Peter Gntert

List of Publications by Citations

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	Torsion angle dynamics for NMR structure calculation with the new program DYANA. *Journal of Molecular Biology*, **1997**, 273, 283-98	6.5	2561
239	The program XEASY for computer-supported NMR spectral analysis of biological macromolecules. *Journal of Biomolecular NMR*, **1995**, 6, 1-10	3	1482
238	Protein NMR structure determination with automated NOE assignment using the new software CANDID and the torsion angle dynamics algorithm DYANA. *Journal of Molecular Biology*, **2002**, 319, 209-27	6.5	1330
237	Automated NMR structure calculation with CYANA. *Methods in Molecular Biology*, **2004**, 278, 353-78	1.4	1018
236	Efficient computation of three-dimensional protein structures in solution from nuclear magnetic resonance data using the program DIANA and the supporting programs CALIBA, HABAS and GLOMSA. *Journal of Molecular Biology*, **1991**, 217, 517-30	6.5	864
235	Atomic-resolution structure of a disease-relevant A(1-42) amyloid fibril. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E4976-84	11.5	557
234	Protein NMR structure determination with automated NOE-identification in the NOESY spectra using the new software ATNOS. *Journal of Biomolecular NMR*, **2002**, 24, 171-89	3	410
233	Optimal isotope labelling for NMR protein structure determinations. *Nature*, **2006**, 440, 52-7	50.4	389
232	Improved efficiency of protein structure calculations from NMR data using the program DIANA with redundant dihedral angle constraints. *Journal of Biomolecular NMR*, **1991**, 1, 447-56	3	328
231	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
230	Protein structure determination in living cells by in-cell NMR spectroscopy. *Nature*, **2009**, 458, 102-5	50.4	267
229	Processing of multi-dimensional NMR data with the new software PROSA. *Journal of Biomolecular NMR*, **1992**, 2, 619-629	3	267
228	Efficient analysis of protein 2D NMR spectra using the software package EASY. *Journal of Biomolecular NMR*, **1991**, 1, 111-30	3	253
227	NMR structure reveals intramolecular regulation mechanism for pheromone binding and release. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 14374-9	11.5	237
226	Atomic-resolution three-dimensional structure of amyloid β fibrils bearing the Osaka mutation. *Angewandte Chemie - International Edition*, **2015**, 54, 331-5	16.4	211
225	Automated NMR protein structure calculation. *Progress in Nuclear Magnetic Resonance Spectroscopy* , **2003**, 43, 105-125	10.4	210
224	Combined automated NOE assignment and structure calculation with CYANA. *Journal of Biomolecular NMR*, **2015**, 62, 453-71	3	202

223	NMR studies in aqueous solution fail to identify significant conformational differences between the monomeric forms of two Alzheimer peptides with widely different plaque-competence, A beta(1-40)(ox) and A beta(1-42)(ox). *FEBS Journal*, **2001**, 268, 5930-6		190
222	Automated structure determination from NMR spectra. *European Biophysics Journal*, **2009**, 38, 129-43	1.9	189
221	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
220	The new program OPAL for molecular dynamics simulations and energy refinements of biological macromolecules. *Journal of Biomolecular NMR*, **1996**, 8, 136-46	3	174
219	Determination of a high-quality nuclear magnetic resonance solution structure of the bovine pancreatic trypsin inhibitor and comparison with three crystal structures. *Journal of Molecular Biology*, **1992**, 227, 757-75	6.5	168
218	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
217	NMR structure of the calreticulin P-domain. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 3133-8	11.5	154
216	NMR structure of the integral membrane protein OmpX. *Journal of Molecular Biology*, **2004**, 336, 1211-21	6.5	152
215	Solution NMR structure of proteorhodopsin. *Angewandte Chemie - International Edition*, **2011**, 50, 11942-6	16.4	150
214	Protein dynamics studied by rotating frame 15N spin relaxation times. *Journal of Biomolecular NMR* , **1993**, 3, 151-64	3	150
213	WeNMR: Structural Biology on the Grid. *Journal of Grid Computing*, **2012**, 10, 743-767	4.2	142
212	Point-centered domain decomposition for parallel molecular dynamics simulation. *Computer Physics Communications*, **2000**, 124, 139-147	4.2	142
211	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
210	Automated protein structure determination from NMR spectra. *Journal of the American Chemical Society*, **2006**, 128, 13112-22	16.4	136
209	Structure calculation of biological macromolecules from NMR data. *Quarterly Reviews of Biophysics*, **1998**, 31, 145-237	7	133
208	Automated combined assignment of NOESY spectra and three-dimensional protein structure determination. *Journal of Biomolecular NMR*, **1997**, 10, 351-62	3	128
207	Structure determination of the Antp (C39----S) homeodomain from nuclear magnetic resonance data in solution using a novel strategy for the structure calculation with the programs DIANA, CALIBA, HABAS and GLOMSA. *Journal of Molecular Biology*, **1991**, 217, 531-40	6.5	124
206	Recommendations of the wwPDB NMR Validation Task Force. *Structure*, **2013**, 21, 1563-70	5.2	117

205	A new algorithm for reliable and general NMR resonance assignment. *Journal of the American Chemical Society*, **2012**, 134, 12817-29	16.4	114
204	Automated sequence-specific NMR assignment of homologous proteins using the program GARANT. *Journal of Biomolecular NMR*, **1996**, 7, 207-13	3	113
203	GARANT-a general algorithm for resonance assignment of multidimensional nuclear magnetic resonance spectra **1997**, 18, 139-149		112
202	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
201	Automated peak picking and peak integration in macromolecular NMR spectra using AUTOPSY. *Journal of Magnetic Resonance*, **1998**, 135, 288-97	3	108
200	Hydration and DNA recognition by homeodomains. *Cell*, **1996**, 85, 1057-65	56.2	104
199	Structural basis for the selectivity of the external thioesterase of the surfactin synthetase. *Nature*, **2008**, 454, 907-11	50.4	103
198	Structural insight into the zinc finger CW domain as a histone modification reader. *Structure*, **2010**, 18, 1127-39	5.2	93
197	NMR structures of three single-residue variants of the human prion protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 8340-5	11.5	92
196	ATP-induced conformational changes of the nucleotide-binding domain of Na,K-ATPase. *Nature Structural and Molecular Biology*, **2003**, 10, 468-74	17.6	88
195	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
194	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
193	Influence of the completeness of chemical shift assignments on NMR structures obtained with automated NOE assignment. *Journal of Structural and Functional Genomics*, **2003**, 4, 179-89		81
192	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
191	NMR structure of the sea urchin (Strongylocentrotus purpuratus) metallothionein MTA. *Journal of Molecular Biology*, **1999**, 291, 417-28	6.5	79
190	Sequence-specific NMR assignment of proteins by global fragment mapping with the program MAPPER. *Journal of Biomolecular NMR*, **2000**, 18, 129-37	3	78
189	NMR structure of the unliganded Bombyx mori pheromone-binding protein at physiological pH. *FEBS Letters*, **2002**, 531, 314-8	3.8	76
188	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

187	Structural basis for phosphorylation-triggered autophagic clearance of Salmonella. *Biochemical Journal*, **2013**, 454, 459-66	3.8	71
186	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
185	Ancestral beta gamma-crystallin precursor structure in a yeast killer toxin. *Nature Structural and Molecular Biology*, **1996**, 3, 662-5	17.6	70
184	Characterization of the interaction of GABARAPL-1 with the LIR motif of NBR1. *Journal of Molecular Biology*, **2011**, 410, 477-87	6.5	68
183	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
182	Nuclear magnetic resonance solution structure of dendrotoxin K from the venom of Dendroaspis polylepis polylepis. *Journal of Molecular Biology*, **1993**, 234, 735-50	6.5	68
181	The NMR solution conformation of unligated human cyclophilin A. *Journal of Molecular Biology*, **1997**, 272, 64-81	6.5	66
180	The program ASNO for computer-supported collection of NOE upper distance constraints as input for protein structure determination. *Journal of Biomolecular NMR*, **1993**, 3, 601	3	65
179	Blind testing of routine, fully automated determination of protein structures from NMR data. *Structure*, **2012**, 20, 227-36	5.2	64
178	Structural basis for the sequence-specific RNA-recognition mechanism of human CUG-BP1 RRM3. *Nucleic Acids Research*, **2009**, 37, 5151-66	20.1	62
177	PSEUDYANA for NMR structure calculation of paramagnetic metalloproteins using torsion angle molecular dynamics. *Journal of Biomolecular NMR*, **1998**, 12, 553-7	3	62
176	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
175	NMR structure of the human doppel protein. *Journal of Molecular Biology*, **2003**, 326, 1549-57	6.5	58
174	SAIL--stereo-array isotope labeling. *Quarterly Reviews of Biophysics*, **2009**, 42, 247-300	7	57
173	NMR structure of the heme chaperone CcmE reveals a novel functional motif. *Structure*, **2002**, 10, 1551-7	5.2	57
172	Solution structure of the RWD domain of the mouse GCN2 protein. *Protein Science*, **2004**, 13, 2089-100	6.3	56
171	POMA: A Complete Mathematica Implementation of the NMR Product-Operator Formalism. *Journal of Magnetic Resonance Series A*, **1993**, 101, 103-105		56
170	Structural basis for the dual RNA-recognition modes of human Tra2-RRM. *Nucleic Acids Research*, **2011**, 39, 1538-53	20.1	54

169	CASD-NMR: critical assessment of automated structure determination by NMR. *Nature Methods*, **2009**, 6, 625-6	21.6	51
168	Nuclear magnetic resonance solution structure of hirudin(1-51) and comparison with corresponding three-dimensional structures determined using the complete 65-residue hirudin polypeptide chain. *Journal of Molecular Biology*, **1992**, 228, 1193-205	6.5	50
167	Conformational analysis of protein and nucleic acid fragments with the new grid search algorithm FOUND. *Journal of Biomolecular NMR*, **1998**, 12, 543-8	3	49
166	NMR structures of 36 and 73-residue fragments of the calreticulin P-domain. *Journal of Molecular Biology*, **2002**, 322, 773-84	6.5	49
165	Integrated NMR and cryo-EM atomic-resolution structure determination of a half-megadalton enzyme complex. *Nature Communications*, **2019**, 10, 2697	17.4	46
164	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
163	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
162	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
161	Automated structure determination of proteins with the SAIL-FLYA NMR method. *Nature Protocols*, **2007**, 2, 2896-902	18.8	45
160	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
159	Solution structure of the PWWP domain of the hepatoma-derived growth factor family. *Protein Science*, **2005**, 14, 756-64	6.3	44
158	NMR studies of the hydration of biological macromolecules. *Faraday Discussions*, **1996**, 103, 245-253	3.6	42
157	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
156	Structure and internal dynamics of the bovine pancreatic trypsin inhibitor in aqueous solution from long-time molecular dynamics simulations. *Proteins: Structure, Function and Bioinformatics*, **1995**, 23, 49-62	4.2	40
155	NMR solution structure of the recombinant tick anticoagulant protein (rTAP), a factor Xa inhibitor from the tick Ornithodoros moubata. *FEBS Letters*, **1994**, 352, 251-7	3.8	40
154	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
153	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
152	Protein structure validation by generalized linear model root-mean-square deviation prediction. *Protein Science*, **2012**, 21, 229-38	6.3	38

151	Solution structure of the extraterminal domain of the bromodomain-containing protein BRD4. *Protein Science*, **2008**, 17, 2174-9	6.3	38
150	NMR solution structure of the periplasmic chaperone FimC. *Nature Structural Biology*, **1998**, 5, 885-90		37
149	Complete relaxation matrix refinement of NMR structures of proteins using analytically calculated dihedral angle derivatives of NOE intensities. *Journal of Biomolecular NMR*, **1991**, 1, 257-69	3	37
148	Automated and assisted RNA resonance assignment using NMR chemical shift statistics. *Nucleic Acids Research*, **2013**, 41, e172	20.1	36
147	Objective identification of residue ranges for the superposition of protein structures. *BMC Bioinformatics*, **2011**, 12, 170	3.6	36
146	NMR protein structure determination in living E. coli cells using nonlinear sampling. *Nature Protocols*, **2010**, 5, 1051-60	18.8	35
145	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
144	A photoswitchable miniprotein based on the sequence of avian pancreatic polypeptide. *Angewandte Chemie - International Edition*, **2006**, 45, 6297-300	16.4	35
143	NMR structure of a variant human prion protein with two disulfide bridges. *Journal of Molecular Biology*, **2003**, 326, 225-34	6.5	35
142	High-Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. *Angewandte Chemie - International Edition*, **2019**, 58, 7284-7288	16.4	34
141	Requirements on paramagnetic relaxation enhancement data for membrane protein structure determination by NMR. *Structure*, **2012**, 20, 1019-27	5.2	33
140	Structural insight into the interaction of ADP-ribose with the PARP WWE domains. *FEBS Letters*, **2012**, 586, 3858-64	3.8	32
139	Automated solid-state NMR resonance assignment of protein microcrystals and amyloids. *Journal of Biomolecular NMR*, **2013**, 56, 243-54	3	32
138	Proteome-wide analysis of phospho-regulated PDZ domain interactions. *Molecular Systems Biology*, **2018**, 14, e8129	12.2	32
137	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
136	Solution structures of the first and fourth TSR domains of F-spondin. *Proteins: Structure, Function and Bioinformatics*, **2006**, 64, 665-72	4.2	31
135	The Exact NOE as an Alternative in Ensemble Structure Determination. *Biophysical Journal*, **2016**, 110, 113-26	2.9	30
134	Crystal structure of a PCP/Sfp complex reveals the structural basis for carrier protein posttranslational modification. *Chemistry and Biology*, **2014**, 21, 552-562		30

133	Solution structure of an atypical WW domain in a novel beta-clam-like dimeric form. *FEBS Letters*, **2007**, 581, 462-8	3.8	30
132	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
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130	Improved in-cell structure determination of proteins at near-physiological concentration. *Scientific Reports*, **2016**, 6, 38312	4.9	29
129	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
128	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
127	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
126	NMR-based automated protein structure determination. *Archives of Biochemistry and Biophysics*, **2017**, 628, 24-32	4.1	27
125	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
124	Impact of protein-protein contacts on the conformation of thrombin-bound hirudin studied by comparison with the nuclear magnetic resonance solution structure of hirudin(1-51). *Journal of Molecular Biology*, **1992**, 228, 1206-11	6.5	27
123	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
122	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
121	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
120	The CUE Domain of Cue1 Aligns Growing Ubiquitin Chains with Ubc7 for Rapid Elongation. *Molecular Cell*, **2016**, 62, 918-928	17.6	25
119	Exclusively NOESY-based automated NMR assignment and structure determination of proteins. *Journal of Biomolecular NMR*, **2011**, 50, 137-46	3	25
118	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
117	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
116	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

115	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
114	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
113	Systematic evaluation of combined automated NOE assignment and structure calculation with CYANA. *Journal of Biomolecular NMR*, **2015**, 62, 81-95	3	23
112	Reliability of exclusively NOESY-based automated resonance assignment and structure determination of proteins. *Journal of Biomolecular NMR*, **2013**, 57, 193-204	3	23
111	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
110	Conformational sampling by NMR solution structures calculated with the program DIANA evaluated by comparison with long-time molecular dynamics calculations in explicit water. *Proteins: Structure, Function and Bioinformatics*, **1996**, 24, 304-13	4.2	23
109	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
108	Solution structure of the rhodanese homology domain At4g01050(175-295) from Arabidopsis thaliana. *Protein Science*, **2005**, 14, 224-30	6.3	22
107	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
106	Peak picking multidimensional NMR spectra with the contour geometry based algorithm CYPICK. *Journal of Biomolecular NMR*, **2017**, 67, 63-76	3	21
105	Multiple-state ensemble structure determination from eNOE spectroscopy. *Molecular Physics*, **2013** , 111, 437-454	1.7	21
104	Structural and functional dissection of the DH and PH domains of oncogenic Bcr-Abl tyrosine kinase. *Nature Communications*, **2017**, 8, 2101	17.4	21
103	Increased reliability of nuclear magnetic resonance protein structures by consensus structure bundles. *Structure*, **2015**, 23, 425-34	5.2	20
102	Structure and dynamics conspire in the evolution of affinity between intrinsically disordered proteins. *Science Advances*, **2018**, 4, eaau4130	14.3	20
101	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
100	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
99	Simultaneous single-structure and bundle representation of protein NMR structures in torsion angle space. *Journal of Biomolecular NMR*, **2012**, 52, 351-64	3	19
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	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
96	Automatic structure-based NMR methyl resonance assignment in large proteins. *Nature Communications*, **2019**, 10, 4922	17.4	18
95	Spontaneous self-assembly of engineered armadillo repeat protein fragments into a folded structure. *Structure*, **2014**, 22, 985-95	5.2	18
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	A Photoswitchable Miniprotein Based on the Sequence of Avian Pancreatic Polypeptide. *Angewandte Chemie*, **2006**, 118, 6445-6448	3.6	18
92	Solution structure of the antifreeze-like domain of human sialic acid synthase. *Protein Science*, **2006**, 15, 1010-6	6.3	18
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90	The three-dimensional structure of human β-endorphin amyloid fibrils. *Nature Structural and Molecular Biology*, **2020**, 27, 1178-1184	17.6	18
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88	Determination of scalar coupling constants by inverse Fourier transformation of in-phase multiplets. *Journal of Magnetic Resonance*, **1992**, 99, 552-560		16
87	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
86	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
85	Solution NMR Structure of Proteorhodopsin. *Angewandte Chemie*, **2011**, 123, 12148-12152	3.6	15
84	Calculating protein structures from NMR data. *Methods in Molecular Biology*, **1997**, 60, 157-94	1.4	15
83	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
82	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
81	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
80	Determination of helix orientations in a flexible DNA by multi-frequency EPR spectroscopy. *Physical Chemistry Chemical Physics*, **2017**, 19, 29801-29811	3.6	14

79	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
78	Stereospecific assignments in proteins using exact NOEs. *Journal of Biomolecular NMR*, **2013**, 57, 211-8	3	14
77	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
76	Symbolic NMR product operator calculations. *International Journal of Quantum Chemistry*, **2006**, 106, 344-350	2.1	14
75	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
74	Automated assignment of methyl NMR spectra from large proteins. *Progress in Nuclear Magnetic Resonance Spectroscopy*, **2020**, 118-119, 54-73	10.4	13
73	Solid-state NMR sequential assignments of the N-terminal domain of HpDnaB helicase. *Biomolecular NMR Assignments*, **2016**, 10, 13-23	0.7	13
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71	The Exact Nuclear Overhauser Enhancement: Recent Advances. *Molecules*, **2017**, 22,	4.8	13
70	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
69	NMR assignment of the SH2 domain from the human feline sarcoma oncogene FES. *Journal of Biomolecular NMR*, **2004**, 30, 463-4	3	13
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