploring the Minimally Frustrated Energy Landscape of Unfolded ACBP. <i>Journal of Molecular Biology</i> , 2014, 426, 722-734.	4.2	17
69	Distinct Ubiquitin Binding Modes Exhibited by SH3 Domains: Molecular Determinants and Functional Implications. <i>PLoS ONE</i> , 2013, 8, e73018.	2.5	17
70	Ensemble Structure of the Highly Flexible Complex Formed between Vesicular Stomatitis Virus Unassembled Nucleoprotein and its Phosphoprotein Chaperone. <i>Journal of Molecular Biology</i> , 2016, 428, 2671-2694.	4.2	16
71	Quantitative Conformational Analysis of Functionally Important Electrostatic Interactions in the Intrinsically Disordered Region of Delta Subunit of Bacterial RNA Polymerase. <i>Journal of the American Chemical Society</i> , 2019, 141, 16817-16828.	13.7	16
72	A Combined NMR and SAXS Analysis of the Partially Folded Cataract-Associated V75D β -Crystallin. <i>Biophysical Journal</i> , 2017, 112, 1135-1146.	0.5	15

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73	Functionally specific binding regions of microtubule-associated protein 2c exhibit distinct conformations and dynamics. <i>Journal of Biological Chemistry</i> , 2018, 293, 13297-13309.	3.4	13
74	Weak self-association of human growth hormone investigated by nitrogen-15 NMR relaxation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 161-172.	2.6	12
75	Characterizing weak protein-protein complexes by NMR residual dipolar couplings. <i>European Biophysics Journal</i> , 2011, 40, 1371-1381.	2.2	10
76	Revealing the mechanism of repressor inactivation during switching of a temperate bacteriophage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20576-20585.	7.1	6
77	Structural basis of the bacteriophage λ CI repressor dimerization and interaction with DNA. <i>FEBS Letters</i> , 2018, 592, 1738-1750.	2.8	5
78	Enthalpy-Entropy Compensation in the Promiscuous Interaction of an Intrinsically Disordered Protein with Homologous Protein Partners. <i>Biomolecules</i> , 2021, 11, 1204.	4.0	5
79	Experimental studies of binding of intrinsically disordered proteins to their partners. , 2019, , 139-187.		3
80	Inside Back Cover: Multi-Timescale Conformational Dynamics of the SH3 Domain of CD2-Associated Protein using NMR Spectroscopy and Accelerated Molecular Dynamics (<i>Angew. Chem. Int. Ed.</i> 25/2012). <i>Angewandte Chemie - International Edition</i> , 2012, 51, 6279-6279.	13.8	0