Markus Zweckstetter

List of Publications by Year
in descending order

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		7069	11899
253	21,623	78	134
papers	citations	h-index	g-index

268	268	268	21484
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	From The Cover: Release of long-range tertiary interactions potentiates aggregation of natively unstructured Â-synuclein. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1430-1435.	3.3	708
2	Prediction of Sterically Induced Alignment in a Dilute Liquid Crystalline Phase:Â Aid to Protein Structure Determination by NMR. Journal of the American Chemical Society, 2000, 122, 3791-3792.	6.6	680
3	VDAC, a multi-functional mitochondrial protein regulating cell life and death. Molecular Aspects of Medicine, 2010, 31, 227-285.	2.7	607
4	Liquidâ€“liquid phase separation of the microtubule-binding repeats of the Alzheimer-related protein Tau. Nature Communications, 2017, 8, 275.	5.8	552
5	Structural Polymorphism of 441-Residue Tau at Single Residue Resolution. PLoS Biology, 2009, 7, e1000034.	2.6	514
6	Structure of the human voltage-dependent anion channel. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15370-15375.	3.3	492
7	RNA polymerase II clustering through carboxy-terminal domain phase separation. Nature Structural and Molecular Biology, 2018, 25, 833-840.	3.6	456
8	Pre-fibrillar Î±-synuclein variants with impaired Î²-structure increase neurotoxicity in Parkinson's disease models. EMBO Journal, 2009, 28, 3256-3268.	3.5	411
9	Tau stabilizes microtubules by binding at the interface between tubulin heterodimers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7501-7506.	3.3	400
10	Structural Ensembles of Intrinsically Disordered Proteins Depend Strongly on Force Field: A Comparison to Experiment. Journal of Chemical Theory and Computation, 2015, 11, 5513-5524.	2.3	368
11	Structural characterization of copper(II) binding to Â-synuclein: Insights into the bioinorganic chemistry of Parkinson's disease. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4294-4299.	3.3	364
12	NMR: prediction of molecular alignment from structure using the PALES software. Nature Protocols, 2008, 3, 679-690.	5.5	332
13	Interaction of Î±-Synuclein with Divalent Metal Ions Reveals Key Differences:Â A Link between Structure, Binding Specificity and Fibrillation Enhancement. Journal of the American Chemical Society, 2006, 128, 9893-9901.	6.6	331
14	Anle138b: a novel oligomer modulator for disease-modifying therapy of neurodegenerative diseases such as prion and Parkinsonâ€™s disease. Acta Neuropathologica, 2013, 125, 795-813.	3.9	327
15	Phosphorylation at Ser-129 but Not the Phosphomimics S129E/D Inhibits the Fibrillation of Î±-Synuclein. Journal of Biological Chemistry, 2008, 283, 16895-16905.	1.6	302
16	NMR Characterization of Long-Range Order in Intrinsically Disordered Proteins. Journal of the American Chemical Society, 2010, 132, 8407-8418.	6.6	276
17	Sites of Tau Important for Aggregation Populate Î²-Structure and Bind to Microtubules and Polyanions. Journal of Biological Chemistry, 2005, 280, 24978-24986.	1.6	275
18	Nucleocapsid protein of SARS-CoV-2 phase separates into RNA-rich polymerase-containing condensates. Nature Communications, 2020, 11, 6041.	5.8	275

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19	Phosphorylation at S87 Is Enhanced in Synucleinopathies, Inhibits Î±-Synuclein Oligomerization, and Influences Synuclein-Membrane Interactions. Journal of Neuroscience, 2010, 30, 3184-3198.	1.7	271
20	Hsp90-Tau Complex Reveals Molecular Basis for Specificity in Chaperone Action. Cell, 2014, 156, 963-974.	13.5	269
21	Mars â€“ robust automatic backbone assignment of proteins. Journal of Biomolecular NMR, 2004, 30, 11-23.	1.6	262
22	Exploring Free-Energy Landscapes of Intrinsically Disordered Proteins at Atomic Resolution Using NMR Spectroscopy. Chemical Reviews, 2014, 114, 6632-6660.	23.0	252
23	NMR of Î±-synucleinâ€“polyamine complexes elucidates the mechanism and kinetics of induced aggregation. EMBO Journal, 2004, 23, 2039-2046.	3.5	231
24	Defining Long-Range Order and Local Disorder in Native Î±-Synuclein Using Residual Dipolar Couplings. Journal of the American Chemical Society, 2005, 127, 17968-17969.	6.6	223
25	Sumoylation inhibits Î±-synuclein aggregation and toxicity. Journal of Cell Biology, 2011, 194, 49-60.	2.3	210
26	Highly Populated Turn Conformations in Natively Unfolded Tau Protein Identified from Residual Dipolar Couplings and Molecular Simulation. Journal of the American Chemical Society, 2007, 129, 5235-5243.	6.6	208
27	Structure of the Mitochondrial Translocator Protein in Complex with a Diagnostic Ligand. Science, 2014, 343, 1363-1366.	6.0	208
28	Phosphorylation of Synucleins by Members of the Polo-like Kinase Family. Journal of Biological Chemistry, 2010, 285, 2807-2822.	1.6	204
29	Structural Properties of Pore-Forming Oligomers of Î±-Synuclein. Journal of the American Chemical Society, 2009, 131, 17482-17489.	6.6	191
30	Î²-Sheet Core of Tau Paired Helical Filaments Revealed by Solid-State NMR. Journal of the American Chemical Society, 2012, 134, 13982-13989.	6.6	176
31	NMR structural and kinetic characterization of a homeodomain diffusing and hopping on nonspecific DNA. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15062-15067.	3.3	172
32	Predictive Atomic Resolution Descriptions of Intrinsically Disordered hTau40 and Î±-Synuclein in Solution from NMR and Small Angle Scattering. Structure, 2014, 22, 238-249.	1.6	171
33	The â€œJawsâ€•of the Tau-Microtubule Interaction. Journal of Biological Chemistry, 2007, 282, 12230-12239.	1.6	167
34	Structure of the IGF-binding domain of the insulin-like growth factor-binding protein-5 (IGFBP-5): implications for IGF and IGF-I receptor interactions. EMBO Journal, 1998, 17, 6558-6572.	3.5	165
35	Familial Mutants of Î±-Synuclein with Increased Neurotoxicity Have a Destabilized Conformation. Journal of Biological Chemistry, 2005, 280, 30649-30652.	1.6	164
36	Lysine/RNA-interactions drive and regulate biomolecular condensation. Nature Communications, 2019, 10, 2909.	5.8	164

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37	Site-Specific Interactions of Cu(II) with Î± and Î²-Synuclein: Bridging the Molecular Gap between Metal Binding and Aggregation. Journal of the American Chemical Society, 2008, 130, 11801-11812.	6.6	160
38	Quantitative Determination of the Conformational Properties of Partially Folded and Intrinsically Disordered Proteins Using NMR Dipolar Couplings. Structure, 2009, 17, 1169-1185.	1.6	160
39	Extracellular phosphorylation of the amyloid Î²-peptide promotes formation of toxic aggregates during the pathogenesis of Alzheimer's disease. EMBO Journal, 2011, 30, 2255-2265.	3.5	160
40	N-truncated amyloid Î² (AÎ²) 4-42 forms stable aggregates and induces acute and long-lasting behavioral deficits. Acta Neuropathologica, 2013, 126, 189-205.	3.9	153
41	Glycation potentiates Î±-synuclein-associated neurodegeneration in synucleinopathies. Brain, 2017, 140, 1399-1419.	3.7	153
42	Structural heterogeneity of Î±-synuclein fibrils amplified from patient brain extracts. Nature Communications, 2019, 10, 5535.	5.8	153
43	Myelin Membrane Assembly Is Driven by a Phase Transition of Myelin Basic Proteins Into a Cohesive Protein Meshwork. PLoS Biology, 2013, 11, e1001577.	2.6	148
44	Extracellular vesicle sorting of Î±-Synuclein is regulated by sumoylation. Acta Neuropathologica, 2015, 129, 695-713.	3.9	136
45	Nuclear localization and phosphorylation modulate pathological effects of alpha-synuclein. Human Molecular Genetics, 2019, 28, 31-50.	1.4	131
46	Folding of the Tau Protein on Microtubules. Angewandte Chemie - International Edition, 2015, 54, 10347-10351.	7.2	130
47	Evaluation of uncertainty in alignment tensors obtained from dipolar couplings. Journal of Biomolecular NMR, 2002, 23, 127-137.	1.6	128
48	Mechanistic Basis of Phenothiazineâ€Driven Inhibition of Tau Aggregation. Angewandte Chemie - International Edition, 2013, 52, 3511-3515.	7.2	127
49	Measurement of long range H,C couplings in natural products in orienting media: a tool for structure elucidation of natural products. Journal of Magnetic Resonance, 2003, 163, 353-359.	1.2	125
50	Fasudil attenuates aggregation of Î±-synuclein in models of Parkinsonâ€™s disease. Acta Neuropathologica Communications, 2016, 4, 39.	2.4	123
51	Entacapone and Tolcapone, Two Catechol O-Methyltransferase Inhibitors, Block Fibril Formation of Î±-Synuclein and Î²-Amyloid and Protect against Amyloid-induced Toxicity. Journal of Biological Chemistry, 2010, 285, 14941-14954.	1.6	119
52	Bioinorganic Chemistry of Parkinsonâ€™s Disease: Structural Determinants for the Copper-Mediated Amyloid Formation of Alpha-Synuclein. Inorganic Chemistry, 2010, 49, 10668-10679.	1.9	119
53	Mapping interactions with the chaperone network reveals factors that protect against tau aggregation. Nature Structural and Molecular Biology, 2018, 25, 384-393.	3.6	119
54	Conformational Changes Specific for Pseudophosphorylation at Serine 262 Selectively Impair Binding of Tau to Microtubules. Biochemistry, 2009, 48, 10047-10055.	1.2	118

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55	Automatic Assignment of the Intrinsically Disordered Protein Tau with 441-Residues. Journal of the American Chemical Society, 2010, 132, 11906-11907.	6.6	114
56	The mechanism of sirtuin 2â€“mediated exacerbation of alpha-synuclein toxicity in models of Parkinson disease. PLoS Biology, 2017, 15, e2000374.	2.6	114
57	Mapping the Potential Energy Landscape of Intrinsically Disordered Proteins at Amino Acid Resolution. Journal of the American Chemical Society, 2012, 134, 15138-15148.	6.6	113
58	Prediction of Charge-Induced Molecular Alignment of Biomolecules Dissolved in Dilute Liquid-Crystalline Phases. Biophysical Journal, 2004, 86, 3444-3460.	0.2	111
59	A Ligand-Induced Switch in the Periplasmic Domain of Sensor Histidine Kinase CitA. Journal of Molecular Biology, 2008, 377, 512-523.	2.0	110
60	Characterization of molecular alignment in aqueous suspensions of Pf1 bacteriophage. , 2001, 20, 365-377.		109
61	Î²-Barrel Mobility Underlies Closure of the Voltage-Dependent Anion Channel. Structure, 2012, 20, 1540-1549.	1.6	104
62	Multivalent cross-linking of actin filaments and microtubules through the microtubule-associated protein Tau. Nature Communications, 2017, 8, 1981.	5.8	104
63	Structural Characterization of the Intrinsically Unfolded Protein Î²-Synuclein, a Natural Negative Regulator of Î±-Synuclein Aggregation. Journal of Molecular Biology, 2007, 372, 708-722.	2.0	102
64	Phosphorylation Drives a Dynamic Switch in Serine/Arginine-Rich Proteins. Structure, 2013, 21, 2162-2174.	1.6	101
65	Imbalance of Hsp70 family variants fosters tau accumulation. FASEB Journal, 2013, 27, 1450-1459.	0.2	100
66	Structural Impact of Tau Phosphorylation at Threonine 231. Structure, 2015, 23, 1448-1458.	1.6	99
67	Structural and mechanistic basis behind the inhibitory interaction of PcTS on Î±-synuclein amyloid fibril formation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21057-21062.	3.3	98
68	Structural characterization of Î±â€synuclein in an aggregation prone state. Protein Science, 2009, 18, 1840-1846.	3.1	97
69	Functional dynamics in the voltage-dependent anion channel. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22546-22551.	3.3	97
70	Aggregation of Î±Synuclein promotes progressive in vivo neurotoxicity in adult rat dopaminergic neurons. Acta Neuropathologica, 2012, 123, 671-683.	3.9	96
71	The NMR Structure of the Sensory Domain of the Membranous Two-component Fumarate Sensor (Histidine Protein Kinase) DcuS of Escherichia coli. Journal of Biological Chemistry, 2003, 278, 39185-39188.	1.6	92
72	Small molecule-mediated stabilization of vesicle-associated helical Î±-synuclein inhibits pathogenic misfolding and aggregation. Nature Communications, 2014, 5, 5857.	5.8	91

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73	Structural Impact of Proline-Directed Pseudophosphorylation at AT8, AT100, and PHF1 Epitopes on 441-Residue Tau. Journal of the American Chemical Society, 2011, 133, 15842-15845.	6.6	90
74	Conkunitzin-S1 Is the First Member of a New Kunitz-type Neurotoxin Family. Journal of Biological Chemistry, 2005, 280, 23766-23770.	1.6	88
75	Effect of Zinc Binding on Î²-Amyloid Structure and Dynamics: Implications for AÎ² Aggregation. Biophysical Journal, 2011, 101, 1202-1211.	0.2	87
76	Structural Characterization of Binding of Cu(II) to Tau Protein. Biochemistry, 2008, 47, 10841-10851.	1.2	85
77	Intrinsically Disordered Proteins: From Sequence and Conformational Properties toward Drug Discovery. ChemBioChem, 2012, 13, 930-950.	1.3	85
78	Î±-Synuclein interacts with the switch region of Rab8a in a Ser129 phosphorylation-dependent manner. Neurobiology of Disease, 2014, 70, 149-161.	2.1	84
79	Phosphorylation of the amyloid Î²-peptide at Ser26 stabilizes oligomeric assembly and increases neurotoxicity. Acta Neuropathologica, 2016, 131, 525-537.	3.9	84
80	Exploring the Structural Details of Cu(I) Binding to Î±-Synuclein by NMR Spectroscopy. Journal of the American Chemical Society, 2011, 133, 194-196.	6.6	83
81	Identification and Characterization of Novel Classes of Macrophage Migration Inhibitory Factor (MIF) Inhibitors with Distinct Mechanisms of Action. Journal of Biological Chemistry, 2010, 285, 26581-26598.	1.6	80
82	Long-Range Correlated Dynamics in Intrinsically Disordered Proteins. Journal of the American Chemical Society, 2014, 136, 16201-16209.	6.6	77
83	Environmental and genetic factors support the dissociation between Î±-synuclein aggregation and toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6506-E6515.	3.3	75
84	The Dynamic Structure of Filamentous Tau. Angewandte Chemie - International Edition, 2011, 50, 11520-11524.	7.2	74
85	Targeting intrinsically disordered proteins in rational drug discovery. Expert Opinion on Drug Discovery, 2016, 11, 65-77.	2.5	74
86	Alpha-synuclein research: defining strategic moves in the battle against Parkinsonâ€™s disease. Npj Parkinson's Disease, 2021, 7, 65.	2.5	74
87	The extracellular human melanoma inhibitory activity (MIA) protein adopts an SH3 domain-like fold. EMBO Journal, 2001, 20, 340-349.	3.5	72
88	Mitogen-activated protein kinases interacting kinases are autoinhibited by a reprogrammed activation segment. EMBO Journal, 2006, 25, 4020-4032.	3.5	71
89	Phosphorylation modifies the molecular stability of Î²-amyloid deposits. Nature Communications, 2016, 7, 11359.	5.8	70
90	Single-Step Determination of Protein Substructures Using Dipolar Couplings:Â Aid to Structural Genomics. Journal of the American Chemical Society, 2001, 123, 9490-9491.	6.6	68

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91	Site-Specific Copper-Catalyzed Oxidation of Î±-Synuclein: Tightening the Link between Metal Binding and Protein Oxidative Damage in Parkinsonâ€™s Disease. Inorganic Chemistry, 2014, 53, 4350-4358.	1.9	68
92	Copper Binding to the N-Terminally Acetylated, Naturally Occurring Form of Alpha-Synuclein Induces Local Helical Folding. Journal of the American Chemical Society, 2015, 137, 6444-6447.	6.6	68
93	Structure and pro-toxic mechanism of the human Hsp90/PPIase/Tau complex. Nature Communications, 2018, 9, 4532.	5.8	68
94	The Native Conformation of the Human VDAC1 Nâ€…Terminus. Angewandte Chemie - International Edition, 2010, 49, 1882-1885.	7.2	67
95	Cholesterol-mediated allosteric regulation of the mitochondrial translocator protein structure. Nature Communications, 2017, 8, 14893.	5.8	67
96	Aggregate Clearance of Î±-Synuclein in Saccharomyces cerevisiae Depends More on Autophagosome and Vacuole Function Than on the Proteasome. Journal of Biological Chemistry, 2012, 287, 27567-27579.	1.6	66
97	Structural and Microtubule Binding Properties of Tau Mutants of Frontotemporal Dementiasâ€. Biochemistry, 2007, 46, 2574-2582.	1.2	65
98	Inhibition of Tau Filament Formation by Conformational Modulation. Journal of the American Chemical Society, 2013, 135, 2853-2862.	6.6	65
99	Phosphorylation of Human Tau Protein by Microtubule Affinity-Regulating Kinase 2. Biochemistry, 2013, 52, 9068-9079.	1.2	65
100	Residue-specific identification of phase separation hot spots of Alzheimer's-related protein tau. Chemical Science, 2019, 10, 6503-6507.	3.7	65
101	The diphenylpyrazole compound anle138b blocks Aî² channels and rescues disease phenotypes in a mouse model for amyloid pathology. EMBO Molecular Medicine, 2018, 10, 32-47.	3.3	63
102	Correlation of Amyloid Fibril Î²â€Structure with the Unfolded State of Î±â€Synuclein. ChemBioChem, 2007, 8, 1671-1674.	1.3	62
103	Amino Acid Bulkiness Defines the Local Conformations and Dynamics of Natively Unfolded Î±-Synuclein and Tau. Journal of the American Chemical Society, 2007, 129, 3032-3033.	6.6	61
104	Is Enantiomer Assignment Possible by NMR Spectroscopy Using Residual Dipolar Couplings from Chiral Nonracemic Alignment Media?â€”A Critical Assessment. Angewandte Chemie - International Edition, 2012, 51, 8388-8391.	7.2	60
105	Lost in translocation: the functions of the 18-kD translocator protein. Trends in Endocrinology and Metabolism, 2015, 26, 349-356.	3.1	60
106	Methylation of Lysine 9 in Histone H3 Directs Alternative Modes of Highly Dynamic Interaction of Heterochromatin Protein hHP1Î² with the Nucleosome. Journal of Biological Chemistry, 2012, 287, 33756-33765.	1.6	58
107	Î²â€synuclein aggregates and induces neurodegeneration in dopaminergic neurons. Annals of Neurology, 2013, 74, 109-118.	2.8	58
108	Diseaseâ€Associated Tau Phosphorylation Hinders Tubulin Assembly within Tau Condensates. Angewandte Chemie - International Edition, 2021, 60, 726-730.	7.2	57

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109	Conformational Dynamics of Intrinsically Disordered Proteins Regulate Biomolecular Condensate Chemistry. Chemical Reviews, 2022, 122, 6719-6748.	23.0	55
110	A Novel SNCA A30G Mutation Causes Familial ParkinsonÊ¼s Disease. Movement Disorders, 2021, 36, 1624-1633.	2.2	54
111	Liquidâ€“liquid phase separation of tau: From molecular biophysics to physiology and disease. Protein Science, 2021, 30, 1294-1314.	3.1	54
112	The Nature of the Stimulus and of the Fumarate Binding Site of the Fumarate Sensor DcuS of Escherichia coli*. Journal of Biological Chemistry, 2005, 280, 20596-20603.	1.6	53
113	Discovery and Structure Activity Relationship of Small Molecule Inhibitors of Toxic Î²-Amyloid-42 Fibril Formation. Journal of Biological Chemistry, 2012, 287, 34786-34800.	1.6	53
114	Small Molecules Detected by Second-Harmonic Generation Modulate the Conformation of Monomeric Î±-Synuclein and Reduce Its Aggregation in Cells. Journal of Biological Chemistry, 2015, 290, 27582-27593.	1.6	53
115	Interplay between tau and Î±â€synuclein liquidâ€“liquid phase separation. Protein Science, 2021, 30, 1326-1336.	3.1	53
116	Parkinson Disease Mutant E46K Enhances Î±-Synuclein Phosphorylation in Mammalian Cell Lines, in Yeast, and in Vivo. Journal of Biological Chemistry, 2015, 290, 9412-9427.	1.6	52
117	A New Class of Isothiocyanate-Based Irreversible Inhibitors of Macrophage Migration Inhibitory Factor. Biochemistry, 2009, 48, 9858-9870.	1.2	51
118	Local and Global Dynamics in Intrinsically Disordered Synuclein. Angewandte Chemie - International Edition, 2018, 57, 15262-15266.	7.2	49
119	Molecular Basis of Small-Molecule Binding to Î±-Synuclein. Journal of the American Chemical Society, 2022, 144, 2501-2510.	6.6	48
120	Global Structure of the Intrinsically Disordered Protein Tau Emerges from Its Local Structure. Jacs Au, 2022, 2, 673-686.	3.6	48
121	Translocator Protein Ligand Protects against Neurodegeneration in the MPTP Mouse Model of Parkinsonism. Journal of Neuroscience, 2019, 39, 3752-3769.	1.7	46
122	Co-factor-free aggregation of tau into seeding-competent RNA-sequestering amyloid fibrils. Nature Communications, 2021, 12, 4231.	5.8	45
123	Structure of the Active Domain of the Herpes Simplex Virus Protein ICP47 in Water/Sodium Dodecyl Sulfate Solution Determined by Nuclear Magnetic Resonance Spectroscopyâ€‚â€¡. Biochemistry, 1999, 38, 13692-13698.	1.2	44
124	Mechanistic basis for the recognition of a misfolded protein by the molecular chaperone Hsp90. Nature Structural and Molecular Biology, 2017, 24, 407-413.	3.6	44
125	Rapid and accurate structure determination of coiled-coil domains using NMR dipolar couplings: Application to cGMP-dependent protein kinase Iα. Protein Science, 2005, 14, 2421-2428.	3.1	43
126	Molten Globule Precursor States Are Conformationally Correlated to Amyloid Fibrils of Human Î²-2-Microglobulin. Journal of the American Chemical Society, 2010, 132, 9223-9225.	6.6	43

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127	Toward the Discovery of Effective Polycyclic Inhibitors of Î±-Synuclein Amyloid Assembly. Journal of Biological Chemistry, 2011, 286, 32036-32044.	1.6	43
128	The Binding Mode of a Tau Peptide with Tubulin. Angewandte Chemie - International Edition, 2018, 57, 3246-3250.	7.2	43
129	Human cyclophilin 40 unravels neurotoxic amyloids. PLoS Biology, 2017, 15, e2001336.	2.6	43
130	Structure of interleukin 16 resembles a PDZ domain with an occluded peptide binding site. Nature Structural and Molecular Biology, 1998, 5, 682-686.	3.6	42
131	The PIP2 binding mode of the C2 domains of rabphilinâ€3A. Protein Science, 2008, 17, 1025-1034.	3.1	42
132	Structure and Functions of Microtubule Associated Proteins Tau and MAP2c: Similarities and Differences. Biomolecules, 2019, 9, 105.	1.8	41
133	The Conformational Flexibility of the Carboxy Terminal Residues 105â^’114 Is a Key Modulator of the Catalytic Activity and Stability of Macrophage Migration Inhibitory Factor. Biochemistry, 2008, 47, 10740-10756.	1.2	40
134	The intermembrane space domain of Tim23 is intrinsically disordered with a distinct binding region for presequences. Protein Science, 2010, 19, 2045-2054.	3.1	40
135	Interaction between Amyloid Beta Peptide and an Aggregation Blocker Peptide Mimicking Islet Amyloid Polypeptide. PLoS ONE, 2011, 6, e20289.	1.1	40
136	An Adiabatic Multiple Spinâ€“Echo Pulse Sequence: Removal of Systematic Errors Due to Pulse Imperfections and Off-Resonance Effects. Journal of Magnetic Resonance, 1998, 133, 134-147.	1.2	39
137	Turn Plasticity Distinguishes Different Modes of Amyloid-Î² Aggregation. Journal of the American Chemical Society, 2014, 136, 4913-4919.	6.6	39
138	Capture of Dense Core Vesicles at Synapses by JNK-Dependent Phosphorylation of Synaptotagmin-4. Cell Reports, 2017, 21, 2118-2133.	2.9	39
139	<scp>NMR</scp> hawkâ€eyed view of <scp>AlphaFold2</scp> structures. Protein Science, 2021, 30, 2333-2337.	3.1	39
140	Pre-Fibrillar Î±-Synuclein Mutants Cause Parkinson's Disease-Like Non-Motor Symptoms in Drosophila. PLoS ONE, 2011, 6, e24701.	1.1	39
141	Structure and DNA-binding properties of the cytolysin regulator CylR2 from Enterococcus faecalis. EMBO Journal, 2004, 23, 3632-3642.	3.5	37
142	Cold denaturation of a protein dimer monitored at atomic resolution. Nature Chemical Biology, 2013, 9, 264-270.	3.9	37
143	Molecular Plasticity of the Human Voltage-Dependent Anion Channel Embedded Into a Membrane. Structure, 2016, 24, 585-594.	1.6	36
144	Backbone assignment of proteins with known structure using residual dipolar couplings. Journal of Biomolecular NMR, 2004, 30, 25-35.	1.6	35

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145	Structural Determinants for Ca2+ and Phosphatidylinositol 4,5-Bisphosphate Binding by the C2A Domain of Rabphilin-3A. Journal of Biological Chemistry, 2008, 283, 35918-35928.	1.6	34
146	Conserved core of amyloid fibrils of wild type and A30P mutant Î±â€synuclein. Protein Science, 2011, 20, 387-395.	3.1	34
147	Simultaneous Assignment and Structure Determination of Protein Backbones by Using NMR Dipolar Couplings. Angewandte Chemie - International Edition, 2004, 43, 3479-3481.	7.2	33
148	Conversion of the Kunitz-Type Module of Collagen VI into a Highly Active Trypsin Inhibitor by Site-Directed Mutagenesis. FEBS Journal, 1996, 238, 333-340.	0.2	32
149	Dissociation of Amyloid Fibrils of Î±â€Synuclein in Supercooled Water. Angewandte Chemie - International Edition, 2008, 47, 5046-5048.	7.2	32
150	Structural Integrity of the A147T Polymorph of Mammalian TSPO. ChemBioChem, 2015, 16, 1483-1489.	1.3	32
151	High-Resolution 3D Structure Determination of Kaliotoxin by Solid-State NMR Spectroscopy. PLoS ONE, 2008, 3, e2359.	1.1	32
152	Prion Protein Helix1 Promotes Aggregation but Is Not Converted into Î²-Sheet. Journal of Biological Chemistry, 2006, 281, 30242-30250.	1.6	31
153	High-resolution structure determination of the CylR2 homodimer using paramagnetic relaxation enhancement and structure-based prediction of molecular alignment. Journal of Biomolecular NMR, 2008, 40, 1-13.	1.6	31
154	Proteasomal degradation of the intrinsically disordered protein tau at single-residue resolution. Science Advances, 2020, 6, eaba3916.	4.7	31
155	Structure of the mammalian TSPO/PBR protein. Biochemical Society Transactions, 2015, 43, 566-571.	1.6	29
156	Yeast reveals similar molecular mechanisms underlying alpha- and beta-synuclein toxicity. Human Molecular Genetics, 2016, 25, 275-290.	1.4	29
157	The potential of zwitterionic nanoliposomes against neurotoxic alpha-synuclein aggregates in Parkinson's Disease. Nanoscale, 2018, 10, 9174-9185.	2.8	29
158	Structure and multiple conformations of the Kunitz-type domain from human type VI collagen Î±3(VI) chain in solution. Structure, 1996, 4, 195-209.	1.6	28
159	Predicting the Rotational Tumbling of Dynamic Multidomain Proteins and Supramolecular Complexes. Angewandte Chemie - International Edition, 2013, 52, 11410-11414.	7.2	28
160	Cooperative structure of the heterotrimeric pre-mRNA retention and splicing complex. Nature Structural and Molecular Biology, 2014, 21, 911-918.	3.6	28
161	The active Hsc70/tau complex can be exploited to enhance tau turnover without damaging microtubule dynamics. Human Molecular Genetics, 2015, 24, 3971-3981.	1.4	28
162	Voltage Dependence of Conformational Dynamics and Subconducting States of VDAC-1. Biophysical Journal, 2016, 111, 1223-1234.	0.2	28

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163	Structure, gating and interactions of the voltage-dependent anion channel. European Biophysics Journal, 2021, 50, 159-172.	1.2	28
164	Nucleotide Interactions of the Human Voltage-dependent Anion Channel. Journal of Biological Chemistry, 2014, 289, 13397-13406.	1.6	27
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