# CITATION REPORT List of articles citing

Domain conformation of tau protein studied by solution small-angle X-ray scattering

DOI: 10.1021/bi800900d Biochemistry, 2008, 47, 10345-53.

Source: https://exaly.com/paper-pdf/43860932/citation-report.pdf

Version: 2024-04-20

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
170	Structural polymorphism of 441-residue tau at single residue resolution. <b>2009</b> , 7, e34		420
169	Biophysical characterization of intrinsically disordered proteins. <b>2009</b> , 19, 23-30		270
168	Methods for structural characterization of prefibrillar intermediates and amyloid fibrils. <i>FEBS Letters</i> , <b>2009</b> , 583, 2600-9	3.8	54
167	Analysis of PKR structure by small-angle scattering. <b>2009</b> , 387, 910-20		36
166	A self-consistent description of the conformational behavior of chemically denatured proteins from NMR and small angle scattering. <i>Biophysical Journal</i> , <b>2009</b> , 97, 2839-45	2.9	83
165	Structural Insights into Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering. <b>2010</b> , 451-47	6	5
164	14-3-3 proteins and regulation of cytoskeleton. <b>2010</b> , 75, 1528-46		51
163	The role of the lipid bilayer in tau aggregation. <i>Biophysical Journal</i> , <b>2010</b> , 98, 2722-30	2.9	78
162	Modeling intrinsically disordered proteins with bayesian statistics. <b>2010</b> , 132, 14919-27		134
161	Small-angle X-ray and neutron scattering as a tool for structural systems biology. <b>2010</b> , 391, 737-43		54
160	Structural analysis of an equilibrium folding intermediate in the apoflavodoxin native ensemble by small-angle X-ray scattering. <b>2011</b> , 406, 604-19		23
159	Oligomerization propensity and flexibility of yeast frataxin studied by X-ray crystallography and small-angle X-ray scattering. <b>2011</b> , 414, 783-97		18
158	Constructing ensembles for intrinsically disordered proteins. <b>2011</b> , 21, 426-31		203
157	Understanding the kinetic roles of the inducer heparin and of rod-like protofibrils during amyloid fibril formation by Tau protein. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 38948-59	5.4	95
156	Structural memory of natively unfolded tau protein detected by small-angle X-ray scattering. <b>2011</b> , 79, 2122-31		44
155	Insights into the molecular activation mechanism of the RhoA-specific guanine nucleotide exchange factor, PDZRhoGEF. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 35163-75	5.4	17
154	A flexible brace maintains the assembly of a hexameric replicative helicase during DNA unwinding. <b>2012</b> , 40, 2271-83		12

## (2012-2012)

153	Using intramolecular disulfide bonds in tau protein to deduce structural features of aggregation-resistant conformations. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 9591-600	5.4	25
152	How random are intrinsically disordered proteins? A small angle scattering perspective. <b>2012</b> , 13, 55-75		225
151	The conformational ensembles of Esynuclein and tau: combining single-molecule FRET and simulations. <i>Biophysical Journal</i> , <b>2012</b> , 103, 1940-9	2.9	101
150	Conformations of microtubule-associated protein Tau mapped by fluorescence resonance energy transfer. <i>Methods in Molecular Biology</i> , <b>2012</b> , 849, 85-99	1.4	6
149	Biochemistry and cell biology of tau protein in neurofibrillary degeneration. <b>2012</b> , 2, a006247		463
148	Continuous thermal collapse of the intrinsically disordered protein tau is driven by its entropic flexible domain. <b>2012</b> , 28, 13405-10		29
147	Evidence for the existence of a secondary pathway for fibril growth during the aggregation of tau. <b>2012</b> , 421, 296-314		45
146	Structure Analysis of Biological Macromolecules by Small-Angle X-ray Scattering. <b>2012</b> , 163-171		
145	Small Angle X-Ray Scattering/Small Angle Neutron Scattering as Methods Complementary to NMR. <b>2012</b> , 562-574		
144	Distance information for disordered proteins from NMR and ESR measurements using paramagnetic spin labels. <i>Methods in Molecular Biology</i> , <b>2012</b> , 895, 127-38	1.4	16
144		1.4	16
	paramagnetic spin labels. <i>Methods in Molecular Biology</i> , <b>2012</b> , 895, 127-38	2.9	
143	paramagnetic spin labels. <i>Methods in Molecular Biology</i> , <b>2012</b> , 895, 127-38  Dynamic rheological properties of native and cross-linked gliadin proteins. <b>2012</b> , 51, 640-6  Dynamical coupling of intrinsically disordered proteins and their hydration water: comparison with		1
143	paramagnetic spin labels. <i>Methods in Molecular Biology</i> , <b>2012</b> , 895, 127-38  Dynamic rheological properties of native and cross-linked gliadin proteins. <b>2012</b> , 51, 640-6  Dynamical coupling of intrinsically disordered proteins and their hydration water: comparison with folded soluble and membrane proteins. <i>Biophysical Journal</i> , <b>2012</b> , 103, 129-36  Analysis of intrinsically disordered proteins by small-angle X-ray scattering. <i>Methods in Molecular</i>	2.9	1 66
143 142 141	Dynamic rheological properties of native and cross-linked gliadin proteins. 2012, 51, 640-6  Dynamical coupling of intrinsically disordered proteins and their hydration water: comparison with folded soluble and membrane proteins. <i>Biophysical Journal</i> , 2012, 103, 129-36  Analysis of intrinsically disordered proteins by small-angle X-ray scattering. <i>Methods in Molecular Biology</i> , 2012, 896, 107-22	2.9	1 66 36
143 142 141 140	Dynamic rheological properties of native and cross-linked gliadin proteins. 2012, 51, 640-6  Dynamical coupling of intrinsically disordered proteins and their hydration water: comparison with folded soluble and membrane proteins. <i>Biophysical Journal</i> , 2012, 103, 129-36  Analysis of intrinsically disordered proteins by small-angle X-ray scattering. <i>Methods in Molecular Biology</i> , 2012, 896, 107-22  Structural analysis of intrinsically disordered proteins by small-angle X-ray scattering. 2012, 8, 151-67	2.9	1 66 36 247
143 142 141 140	Dynamic rheological properties of native and cross-linked gliadin proteins. 2012, 51, 640-6  Dynamical coupling of intrinsically disordered proteins and their hydration water: comparison with folded soluble and membrane proteins. <i>Biophysical Journal</i> , 2012, 103, 129-36  Analysis of intrinsically disordered proteins by small-angle X-ray scattering. <i>Methods in Molecular Biology</i> , 2012, 896, 107-22  Structural analysis of intrinsically disordered proteins by small-angle X-ray scattering. 2012, 8, 151-67  Molecular dynamics simulation of intrinsically disordered proteins. 2012, 38, 139-143  Tau and Amyloid-? Conformational Change to ? -Sheet Structures as Effectors in the Development	2.9	1 66 36 247

135	Temperature and solvent dependence of the dynamical landscape of tau protein conformations. <b>2012</b> , 38, 169-79	8
134	Inhibition of tau filament formation by conformational modulation. <b>2013</b> , 135, 2853-62	51
133	Structure Analysis of Biological Macromolecules by Small-Angle X-ray Scattering. 2013, 343-351	
132	Mechanical properties of doubly stabilized microtubule filaments. <i>Biophysical Journal</i> , <b>2013</b> , 104, 1517-2 <u>8</u> .9	55
131	Intracerebral propagation of Alzheimer <b>s</b> disease: strengthening evidence of a herpes simplex virus etiology. <b>2013</b> , 9, 169-75	61
130	Microstructure and dielectric property study of polyimide/BaTiO3 nanocomposite films. 2013, 544, 116-119	19
129	Mechanistic basis of phenothiazine-driven inhibition of Tau aggregation. 2013, 52, 3511-5	101
128	Super-resolution in solution X-ray scattering and its applications to structural systems biology. <b>2013</b> , 42, 415-41	157
127	Mechanistic studies unravel the complexity inherent in tau aggregation leading to Alzheimer's disease and the tauopathies. <i>Biochemistry</i> , <b>2013</b> , 52, 4107-26	45
126	Transient tertiary structures in tau, an intrinsically disordered protein. <b>2013</b> , 39, 1084-1092	7
125	Advancing Methods for Biomolecular Crystallography. 2013,	1
124	Introduction. <b>2013</b> , 1-10	4
123	Mechanismus der Phenothiazin-induzierten Hemmung der Tau-Aggregation. 2013, 125, 3596-3600	4
122	Simulated cytoskeletal collapse via tau degradation. <b>2014</b> , 9, e104965	4
121	Advances in Small- and Wide-Angle X-ray Scattering SAXS and WAXS of Proteins. 2014, 1-34	3
120	Predictive atomic resolution descriptions of intrinsically disordered hTau40 and Esynuclein in solution from NMR and small angle scattering. <i>Structure</i> , <b>2014</b> , 22, 238-49	143
119	Hsp90-Tau complex reveals molecular basis for specificity in chaperone action. <b>2014</b> , 156, 963-74	198
118	Structural Insight into Tau Protein's Paradox of Intrinsically Disordered Behavior, Self-Acetylation Activity, and Aggregation. <i>Journal of Physical Chemistry Letters</i> , <b>2014</b> , 5, 3026-3031	65

## (2016-2014)

117	Exploring free-energy landscapes of intrinsically disordered proteins at atomic resolution using NMR spectroscopy. <b>2014</b> , 114, 6632-60		197
116	Single-molecule tracking of tau reveals fast kiss-and-hop interaction with microtubules in living neurons. <b>2014</b> , 25, 3541-51		101
115	Hyperphosphorylation of intrinsically disordered tau protein induces an amyloidogenic shift in its conformational ensemble. <b>2015</b> , 10, e0120416		53
114	Cellular factors modulating the mechanism of tau protein aggregation. <i>Cellular and Molecular Life Sciences</i> , <b>2015</b> , 72, 1863-79	10.3	42
113	Structural Impact of Tau Phosphorylation at Threonine 231. <i>Structure</i> , <b>2015</b> , 23, 1448-1458	5.2	70
112	In vitro effect of temperature on the conformational structure and collagen binding of SdrF, a Staphylococcus epidermidis adhesin. <b>2015</b> , 99, 5593-603		4
111	Assembly and Disassembly of Protein Aggregates. <b>2015</b> , 229-276		
110	Direct force measurements reveal that protein Tau confers short-range attractions and isoform-dependent steric stabilization to microtubules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E6416-25	11.5	34
109	Application of SAXS for the Structural Characterization of IDPs. 2015, 870, 261-89		23
108	Molecular Dynamics Simulations of a Powder Model of the Intrinsically Disordered Protein Tau. Journal of Physical Chemistry B, <b>2015</b> , 119, 12580-9	3.4	13
107	Finding Our Way in the Dark Proteome. <b>2016</b> , 138, 9730-42		93
106	Frontier methods in coherent X-ray diffraction for high-resolution structure determination. <b>2016</b> , 49,		8
105	Regulation of Microtubule Assembly by Tau and not by Pin1. <b>2016</b> , 428, 1742-59		16
104	How Does Hyperphopsphorylation Promote Tau Aggregation and Modulate Filament Structure and Stability?. <b>2016</b> , 7, 565-75		23
103	Ensemble Structure of the Highly Flexible Complex Formed between Vesicular Stomatitis Virus Unassembled Nucleoprotein and its Phosphoprotein Chaperone. <b>2016</b> , 428, 2671-94		13
102	Globular-disorder transition in proteins: a compromise between hydrophobic and electrostatic interactions?. <b>2016</b> , 18, 23207-14		5
101	Tau mediates microtubule bundle architectures mimicking fascicles of microtubules found in the axon initial segment. <i>Nature Communications</i> , <b>2016</b> , 7, 12278	17.4	33
100	Sequence Determinants of the Conformational Properties of an Intrinsically Disordered Protein Prior to and upon Multisite Phosphorylation. <b>2016</b> , 138, 15323-15335		142

99	Analysis of biostructural changes, dynamics, and interactions - Small-angle X-ray scattering to the rescue. <b>2016</b> , 602, 69-79		24
98	Characterizing Structural Stability of Amyloid Motif Fibrils Mediated by Water Molecules. <b>2017</b> , 18, 817-8	827	6
97	Discrete Molecular Dynamics Approach to the Study of Disordered and Aggregating Proteins. <i>Journal of Chemical Theory and Computation</i> , <b>2017</b> , 13, 1454-1461	6.4	14
96	Time course of Tau toxicity and pharmacologic prevention in a cell[model of Tauopathy. 2017, 57, 47-63		16
95	Glycan Determinants of Heparin-Tau Interaction. <i>Biophysical Journal</i> , <b>2017</b> , 112, 921-932	2.9	47
94	Thermal compaction of the intrinsically disordered protein tau: entropic, structural, and hydrophobic factors. <b>2017</b> , 19, 8435-8446		22
93	Conformational Dynamics of Intracellular Tau Protein Revealed by CD and SAXS. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1523, 3-20	1.4	22
92	Global Conformation of Tau Protein Mapped by Raman Spectroscopy. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1523, 21-31	1.4	18
91	Exploring the Aggregation Mechanism of Intrinsically Disordered Tau Protein. 2017, 51-71		
90	Amyloidogenesis of Tau protein. <b>2017</b> , 26, 2126-2150		56
89	Small-angle scattering studies of intrinsically disordered proteins and their complexes. <b>2017</b> , 42, 15-23		54
88	Paclitaxel suppresses Tau-mediated microtubule bundling in a concentration-dependent manner. <b>2017</b> , 1861, 3456-3463		8
87	Structural Characterization of Highly Flexible Proteins by Small-Angle Scattering. 2017, 1009, 107-129		21
86	Structure-Property Relationship of Amyloidogenic Prion Nanofibrils. 2017,		
85	The Rational Discovery of a Tau Aggregation Inhibitor. <i>Biochemistry</i> , <b>2018</b> , 57, 6099-6107	3.2	15
84	Untangling Tau and Iron: Exploring the Interaction Between Iron and Tau in Neurodegeneration. <b>2018</b> , 11, 276		32
83	Dependence of the Formation of Tau and AlPeptide Mixed Aggregates on the Secondary Structure of the N-Terminal Region of All Journal of Physical Chemistry B, <b>2018</b> , 122, 7049-7056	3.4	13
82	Conformational heterogeneity of tau: Implication on intrinsic disorder, acid stability and fibrillation in Alzheimer disease. <b>2018</b> , 241, 27-37		17

## (2020-2018)

81	Charge fluctuation effects on the shape of flexible polyampholytes with applications to intrinsically disordered proteins. <b>2018</b> , 149, 163323		36
80	Amyloidogenic cross-seeding of Tau protein: Transient emergence of structural variants of fibrils. <b>2018</b> , 13, e0201182		18
79	Insight into the Structure of the "Unstructured" Tau Protein. Structure, 2019, 27, 1710-1715.e4	5.2	27
78	Dynamic structural determinants underlie the neurotoxicity of the N-terminal tau 26-44 peptide in Alzheimers disease and other human tauopathies. <b>2019</b> , 141, 278-289		11
77	Dynamical decoration of stabilized-microtubules by Tau-proteins. <i>Scientific Reports</i> , <b>2019</b> , 9, 12473	4.9	8
76	Tau local structure shields anamyloid-forming motif and controls aggregation propensity. <i>Nature Communications</i> , <b>2019</b> , 10, 2493	17.4	56
75	14-3-3/Tau Interaction and Tau Amyloidogenesis. <i>Journal of Molecular Neuroscience</i> , <b>2019</b> , 68, 620-630	3.3	11
74	Mechanistic approaches to understand the prion-like propagation of aggregates of the human tau protein. <b>2019</b> , 1867, 922-932		7
73	Sequence Effects on Size, Shape, and Structural Heterogeneity in Intrinsically Disordered Proteins. Journal of Physical Chemistry B, <b>2019</b> , 123, 3462-3474	3.4	61
72	Effect of Polymer Chain Density on Protein-Polymer Conjugate Conformation. <i>Biomacromolecules</i> , <b>2019</b> , 20, 1944-1955	6.9	15
71	Advances in Small and Wide-Angle X-Ray Scattering from Proteins and Macromolecular Solutions. <b>2019</b> , 1-39		
70	Realistic Ensemble Models of Intrinsically Disordered Proteins Using a Structure-Encoding Coil Database. <i>Structure</i> , <b>2019</b> , 27, 381-391.e2	5.2	28
69	Hierarchical Ensembles of Intrinsically Disordered Proteins at Atomic Resolution in Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , <b>2020</b> , 16, 725-737	6.4	33
68	Exploring Particle Aggregation Using Small Angle Scattering Techniques. <i>ACS Symposium Series</i> , <b>2020</b> , 201-257	0.4	2
67	Lipid membrane templated misfolding and self-assembly of intrinsically disordered tau protein. <i>Scientific Reports</i> , <b>2020</b> , 10, 13324	4.9	11
66	The Iron Chelator Deferiprone Improves the Phenotype in a Mouse Model of Tauopathy. <i>Journal of Alzheimerys Disease</i> , <b>2020</b> , 77, 753-771	4.3	14
65	Thermal Compaction of Disordered and Elastin-like Polypeptides: A Temperature-Dependent, Sequence-Specific Coarse-Grained Simulation Model. <i>Biomacromolecules</i> , <b>2020</b> , 21, 3523-3538	6.9	5
64	The Positive Side of the Alzheimer's Disease Amyloid Cross-Interactions: The Case of the All-42 Peptide with Tau, TTR, CysC, and ApoA1. <i>Molecules</i> , <b>2020</b> , 25,	4.8	22

63	Pseudo-Improper-Dihedral Model for Intrinsically Disordered Proteins. <i>Journal of Chemical Theory and Computation</i> , <b>2020</b> , 16, 4726-4733	6.4	9
62	Impact of the Hereditary P301L Mutation on the Correlated Conformational Dynamics of Human Tau Protein Revealed by the Paramagnetic Relaxation Enhancement NMR Experiments.  International Journal of Molecular Sciences, 2020, 21,	6.3	6
61	Prediction of human tau 3D structure, and interplay between O-EGlcNAc and phosphorylation modifications in Alzheimer's disease: C. Lelegans as a suitable model to study these interactions in Livivo. Biochemical and Biophysical Research Communications, 2020, 528, 466-472	3.4	1
60	A Novel Tau Antibody Detecting the First Amino-Terminal Insert Reveals Conformational Differences Among Tau Isoforms. <i>Frontiers in Molecular Biosciences</i> , <b>2020</b> , 7, 48	5.6	O
59	Structural basis of the interplay between Esynuclein and Tau in regulating pathological amyloid aggregation. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 7470-7480	5.4	17
58	The structure and phase of tau: from monomer to amyloid filament. <i>Cellular and Molecular Life Sciences</i> , <b>2021</b> , 78, 1873-1886	10.3	7
57	Structural and dynamics analysis of intrinsically disordered proteins by high-speed atomic force microscopy. <i>Nature Nanotechnology</i> , <b>2021</b> , 16, 181-189	28.7	21
56	Liquid-Liquid Phase Separation of Tau Protein Is Encoded at the Monomeric Level. <i>Journal of Physical Chemistry Letters</i> , <b>2021</b> , 12, 2576-2586	6.4	15
55	Comment on the Optimal Parameters to Derive Intrinsically Disordered Protein Conformational Ensembles from Small-Angle X-ray Scattering Data Using the Ensemble Optimization Method. <i>Journal of Chemical Theory and Computation</i> , <b>2021</b> , 17, 2014-2021	6.4	2
54	Structural Proteomics Methods to Interrogate the Conformations and Dynamics of Intrinsically Disordered Proteins. <i>Frontiers in Chemistry</i> , <b>2021</b> , 9, 603639	5	8
53	Conformational landscape of full-length Smad proteins.		1
52	Refining conformational ensembles of flexible proteins against small-angle X-ray scattering data.		1
51	Misfolding and Self-Assembly Dynamics of Microtubule-Binding Repeats of the Alzheimer-Related Protein Tau. <i>Journal of Chemical Information and Modeling</i> , <b>2021</b> , 61, 2916-2925	6.1	8
50	Accurate model of liquid-liquid phase behaviour of intrinsically-disordered proteins from optimization of single-chain properties.		4
49	The disease associated Tau35 fragment has an increased propensity to aggregate compared to full-length tau.		
48	The Structure Biology of Tau and Clue for Aggregation Inhibitor Design. <i>Protein Journal</i> , <b>2021</b> , 40, 656-6	568)	1
47	Conformational landscape of multidomain SMAD proteins. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 5210-5224	6.8	1
46	Structural Analyses of Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2141, 249-269	1.4	2

45	Predicting Conformational Properties of Intrinsically Disordered Proteins from Sequence. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2141, 347-389	1.4	3
44	Small-Angle X-Ray Scattering Study on Nanostructures of Polyimide Films. <i>Chinese Physics Letters</i> , <b>2010</b> , 27, 096103	1.8	6
43	Sequence effects on size, shape, and structural heterogeneity in Intrinsically Disordered Proteins.		2
42	Investigating increasingly complex macromolecular systems with small-angle X-ray scattering. <i>IUCrJ</i> , <b>2014</b> , 1, 523-9	4.7	13
41	Extracellular truncated tau causes early presynaptic dysfunction associated with Alzheimer\$ disease and other tauopathies. <i>Oncotarget</i> , <b>2017</b> , 8, 64745-64778	3.3	38
40	Improving the global dimensions of intrinsically disordered proteins in Martini 3.		1
39	Refining conformational ensembles of flexible proteins against small-angle x-ray scattering data. <i>Biophysical Journal</i> , <b>2021</b> , 120, 5124-5135	2.9	5
38	References. 575-608		
37	Charge fluctuation effects on the shape of flexible polyampholytes with applications to Intrinsically disordered proteins.		
36	Tau local structure shields amyloid motif and controls aggregation propensity.		1
35	Dynamical decoration of stabilized-microtubules by tau-proteins.		
34	Hierarchical Ensembles of Intrinsically Disordered Proteins at Atomic Resolution in Molecular Dynamics Simulations.		
33	To target Tau pathologies, we must embrace and reconstruct their complexities. <i>Neurobiology of Disease</i> , <b>2021</b> , 161, 105536	7.5	3
32	The Disease Associated Tau35 Fragment has an Increased Propensity to Aggregate Compared to Full-Length Tau. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 779240	5.6	1
31	Accurate model of liquid-liquid phase behavior of intrinsically disordered proteins from optimization of single-chain properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	18
30	Dynamic interactions and Ca-binding modulate the holdase-type chaperone activity of S100B preventing tau aggregation and seeding. <i>Nature Communications</i> , <b>2021</b> , 12, 6292	17.4	0
29	Lipid membrane templated misfolding and self-assembly of intrinsically disordered tau protein.		
28	Global Structure of the Intrinsically Disordered Protein Tau Emerges from its Local Structure.		1

27 Biomolecular Tau condensation is linked to Tau accumulation at the nuclear envelope.

26	Neuropathological Mechanisms of EN-Methylamino-L-Alanine (BMAA) with a Focus on Iron Overload and Ferroptosis <i>Neurotoxicity Research</i> , <b>2022</b> , 1	4.3	O
25	Protein Dynamics to Define and Refine Disordered Protein Ensembles <i>Journal of Physical Chemistry B</i> , <b>2022</b> ,	3.4	1
24	Sequence-Dependent Backbone Dynamics of Intrinsically Disordered Proteins.		O
23	The Role of Post-Translational Modifications on the Structure and Function of Tau Protein <i>Journal of Molecular Neuroscience</i> , <b>2022</b> , 1	3.3	1
22	Global Structure of the Intrinsically Disordered Protein Tau Emerges from Its Local Structure <i>Jacs Au</i> , <b>2022</b> , 2, 673-686		4
21	Interaction kinetics reveal distinct properties of conformational ensembles of three-repeat and four-repeat tau proteins <i>FEBS Letters</i> , <b>2022</b> ,	3.8	O
20	Molecular crowding and RNA synergize to promote phase separation, microtubule interaction, and seeding of Tau condensates <i>EMBO Journal</i> , <b>2022</b> , e108882	13	3
19	Improving Martini 3 for Disordered and Multidomain Proteins <i>Journal of Chemical Theory and Computation</i> , <b>2022</b> ,	6.4	5
18	Intrinsically Disordered Proteins (IDPs). Nanoscience and Technology, 2022, 201-225	0.6	
17	Table_1.docx. <b>2020</b> ,		
16	Table_2.docx. <b>2020</b> ,		
15	Prion-like strain effects in tauopathies Cell and Tissue Research, 2022, 1	4.2	O
14	Assessment of models for calculating the hydrodynamic radius of intrinsically disordered proteins.		O
13	PP2A is activated by cytochrome c upon formation of a diffuse encounter complex with SET/TAF-III <i>Computational and Structural Biotechnology Journal</i> , <b>2022</b> , 20, 3695-3707	6.8	
12	Improved Predictions of Phase Behaviour of Intrinsically Disordered Proteins by Tuning the Interaction Range.		
11	Complexes of tubulin oligomers and tau form an intervening network cross-bridging microtubules into bundles.		
10	FTD-tau S320F mutation stabilizes local structure and allosterically promotes amyloid motif-dependent aggregation.		

### CITATION REPORT

9	Improved predictions of phase behaviour of intrinsically disordered proteins by tuning the interaction range. 2, 94	0
8	Sequence-Dependent Backbone Dynamics of Intrinsically Disordered Proteins.	O
7	Functional Implications of Dynamic Structures of Intrinsically Disordered Proteins Revealed by High-Speed AFM Imaging. <b>2022</b> , 12, 1876	О
6	Assessment of models for calculating thelhydrodynamic radius of intrinsically disordered proteins. <b>2022</b> ,	1
5	Investigation of the Structure of Full-Length Tau Proteins with Coarse-Grained and All-Atom Molecular Dynamics Simulations.	О
4	Improved predictions of phase behaviour of intrinsically disordered proteins by tuning the interaction range. 2, 94	1
3	Inhibition and Disassembly of Tau Aggregates by Engineered Graphene Quantum Dots.	О
2	Initiation and modulation of Tau protein phase separation by the drug suramin. 2023, 13,	О
1	FTD-tau S320F mutation stabilizes local structure and allosterically promotes amyloid motif-dependent aggregation. <b>2023</b> , 14,	O