Peter Gntert

List of Publications by Year in Descending Order

240 papers	**19,505** citations	**62** h-index	**136** g-index
250 ext. papers	**21,003** ext. citations	**7.1** avg, IF	**6.81** L-index

#	Paper	IF	Citations
240	Atomic-resolution chemical characterization of (2x)72-kDa tryptophan synthase via four- and five-dimensional H-detected solid-state NMR.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	6
239	Optimization and validation of multi-state NMR protein structures using structural correlations.. *Journal of Biomolecular NMR*, **2022**, 1	3	0
238	A B-factor for NOEs?. *Journal of Magnetic Resonance*, **2022**, 338, 107189	3	0
237	H, C and N resonance assignments and solution structures of the two RRM domains of Matrin-3. *Biomolecular NMR Assignments*, **2021**, 1	0.7	
236	Paramagnetic Solid-State NMR to Localize the Metal-Ion Cofactor in an Oligomeric DnaB Helicase. *Chemistry - A European Journal*, **2021**, 27, 7745-7755	4.8	4
235	Evaluation of Multi-Objective Optimization Algorithms for NMR Chemical Shift Assignment. *Molecules*, **2021**, 26,	4.8	1
234	H, C and N resonance assignment of the YTH domain of YTHDC2. *Biomolecular NMR Assignments*, **2021**, 15, 1-7	0.7	0
233	An automated iterative approach for protein structure refinement using pseudocontact shifts. *Journal of Biomolecular NMR*, **2021**, 75, 319-334	3	2
232	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	16.4	22
231	Automated assignment of methyl NMR spectra from large proteins. *Progress in Nuclear Magnetic Resonance Spectroscopy*, **2020**, 118-119, 54-73	10.4	13
230	Backbone and methyl assignment of bacteriorhodopsin incorporated into nanodiscs. *Journal of Biomolecular NMR*, **2020**, 74, 45-60	3	7
229	The three-dimensional structure of human Ɛ-endorphin amyloid fibrils. *Nature Structural and Molecular Biology*, **2020**, 27, 1178-1184	17.6	18
228	Protein Allostery at Atomic Resolution. *Angewandte Chemie - International Edition*, **2020**, 59, 22132-22139	16.4	6
227	Protein Allostery at Atomic Resolution. *Angewandte Chemie*, **2020**, 132, 22316-22323	3.6	
226	Dynamics of Bacteriorhodopsin in the Dark-Adapted State from Solution Nuclear Magnetic Resonance Spectroscopy. *Angewandte Chemie - International Edition*, **2020**, 59, 20965-20972	16.4	1
225	Dynamics of Bacteriorhodopsin in the Dark-Adapted State from Solution Nuclear Magnetic Resonance Spectroscopy. *Angewandte Chemie*, **2020**, 132, 21151-21158	3.6	1
224	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	10.2	16

223	The Solution Structure and Dynamics of Cd-Metallothionein from Reveal Optimization for Binding Cd over Zn. *Biochemistry*, **2019**, 58, 4570-4581	3.2	10
222	Integrated NMR and cryo-EM atomic-resolution structure determination of a half-megadalton enzyme complex. *Nature Communications*, **2019**, 10, 2697	17.4	46
221	Protein Structure Determination in Living Cells. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	12
220	Global response of diacylglycerol kinase towards substrate binding observed by 2D and 3D MAS NMR. *Scientific Reports*, **2019**, 9, 3995	4.9	8
219	High-Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. *Angewandte Chemie - International Edition*, **2019**, 58, 7284-7288	16.4	34
218	High-Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. *Angewandte Chemie*, **2019**, 131, 7362-7366	3.6	5
217	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	5.6	12
216	Automatic structure-based NMR methyl resonance assignment in large proteins. *Nature Communications*, **2019**, 10, 4922	17.4	18
215	CYANA **2019**, 1-2		
214	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	11.5	19
213	Chain Assembly and Disassembly Processes Differently Affect the Conformational Space of Ubiquitin Chains. *Structure*, **2018**, 26, 249-258.e4	5.2	11
212	Noise peak filtering in multi-dimensional NMR spectra using convolutional neural networks. *Bioinformatics*, **2018**, 34, 4300-4301	7.2	12
211	Extending the Applicability of Exact Nuclear Overhauser Enhancements to Large Proteins and RNA. *ChemBioChem*, **2018**, 19, 1695	3.8	9
210	High-resolution small RNA structures from exact nuclear Overhauser enhancement measurements without additional restraints. *Communications Biology*, **2018**, 1, 61	6.7	12
209	Structural investigation of glycan recognition by the ERAD quality control lectin Yos9. *Journal of Biomolecular NMR*, **2018**, 72, 1-10	3	4
208	Automated Structure Determination from NMR Spectra **2018**, 401-418		
207	Fully automated assignment of methyl resonances of a 36 kDa protein dimer from sparse NOESY data. *Journal of Physics: Conference Series*, **2018**, 1036, 012008	0.3	1
206	Structure and dynamics conspire in the evolution of affinity between intrinsically disordered proteins. *Science Advances*, **2018**, 4, eaau4130	14.3	20

No.	Reference	IF	Cit.
205	Proteome-wide analysis of phospho-regulated PDZ domain interactions. *Molecular Systems Biology*, **2018**, 14, e8129	12.2	32
204	Regulation of the Activity in the p53 Family Depends on the Organization of the Transactivation Domain. *Structure*, **2018**, 26, 1091-1100.e4	5.2	10
203	Peak picking multidimensional NMR spectra with the contour geometry based algorithm CYPICK. *Journal of Biomolecular NMR*, **2017**, 67, 63-76	3	21
202	NMR-based automated protein structure determination. *Archives of Biochemistry and Biophysics*, **2017**, 628, 24-32	4.1	27
201	Solution structure of discoidal high-density lipoprotein particles with a shortened apolipoprotein A-I. *Nature Structural and Molecular Biology*, **2017**, 24, 187-193	17.6	85
200	Determination of helix orientations in a flexible DNA by multi-frequency EPR spectroscopy. *Physical Chemistry Chemical Physics*, **2017**, 19, 29801-29811	3.6	14
199	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	6.3	5
198	Structural and functional dissection of the DH and PH domains of oncogenic Bcr-Abl tyrosine kinase. *Nature Communications*, **2017**, 8, 2101	17.4	21
197	The Exact Nuclear Overhauser Enhancement: Recent Advances. *Molecules*, **2017**, 22,	4.8	13
196	Automated Structure Determination from NMR Spectra **2017**, 1-18		1
195	Atomic-resolution structure of a disease-relevant Aβ(1-42) amyloid fibril. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E4976-84	11.5	557
194	NMR Investigation of Structures of G-protein Coupled Receptor Folding Intermediates. *Journal of Biological Chemistry*, **2016**, 291, 27170-27186	5.4	6
193	The CUE Domain of Cue1 Aligns Growing Ubiquitin Chains with Ubc7 for Rapid Elongation. *Molecular Cell*, **2016**, 62, 918-928	17.6	25
192	NMR-Based Determination of the 3D Structure of the Ligand-Protein Interaction Site without Protein Resonance Assignment. *Journal of the American Chemical Society*, **2016**, 138, 4393-400	16.4	38
191	The Exact NOE as an Alternative in Ensemble Structure Determination. *Biophysical Journal*, **2016**, 110, 113-26	2.9	30
190	Solid-state NMR sequential assignments of the N-terminal domain of HpDnaB helicase. *Biomolecular NMR Assignments*, **2016**, 10, 13-23	0.7	13
189	Protein NMR Structure Refinement based on Bayesian Inference. *Journal of Physics: Conference Series*, **2016**, 699, 012005	0.3	8
188	Improved in-cell structure determination of proteins at near-physiological concentration. *Scientific Reports*, **2016**, 6, 38312	4.9	29

187	Solid-state NMR sequential assignment of an Amyloid-β(1-42) fibril polymorph. *Biomolecular NMR Assignments*, **2016**, 10, 269-76	0.7	17
186	Mechanism of TAp73 inhibition by ΔNp63 and structural basis of p63/p73 hetero-tetramerization. *Cell Death and Differentiation*, **2016**, 23, 1930-1940	12.7	22
185	Increased reliability of nuclear magnetic resonance protein structures by consensus structure bundles. *Structure*, **2015**, 23, 425-34	5.2	20
184	The RING domain of human promyelocytic leukemia protein (PML). *Journal of Biomolecular NMR*, **2015**, 61, 173-80	3	4
183	Systematic evaluation of combined automated NOE assignment and structure calculation with CYANA. *Journal of Biomolecular NMR*, **2015**, 62, 81-95	3	23
182	Combined automated NOE assignment and structure calculation with CYANA. *Journal of Biomolecular NMR*, **2015**, 62, 453-71	3	202
181	Complementarity and congruence between exact NOEs and traditional NMR probes for spatial decoding of protein dynamics. *Journal of Structural Biology*, **2015**, 191, 306-17	3.4	14
180	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	3	13
179	Atomic-resolution three-dimensional structure of amyloid β fibrils bearing the Osaka mutation. *Angewandte Chemie - International Edition*, **2015**, 54, 331-5	16.4	211
178	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	1.2	10
177	Die atomare dreidimensionale Struktur von Amyloid-β-Fibrillen mit der Osaka-Mutation. *Angewandte Chemie*, **2015**, 127, 337-342	3.6	12
176	A Structural Ensemble for the Enzyme Cyclophilin Reveals an Orchestrated Mode of Action at Atomic Resolution. *Angewandte Chemie - International Edition*, **2015**, 54, 11657-61	16.4	23
175	A Structural Ensemble for the Enzyme Cyclophilin Reveals an Orchestrated Mode of Action at Atomic Resolution. *Angewandte Chemie*, **2015**, 127, 11823-11827	3.6	1
174	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. *Nature Structural and Molecular Biology*, **2015**, 22, 433-4	17.6	26
173	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, 200-5	3.4	4
172	Automated structure determination from NMR spectra. *Methods in Molecular Biology*, **2015**, 1261, 303-29	2.4	9
171	Peak picking NMR spectral data using non-negative matrix factorization. *BMC Bioinformatics*, **2014**, 15, 46	3.6	13
170	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	3	15

No.	Reference	IF	Cit
169	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, 53-9	3	27
168	Automated resonance assignment of the 21kDa stereo-array isotope labeled thioldisulfide oxidoreductase DsbA. *Journal of Magnetic Resonance*, **2014**, 249, 88-93	3	7
167	Spontaneous self-assembly of engineered armadillo repeat protein fragments into a folded structure. *Structure*, **2014**, 22, 985-95	5.2	18
166	Structural features of peptoid-peptide hybrids in lipid-water interfaces. *FEBS Letters*, **2014**, 588, 3291-7	3.8	7
165	RBFOX and SUP-12 sandwich a G base to cooperatively regulate tissue-specific splicing. *Nature Structural and Molecular Biology*, **2014**, 21, 778-86	17.6	24
164	Influence of NMR Data Completeness on Structure Determinations of Homodimeric Proteins. *Journal of the Chinese Chemical Society*, **2014**, 61, 1297-1306	1.5	
163	Identification of residues required for stalled-ribosome rescue in the codon-independent release factor YaeJ. *Nucleic Acids Research*, **2014**, 42, 3152-63	20.1	28
162	Novel RNA recognition motif domain in the cytoplasmic polyadenylation element binding protein 3. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 2879-86	4.2	2
161	Crystal structure of a PCP/Sfp complex reveals the structural basis for carrier protein posttranslational modification. *Chemistry and Biology*, **2014**, 21, 552-562		30
160	Multiple-state ensemble structure determination from eNOE spectroscopy. *Molecular Physics*, **2013**, 111, 437-454	1.7	21
159	Prediction of peak overlap in NMR spectra. *Journal of Biomolecular NMR*, **2013**, 56, 113-23	3	
158	Peakmatch: a simple and robust method for peak list matching. *Journal of Biomolecular NMR*, **2013**, 55, 267-77	3	7
157	(1)H, (13)C, and (15)N resonance assignments of the dsRBDs of mouse RNA helicase A. *Biomolecular NMR Assignments*, **2013**, 7, 69-72	0.7	1
156	Reliability of exclusively NOESY-based automated resonance assignment and structure determination of proteins. *Journal of Biomolecular NMR*, **2013**, 57, 193-204	3	23
155	Stereospecific assignments in proteins using exact NOEs. *Journal of Biomolecular NMR*, **2013**, 57, 211-8	3	14
154	Estimating structure quality trends in the Protein Data Bank by equivalent resolution. *Computational Biology and Chemistry*, **2013**, 46, 8-15	3.6	11
153	Recommendations of the wwPDB NMR Validation Task Force. *Structure*, **2013**, 21, 1563-70	5.2	117
152	Automated solid-state NMR resonance assignment of protein microcrystals and amyloids. *Journal of Biomolecular NMR*, **2013**, 56, 243-54	3	32

151	Molecular crowding drives active Pin1 into nonspecific complexes with endogenous proteins prior to substrate recognition. *Journal of the American Chemical Society*, **2013**, 135, 13796-803	16.4	60
150	Structural basis for phosphorylation-triggered autophagic clearance of Salmonella. *Biochemical Journal*, **2013**, 454, 459-66	3.8	71
149	Automated and assisted RNA resonance assignment using NMR chemical shift statistics. *Nucleic Acids Research*, **2013**, 41, e172	20.1	36
148	NMR solution structure of a Chymotrypsin inhibitor from the Taiwan cobra Naja naja atra. *Molecules*, **2013**, 18, 8906-18	4.8	4
147	Effects of NMR spectral resolution on protein structure calculation. *PLoS ONE*, **2013**, 8, e68567	3.7	7
146	Blind testing of routine, fully automated determination of protein structures from NMR data. *Structure*, **2012**, 20, 227-36	5.2	64
145	Requirements on paramagnetic relaxation enhancement data for membrane protein structure determination by NMR. *Structure*, **2012**, 20, 1019-27	5.2	33
144	The First structure of a lantibiotic immunity protein, SpaI from Bacillus subtilis, reveals a novel fold. *Journal of Biological Chemistry*, **2012**, 287, 35286-35298	5.4	19
143	WeNMR: Structural Biology on the Grid. *Journal of Grid Computing*, **2012**, 10, 743-767	4.2	142
142	Structural insight into the interaction of ADP-ribose with the PARP WWE domains. *FEBS Letters*, **2012**, 586, 3858-64	3.8	32
141	Discrete three-dimensional representation of macromolecular motion from eNOE-based ensemble calculation. *Chimia*, **2012**, 66, 787-90	1.3	8
140	Solution structure and siRNA-mediated knockdown analysis of the mitochondrial disease-related protein C12orf65. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 2629-42	4.2	26
139	Spatial elucidation of motion in proteins by ensemble-based structure calculation using exact NOEs. *Nature Structural and Molecular Biology*, **2012**, 19, 1053-7	17.6	73
138	Influence of ¹H chemical shift assignments of the interface residues on structure determinations of homodimeric proteins. *Journal of Magnetic Resonance*, **2012**, 222, 96-104	3	6
137	A new algorithm for reliable and general NMR resonance assignment. *Journal of the American Chemical Society*, **2012**, 134, 12817-29	16.4	114
136	Characterization of molecular interactions between ACP and halogenase domains in the Curacin A polyketide synthase. *ACS Chemical Biology*, **2012**, 7, 378-86	4.9	29
135	Protein structure validation by generalized linear model root-mean-square deviation prediction. *Protein Science*, **2012**, 21, 229-38	6.3	38
134	Solution structure of the splicing factor motif of the human Prp18 protein. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 968-74	4.2	3

133	Solution structures of the double-stranded RNA-binding domains from RNA helicase A. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1699-706	4.2	5
132	Fast automated NMR spectroscopy of short-lived biological samples. *ChemBioChem*, **2012**, 13, 964-7	3.8	2
131	A universal expression tag for structural and functional studies of proteins. *ChemBioChem*, **2012**, 13, 959-63	3.8	29
130	Simultaneous single-structure and bundle representation of protein NMR structures in torsion angle space. *Journal of Biomolecular NMR*, **2012**, 52, 351-64	3	19
129	Comparative NMR analysis of an 80-residue G protein-coupled receptor fragment in two membrane mimetic environments. *Biochimica Et Biophysica Acta - Biomembranes*, **2011**, 1808, 2674-84	3.8	11
128	Characterization of the interaction of GABARAPL-1 with the LIR motif of NBR1. *Journal of Molecular Biology*, **2011**, 410, 477-87	6.5	68
127	Structural insights into Rcs phosphotransfer: the newly identified RcsD-ABL domain enhances interaction with the response regulator RcsB. *Structure*, **2011**, 19, 577-87	5.2	14
126	Structure-guided fragment-based in silico drug design of dengue protease inhibitors. *Journal of Computer-Aided Molecular Design*, **2011**, 25, 263-74	4.2	46
125	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	3	40
124	Exclusively NOESY-based automated NMR assignment and structure determination of proteins. *Journal of Biomolecular NMR*, **2011**, 50, 137-46	3	25
123	Objective identification of residue ranges for the superposition of protein structures. *BMC Bioinformatics*, **2011**, 12, 170	3.6	36
122	Structures of the first and second double-stranded RNA-binding domains of human TAR RNA-binding protein. *Protein Science*, **2011**, 20, 118-30	6.3	45
121	Calculation of Structures from NMR Restraints **2011**, 159-192		
120	Solution NMR Structure of Proteorhodopsin. *Angewandte Chemie*, **2011**, 123, 12148-12152	3.6	15
119	Solution NMR structure of proteorhodopsin. *Angewandte Chemie - International Edition*, **2011**, 50, 11942-6	16.4	150
118	Structural basis for the dual RNA-recognition modes of human Tra2-β RRM. *Nucleic Acids Research*, **2011**, 39, 1538-53	20.1	54
117	NMR protein structure determination in living E. coli cells using nonlinear sampling. *Nature Protocols*, **2010**, 5, 1051-60	18.8	35
116	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, 9644-9	11.5	68

115	Solution structure of the catalytic domain of the mitochondrial protein ICT1 that is essential for cell vitality. *Journal of Molecular Biology*, **2010**, 404, 260-73	6.5	44
114	Solution structure of polytheonamide B, a highly cytotoxic nonribosomal polypeptide from marine sponge. *Journal of the American Chemical Society*, **2010**, 132, 12941-5	16.4	71
113	Determinants of activity in glutaredoxins: an in vitro evolved Grx1-like variant of Escherichia coli Grx3. *Biochemical Journal*, **2010**, 430, 487-95	3.8	7
112	Structural insight into the zinc finger CW domain as a histone modification reader. *Structure*, **2010**, 18, 1127-39	5.2	93
111	Structural basis for the sequence-specific RNA-recognition mechanism of human CUG-BP1 RRM3. *Nucleic Acids Research*, **2009**, 37, 5151-66	20.1	62
110	Automated assignment of NMR chemical shifts using peak-particle dynamics simulation with the DYNASSIGN algorithm. *Journal of Biomolecular NMR*, **2009**, 43, 97-109	3	24
109	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, 261-72	3	25
108	Automated structure determination from NMR spectra. *European Biophysics Journal*, **2009**, 38, 129-43	1.9	189
107	Solution structure of the GUCT domain from human RNA helicase II/Gu beta reveals the RRM fold, but implausible RNA interactions. *Proteins: Structure, Function and Bioinformatics*, **2009**, 74, 133-44	4.2	9
106	Structure of the Cdt1 C-terminal domain: conservation of the winged helix fold in replication licensing factors. *Protein Science*, **2009**, 18, 2252-64	6.3	28
105	Solution structure of the cysteine-rich domain in Fn14, a member of the tumor necrosis factor receptor superfamily. *Protein Science*, **2009**, 18, 650-6	6.3	24
104	Protein structure determination in living cells by in-cell NMR spectroscopy. *Nature*, **2009**, 458, 102-5	50.4	267
103	Conformational stability and activity of p73 require a second helix in the tetramerization domain. *Cell Death and Differentiation*, **2009**, 16, 1582-9	12.7	46
102	CASD-NMR: critical assessment of automated structure determination by NMR. *Nature Methods*, **2009**, 6, 625-6	21.6	51
101	The beta(E)-domain of wheat E(c)-1 metallothionein: a metal-binding domain with a distinctive structure. *Journal of Molecular Biology*, **2009**, 387, 207-18	6.5	80
100	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, 478-95	6.5	26
99	SAIL--stereo-array isotope labeling. *Quarterly Reviews of Biophysics*, **2009**, 42, 247-300	7	57
98	Solution structure of the RNA binding domain in the human muscleblind-like protein 2. *Protein Science*, **2009**, 18, 80-91	6.3	19

97	Structural basis for the selectivity of the external thioesterase of the surfactin synthetase. *Nature*, **2008**, 454, 907-11	50.4	103
96	Solution structure of the extraterminal domain of the bromodomain-containing protein BRD4. *Protein Science*, **2008**, 17, 2174-9	6.3	38
95	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, 608-22	6.5	87
94	Structural basis of the role of the NikA ribbon-helix-helix domain in initiating bacterial conjugation. *Journal of Molecular Biology*, **2008**, 384, 690-701	6.5	18
93	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, 6437-50	3.2	15
92	The RRM domain of poly(A)-specific ribonuclease has a noncanonical binding site for mRNA cap analog recognition. *Nucleic Acids Research*, **2008**, 36, 4754-67	20.1	39
91	Transmembrane segment enhanced labeling as a tool for the backbone assignment of alpha-helical membrane proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 8262-7	11.5	35
90	Complex assembly mechanism and an RNA-binding mode of the human p14-SF3b155 spliceosomal protein complex identified by NMR solution structure and functional analyses. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 1617-36	4.2	13
89	Structure of the putative 32 kDa myrosinase-binding protein from Arabidopsis (At3g16450.1) determined by SAIL-NMR. *FEBS Journal*, **2008**, 275, 5873-84	5.7	25
88	Automated structure determination of proteins with the SAIL-FLYA NMR method. *Nature Protocols*, **2007**, 2, 2896-902	18.8	45
87	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	3	137
86	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, 9236-41	11.5	109
85	Solution structure of an atypical WW domain in a novel beta-clam-like dimeric form. *FEBS Letters*, **2007**, 581, 462-8	3.8	30
84	Solution structures of the SURP domains and the subunit-assembly mechanism within the splicing factor SF3a complex in 17S U2 snRNP. *Structure*, **2006**, 14, 1677-89	5.2	19
83	A photoswitchable miniprotein based on the sequence of avian pancreatic polypeptide. *Angewandte Chemie - International Edition*, **2006**, 45, 6297-300	16.4	35
82	Fully automated structure determinations of the Fes SH2 domain using different sets of NMR spectra. *Magnetic Resonance in Chemistry*, **2006**, 44 Spec No, S83-8	2.1	9
81	Evaluation of stereo-array isotope labeling (SAIL) patterns for automated structural analysis of proteins with CYANA. *Magnetic Resonance in Chemistry*, **2006**, 44 Spec No, S152-7	2.1	28
80	A Photoswitchable Miniprotein Based on the Sequence of Avian Pancreatic Polypeptide. *Angewandte Chemie*, **2006**, 118, 6445-6448	3.6	18

79	NMR structure of the R-module: a parallel beta-roll subunit from an Azotobacter vinelandii mannuronan C-5 epimerase. *Journal of Biological Chemistry*, **2006**, 281, 7350-6	5.4	31
78	Automated protein structure determination from NMR spectra. *Journal of the American Chemical Society*, **2006**, 128, 13112-22	16.4	136
77	Symbolic NMR product operator calculations. *International Journal of Quantum Chemistry*, **2006**, 106, 344-350	2.1	14
76	Solution structures of the first and fourth TSR domains of F-spondin. *Proteins: Structure, Function and Bioinformatics*, **2006**, 64, 665-72	4.2	31
75	Optimal isotope labelling for NMR protein structure determinations. *Nature*, **2006**, 440, 52-7	50.4	389
74	Solution structure of the antifreeze-like domain of human sialic acid synthase. *Protein Science*, **2006**, 15, 1010-6	6.3	18
73	Solution structure of the rhodanese homology domain At4g01050(175-295) from Arabidopsis thaliana. *Protein Science*, **2005**, 14, 224-30	6.3	22
72	Solution structure of the PWWP domain of the hepatoma-derived growth factor family. *Protein Science*, **2005**, 14, 756-64	6.3	44
71	NMR solution structure of the monomeric form of the bacteriophage lambda capsid stabilizing protein gpD. *Journal of Biomolecular NMR*, **2005**, 31, 351-6	3	15
70	Solution structure of the Src homology 2 domain from the human feline sarcoma oncogene Fes. *Journal of Biomolecular NMR*, **2005**, 31, 357-61	3	15
69	Solution structure of the mouse enhancer of rudimentary protein reveals a novel fold. *Journal of Biomolecular NMR*, **2005**, 32, 329-34	3	13
68	RECOORD: a recalculated coordinate database of 500+ proteins from the PDB using restraints from the BioMagResBank. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 662-72	4.2	285
67	Prion protein NMR structures of chickens, turtles, and frogs. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 651-5	11.5	154
66	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, 640-5	11.5	178
65	Solution structure of the RWD domain of the mouse GCN2 protein. *Protein Science*, **2004**, 13, 2089-100	6.3	56
64	Assignments of 1H and 15N resonances of the bacteriophage lambda capsid stabilizing protein gpD. *Journal of Biomolecular NMR*, **2004**, 28, 89-90	3	3
63	NMR assignment of the hypothetical ENTH-VHS domain At3g16270 from Arabidopsis thaliana. *Journal of Biomolecular NMR*, **2004**, 29, 205-6	3	18
62	NMR assignment of the hypothetical rhodanese domain At4g01050 from Arabidopsis thaliana. *Journal of Biomolecular NMR*, **2004**, 29, 207-8	3	12

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61	NMR assignment of the SH2 domain from the human feline sarcoma oncogene FES. *Journal of Biomolecular NMR*, **2004**, 30, 463-4	3	13
60	Automated NMR structure calculation with CYANA. *Methods in Molecular Biology*, **2004**, 278, 353-78	1.4	1018
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