Markus Zweckstetter

List of Publications by Year in descending order

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253 papers 21,623 citations

78 h-index 134 g-index

268 all docs

268 docs citations

268 times ranked 23777 citing authors

#	Article	IF	CITATIONS
1	The pathogenic R5L mutation disrupts formation of Tau complexes on the microtubule by altering local N-terminal structure. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119 , .	3.3	8
2	Molecular Basis of Small-Molecule Binding to \hat{l}_{\pm} -Synuclein. Journal of the American Chemical Society, 2022, 144, 2501-2510.	6.6	48
3	Dynamical component exchange in a model phase separating system: an NMR-based approach. Physical Chemistry Chemical Physics, 2022, 24, 6169-6175.	1.3	4
4	Conformational Dynamics of Intrinsically Disordered Proteins Regulate Biomolecular Condensate Chemistry. Chemical Reviews, 2022, 122, 6719-6748.	23.0	55
5	Global Structure of the Intrinsically Disordered Protein Tau Emerges from Its Local Structure. Jacs Au, 2022, 2, 673-686.	3.6	48
6	A NAC domain mutation (E83Q) unlocks the pathogenicity of human alpha-synuclein and recapitulates its pathological diversity. Science Advances, 2022, 8, eabn0044.	4.7	20
7	Hsp multichaperone complex buffers pathologically modified Tau. Nature Communications, 2022, 13, .	5.8	11
8	Aromaticity at position 39 in αâ€synuclein: A modulator of amyloid fibril assembly and membraneâ€bound conformations. Protein Science, 2022, 31, .	3.1	7
9	Diseaseâ€Associated Tau Phosphorylation Hinders Tubulin Assembly within Tau Condensates. Angewandte Chemie - International Edition, 2021, 60, 726-730.	7.2	57
10	Die krankheitsassoziierte Tauâ€Phosphorylierung behindert die Tubulinpolymerisation in Tauâ€Kondensaten. Angewandte Chemie, 2021, 133, 737-741.	1.6	0
11	Interplay between tau and αâ€synuclein liquid–liquid phase separation. Protein Science, 2021, 30, 1326-1336.	3.1	53
12	Structural Flexibility of Cyclosporine A Is Mediated by Amide ⟨i⟩Cis⟨ i⟩–⟨i⟩Trans⟨ i⟩ Isomerization and the Chameleonic Roles of Calcium. Journal of Physical Chemistry B, 2021, 125, 1378-1391.	1.2	8
13	A Novel SNCA A30G Mutation Causes Familial Parkinson $\hat{E}^{1}\!\!/\!\!4$ s Disease. Movement Disorders, 2021, 36, 1624-1633.	2.2	54
14	Structure, gating and interactions of the voltage-dependent anion channel. European Biophysics Journal, 2021, 50, 159-172.	1.2	28
15	Extending the applicability of P3D for structure determination of small molecules. Magnetic Resonance, 2021, 2, 105-116.	0.8	8
16	Liquid–liquid phase separation of tau: From molecular biophysics to physiology and disease. Protein Science, 2021, 30, 1294-1314.	3.1	54
17	Low-Expressing Synucleinopathy Mouse Models Based on Oligomer-Forming Mutations and C-Terminal Truncation of ݱ-Synuclein. Frontiers in Neuroscience, 2021, 15, 643391.	1.4	4
18	Proline/arginine dipeptide repeat polymers derail protein folding in amyotrophic lateral sclerosis. Nature Communications, 2021, 12, 3396.	5.8	14

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19	Structure of serotonin receptors: molecular underpinning of receptor activation and modulation. Signal Transduction and Targeted Therapy, 2021, 6, 243.	7.1	3
20	Introduction: Biophysics of biomolecular condensates. Protein Science, 2021, 30, 1274-1276.	3.1	0
21	Alpha-synuclein research: defining strategic moves in the battle against Parkinson's disease. Npj Parkinson's Disease, 2021, 7, 65.	2.5	74
22	Co-factor-free aggregation of tau into seeding-competent RNA-sequestering amyloid fibrils. Nature Communications, 2021, 12, 4231.	5.8	45
23	<scp>NMR</scp> hawkâ€eyed view of <scp>AlphaFold2</scp> structures. Protein Science, 2021, 30, 2333-2337.	3.1	39
24	Membrane-embedded TSPO: an NMR view. European Biophysics Journal, 2021, 50, 173-180.	1.2	3
25	Biomolecular condensation of the microtubule-associated protein tau. Seminars in Cell and Developmental Biology, 2020, 99, 202-214.	2.3	27
26	Molecular characterization of an aggregation-prone variant of alpha-synuclein used to model synucleinopathies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140298.	1.1	10
27	The Molecular Basis of the Interaction of Cyclophilinâ€A with α‧ynuclein. Angewandte Chemie, 2020, 132, 5692-5695.	1.6	0
28	The Molecular Basis of the Interaction of Cyclophilinâ€A with α‧ynuclein. Angewandte Chemie - International Edition, 2020, 59, 5643-5646.	7.2	20
29	Molecular basis of the interaction of Hsp90 with its coâ€chaperone Hop. Protein Science, 2020, 29, 2422-2432.	3.1	15
30	Catalysis of proline isomerization and molecular chaperone activity in a tug-of-war. Nature Communications, 2020, 11, 6046.	5.8	18
31	Nucleocapsid protein of SARS-CoV-2 phase separates into RNA-rich polymerase-containing condensates. Nature Communications, 2020, 11, 6041.	5.8	275
32	Proteasomal degradation of the intrinsically disordered protein tau at single-residue resolution. Science Advances, 2020, 6, eaba3916.	4.7	31
33	Solid-phase fluorescent BODIPY–peptide synthesis <i>via in situ</i> dipyrrin construction. Chemical Science, 2020, 11, 11266-11273.	3.7	22
34	Structural analysis of the intrinsically disordered splicing factor Spp2 and its binding to the DEAH-box ATPase Prp2. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2948-2956.	3.3	27
35	Bestimmung komplexer kleiner Molek $\tilde{A}^{1/4}$ lstrukturen mittels molekularer Ausrichtungssimulation. Angewandte Chemie, 2020, 132, 6230-6235.	1.6	5
36	Determination of Complex Smallâ€Molecule Structures Using Molecular Alignment Simulation. Angewandte Chemie - International Edition, 2020, 59, 6172-6176.	7.2	25

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37	Towards a consensus on developmental regression. Neuroscience and Biobehavioral Reviews, 2019, 107, 3-5.	2.9	14
38	Dynamic Aha1 co haperone binding to human Hsp90. Protein Science, 2019, 28, 1545-1551.	3.1	19
39	Lysine/RNA-interactions drive and regulate biomolecular condensation. Nature Communications, 2019, 10, 2909.	5.8	164
40	Reorientational Dynamics of Amyloid-β from NMR Spin Relaxation and Molecular Simulation. Journal of Physical Chemistry Letters, 2019, 10, 3369-3375.	2.1	26
41	Residue-specific identification of phase separation hot spots of Alzheimer's-related protein tau. Chemical Science, 2019, 10, 6503-6507.	3.7	65
42	Structure and Functions of Microtubule Associated Proteins Tau and MAP2c: Similarities and Differences. Biomolecules, 2019, 9, 105.	1.8	41
43	In response to: The validity of 18F-GE180 as a TSPO imaging agent. European Journal of Nuclear Medicine and Molecular Imaging, 2019, 46, 1208-1211.	3.3	19
44	Translocator Protein Ligand Protects against Neurodegeneration in the MPTP Mouse Model of Parkinsonism. Journal of Neuroscience, 2019, 39, 3752-3769.	1.7	46
45	Structural heterogeneity of \hat{l}_{\pm} -synuclein fibrils amplified from patient brain extracts. Nature Communications, 2019, 10, 5535.	5.8	153
46	Nuclear localization and phosphorylation modulate pathological effects of alpha-synuclein. Human Molecular Genetics, 2019, 28, 31-50.	1.4	131
47	Upregulated levels and pathological aggregation of abnormally phosphorylated Tau-protein in children with neurodevelopmental disorders. Neuroscience and Biobehavioral Reviews, 2019, 98, 1-9.	2.9	23
48	Challenges and approaches to understand cholesterol-binding impact on membrane protein function: an NMR view. Cellular and Molecular Life Sciences, 2018, 75, 2137-2151.	2.4	16
49	The Binding Mode of a Tau Peptide with Tubulin. Angewandte Chemie - International Edition, 2018, 57, 3246-3250.	7.2	43
50	Der Bindungsmodus eines Tauâ€Peptids mit Tubulin. Angewandte Chemie, 2018, 130, 3301-3305.	1.6	3
51	The potential of zwitterionic nanoliposomes against neurotoxic alpha-synuclein aggregates in Parkinson's Disease. Nanoscale, 2018, 10, 9174-9185.	2.8	29
52	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
53	Insights into Cholesterol/Membrane Protein Interactions Using Paramagnetic Solidâ€5tate NMR. Chemistry - A European Journal, 2018, 24, 17606-17611.	1.7	16
54	Interaction of Cu(<scp>i</scp>) with the Met-X ₃ -Met motif of alpha-synuclein: binding ligands, affinity and structural features. Metallomics, 2018, 10, 1383-1389.	1.0	16

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55	Structure and pro-toxic mechanism of the human Hsp90/PPlase/Tau complex. Nature Communications, 2018, 9, 4532.	5.8	68
56	Local and Global Dynamics in Intrinsically Disordered Synuclein. Angewandte Chemie - International Edition, 2018, 57, 15262-15266.	7.2	49
57	Lokale und globale Dynamik im ungeordneten Synukleinâ€Protein. Angewandte Chemie, 2018, 130, 15482-15486.	1.6	0
58	RNA polymerase II clustering through carboxy-terminal domain phase separation. Nature Structural and Molecular Biology, 2018, 25, 833-840.	3.6	456
59	Functionally specific binding regions of microtubule-associated protein 2c exhibit distinct conformations and dynamics. Journal of Biological Chemistry, 2018, 293, 13297-13309.	1.6	13
60	The diphenylpyrazole compound anle 138b blocks $\hat{Al^2}$ channels and rescues disease phenotypes in a mouse model for amyloid pathology. EMBO Molecular Medicine, 2018, 10, 32-47.	3.3	63
61	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
62	Glycation potentiates \hat{l} ±-synuclein-associated neurodegeneration in synucleinopathies. Brain, 2017, 140, 1399-1419.	3.7	153
63	Cholesterol-mediated allosteric regulation of the mitochondrial translocator protein structure. Nature Communications, 2017, 8, 14893.	5.8	67
64	Liquid–liquid phase separation of the microtubule-binding repeats of the Alzheimer-related protein Tau. Nature Communications, 2017, 8, 275.	5.8	552
65	Smallâ€Moleculeâ€Induced Soluble Oligomers of αâ€Synuclein with Helical Structure. Chemistry - A European Journal, 2017, 23, 13010-13014.	1.7	14
66	Bioinorganic Chemistry of Parkinson's Disease: Affinity and Structural Features of Cu(I) Binding to the Full-Length β-Synuclein Protein. Inorganic Chemistry, 2017, 56, 10387-10395.	1.9	9
67	Multivalent cross-linking of actin filaments and microtubules through the microtubule-associated protein Tau. Nature Communications, 2017, 8, 1981.	5.8	104
68	Capture of Dense Core Vesicles at Synapses by JNK-Dependent Phosphorylation of Synaptotagmin-4. Cell Reports, 2017, 21, 2118-2133.	2.9	39
69	The mechanism of sirtuin 2–mediated exacerbation of alpha-synuclein toxicity in models of Parkinson disease. PLoS Biology, 2017, 15, e2000374.	2.6	114
70	Human cyclophilin 40 unravels neurotoxic amyloids. PLoS Biology, 2017, 15, e2001336.	2.6	43
71	Elucidating the structure of an infectious protein. PLoS Pathogens, 2017, 13, e1006229.	2.1	15
72	The protonation state of histidine 111 regulates the aggregation of the evolutionary most conserved region of the human prion protein. Protein Science, 2016, 25, 1563-1567.	3.1	4

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73	Remodeling of the conformational ensemble of the repeat domain of tau by an aggregation enhancer. Protein Science, 2016, 25, 1010-1020.	3.1	27
74	Solidâ€Phase Synthesis and Characterization of Nâ€Terminally Elongated Aβ _{â^³3–<i>x</i>} â€Peptides. Chemistry - A European Journal, 2016, 22, 8685-8693.	1.7	8
75	Phosphorylation modifies the molecular stability of \hat{l}^2 -amyloid deposits. Nature Communications, 2016, 7, 11359.	5.8	70
76	Phosphorylation of the amyloid \hat{l}^2 -peptide at Ser26 stabilizes oligomeric assembly and increases neurotoxicity. Acta Neuropathologica, 2016, 131, 525-537.	3.9	84
77	Environmental and genetic factors support the dissociation between α-synuclein aggregation and toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6506-E6515.	3.3	75
78	Voltage Dependence of Conformational Dynamics and Subconducting States of VDAC-1. Biophysical Journal, 2016, 111, 1223-1234.	0.2	28
79	Phosphorylation Interferes with Maturation of Amyloid- \hat{l}^2 Fibrillar Structure in the N Terminus. Journal of Biological Chemistry, 2016, 291, 16059-16067.	1.6	22
80	Structure of Monomeric Transthyretin Carrying the Clinically Important T119M Mutation. Angewandte Chemie - International Edition, 2016, 55, 16168-16171.	7.2	15
81	Highâ€Resolution NMR Determination of the Dynamic Structure of Membrane Proteins. Angewandte Chemie - International Edition, 2016, 55, 10518-10521.	7.2	25
82	Struktur eines monomeren Transthyretin mit der klinisch wichtigen T119Mâ€Mutation. Angewandte Chemie, 2016, 128, 16402-16405.	1.6	0
83	Fasudil attenuates aggregation of α-synuclein in models of Parkinson's disease. Acta Neuropathologica Communications, 2016, 4, 39.	2.4	123
84	Targeting intrinsically disordered proteins in rational drug discovery. Expert Opinion on Drug Discovery, 2016, 11, 65-77.	2.5	74
85	Molecular Plasticity of the Human Voltage-Dependent Anion Channel Embedded Into a Membrane. Structure, 2016, 24, 585-594.	1.6	36
86	Yeast reveals similar molecular mechanisms underlying alpha- and beta-synuclein toxicity. Human Molecular Genetics, 2016, 25, 275-290.	1.4	29
87	Backbone and side-chain resonance assignment of the A147T polymorph of mouse TSPO in complex with a high-affinity radioligand. Biomolecular NMR Assignments, 2016, 10, 79-83.	0.4	8
88	Retention and splicing complex (RES) – the importance of cooperativity. RNA Biology, 2016, 13, 128-133.	1.5	12
89	Structures of intermediates during RES complex assembly. Scientific Reports, 2015, 5, 12545.	1.6	7
90	Structure of the mammalian TSPO/PBR protein. Biochemical Society Transactions, 2015, 43, 566-571.	1.6	29

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91	Conformational Flexibility in the Transmembrane Protein TSPO. Chemistry - A European Journal, 2015, 21, 16555-16563.	1.7	23
92	Structural Integrity of the A147T Polymorph of Mammalian TSPO. ChemBioChem, 2015, 16, 1483-1489.	1.3	32
93	Multiple Paramagnetic Effects through a Tagged Reporter Protein. Angewandte Chemie - International Edition, 2015, 54, 336-339.	7.2	15
94	Folding of the Tau Protein on Microtubules. Angewandte Chemie - International Edition, 2015, 54, 10347-10351.	7.2	130
95	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
96	HYCUD: a computational tool for prediction of effective rotational correlation time in flexible proteins. Bioinformatics, 2015, 31, 1319-1321.	1.8	10
97	Lost in translocation: the functions of the 18-kD translocator protein. Trends in Endocrinology and Metabolism, 2015, 26, 349-356.	3.1	60
98	Solid-state NMR, electrophysiology and molecular dynamics characterization of human VDAC2. Journal of Biomolecular NMR, 2015, 61, 311-320.	1.6	26
99	Small Molecules Detected by Second-Harmonic Generation Modulate the Conformation of Monomeric α-Synuclein and Reduce Its Aggregation in Cells. Journal of Biological Chemistry, 2015, 290, 27582-27593.	1.6	53
100	Structural Impact of Tau Phosphorylation at Threonine 231. Structure, 2015, 23, 1448-1458.	1.6	99
101	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
102	Extracellular vesicle sorting of \hat{l}_{\pm} -Synuclein is regulated by sumoylation. Acta Neuropathologica, 2015, 129, 695-713.	3.9	136
103	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
104	Parkinson Disease Mutant E46K Enhances α-Synuclein Phosphorylation in Mammalian Cell Lines, in Yeast, and in Vivo. Journal of Biological Chemistry, 2015, 290, 9412-9427.	1.6	52
105	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
106	Improved validation of IDP ensembles by one-bond Cα–Hα scalar couplings. Journal of Biomolecular NMR, 2015, 63, 299-307.	1.6	4
107	Bioinorganic chemistry of synucleinopathies: Deciphering the binding features of Met motifs and His-50 in AS–Cu(I) interactions. Journal of Inorganic Biochemistry, 2014, 141, 208-211.	1.5	22
108	A six-dimensional alpha proton detection-based APSY experiment for backbone assignment of intrinsically disordered proteins. Journal of Biomolecular NMR, 2014, 60, 231-240.	1.6	17

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109	Small molecule-mediated stabilization of vesicle-associated helical α-synuclein inhibits pathogenic misfolding and aggregation. Nature Communications, 2014, 5, 5857.	5.8	91
110	Long-Range Correlated Dynamics in Intrinsically Disordered Proteins. Journal of the American Chemical Society, 2014, 136, 16201-16209.	6.6	77
111	Cooperative structure of the heterotrimeric pre-mRNA retention and splicing complex. Nature Structural and Molecular Biology, 2014, 21, 911-918.	3.6	28
112	Interaction of the Intermembrane Space Domain of Tim23 Protein with Mitochondrial Membranes. Journal of Biological Chemistry, 2014, 289, 34620-34626.	1.6	15
113	Predictive Atomic Resolution Descriptions of Intrinsically Disordered hTau40 and α-Synuclein in Solution from NMR and Small Angle Scattering. Structure, 2014, 22, 238-249.	1.6	171
114	Structure of the Mitochondrial Translocator Protein in Complex with a Diagnostic Ligand. Science, 2014, 343, 1363-1366.	6.0	208
115	Hsp90-Tau Complex Reveals Molecular Basis for Specificity in Chaperone Action. Cell, 2014, 156, 963-974.	13.5	269
116	Internalization routes of cellâ€penetrating melanoma antigen peptides into human dendritic cells. Experimental Dermatology, 2014, 23, 20-26.	1.4	6
117	Nucleotide Interactions of the Human Voltage-dependent Anion Channel. Journal of Biological Chemistry, 2014, 289, 13397-13406.	1.6	27
118	Toward the functional oligomerization state of tryptophanâ€rich sensory proteins. Protein Science, 2014, 23, 1154-1160.	3.1	8
119	Turn Plasticity Distinguishes Different Modes of Amyloid- \hat{l}^2 Aggregation. Journal of the American Chemical Society, 2014, 136, 4913-4919.	6.6	39
120	Molecular Basis of the Dynamic Structure of the TIM23 Complex in the Mitochondrial Intermembrane Space. Structure, 2014, 22, 1501-1511.	1.6	22
121	Exploring Free-Energy Landscapes of Intrinsically Disordered Proteins at Atomic Resolution Using NMR Spectroscopy. Chemical Reviews, 2014, 114, 6632-6660.	23.0	252
122	\hat{l}_{\pm} -Synuclein interacts with the switch region of Rab8a in a Ser129 phosphorylation-dependent manner. Neurobiology of Disease, 2014, 70, 149-161.	2.1	84
123	Characterization of the effects of phosphorylation by CK2 on the structure and binding properties of human HP1 \hat{l}^2 . FEBS Letters, 2014, 588, 1094-1099.	1.3	11
124	Site-Specific Copper-Catalyzed Oxidation of α-Synuclein: Tightening the Link between Metal Binding and Protein Oxidative Damage in Parkinson's Disease. Inorganic Chemistry, 2014, 53, 4350-4358.	1.9	68
125	Detection of a transient intramolecular hydrogen bond using 1JNH scalar couplings. Journal of Magnetic Resonance, 2014, 243, 93-97.	1.2	3
126	NMR-Based Detection of Hydrogen/Deuterium Exchange in Liposome-Embedded Membrane Proteins. PLoS ONE, 2014, 9, e112374.	1.1	3

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127	Inhibition of Tau Filament Formation by Conformational Modulation. Journal of the American Chemical Society, 2013, 135, 2853-2862.	6.6	65
128	N-truncated amyloid \hat{l}^2 (A \hat{l}^2) 4-42 forms stable aggregates and induces acute and long-lasting behavioral deficits. Acta Neuropathologica, 2013, 126, 189-205.	3.9	153
129	Phosphorylation Drives a Dynamic Switch in Serine/Arginine-Rich Proteins. Structure, 2013, 21, 2162-2174.	1.6	101
130	Predicting the Rotational Tumbling of Dynamic Multidomain Proteins and Supramolecular Complexes. Angewandte Chemie - International Edition, 2013, 52, 11410-11414.	7.2	28
131	Cold denaturation of a protein dimer monitored at atomic resolution. Nature Chemical Biology, 2013, 9, 264-270.	3.9	37
132	Mechanistic Basis of Phenothiazineâ€Driven Inhibition of Tau Aggregation. Angewandte Chemie - International Edition, 2013, 52, 3511-3515.	7.2	127
133	Anle138b: a novel oligomer modulator for disease-modifying therapy of neurodegenerative diseases such as prion and Parkinson's disease. Acta Neuropathologica, 2013, 125, 795-813.	3.9	327
134	Nâ€"H Spinâ€"Spin Couplings: Probing Hydrogen Bonds in Proteins. Angewandte Chemie - International Edition, 2013, 52, 3525-3528.	7.2	16
135	Imbalance of Hsp70 family variants fosters tau accumulation. FASEB Journal, 2013, 27, 1450-1459.	0.2	100
136	Phosphorylation of Human Tau Protein by Microtubule Affinity-Regulating Kinase 2. Biochemistry, 2013, 52, 9068-9079.	1.2	65
137	$\hat{l}^2 \hat{a} \in \mathbf{s}$ ynuclein aggregates and induces neurodegeneration in dopaminergic neurons. Annals of Neurology, 2013, 74, 109-118.	2.8	58
138	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
139	Conserved amyloid core structure of stop mutants of the human prion protein. Prion, 2013, 7, 193-197.	0.9	12
140	Burial of the Polymorphic Residue 129 in Amyloid Fibrils of Prion Stop Mutants. Journal of Biological Chemistry, 2013, 288, 2994-3002.	1.6	17
141	Structural Plasticity in Human Heterochromatin Protein $1\hat{l}^2$. PLoS ONE, 2013, 8, e60887.	1.1	24
142	Discovery and Structure Activity Relationship of Small Molecule Inhibitors of Toxic Î ² -Amyloid-42 Fibril Formation. Journal of Biological Chemistry, 2012, 287, 34786-34800.	1.6	53
143	Methylation of Lysine 9 in Histone H3 Directs Alternative Modes of Highly Dynamic Interaction of Heterochromatin Protein hHP1 $\hat{1}^2$ with the Nucleosome. Journal of Biological Chemistry, 2012, 287, 33756-33765.	1.6	58
144	Aggregate Clearance of α-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

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145	Determination of amyloid core structure using chemical shifts. Protein Science, 2012, 21, 1948-1953.	3.1	12
146	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
147	l̂ ² -Barrel Mobility Underlies Closure of the Voltage-Dependent Anion Channel. Structure, 2012, 20, 1540-1549.	1.6	104
148	Cold-Induced Changes in the Protein Ubiquitin. PLoS ONE, 2012, 7, e37270.	1.1	9
149	Characterization of Molecular Determinants of the Conformational Stability of Macrophage Migration Inhibitory Factor: Leucine 46 Hydrophobic Pocket. PLoS ONE, 2012, 7, e45024.	1.1	9
150	\hat{l}^2 -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
151	Is Enantiomer Assignment Possible by NMR Spectroscopy Using Residual Dipolar Couplings from Chiral Nonracemic Alignment Media?—A Critical Assessment. Angewandte Chemie - International Edition, 2012, 51, 8388-8391.	7.2	60
152	Intrinsically Disordered Proteins: From Sequence and Conformational Properties toward Drug Discovery. ChemBioChem, 2012, 13, 930-950.	1.3	85
153	Aggregation of αSynuclein promotes progressive in vivo neurotoxicity in adult rat dopaminergic neurons. Acta Neuropathologica, 2012, 123, 671-683.	3.9	96
154	Exploring the Structural Details of Cu(I) Binding to \hat{l}_{\pm} -Synuclein by NMR Spectroscopy. Journal of the American Chemical Society, 2011, 133, 194-196.	6.6	83
155	Toward the Discovery of Effective Polycyclic Inhibitors of α-Synuclein Amyloid Assembly. Journal of Biological Chemistry, 2011, 286, 32036-32044.	1.6	43
156	Effect of Zinc Binding on \hat{l}^2 -Amyloid Structure and Dynamics: Implications for A \hat{l}^2 Aggregation. Biophysical Journal, 2011, 101, 1202-1211.	0.2	87
157	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
158	Interaction between Amyloid Beta Peptide and an Aggregation Blocker Peptide Mimicking Islet Amyloid Polypeptide. PLoS ONE, 2011, 6, e20289.	1.1	40
159	Extracellular phosphorylation of the amyloid \hat{l}^2 -peptide promotes formation of toxic aggregates during the pathogenesis of Alzheimer's disease. EMBO Journal, 2011, 30, 2255-2265.	3.5	160
160	Integrated analysis of the conformation of a protein-linked spin label by crystallography, EPR and NMR spectroscopy. Journal of Biomolecular NMR, 2011, 49, 111-119.	1.6	23
161	Conserved core of amyloid fibrils of wild type and A30P mutant αâ€synuclein. Protein Science, 2011, 20, 387-395.	3.1	34
162	The Dynamic Structure of Filamentous Tau. Angewandte Chemie - International Edition, 2011, 50, 11520-11524.	7.2	74

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163	The <i>Caenorhabditis elegans </i> GARP complex contains the conserved Vps51 subunit and is required to maintain lysosomal morphology. Molecular Biology of the Cell, 2011, 22, 2564-2578.	0.9	25
164	Sumoylation inhibits α-synuclein aggregation and toxicity. Journal of Cell Biology, 2011, 194, 49-60.	2.3	210
165	Pre-Fibrillar α-Synuclein Mutants Cause Parkinson's Disease-Like Non-Motor Symptoms in Drosophila. PLoS ONE, 2011, 6, e24701.	1.1	39
166	NMR Characterization of Long-Range Order in Intrinsically Disordered Proteins. Journal of the American Chemical Society, 2010, 132, 8407-8418.	6.6	276
167	Characterization of Amyloid Fibrils of Human βâ€2â€Microglobulin by Highâ€Resolution Magicâ€Angle Spinning NMR. ChemBioChem, 2010, 11, 1829-1832.	1.3	6
168	The Native Conformation of the Human VDAC1 Nâ€Terminus. Angewandte Chemie - International Edition, 2010, 49, 1882-1885.	7.2	67
169	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
170	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
171	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
172	Entacapone and Tolcapone, Two Catechol O-Methyltransferase Inhibitors, Block Fibril Formation of \hat{l}_{2} -Amyloid and Protect against Amyloid-induced Toxicity. Journal of Biological Chemistry, 2010, 285, 14941-14954.	1.6	119
173	Phosphorylation at S87 Is Enhanced in Synucleinopathies, Inhibits α-Synuclein Oligomerization, and Influences Synuclein-Membrane Interactions. Journal of Neuroscience, 2010, 30, 3184-3198.	1.7	271
174	Bioinorganic Chemistry of Parkinson's Disease: Structural Determinants for the Copper-Mediated Amyloid Formation of Alpha-Synuclein. Inorganic Chemistry, 2010, 49, 10668-10679.	1.9	119
175	Molten Globule Precursor States Are Conformationally Correlated to Amyloid Fibrils of Human β-2-Microglobulin. Journal of the American Chemical Society, 2010, 132, 9223-9225.	6.6	43
176	Automatic Assignment of the Intrinsically Disordered Protein Tau with 441-Residues. Journal of the American Chemical Society, 2010, 132, 11906-11907.	6.6	114
177	Phosphorylation of Synucleins by Members of the Polo-like Kinase Family. Journal of Biological Chemistry, 2010, 285, 2807-2822.	1.6	204
178	VDAC, a multi-functional mitochondrial protein regulating cell life and death. Molecular Aspects of Medicine, 2010, 31, 227-285.	2.7	607
179	Structural Polymorphism of 441-Residue Tau at Single Residue Resolution. PLoS Biology, 2009, 7, e1000034.	2.6	514
180	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

#	Article	IF	CITATIONS
181	Amyloidogenic potential of αâ€chymotrypsin in different conformational states. Biopolymers, 2009, 91, 28-36.	1.2	19
182	Structural characterization of αâ€synuclein in an aggregation prone state. Protein Science, 2009, 18, 1840-1846.	3.1	97
183	Pre-fibrillar α-synuclein variants with impaired \hat{I}^2 -structure increase neurotoxicity in Parkinson's disease models. EMBO Journal, 2009, 28, 3256-3268.	3.5	411
184	Conformational Changes Specific for Pseudophosphorylation at Serine 262 Selectively Impair Binding of Tau to Microtubules. Biochemistry, 2009, 48, 10047-10055.	1.2	118
185	A New Class of Isothiocyanate-Based Irreversible Inhibitors of Macrophage Migration Inhibitory Factor. Biochemistry, 2009, 48, 9858-9870.	1.2	51
186	Structural Properties of Pore-Forming Oligomers of \hat{l} ±-Synuclein. Journal of the American Chemical Society, 2009, 131, 17482-17489.	6.6	191
187	Structural and mechanistic basis behind the inhibitory interaction of PcTS on α-synuclein amyloid fibril formation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21057-21062.	3.3	98
188	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
189	Dissociation of Amyloid Fibrils of αâ€Synuclein in Supercooled Water. Angewandte Chemie - International Edition, 2008, 47, 5046-5048.	7.2	32
190	Cover Picture: Dissociation of Amyloid Fibrils of α-Synuclein in Supercooled Water (Angew. Chem. Int.) Tj ETQq0) 0 0 rgBT 7.2	/Overlock 10
191	Titelbild: Dissociation of Amyloid Fibrils of \hat{l}_{\pm} -Synuclein in Supercooled Water (Angew. Chem. 27/2008). Angewandte Chemie, 2008, 120, 5017-5017.	1.6	0
192	Assignmentâ€free solution NMR method reveals CesT as an unswapped homodimer. Protein Science, 2008, 17, 2015-2019.	3.1	6
193	The PIP2 binding mode of the C2 domains of rabphilinâ€3A. Protein Science, 2008, 17, 1025-1034.	3.1	42
194	NMR: prediction of molecular alignment from structure using the PALES software. Nature Protocols, 2008, 3, 679-690.	5 . 5	332
195	Structural Characterization of Binding of Cu(II) to Tau Protein. Biochemistry, 2008, 47, 10841-10851.	1.2	85
196	Site-Specific Interactions of Cu(II) with \hat{l}_{\pm} and \hat{l}_{-} -Synuclein: Bridging the Molecular Gap between Metal Binding and Aggregation. Journal of the American Chemical Society, 2008, 130, 11801-11812.	6.6	160
197	A Ligand-Induced Switch in the Periplasmic Domain of Sensor Histidine Kinase CitA. Journal of Molecular Biology, 2008, 377, 512-523.	2.0	110
198	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

#	Article	IF	Citations
199	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
200	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
201	Phosphorylation at Ser-129 but Not the Phosphomimics S129E/D Inhibits the Fibrillation of $\hat{l}\pm$ -Synuclein. Journal of Biological Chemistry, 2008, 283, 16895-16905.	1.6	302
202	High-Resolution 3D Structure Determination of Kaliotoxin by Solid-State NMR Spectroscopy. PLoS ONE, 2008, 3, e2359.	1.1	32
203	The C2A-C2B Linker Defines the High Affinity Ca2+ Binding Mode of Rabphilin-3A. Journal of Biological Chemistry, 2007, 282, 5015-5025.	1.6	16
204	The "Jaws―of the Tau-Microtubule Interaction. Journal of Biological Chemistry, 2007, 282, 12230-12239.	1.6	167
205	Structural Characterization of the Intrinsically Unfolded Protein β-Synuclein, a Natural Negative Regulator of α-Synuclein Aggregation. Journal of Molecular Biology, 2007, 372, 708-722.	2.0	102
206	Amino Acid Bulkiness Defines the Local Conformations and Dynamics of Natively Unfolded \hat{l}_{\pm} -Synuclein and Tau. Journal of the American Chemical Society, 2007, 129, 3032-3033.	6.6	61
207	Structural and Microtubule Binding Properties of Tau Mutants of Frontotemporal Dementiasâ€. Biochemistry, 2007, 46, 2574-2582.	1.2	65
208	Correlation of Amyloid Fibril βâ€Structure with the Unfolded State of αâ€Synuclein. ChemBioChem, 2007, 8, 1671-1674.	1.3	62
209	Fast High-Resolution Protein Structure Determination by Using Unassigned NMR Data. Angewandte Chemie - International Edition, 2007, 46, 1176-1179.	7.2	13
210	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
211	Interaction of α-Synuclein with Divalent Metal Ions Reveals Key Differences: A Link between Structure, Binding Specificity and Fibrillation Enhancement. Journal of the American Chemical Society, 2006, 128, 9893-9901.	6.6	331
212	Production of recombinant Conkunitzin-S1 in Escherichia coli. Protein Expression and Purification, 2006, 47, 640-644.	0.6	21
213	NMR in the SPINE Structural Proteomics project. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1150-1161.	2.5	12
214	Mitogen-activated protein kinases interacting kinases are autoinhibited by a reprogrammed activation segment. EMBO Journal, 2006, 25, 4020-4032.	3.5	71
215	1H, 15N, and 13C Resonance Assignment of the C2A Domain of Rabphilin3A. Journal of Biomolecular NMR, 2006, 36, 20-20.	1.6	2
216	Prediction of charge-induced molecular alignment: residual dipolar couplings at pHÂ3 and alignment in surfactant liquid crystalline phases. European Biophysics Journal, 2006, 35, 170-180.	1.2	11

#	Article	IF	Citations
217	Charge-Induced Molecular Alignment of Intrinsically Disordered Proteins. Angewandte Chemie - International Edition, 2006, 45, 7012-7015.	7.2	17
218	Prion Protein Helix 1 Promotes Aggregation but Is Not Converted into \hat{l}^2 -Sheet. Journal of Biological Chemistry, 2006, 281, 30242-30250.	1.6	31
219	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
220	Tailor made activation segment for autoinhibition. Acta Crystallographica Section A: Foundations and Advances, 2006, 62, s156-s156.	0.3	0
221	Simultaneous measurement of protein one-bond residual dipolar couplings without increased resonance overlap. Journal of Magnetic Resonance, 2005, 174, 245-253.	1.2	14
222	Rapid and accurate structure determination of coiled-coil domains using NMR dipolar couplings: Application to cGMP-dependent protein kinase l $\hat{l}\pm$. Protein Science, 2005, 14, 2421-2428.	3.1	43
223	Letter to the Editor: Backbone resonance assignment of the homodimeric, 35ÂkDa chaperone CesT from enteropathogenic Escherichia coli. Journal of Biomolecular NMR, 2005, 31, 377-378.	1.6	1
224	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
225	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
226	Conkunitzin-S1 Is the First Member of a New Kunitz-type Neurotoxin Family. Journal of Biological Chemistry, 2005, 280, 23766-23770.	1.6	88
227	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
228	Familial Mutants of \hat{l}_{\pm} -Synuclein with Increased Neurotoxicity Have a Destabilized Conformation. Journal of Biological Chemistry, 2005, 280, 30649-30652.	1.6	164
229	Determination of the Packing Mode of the Coiled-Coil Domain of cGMP-Dependent Protein Kinase \hat{l}^{\pm} in Solution Using Charge-Predicted Dipolar Couplings. Journal of the American Chemical Society, 2005, 127, 11918-11919.	6.6	9
230	Sites of Tau Important for Aggregation Populate \hat{l}^2 -Structure and Bind to Microtubules and Polyanions. Journal of Biological Chemistry, 2005, 280, 24978-24986.	1.6	275
231	Defining Long-Range Order and Local Disorder in Native α-Synuclein Using Residual Dipolar Couplings. Journal of the American Chemical Society, 2005, 127, 17968-17969.	6.6	223
232	NMR of α-synuclein–polyamine complexes elucidates the mechanism and kinetics of induced aggregation. EMBO Journal, 2004, 23, 2039-2046.	3.5	231
233	Structure and DNA-binding properties of the cytolysin regulator CylR2 from Enterococcus faecalis. EMBO Journal, 2004, 23, 3632-3642.	3.5	37
234	Mars $\hat{a}\in$ robust automatic backbone assignment of proteins. Journal of Biomolecular NMR, 2004, 30, 11-23.	1.6	262

#	Article	IF	Citations
235	Backbone assignment of proteins with known structure using residual dipolar couplings. Journal of Biomolecular NMR, 2004, 30, 25-35.	1.6	35
236	Expression, purification, crystallization and preliminary crystallographic studies of theEnterococcus faecaliscytolysin repressor CylR2. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 746-748.	2.5	7
237	Simultaneous Assignment and Structure Determination of Protein Backbones by Using NMR Dipolar Couplings. Angewandte Chemie - International Edition, 2004, 43, 3479-3481.	7.2	33
238	Prediction of Charge-Induced Molecular Alignment of Biomolecules Dissolved in Dilute Liquid-Crystalline Phases. Biophysical Journal, 2004, 86, 3444-3460.	0.2	111
239	Determination of molecular alignment tensors without backbone resonance assignment: Aid to rapid analysis of protein-protein interactions. Journal of Biomolecular NMR, 2003, 27, 41-56.	1.6	15
240	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
241	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
242	Evaluation of uncertainty in alignment tensors obtained from dipolar couplings. Journal of Biomolecular NMR, 2002, 23, 127-137.	1.6	128
243	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
244	Characterization of molecular alignment in aqueous suspensions of Pf1 bacteriophage. , 2001, 20, 365-377.		109
245	The extracellular human melanoma inhibitory activity (MIA) protein adopts an SH3 domain-like fold. EMBO Journal, 2001, 20, 340-349.	3.5	72
246	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
247	Robust refocusing of 13C magnetization in multidimensional NMR experiments by adiabatic fast passage pulses., 1999, 15, 331-334.		11
248	Structure of the Active Domain of the Herpes Simplex Virus Protein ICP47 in Water/Sodium Dodecyl Sulfate Solution Determined by Nuclear Magnetic Resonance Spectroscopyâ€,‡. Biochemistry, 1999, 38, 13692-13698.	1.2	44
249	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
250	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
251	An Adiabatic Multiple Spin–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
252	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

#	Article	lF	CITATIONS
253	Structure and multiple conformations of the Kunitz-type domain from human type VI collagen $\hat{l}\pm 3$ (VI) chain in solution. Structure, 1996, 4, 195-209.	1.6	28