

Thomas Szyperski

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

93
papers

5,861
citations

35
h-index

76
g-index

132
ext. papers

6,340
ext. citations

8.5
avg, IF

5.36
L-index

#	Paper	IF	Citations
93	Perturbing the energy landscape for improved packing during computational protein design. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 436-449	4.2	22
92	Evolutionary coupling saturation mutagenesis: Coevolution-guided identification of distant sites influencing <i>Bacillus naganensis</i> pullulanase activity. <i>FEBS Letters</i> , 2020 , 594, 799-812	3.8	10
91	Structural Basis by Which the N-Terminal Polypeptide Segment of Lipase Regulates Its Substrate Binding Affinity. <i>Biochemistry</i> , 2019 , 58, 3943-3954	3.2	9
90	Development of a Fragment-Based Screening Assay for the Focal Adhesion Targeting Domain Using SPR and NMR. <i>Molecules</i> , 2019 , 24,	4.8	8
89	Folding and Assembly of Short $\alpha\beta$ -Hybrid Peptides: Minor Variations in Sequence and Drastic Differences in Higher-Level Structures. <i>Journal of the American Chemical Society</i> , 2019 , 141, 14239-14248	16.4	10
88	The operon protects from copper toxicity: CopL is an extracellular membrane-associated copper-binding protein. <i>Journal of Biological Chemistry</i> , 2019 , 294, 4027-4044	5.4	23
87	Cytosolic expression, solution structures, and molecular dynamics simulation of genetically encodable disulfide-rich de novo designed peptides. <i>Protein Science</i> , 2018 , 27, 1611-1623	6.3	11
86	Room Temperature X-Ray Crystallography Reveals Conformational Heterogeneity of Engineered Proteins. <i>Structure</i> , 2017 , 25, 691-692	5.2	1
85	C metabolic flux profiling of <i>Pichia pastoris</i> grown in aerobic batch cultures on glucose revealed high relative anabolic use of TCA cycle and limited incorporation of provided precursors of branched-chain amino acids. <i>FEBS Journal</i> , 2017 , 284, 3100-3113	5.7	8
84	Accurate de novo design of hyperstable constrained peptides. <i>Nature</i> , 2016 , 538, 329-335	50.4	231
83	Metabolomics of biomarker discovery in ovarian cancer: a systematic review of the current literature. <i>Metabolomics</i> , 2016 , 12, 1	4.7	42
82	Aromatic oligureas as hosts for anions and cations. <i>Chemical Communications</i> , 2016 , 52, 9905-8	5.8	9
81	A community resource of experimental data for NMR / X-ray crystal structure pairs. <i>Protein Science</i> , 2016 , 25, 30-45	6.3	10
80	Discrete stacking of aromatic oligoamide macrocycles. <i>Journal of the American Chemical Society</i> , 2015 , 137, 5879-82	16.4	27
79	Solution NMR Experiment for Measurement of $(15)\text{N}$ - $(1)\text{H}$ Residual Dipolar Couplings in Large Proteins and Supramolecular Complexes. <i>Journal of the American Chemical Society</i> , 2015 , 137, 11242-5	16.4	7
78	Polypeptide backbone, C α and methyl group resonance assignments of the 24 kDa plectin repeat domain 6 from human protein plectin. <i>Biomolecular NMR Assignments</i> , 2015 , 9, 135-138	0.7	
77	Solution NMR structures of homeodomains from human proteins ALX4, ZHX1, and CASP8AP2 contribute to the structural coverage of the Human Cancer Protein Interaction Network. <i>Journal of Structural and Functional Genomics</i> , 2014 , 15, 201-7		1

76	Solution NMR structures of immunoglobulin-like domains 7 and 12 from obscurin-like protein 1 contribute to the structural coverage of the Human Cancer Protein Interaction Network. <i>Journal of Structural and Functional Genomics</i> , 2014 , 15, 209-14		
75	High-quality NMR structure of human anti-apoptotic protein domain Mcl-1(171-327) for cancer drug design. <i>PLoS ONE</i> , 2014 , 9, e96521	3.7	20
74	Structural and functional characterization of DUF1471 domains of Salmonella proteins SrfN, YdgH/SssB, and YahO. <i>PLoS ONE</i> , 2014 , 9, e101787	3.7	8
73	Spatially selective heteronuclear multiple-quantum coherence spectroscopy for biomolecular NMR studies. <i>ChemPhysChem</i> , 2014 , 15, 1872-9	3.2	6
72	Identification of low-molecular-weight compounds inhibiting growth of corynebacteria: potential lead compounds for antibiotics. <i>ChemMedChem</i> , 2014 , 9, 282-5	3.7	3
71	Solution NMR structure of the helicase associated domain BVU_0683(627-691) from <i>Bacteroides vulgatus</i> provides first structural coverage for protein domain family PF03457 and indicates domain binding to DNA. <i>Journal of Structural and Functional Genomics</i> , 2013 , 14, 19-24		
70	Solution NMR structure of CD1104B from pathogenic <i>Clostridium difficile</i> reveals a distinct helical architecture and provides first structural representative of protein domain family PF14203. <i>Journal of Structural and Functional Genomics</i> , 2013 , 14, 155-60		1
69	Protein conformational space populated in solution probed with aromatic residual dipolar (13) C-(1) H couplings. <i>ChemBioChem</i> , 2013 , 14, 684-8	3.8	12
68	Solution NMR structures provide first structural coverage of the large protein domain family PF08369 and complementary structural coverage of dark operative protochlorophyllide oxidoreductase complexes. <i>Journal of Structural and Functional Genomics</i> , 2013 , 14, 119-26		
67	Increasing sequence diversity with flexible backbone protein design: the complete redesign of a protein hydrophobic core. <i>Structure</i> , 2012 , 20, 1086-96	5.2	45
66	(1)H NMR based profiling of spent culture media cannot predict success of implantation for day 3 human embryos. <i>Journal of Assisted Reproduction and Genetics</i> , 2012 , 29, 1435-42	3.4	14
65	GFT projection NMR for efficient (1)H/ (13)C sugar spin system identification in nucleic acids. <i>Journal of Biomolecular NMR</i> , 2012 , 54, 337-42	3	4
64	Highly precise measurement of kinetic isotope effects using 1H-detected 2D [13C,1H]-HSQC NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2012 , 134, 20589-92	16.4	32
63	Solution NMR structures reveal unique homodimer formation by a winged helix-turn-helix motif and provide first structures for protein domain family PF10771. <i>Journal of Structural and Functional Genomics</i> , 2012 , 13, 1-7		2
62	Solution NMR structures reveal a distinct architecture and provide first structures for protein domain family PF04536. <i>Journal of Structural and Functional Genomics</i> , 2012 , 13, 9-14		7
61	NMR structure of lipoprotein YxeF from <i>Bacillus subtilis</i> reveals a calycin fold and distant homology with the lipocalin Blc from <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2012 , 7, e37404	3.7	4
60	Theory of mirrored time domain sampling for NMR spectroscopy. <i>Journal of Magnetic Resonance</i> , 2011 , 213, 46-57	3	2
59	NMR-based structural biology of proteins in supercooled water. <i>Journal of Structural and Functional Genomics</i> , 2011 , 12, 1-7		13

58	Solution NMR structure of MED25(391-543) comprising the activator-interacting domain (ACID) of human mediator subunit 25. <i>Journal of Structural and Functional Genomics</i> , 2011 , 12, 159-66		13
57	Diagnosis of early stage ovarian cancer by ¹ H NMR metabonomics of serum explored by use of a microflow NMR probe. <i>Journal of Proteome Research</i> , 2011 , 10, 1765-71	5.6	58
56	NMR structure determination for larger proteins using backbone-only data. <i>Science</i> , 2010 , 327, 1014-8	33.3	220
55	Solution NMR structures of proteins VPA0419 from <i>Vibrio parahaemolyticus</i> and yjiS from <i>Shigella flexneri</i> provide structural coverage for protein domain family PFAM 04175. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 779-84	4.2	
54	Advances in protein NMR provided by the NIGMS Protein Structure Initiative: impact on drug discovery. <i>Current Opinion in Drug Discovery & Development</i> , 2010 , 13, 335-49		7
53	Analysis of the varicella-zoster virus IE62 N-terminal acidic transactivating domain and its interaction with the human mediator complex. <i>Journal of Virology</i> , 2009 , 83, 6300-5	6.6	23
52	Clean Absorption-Mode NMR Data Acquisition. <i>Angewandte Chemie</i> , 2009 , 121, 1507-1511	3.6	2
51	Standard operating procedure for metabonomics studies of blood serum and plasma samples using a ¹ H-NMR micro-flow probe. <i>Magnetic Resonance in Chemistry</i> , 2009 , 47 Suppl 1, S81-5	2.1	13
50	Clean absorption-mode NMR data acquisition. <i>Angewandte Chemie - International Edition</i> , 2009 , 48, 1479-84	1.84	4
49	Unique opportunities for NMR methods in structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2009 , 10, 101-6		15
48	Clean absorption mode NMR data acquisition based on time-proportional phase incrementation. <i>Journal of Structural and Functional Genomics</i> , 2009 , 10, 227-32		4
47	Consistent blind protein structure generation from NMR chemical shift data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 4685-90	11.5	665
46	Simultaneously cycled NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2008 , 130, 4925-33	16.4	8
45	On NMR-based Structural Proteomics 2008 , 307-329		
44	Structure of the protein BPTI derived with NOESY in supercooled water: validation and refinement of solution structures. <i>Angewandte Chemie - International Edition</i> , 2008 , 47, 324-6	16.4	5
43	J-GFT NMR for precise measurement of mutually correlated nuclear spin-spin couplings. <i>Journal of the American Chemical Society</i> , 2007 , 129, 680-92	16.4	24
42	Metabolic flux profiling of <i>Pichia pastoris</i> grown on glycerol/methanol mixtures in chemostat cultures at low and high dilution rates. <i>Microbiology (United Kingdom)</i> , 2007 , 153, 281-90	2.9	74
41	Combined NMR-observation of cold denaturation in supercooled water and heat denaturation enables accurate measurement of $\Delta C(p)$ of protein unfolding. <i>European Biophysics Journal</i> , 2006 , 35, 363-6	1.9	35

40	Principles and applications of GFT projection NMR spectroscopy. <i>Magnetic Resonance in Chemistry</i> , 2006 , 44 Spec No, S51-60	2.1	46
39	Probing structure and functional dynamics of (large) proteins with aromatic rings: L-GFT-TROSY (4,3)D HCCH NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2005 , 127, 14578-9	16.4	31
38	G-matrix Fourier transform NOESY-based protocol for high-quality protein structure determination. <i>Journal of the American Chemical Society</i> , 2005 , 127, 9085-99	16.4	54
37	Resonance assignment of proteins with high shift degeneracy based on 5D spectral information encoded in G2FT NMR experiments. <i>Journal of the American Chemical Society</i> , 2005 , 127, 4554-5	16.4	34
36	NMR solution structure of <i>Thermotoga maritima</i> protein TM1509 reveals a Zn-metalloprotease-like tertiary structure. <i>Journal of Structural and Functional Genomics</i> , 2005 , 6, 51-62		19
35	An integrated platform for automated analysis of protein NMR structures. <i>Methods in Enzymology</i> , 2005 , 394, 111-41	1.7	59
34	Rapid NMR data collection. <i>Methods in Enzymology</i> , 2005 , 394, 78-108	1.7	78
33	NMR data collection and analysis protocol for high-throughput protein structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 10487-92	11.5	101
32	Amino acid biosynthesis and metabolic flux profiling of <i>Pichia pastoris</i> . <i>FEBS Journal</i> , 2004 , 271, 2462-70		74
31	GFT NMR experiments for polypeptide backbone and ¹³ Cβ chemical shift assignment. <i>Journal of Biomolecular NMR</i> , 2004 , 28, 117-30	3	37
30	A generalized approach to automated NMR peak list editing: application to reduced dimensionality triple resonance spectra. <i>Journal of Magnetic Resonance</i> , 2004 , 170, 263-77	3	36
29	The phosphoenolpyruvate carboxykinase also catalyzes C3 carboxylation at the interface of glycolysis and the TCA cycle of <i>Bacillus subtilis</i> . <i>Metabolic Engineering</i> , 2004 , 6, 277-84	9.7	45
28	G-matrix Fourier transform NMR spectroscopy for complete protein resonance assignment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 9642-7	11.5	118
27	GFT NMR, a new approach to rapidly obtain precise high-dimensional NMR spectral information. <i>Journal of the American Chemical Society</i> , 2003 , 125, 1385-93	16.4	322
26	Metabolic-flux profiling of the yeasts <i>Saccharomyces cerevisiae</i> and <i>Pichia stipitis</i> . <i>Eukaryotic Cell</i> , 2003 , 2, 170-80		133
25	Protein dynamics in supercooled water: the search for slow motional modes. <i>Journal of Biomolecular NMR</i> , 2002 , 23, 63-7	3	30
24	Reduced-dimensionality NMR spectroscopy for high-throughput protein resonance assignment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 8009-14	11.5	165
23	Metabolic flux responses to pyruvate kinase knockout in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2002 , 184, 152-64	3.5	228

22	Strukturelle Genomik. <i>Nachrichten Aus Der Chemie</i> , 2002 , 50, 1128-1131	0.1	3
21	Intracellular carbon fluxes in riboflavin-producing <i>Bacillus subtilis</i> during growth on two-carbon substrate mixtures. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 1760-71	4.8	64
20	Central carbon metabolism of <i>Saccharomyces cerevisiae</i> explored by biosynthetic fractional (¹³ C) labeling of common amino acids. <i>FEBS Journal</i> , 2001 , 268, 2464-79		133
19	Aromatic ring-flipping in supercooled water: implications for NMR-based structural biology of proteins. <i>Journal of the American Chemical Society</i> , 2001 , 123, 388-97	16.4	65
18	Metabolic flux response to phosphoglucose isomerase knock-out in <i>Escherichia coli</i> and impact of overexpression of the soluble transhydrogenase UdhA. <i>FEMS Microbiology Letters</i> , 2001 , 204, 247-52	2.9	147
17	Dissection of central carbon metabolism of hemoglobin-expressing <i>Escherichia coli</i> by ¹³ C nuclear magnetic resonance flux distribution analysis in microaerobic bioprocesses. <i>Applied and Environmental Microbiology</i> , 2001 , 67, 680-7	4.8	33
16	Toward Structural Biology in Supercooled Water. <i>Journal of the American Chemical Society</i> , 2000 , 122, 3230-3231	16.4	41
15	Metabolic flux ratio analysis of genetic and environmental modulations of <i>Escherichia coli</i> central carbon metabolism. <i>Journal of Bacteriology</i> , 1999 , 181, 6679-88	3.5	323
14	Bioreaction network topology and metabolic flux ratio analysis by biosynthetic fractional ¹³ C labeling and two-dimensional NMR spectroscopy. <i>Metabolic Engineering</i> , 1999 , 1, 189-97	9.7	96
13	The 2D [³¹ P] spin-echo-difference constant-time [¹³ C, ¹ H]-HMQC experiment for simultaneous determination of ³ J(H ₃ W) and ³ J(C ₄ W) in ¹³ C-labeled nucleic acids and their protein complexes. <i>Journal of Magnetic Resonance</i> , 1999 , 140, 491-4	3	18
12	Conformational changes of the BS2 operator DNA upon complex formation with the Antennapedia homeodomain studied by NMR with ¹³ C/ ¹⁵ N-labeled DNA. <i>Journal of Molecular Biology</i> , 1999 , 292, 609-17	6.5	11
11	Amino acid biosynthesis in the halophilic archaeon <i>Haloarcula hispanica</i> . <i>Journal of Bacteriology</i> , 1999 , 181, 3226-37	3.5	36
10	Sequential resonance assignment of medium-sized ¹⁵ N/ ¹³ C-labeled proteins with projected 4D triple resonance NMR experiments. <i>Journal of Biomolecular NMR</i> , 1998 , 11, 387-405	3	25
9	Measurement of Deoxyribose ³ J _{HH} Scalar Couplings Reveals Protein Binding-Induced Changes in the Sugar Puckers of the DNA. <i>Journal of the American Chemical Society</i> , 1998 , 120, 821-822	16.4	16
8	¹³ C-NMR, MS and metabolic flux balancing in biotechnology research. <i>Quarterly Reviews of Biophysics</i> , 1998 , 31, 41-106	7	194
7	Measurement of ³ J _{C2P} Scalar Couplings in a 17 kDa Protein Complex with ¹³ C, ¹⁵ N-Labeled DNA Distinguishes the BI and BII Phosphate Conformations of the DNA. <i>Journal of the American Chemical Society</i> , 1997 , 119, 9901-9902	16.4	30
6	Metabolic fluxes in riboflavin-producing <i>Bacillus subtilis</i> . <i>Nature Biotechnology</i> , 1997 , 15, 448-52	44.5	221
5	Detecting and dissecting metabolic fluxes using biosynthetic fractional ¹³ C labeling and two-dimensional NMR spectroscopy. <i>Trends in Biotechnology</i> , 1996 , 14, 453-459	15.1	58

4	Biosynthetically directed fractional ¹³ C-labeling of proteinogenic amino acids. An efficient analytical tool to investigate intermediary metabolism. <i>FEBS Journal</i> , 1995 , 232, 433-48		305
3	Support of ¹ H NMR assignments in proteins by biosynthetically directed fractional ¹³ C-labeling. <i>Journal of Biomolecular NMR</i> , 1992 , 2, 323-34	3	88
2	Stereospecific nuclear magnetic resonance assignments of the methyl groups of valine and leucine in the DNA-binding domain of the 434 repressor by biosynthetically directed fractional ¹³ C labeling. <i>Biochemistry</i> , 1989 , 28, 7510-6	3.2	564
1	Metabolic flux response to phosphoglucose isomerase knock-out in <i>Escherichia coli</i> and impact of overexpression of the soluble transhydrogenase UdhA		8