Peter GÃ¼ntert

List of Publications by Year
in descending order

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238 papers	22,214 citations	15503 65 h-index	10445 139 g-index
251 all docs	251 docs citations	251 times ranked	16875 citing authors

#	Article	IF	Citations
1	1H, 13C and 15N resonance assignments and solution structures of the two RRM domains of Matrin-3. Biomolecular NMR Assignments, 2022, 16, 41-49.	0.8	3
2	Atomic-resolution chemical characterization of (2x)72-kDa tryptophan synthase via four- and five-dimensional ¹ H-detected solid-state NMR. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	31
3	Optimization and validation of multi-state NMR protein structures using structural correlations. Journal of Biomolecular NMR, 2022, , 1.	2.8	6
4	PDBcor: An automated correlation extraction calculator for multi-state protein structures. Structure, 2022, 30, 646-652.e2.	3.3	5
5	A B-factor for NOEs?. Journal of Magnetic Resonance, 2022, 338, 107189.	2.1	5
6	1H, 13C and 15N resonance assignment of the YTH domain of YTHDC2. Biomolecular NMR Assignments, 2021, 15, 1-7.	0.8	2
7	Paramagnetic Solidâ€State NMR to Localize the Metalâ€Ion Cofactor in an Oligomeric DnaB Helicase. Chemistry - A European Journal, 2021, 27, 7745-7755.	3.3	8
8	Evaluation of Multi-Objective Optimization Algorithms for NMR Chemical Shift Assignment. Molecules, 2021, 26, 3699.	3.8	1
9	An automated iterative approach for protein structure refinement using pseudocontact shifts. Journal of Biomolecular NMR, 2021, 75, 319-334.	2.8	5
10	On the Entropy of a One-Dimensional Gas with and without Mixing Using Sinai Billiard. Entropy, 2021, 23, 1188.	2.2	0
11	An atypical LIR motif within UBA5 (ubiquitin like modifier activating enzyme 5) interacts with GABARAP proteins and mediates membrane localization of UBA5. Autophagy, 2020, 16, 256-270.	9.1	41
12	Backbone and methyl assignment of bacteriorhodopsin incorporated into nanodiscs. Journal of Biomolecular NMR, 2020, 74, 45-60.	2.8	14
13	The three-dimensional structure of human Î²-endorphin amyloid fibrils. Nature Structural and Molecular Biology, 2020, 27, 1178-1184.	8.2	46
14	Protein Allostery at Atomic Resolution. Angewandte Chemie - International Edition, 2020, 59, 22132-22139.	13.8	21
15	Protein Allostery at Atomic Resolution. Angewandte Chemie, 2020, 132, 22316-22323.	2.0	1
16	Dynamics of Bacteriorhodopsin in the Darkâ€Adapted State from Solution Nuclear Magnetic Resonance Spectroscopy. Angewandte Chemie - International Edition, 2020, 59, 20965-20972.	13.8	6
17	Dynamics of Bacteriorhodopsin in the Darkâ€Adapted State from Solution Nuclear Magnetic Resonance Spectroscopy. Angewandte Chemie, 2020, 132, 21151-21158.	2.0	1
18	Automated Backbone NMR Resonance Assignment of Large Proteins Using Redundant Linking from a Single Simultaneous Acquisition. Journal of the American Chemical Society, 2020, 142, 5793-5799.	13.7	41

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19	Automated assignment of methyl NMR spectra from large proteins. Progress in Nuclear Magnetic Resonance Spectroscopy, 2020, 118-119, 54-73.	7.5	23
20	Including Protons in Solid-State NMR Resonance Assignment and Secondary Structure Analysis: The Example of RNA Polymerase II Subunits Rpo4/7. Frontiers in Molecular Biosciences, 2019, 6, 100.	3.5	14
21	Automatic structure-based NMR methyl resonance assignment in large proteins. Nature Communications, 2019, 10, 4922.	12.8	30
22	The Solution Structure and Dynamics of Cd-Metallothionein from Helix pomatia Reveal Optimization for Binding Cd over Zn. Biochemistry, 2019, 58, 4570-4581.	2.5	16
23	Integrated NMR and cryo-EM atomic-resolution structure determination of a half-megadalton enzyme complex. Nature Communications, 2019, 10, 2697.	12.8	80
24	Protein Structure Determination in Living Cells. International Journal of Molecular Sciences, 2019, 20, 2442.	4.1	25
25	Global response of diacylglycerol kinase towards substrate binding observed by 2D and 3D MAS NMR. Scientific Reports, 2019, 9, 3995.	3.3	14
26	Highâ€Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. Angewandte Chemie - International Edition, 2019, 58, 7284-7288.	13.8	52
27	Highâ€Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. Angewandte Chemie, 2019, 131, 7362-7366.	2.0	9
28	CYANA. , 2019, , 1-2.		0
29	Protein aggregation of the p63 transcription factor underlies severe skin fragility in AEC syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E906-E915.	7.1	26
30	Chain Assembly and Disassembly Processes Differently Affect the Conformational Space of Ubiquitin Chains. Structure, 2018, 26, 249-258.e4.	3.3	16
31	Fully automated assignment of methyl resonances of a 36 kDa protein dimer from sparse NOESY data. Journal of Physics: Conference Series, 2018, 1036, 012008.	0.4	2
32	Structure and dynamics conspire in the evolution of affinity between intrinsically disordered proteins. Science Advances, 2018, 4, eaau4130.	10.3	38
33	Proteomeâ€wide analysis of phosphoâ€regulated <scp>PDZ</scp> domain interactions. Molecular Systems Biology, 2018, 14, e8129.	7.2	48
34	Regulation of the Activity in the p53 Family Depends on the Organization of the Transactivation Domain. Structure, 2018, 26, 1091-1100.e4.	3.3	18
35	Noise peak filtering in multi-dimensional NMR spectra using convolutional neural networks. Bioinformatics, 2018, 34, 4300-4301.	4.1	22
36	Extending the Applicability of Exact Nuclear Overhauser Enhancements to Large Proteins and RNA. ChemBioChem, 2018, 19, 1695-1701.	2.6	15

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37	High-resolution small RNA structures from exact nuclear Overhauser enhancement measurements without additional restraints. Communications Biology, 2018, 1, 61.	4.4	23
38	Structural investigation of glycan recognition by the ERAD quality control lectin Yos9. Journal of Biomolecular NMR, 2018, 72, 1-10.	2.8	5
39	Automated Structure Determination from NMR Spectra. , 2018, , 401-418.		0
40	Peak picking multidimensional NMR spectra with the contour geometry based algorithm CYPICK. Journal of Biomolecular NMR, 2017, 67, 63-76.	2.8	26
41	NMR-based automated protein structure determination. Archives of Biochemistry and Biophysics, 2017, 628, 24-32.	3.0	35
42	Solution structure of discoidal high-density lipoprotein particles with a shortened apolipoprotein A-I. Nature Structural and Molecular Biology, 2017, 24, 187-193.	8.2	105
43	Determination of helix orientations in a flexible DNA by multi-frequency EPR spectroscopy. Physical Chemistry Chemical Physics, 2017, 19, 29801-29811.	2.8	18
44	Solution structure of the first RNA recognition motif domain of human spliceosomal protein SF3b49 and its mode of interaction with a SF3b145 fragment. Protein Science, 2017, 26, 280-291.	7.6	5
45	Structural and functional dissection of the DH and PH domains of oncogenic Bcr-Abl tyrosine kinase. Nature Communications, 2017, 8, 2101.	12.8	33
46	The Exact Nuclear Overhauser Enhancement: Recent Advances. Molecules, 2017, 22, 1176.	3.8	26
47	Automated Structure Determination from NMR Spectra. , 2017, , 1-18.		1
48	Protein NMR Structure Refinement based on Bayesian Inference. Journal of Physics: Conference Series, 2016, 699, 012005.	0.4	10
49	Improved in-cell structure determination of proteins at near-physiological concentration. Scientific Reports, 2016, 6, 38312.	3.3	43
50	Solid-state NMR sequential assignment of an Amyloid-Î²(1â€“42) fibril polymorph. Biomolecular NMR Assignments, 2016, 10, 269-276.	0.8	18
51	Mechanism of TAp73 inhibition by Î”Np63 and structural basis of p63/p73 hetero-tetramerization. Cell Death and Differentiation, 2016, 23, 1930-1940.	11.2	29
52	Atomic-resolution structure of a disease-relevant AÎ²(1â€“42) amyloid fibril. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4976-84.	7.1	712
53	NMR Investigation of Structures of G-protein Coupled Receptor Folding Intermediates. Journal of Biological Chemistry, 2016, 291, 27170-27186.	3.4	6
54	The CUE Domain of Cue1 Aligns Growing Ubiquitin Chains with Ubc7 for Rapid Elongation. Molecular Cell, 2016, 62, 918-928.	9.7	34

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55	NMR-Based Determination of the 3D Structure of the Ligandâ€“Protein Interaction Site without Protein Resonance Assignment. Journal of the American Chemical Society, 2016, 138, 4393-4400.	13.7	46
56	The Exact NOE as an Alternative in Ensemble Structure Determination. Biophysical Journal, 2016, 110, 113-126.	0.5	39
57	Solid-state NMR sequential assignments of the N-terminal domain of HpDnaB helicase. Biomolecular NMR Assignments, 2016, 10, 13-23.	0.8	16
58	Compiled data set of exact NOE distance limits, residual dipolar couplings and scalar couplings for the protein GB3. Data in Brief, 2015, 5, 99-106.	1.0	11
59	A Structural Ensemble for the Enzyme Cyclophilin Reveals an Orchestrated Mode of Action at Atomic Resolution. Angewandte Chemie - International Edition, 2015, 54, 11657-11661.	13.8	30
60	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology, 2015, 22, 433-434.	8.2	40
61	Evaluation of the reliability of the maximum entropy method for reconstructing 3D and 4D NOESY-type NMR spectra of proteins. Biochemical and Biophysical Research Communications, 2015, 457, 200-205.	2.1	5
62	Increased Reliability of Nuclear Magnetic Resonance Protein Structures by Consensus Structure Bundles. Structure, 2015, 23, 425-434.	3.3	26
63	The RING domain of human promyelocytic leukemia protein (PML). Journal of Biomolecular NMR, 2015, 61, 173-180.	2.8	6
64	Systematic evaluation of combined automated NOE assignment and structure calculation with CYANA. Journal of Biomolecular NMR, 2015, 62, 81-95.	2.8	35
65	Combined automated NOE assignment and structure calculation with CYANA. Journal of Biomolecular NMR, 2015, 62, 453-471.	2.8	329
66	Complementarity and congruence between exact NOEs and traditional NMR probes for spatial decoding of protein dynamics. Journal of Structural Biology, 2015, 191, 306-317.	2.8	19
67	NMR structure calculation for all small molecule ligands and non-standard residues from the PDB Chemical Component Dictionary. Journal of Biomolecular NMR, 2015, 63, 21-37.	2.8	26
68	Atomicâ€Resolution Threeâ€Dimensional Structure of Amyloid Î² Fibrils Bearing the Osaka Mutation. Angewandte Chemie - International Edition, 2015, 54, 331-335.	13.8	245
69	Automated Structure Determination from NMR Spectra. Methods in Molecular Biology, 2015, 1261, 303-329.	0.9	13
70	Identification of residues required for stalled-ribosome rescue in the codon-independent release factor YaeJ. Nucleic Acids Research, 2014, 42, 3152-3163.	14.5	31
71	Novel RNA recognition motif domain in the cytoplasmic polyadenylation element binding protein 3. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2879-2886.	2.6	4
72	Crystal Structure of a PCP/Sfp Complex Reveals the Structural Basis for Carrier Protein Posttranslational Modification. Chemistry and Biology, 2014, 21, 552-562.	6.0	37

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73	Peak picking NMR spectral data using non-negative matrix factorization. BMC Bioinformatics, 2014, 15, 46.	2.6	17
74	Automated NMR resonance assignment strategy for RNA via the phosphodiester backbone based on high-dimensional through-bond APSY experiments. Journal of Biomolecular NMR, 2014, 59, 87-93.	2.8	16
75	Towards a true protein movie: A perspective on the potential impact of the ensemble-based structure determination using exact NOEs. Journal of Magnetic Resonance, 2014, 241, 53-59.	2.1	31
76	Automated resonance assignment of the 21 kDa stereo-array isotope labeled thioldisulfide oxidoreductase DsbA. Journal of Magnetic Resonance, 2014, 249, 88-93.	2.1	7
77	Spontaneous Self-Assembly of Engineered Armadillo Repeat Protein Fragments into a Folded Structure. Structure, 2014, 22, 985-995.	3.3	19
78	Structural features of peptoid-peptide hybrids in lipid-water interfaces. FEBS Letters, 2014, 588, 3291-3297.	2.8	8
79	RBFOX and SUP-12 sandwich a G base to cooperatively regulate tissue-specific splicing. Nature Structural and Molecular Biology, 2014, 21, 778-786.	8.2	27
80	Influence of NMR Data Completeness on Structure Determinations of Homodimeric Proteins. Journal of the Chinese Chemical Society, 2014, 61, 1297-1306.	1.4	0
81	Multiple-state ensemble structure determination from eNOE spectroscopy. Molecular Physics, 2013, 111, 437-454.	1.7	28
82	Prediction of peak overlap in NMR spectra. Journal of Biomolecular NMR, 2013, 56, 113-123.	2.8	0
83	Peakmatch: a simple and robust method for peak list matching. Journal of Biomolecular NMR, 2013, 55, 267-277.	2.8	9
84	1H, 13C, and 15N resonance assignments of the dsRBDs of mouse RNA helicase A. Biomolecular NMR Assignments, 2013, 7, 69-72.	0.8	1
85	Reliability of exclusively NOESY-based automated resonance assignment and structure determination of proteins. Journal of Biomolecular NMR, 2013, 57, 193-204.	2.8	24
86	Stereospecific assignments in proteins using exact NOEs. Journal of Biomolecular NMR, 2013, 57, 211-218.	2.8	16
87	Estimating structure quality trends in the Protein Data Bank by equivalent resolution. Computational Biology and Chemistry, 2013, 46, 8-15.	2.3	13
88	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-1570.	3.3	151
89	Automated solid-state NMR resonance assignment of protein microcrystals and amyloids. Journal of Biomolecular NMR, 2013, 56, 243-254.	2.8	39
90	Molecular Crowding Drives Active Pin1 into Nonspecific Complexes with Endogenous Proteins Prior to Substrate Recognition. Journal of the American Chemical Society, 2013, 135, 13796-13803.	13.7	76

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91	Structural basis for phosphorylation-triggered autophagic clearance of Salmonella. Biochemical Journal, 2013, 454, 459-466.	3.7	92
92	Automated and assisted RNA resonance assignment using NMR chemical shift statistics. Nucleic Acids Research, 2013, 41, e172-e172.	14.5	42
93	NMR Solution Structure of a Chymotrypsin Inhibitor from the Taiwan Cobra Naja naja atra. Molecules, 2013, 18, 8906-8918.	3.8	4
94	Effects of NMR Spectral Resolution on Protein Structure Calculation. PLoS ONE, 2013, 8, e68567.	2.5	10
95	The First Structure of a Lantibiotic Immunity Protein, SpaI from Bacillus subtilis, Reveals a Novel Fold. Journal of Biological Chemistry, 2012, 287, 35286-35298.	3.4	20
96	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	3.9	170
97	Structural insight into the interaction of ADPâ€ribose with the PARP WWE domains. FEBS Letters, 2012, 586, 3858-3864.	2.8	47
98	Discrete Three-dimensional Representation of Macromolecular Motion from eNOE-based Ensemble Calculation. Chimia, 2012, 66, 787.	0.6	10
99	Solution structure and siRNAâ€mediated knockdown analysis of the mitochondrial diseaseâ€related protein C12orf65. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2629-2642.	2.6	27
100	Spatial elucidation of motion in proteins by ensemble-based structure calculation using exact NOEs. Nature Structural and Molecular Biology, 2012, 19, 1053-1057.	8.2	92
101	Influence of 1H chemical shift assignments of the interface residues on structure determinations of homodimeric proteins. Journal of Magnetic Resonance, 2012, 222, 96-104.	2.1	6
102	A New Algorithm for Reliable and General NMR Resonance Assignment. Journal of the American Chemical Society, 2012, 134, 12817-12829.	13.7	153
103	Characterization of Molecular Interactions between ACP and Halogenase Domains in the Curacin A Polyketide Synthase. ACS Chemical Biology, 2012, 7, 378-386.	3.4	35
104	Protein structure validation by generalized linear model rootâ€meanâ€square deviation prediction. Protein Science, 2012, 21, 229-238.	7.6	45
105	Solution structure of the splicing factor motif of the human Prp18 protein. Proteins: Structure, Function and Bioinformatics, 2012, 80, 968-974.	2.6	3
106	Solution structures of the doubleâ€stranded RNAâ€binding domains from rna helicase A. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1699-1706.	2.6	7
107	Fast Automated NMR Spectroscopy of Shortâ€Lived Biological Samples. ChemBioChem, 2012, 13, 964-967.	2.6	2
108	A Universal Expression Tag for Structural and Functional Studies of Proteins. ChemBioChem, 2012, 13, 959-963.	2.6	38

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109	Simultaneous single-structure and bundle representation of protein NMR structures in torsion angle space. Journal of Biomolecular NMR, 2012, 52, 351-364.	2.8	27
110	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	3.3	75
111	Requirements on Paramagnetic Relaxation Enhancement Data for Membrane Protein Structure Determination by NMR. Structure, 2012, 20, 1019-1027.	3.3	35
112	Comparative NMR analysis of an 80-residue G protein-coupled receptor fragment in two membrane mimetic environments. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 2674-2684.	2.6	13
113	Characterization of the Interaction of GABARAPL-1 with the LIR Motif of NBR1. Journal of Molecular Biology, 2011, 410, 477-487.	4.2	86
114	Structural Insights into Rcs Phosphotransfer: The Newly Identified RcsD-ABL Domain Enhances Interaction with the Response Regulator RcsB. Structure, 2011, 19, 577-587.	3.3	14
115	Structure-guided fragment-based in silico drug design of dengue protease inhibitors. Journal of Computer-Aided Molecular Design, 2011, 25, 263-274.	2.9	51
116	Optimization of amino acid type-specific 13C and 15N labeling for the backbone assignment of membrane proteins by solution- and solid-state NMR with the UPLABEL algorithm. Journal of Biomolecular NMR, 2011, 49, 75-84.	2.8	41
117	Exclusively NOESY-based automated NMR assignment and structure determination of proteins. Journal of Biomolecular NMR, 2011, 50, 137-146.	2.8	26
118	Objective identification of residue ranges for the superposition of protein structures. BMC Bioinformatics, 2011, 12, 170.	2.6	53
119	Structures of the first and second doubleâ€stranded RNAâ€binding domains of human TAR RNAâ€binding protein. Protein Science, 2011, 20, 118-130.	7.6	50
120	Solution NMR Structure of Proteorhodopsin. Angewandte Chemie - International Edition, 2011, 50, 11942-11946.	13.8	162
121	Structural basis for the dual RNA-recognition modes of human Tra2-Î² RRM. Nucleic Acids Research, 2011, 39, 1538-1553.	14.5	62
122	Determinants of activity in glutaredoxins: an in vitro evolved Grx1-like variant of Escherichia coli Grx3. Biochemical Journal, 2010, 430, 487-495.	3.7	10
123	Structural Insight into the Zinc Finger CW Domain as a Histone Modification Reader. Structure, 2010, 18, 1127-1139.	3.3	103
124	NMR protein structure determination in living E. coli cells using nonlinear sampling. Nature Protocols, 2010, 5, 1051-1060.	12.0	42
125	Structural investigation of the C-terminal catalytic fragment of presenilin 1. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9644-9649.	7.1	72
126	Solution Structure of the Catalytic Domain of the Mitochondrial Protein ICT1 That Is Essential for Cell Vitality. Journal of Molecular Biology, 2010, 404, 260-273.	4.2	48

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127	Solution Structure of Polytheonamide B, a Highly Cytotoxic Nonribosomal Polypeptide from Marine Sponge. Journal of the American Chemical Society, 2010, 132, 12941-12945.	13.7	80
128	Solution structure of the RNA binding domain in the human muscleblindâ€like protein 2. Protein Science, 2009, 18, 80-91.	7.6	20
129	Structural basis for the sequence-specific RNA-recognition mechanism of human CUG-BP1 RRM3. Nucleic Acids Research, 2009, 37, 5151-5166.	14.5	67
130	Automated assignment of NMR chemical shifts using peak-particle dynamics simulation with the DYNASSIGN algorithm. Journal of Biomolecular NMR, 2009, 43, 97-109.	2.8	24
131	Automated NMR structure determination of stereo-array isotope labeled ubiquitin from minimal sets of spectra using the SAIL-FLYA system. Journal of Biomolecular NMR, 2009, 44, 261-272.	2.8	27
132	Automated structure determination from NMR spectra. European Biophysics Journal, 2009, 38, 129-143.	2.2	227
133	Solution structure of the GUCT domain from human RNA helicase II/GuÎ² reveals the RRM fold, but implausible RNA interactions. Proteins: Structure, Function and Bioinformatics, 2009, 74, 133-144.	2.6	11
134	Structure of the Cdt1 Câ€terminal domain: Conservation of the winged helix fold in replication licensing factors. Protein Science, 2009, 18, 2252-2264.	7.6	33
135	Solution structure of the cysteineâ€rich domain in Fn14, a member of the tumor necrosis factor receptor superfamily. Protein Science, 2009, 18, 650-656.	7.6	26
136	Protein structure determination in living cells by in-cell NMR spectroscopy. Nature, 2009, 458, 102-105.	27.8	317
137	Conformational stability and activity of p73 require a second helix in the tetramerization domain. Cell Death and Differentiation, 2009, 16, 1582-1589.	11.2	53
138	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	19.0	80
139	The Î²E-Domain of Wheat Ec-1 Metallothionein: A Metal-Binding Domain with a Distinctive Structure. Journal of Molecular Biology, 2009, 387, 207-218.	4.2	88
140	Structural and Functional Characterization of the NHR1 Domain of the Drosophila Neuralized E3 Ligase in the Notch Signaling Pathway. Journal of Molecular Biology, 2009, 393, 478-495.	4.2	27
141	SAIL â€“ stereo-array isotope labeling. Quarterly Reviews of Biophysics, 2009, 42, 247-300.	5.7	64
142	Solution structure of the rhodanese homology domain At4g01050(175-295) from Arabidopsis thaliana. Protein Science, 2009, 14, 224-230.	7.6	24
143	Complex assembly mechanism and an RNAâ€binding mode of the human p14â€SF3b155 spliceosomal protein complex identified by NMR solution structure and functional analyses. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1617-1636.	2.6	15
144	Structure of the putative 32â€ƒkDa myrosinaseâ€binding protein from Arabidopsis (At3g16450.1) determined by SAILâ€NMR. FEBS Journal, 2008, 275, 5873-5884.	4.7	28

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145	Structural basis for the selectivity of the external thioesterase of the surfactin synthetase. Nature, 2008, 454, 907-911.	27.8	112
146	Solution structure of the extraterminal domain of the bromodomainâ€containing protein BRD4. Protein Science, 2008, 17, 2174-2179.	7.6	43
147	Solution Structure of the C-terminal Dimerization Domain of SARS Coronavirus Nucleocapsid Protein Solved by the SAIL-NMR Method. Journal of Molecular Biology, 2008, 380, 608-622.	4.2	111
148	Structural Basis of the Role of the NikA Ribbon-Helix-Helix Domain in Initiating Bacterial Conjugation. Journal of Molecular Biology, 2008, 384, 690-701.	4.2	21
149	Solution Structure of the Second RNA Recognition Motif (RRM) Domain of Murine T Cell Intracellular Antigen-1 (TIA-1) and Its RNA Recognition Mode. Biochemistry, 2008, 47, 6437-6450.	2.5	16
150	The RRM domain of poly(A)-specific ribonuclease has a noncanonical binding site for mRNA cap analog recognition. Nucleic Acids Research, 2008, 36, 4754-4767.	14.5	41
151	Transmembrane segment enhanced labeling as a tool for the backbone assignment of Î±-helical membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8262-8267.	7.1	38
152	Structural insight into dimeric interaction of the SARAH domains from Mst1 and RASSF family proteins in the apoptosis pathway. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9236-9241.	7.1	124
153	Solution structure of an atypical WW domain in a novel Î²-clam-like dimeric form. FEBS Letters, 2007, 581, 462-468.	2.8	33
154	Automated structure determination of proteins with the SAIL-FLYA NMR method. Nature Protocols, 2007, 2, 2896-2902.	12.0	48
155	KUJIRA, a package of integrated modules for systematic and interactive analysis of NMR data directed to high-throughput NMR structure studies. Journal of Biomolecular NMR, 2007, 39, 31-52.	2.8	153
156	Automated Protein Structure Determination from NMR Spectra. Journal of the American Chemical Society, 2006, 128, 13112-13122.	13.7	161
157	Symbolic NMR product operator calculations. International Journal of Quantum Chemistry, 2006, 106, 344-350.	2.0	15
158	Solution structures of the first and fourth TSR domains of F-spondin. Proteins: Structure, Function and Bioinformatics, 2006, 64, 665-672.	2.6	36
159	Optimal isotope labelling for NMR protein structure determinations. Nature, 2006, 440, 52-57.	27.8	442
160	Solution structure of the antifreeze-like domain of human sialic acid synthase. Protein Science, 2006, 15, 1010-1016.	7.6	20
161	Solution Structures of the SURP Domains and the Subunit-Assembly Mechanism within the Splicing Factor SF3a Complex in 17S U2 snRNP. Structure, 2006, 14, 1677-1689.	3.3	22
162	A Photoswitchable Miniprotein Based on the Sequence of Avian Pancreatic Polypeptide. Angewandte Chemie - International Edition, 2006, 45, 6297-6300.	13.8	36

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163	Fully automated structure determinations of the Fes SH2 domain using different sets of NMR spectra. Magnetic Resonance in Chemistry, 2006, 44, S83-S88.	1.9	10
164	Evaluation of stereo-array isotope labeling (SAIL) patterns for automated structural analysis of proteins with CYANA. Magnetic Resonance in Chemistry, 2006, 44, S152-S157.	1.9	32
165	NMR Structure of the R-module. Journal of Biological Chemistry, 2006, 281, 7350-7356.	3.4	39
166	Solution structure of the PWWP domain of the hepatoma-derived growth factor family. Protein Science, 2005, 14, 756-764.	7.6	48
167	NMR solution structure of the monomeric form of the bacteriophage Î» capsid stabilizing protein gpD. Journal of Biomolecular NMR, 2005, 31, 351-356.	2.8	16
168	Solution structure of the Src homology 2 domain fromâ£the human feline sarcoma oncogene Fes. Journal of Biomolecular NMR, 2005, 31, 357-361.	2.8	16
169	Solution Structure of the Mouse Enhancer of Rudimentary Protein Reveals a Novel Fold. Journal of Biomolecular NMR, 2005, 32, 329-334.	2.8	17
170	RECOORD: A recalculated coordinate database of 500+ proteins from the PDB using restraints from the BioMagResBank. Proteins: Structure, Function and Bioinformatics, 2005, 59, 662-672.	2.6	323
171	Prion protein NMR structures of chickens, turtles, and frogs. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 651-655.	7.1	161
172	Prion protein NMR structures of cats, dogs, pigs, and sheep. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 640-645.	7.1	203
173	Solution structure of the RWD domain of the mouse GCN2 protein. Protein Science, 2004, 13, 2089-2100.	7.6	66
174	Letter to the Editor: Assignments of1H and15N resonances of the bacteriophage Î» capsid stabilizing protein gpD. Journal of Biomolecular NMR, 2004, 28, 89-90.	2.8	3
175	Letter to the Editor: NMR assignment of the hypothetical ENTH-VHS domain At3g16270 from Arabidopsis thaliana. Journal of Biomolecular NMR, 2004, 29, 205-206.	2.8	18
176	Letter to the Editor: NMR assignment of the hypothetical rhodanese domain At4g01050 from Arabidopsis thaliana. Journal of Biomolecular NMR, 2004, 29, 207-208.	2.8	12
177	Letter to the Editor: NMR assignment of the SH2 domain from the human feline sarcoma oncogene FES. Journal of Biomolecular NMR, 2004, 30, 463-464.	2.8	13
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