

Shan-Ho Chou

List of Publications by Year in descending order

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129
papers

4,076
citations

136740

32
h-index

138251

58
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135
all docs

135
docs citations

135
times ranked

3104
citing authors

#	ARTICLE	IF	CITATIONS
1	A "time bomb"™ in the human intestine—the multiple emergence and spread of antibiotic-resistant bacteria. <i>Environmental Microbiology</i> , 2022, 24, 1231-1246.	1.8	5
2	Sequence Conservation, Domain Architectures, and Phylogenetic Distribution of the HD-GYP Type c-di-GMP Phosphodiesterases. <i>Journal of Bacteriology</i> , 2022, 204, jb0056121.	1.0	15
3	The RNA Chaperone Protein Hfq Regulates the Characteristic Sporulation and Insecticidal Activity of <i>Bacillus thuringiensis</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 884528.	1.5	0
4	Bio-hybrid nanoarchitectonics of nanoflower-based ELISA method for the detection of <i>Staphylococcus aureus</i> . <i>Sensors and Actuators B: Chemical</i> , 2022, 366, 132005.	4.0	20
5	A non-flagellated, predatory soil bacterium reprograms a chemosensory system to control antifungal antibiotic production via cyclic c-di-GMP signalling. <i>Environmental Microbiology</i> , 2021, 23, 878-892.	1.8	11
6	Coordinated control of the type IV pili and c-di-GMP-dependent antifungal antibiotic production in <i>Lysobacter</i> by the response regulator PilR. <i>Molecular Plant Pathology</i> , 2021, 22, 602-617.	2.0	14
7	Which Is Stronger? A Continuing Battle Between Cry Toxins and Insects. <i>Frontiers in Microbiology</i> , 2021, 12, 665101.	1.5	17
8	<i>Lysobacter enzymogenes</i> antagonizes soilborne bacteria using the type IV secretion system. <i>Environmental Microbiology</i> , 2021, 23, 4673-4688.	1.8	18
9	Antifungal weapons of <i>Lysobacter</i> , a mighty biocontrol agent. <i>Environmental Microbiology</i> , 2021, 23, 5704-5715.	1.8	34
10	The Multiple Regulatory Relationship Between RNA-Chaperone Hfq and the Second Messenger c-di-GMP. <i>Frontiers in Microbiology</i> , 2021, 12, 689619.	1.5	6
11	Clp is a "busy" transcription factor in the bacterial warrior, <i>Lysobacter enzymogenes</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3564-3572.	1.9	11
12	The spatial position effect: synthetic biology enters the era of 3D genomics. <i>Trends in Biotechnology</i> , 2021, , .	4.9	1
13	Ways to control harmful biofilms: prevention, inhibition, and eradication. <i>Critical Reviews in Microbiology</i> , 2021, 47, 57-78.	2.7	38
14	Bacterial quorum sensing quenching activity of <i>Lysobacter leucyl</i> aminopeptidase acts by interacting with autoinducer synthase. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6179-6190.	1.9	4
15	ClpP mediates antagonistic interaction of <i>Lysobacter enzymogenes</i> with a crop fungal pathogen. <i>Biological Control</i> , 2020, 140, 104125.	1.4	6
16	A YajQ-like, cyclic c-di-GMP-dependent system regulating biosynthesis of an antifungal antibiotic in a crop-protecting bacterium, <i>Lysobacter enzymogenes</i> . <i>Molecular Plant Pathology</i> , 2020, 21, 218-229.	2.0	20
17	2-Methylcitrate cycle: a well-regulated controller of <i>Bacillus</i> sporulation. <i>Environmental Microbiology</i> , 2020, 22, 1125-1140.	1.8	19
18	An intrinsic mechanism for coordinated production of the contact-dependent and contact-independent weapon systems in a soil bacterium. <i>PLoS Pathogens</i> , 2020, 16, e1008967.	2.1	24

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19	6S-1 RNA Contributes to Sporulation and Parasporal Crystal Formation in <i>Bacillus thuringiensis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 604458.	1.5	5
20	Functional divergence of flagellar type III secretion system: A case study in a non-flagellated, predatory bacterium. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3368-3376.	1.9	7
21	The Homologous Components of Flagellar Type III Protein Apparatus Have Acquired a Novel Function to Control Twitching Motility in a Non-Flagellated Biocontrol Bacterium. <i>Biomolecules</i> , 2020, 10, 733.	1.8	12
22	A decade of research on the second messenger c-di-AMP. <i>FEMS Microbiology Reviews</i> , 2020, 44, 701-724.	3.9	74
23	A non-flagellated biocontrol bacterium employs a PilZ-PilB complex to provoke twitching motility associated with its predation behavior. <i>Phytopathology Research</i> , 2020, 2, .	0.9	4
24	Cyclic di-GMP in <i>Streptomyces</i> : A New Conformation, New Binding Mode, New Receptor, and a New Mechanism to Control Cell Development. <i>Molecular Cell</i> , 2020, 77, 443-445.	4.5	5
25	Cyclic di-AMP, a second messenger of primary importance: tertiary structures and binding mechanisms. <i>Nucleic Acids Research</i> , 2020, 48, 2807-2829.	6.5	66
26	Knockout of Diguanylate Cyclase Genes in <i>Lysobacter</i> enzymogenes to Improve Production of Antifungal Factor and Increase Its Application in Seed Coating. <i>Current Microbiology</i> , 2020, 77, 1006-1015.	1.0	10
27	Structural Conservation and Diversity of PilZ-Related Domains. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	24
28	Cyclic di-GMP Signaling in the Phytopathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> . , 2020, , 427-442.		0
29	Cyclic di-GMP-Dependent Regulation of Antibiotic Biosynthesis in <i>Lysobacter</i> . , 2020, , 329-336.		1
30	Noncanonical Cyclic di-GMP Binding Modes. , 2020, , 125-134.		0
31	A c-di-AMP riboswitch controlling <i>kdpFABC</i> operon transcription regulates the potassium transporter system in <i>Bacillus thuringiensis</i> . <i>Communications Biology</i> , 2019, 2, 151.	2.0	31
32	Spermidine plays a significant role in stabilizing a master transcription factor Clp to promote antifungal activity in <i>Lysobacter</i> enzymogenes. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1811-1822.	1.7	7
33	Insights into the distinct cooperation between the transcription factor Clp and Le DSF signaling in the regulation of antifungal factors in <i>Lysobacter</i> enzymogenes OH11. <i>Biological Control</i> , 2018, 120, 52-58.	1.4	7
34	Sigma factor RpoN employs a dual transcriptional regulation for controlling twitching motility and biofilm formation in <i>Lysobacter</i> enzymogenes OH11. <i>Current Genetics</i> , 2018, 64, 515-527.	0.8	8
35	Signaling specificity in the c-di-GMP-dependent network regulating antibiotic synthesis in <i>Lysobacter</i> . <i>Nucleic Acids Research</i> , 2018, 46, 9276-9288.	6.5	55
36	Two direct gene targets contribute to Clp-dependent regulation of type IV pilus-mediated twitching motility in <i>Lysobacter</i> enzymogenes OH11. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7509-7519.	1.7	15

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37	c-di-GMP Regulates Various Phenotypes and Insecticidal Activity of Gram-Positive <i>Bacillus thuringiensis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 45.	1.5	39
38	Genome-wide Analysis of the Distribution of Riboswitches and Function Analyses of the Corresponding Downstream Genes in Prokaryotes. <i>Current Bioinformatics</i> , 2018, 14, 53-61.	0.7	1
39	Parity-dependent hairpin configurations of repetitive DNA sequence promote slippage associated with DNA expansion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9535-9540.	3.3	31
40	Regulation of Inducible Potassium Transporter KdpFABC by the KdpD/KdpE Two-Component System in <i>Mycobacterium smegmatis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 570.	1.5	36
41	Transcriptome Landscape of <i>Mycobacterium smegmatis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2505.	1.5	64
42	A TonB-dependent receptor regulates antifungal HSAF biosynthesis in <i>Lysobacter</i> . <i>Scientific Reports</i> , 2016, 6, 26881.	1.6	22
43	DgcA, a diguanylate cyclase from <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> regulates bacterial pathogenicity on rice. <i>Scientific Reports</i> , 2016, 6, 25978.	1.6	25
44	Cyclic di-GMP contributes to adaption and virulence of <i>Bacillus thuringiensis</i> through a riboswitch-regulated collagen adhesion protein. <i>Scientific Reports</i> , 2016, 6, 28807.	1.6	50
45	Direct Regulation of Extracellular Chitinase Production by the Transcription Factor <i>LeClp</i> in <i>Lysobacter enzymogenes</i> OH11. <i>Phytopathology</i> , 2016, 106, 971-977.	1.1	27
46	Functional and genomic insights into the pathogenesis of <i>Burkholderia</i> species to rice. <i>Environmental Microbiology</i> , 2016, 18, 780-790.	1.8	25
47	Nucleotide binding by the widespread high-affinity cyclic di-GMP receptor MshEN domain. <i>Nature Communications</i> , 2016, 7, 12481.	5.8	129
48	Characterization of a natural triple-tandem c-di-GMP riboswitch and application of the riboswitch-based dual-fluorescence reporter. <i>Scientific Reports</i> , 2016, 6, 20871.	1.6	96
49	Diversity of Cyclic Di-GMP-Binding Proteins and Mechanisms. <i>Journal of Bacteriology</i> , 2016, 198, 32-46.	1.0	244
50	Complete Genome Sequence of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strain 17 from Taiwan. <i>Genome Announcements</i> , 2015, 3, .	0.8	18
51	Structure and dynamics of polymyxin-resistance-associated response regulator PmrA in complex with promoter DNA. <i>Nature Communications</i> , 2015, 6, 8838.	5.8	54
52	Backbone resonance assignments of the 54 kDa dimeric C-terminal domain of murine STING in complex with DMXAA. <i>Biomolecular NMR Assignments</i> , 2015, 9, 271-274.	0.4	4
53	Structural Insights into the Distinct Binding Mode of Cyclic Di-AMP with <i>SaCpaA_RCK</i> . <i>Biochemistry</i> , 2015, 54, 4936-4951.	1.2	48
54	Solution structure and tandem DNA recognition of the C-terminal effector domain of PmrA from <i>Klebsiella pneumoniae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 4080-4093.	6.5	24

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55	Crystal Structure of a Conserved Hypothetical Protein MJ0927 from <i>Methanocaldococcus jannaschii</i> Reveals a Novel Quaternary Assembly in the Nif3 Family. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	2
56	Crystallization of the N-terminal regulatory domain of the enhancer-binding protein FleQ from <i>Stenotrophomonas maltophilia</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 326-330.	0.4	6
57	A cyclic GMP-dependent signalling pathway regulates bacterial phytopathogenesis. <i>EMBO Journal</i> , 2013, 32, 2430-2438.	3.5	46
58	A cyclic GMP-dependent signalling pathway regulates bacterial phytopathogenesis. <i>EMBO Journal</i> , 2013, 32, 2779-2781.	3.5	1
59	Novel c-di-GMP recognition modes of the mouse innate immune adaptor protein STING. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 352-366.	2.5	36
60	Functional Divergence of FimX in PilZ Binding and Type IV Pilus Regulation. <i>Journal of Bacteriology</i> , 2012, 194, 5922-5931.	1.0	22
61	Structural polymorphism of c-di-GMP bound to an EAL domain and in complex with a type II PilZ-domain protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1380-1392.	2.5	42
62	Crystallization studies of the murine c-di-GMP sensor protein STING. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 906-910.	0.7	9
63	Crystallization and preliminary X-ray diffraction studies of <i>Xanthomonas campestris</i> PNPase in the presence of c-di-GMP. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1247-1250.	0.7	5
64	Crystallization and preliminary X-ray diffraction characterization of the XccFimXEAL-c-di-GMP and XccFimXEAL-c-di-GMP-XccPilZ complexes from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 301-305.	0.7	5
65	A Novel Tetrameric PilZ Domain Structure from Xanthomonads. <i>PLoS ONE</i> , 2011, 6, e22036.	1.1	20
66	The structure and inhibition of a GGDEF diguanylate cyclase complexed with (c-di-GMP) ₂ at the active site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 997-1008.	2.5	48
67	Delicate conformational changes of a protein in the CRP family lead to dramatic functional changes via binding of an alternate secondary messenger molecule. <i>Virulence</i> , 2011, 2, 152-157.	1.8	2
68	Structure of <i>Stenotrophomonas maltophilia</i> FeoA complexed with zinc: a unique prokaryotic SH3-domain protein that possibly acts as a bacterial ferrous iron-transport activating factor. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 636-642.	0.7	29
69	Lipid Bilayer-Assisted Release of an Eneidine Antibiotic from Neocarzinostatin Chromoprotein. <i>Biochemistry</i> , 2010, 49, 7722-7732.	1.2	1
70	The cAMP Receptor-Like Protein CLP Is a Novel c-di-GMP Receptor Linking Cell-Cell Signaling to Virulence Gene Expression in <i>Xanthomonas campestris</i> . <i>Journal of Molecular Biology</i> , 2010, 396, 646-662.	2.0	191
71	XC1028 from <i>Xanthomonas campestris</i> adopts a PilZ domain-like structure without a c-di-GMP switch. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 282-288.	1.5	43
72	<i>Xanthomonas campestris</i> PqqD in the pyrroloquinoline quinone biosynthesis operon adopts a novel saddle-like fold that possibly serves as a PQQ carrier. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 1042-1048.	1.5	33

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73	Crystallization and preliminary X-ray diffraction characterization of an essential protein from <i>Xanthomonas campestris</i> that contains a noncanonical PilZ signature motif yet is critical for pathogenicity. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1056-1059.	0.7	4
74	Unique GTP-Binding Pocket and Allostery of Uridylate Kinase from a Gram-Negative Phytopathogenic Bacterium. <i>Journal of Molecular Biology</i> , 2009, 385, 1113-1126.	2.0	10
75	Insights into the Alkyl Peroxide Reduction Pathway of <i>Xanthomonas campestris</i> Bacterioferritin Comigratory Protein from the Trapped Intermediate-Ligand Complex Structures. <i>Journal of Molecular Biology</i> , 2009, 390, 951-966.	2.0	28
76	Crystal structure of DFA0005 complexed with α -ketoglutarate: A novel member of the ICL/PEPM superfamily from alkali-tolerant <i>Deinococcus ficus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 362-371.	1.5	0
77	Crystal Structure of the C-Terminal Domain of a Flagellar Hook-Capping Protein from <i>Xanthomonas campestris</i> . <i>Journal of Molecular Biology</i> , 2008, 381, 189-199.	2.0	22
78	The First Crystal Structure of Gluconolactonase Important in the Glucose Secondary Metabolic Pathways. <i>Journal of Molecular Biology</i> , 2008, 384, 604-614.	2.0	31
79	The crystallization of apo-form UMP kinase from <i>Xanthomonas campestris</i> significantly improved in a strong magnetic field. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 438-442.	0.7	5
80	XC5848, an ORF protein from <i>Xanthomonas campestris</i> , adopts a novel variant of Sm-like motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 1006-1010.	1.5	5
81	The crystal structure of XC1258 from <i>Xanthomonas campestris</i> : A putative prokaryotic Nit protein with an arsenic adduct in the active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 665-671.	1.5	12
82	A model for enediyne antibiotic transport/release. <i>FASEB Journal</i> , 2007, 21, A628.	0.2	0
83	Structure of XC6422 from <i>Xanthomonas campestris</i> at 1.6 Å resolution: a small serine β -hydrolase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 498-503.	0.7	3
84	Cloning, crystallization and preliminary X-ray study of XC1258, a CN-hydrolase superfamily protein from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 999-1002.	0.7	2
85	The crystal structure of XC1739: A putative multiple antibiotic-resistance repressor (MarR) from <i>Xanthomonas campestris</i> at 1.8 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 239-242.	1.5	11
86	Crystal structure of a putative acyl-CoA thioesterase from <i>Xanthomonas campestris</i> (XC229) adopts a tetrameric hotdog fold of β mode. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 823-826.	1.5	3
87	Crystal structure of the conserved hypothetical cytosolic protein Xcc0516 from <i>Xanthomonas campestris</i> reveals a novel quaternary structure assembled by five four-helix bundles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 783-786.	1.5	7
88	Crystal structure of XC5357 from <i>Xanthomonas campestris</i> : A putative tetracenomycin polyketide synthesis protein adopting a novel cupin subfamily structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 1046-1050.	1.5	4
89	The crystal structure of XC847 from <i>Xanthomonas campestris</i> : A β -oligoribonuclease of DnaQ fold family with a novel opposingly shifted helix. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 1036-1040.	1.5	22
90	A New Model for Ligand Release. <i>Journal of Biological Chemistry</i> , 2006, 281, 16025-16033.	1.6	11

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91	DNA aptamers as potential anti-HIV agents. <i>Trends in Biochemical Sciences</i> , 2005, 30, 231-234.	3.7	70
92	Letter to the Editor: NMR structure note ? Solution structure of a bacterial BolA-like protein XC975 from a plant pathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Journal of Biomolecular NMR</i> , 2005, 31, 167-172.	1.6	12
93	A putative polyketide-synthesis protein XC5357 from <i>Xanthomonas campestris</i> : heterologous expression, crystallization and preliminary X-ray analysis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 697-699.	0.7	2
94	Cloning, purification crystallization and preliminary X-ray characterization of a conserved hypothetical protein XC6422 from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 703-705.	0.7	1
95	Cloning, purification, crystallization and preliminary X-ray crystallographic analysis of XC847, a $3\text{â}\text{€}^2\text{-5\text{â}\text{€}^2$ oligoribonuclease from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 902-905.	0.7	19
96	Preparation of amino-acid-type selective isotope labeling of protein expressed in <i>Pichia pastoris</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 279-287.	1.5	34
97	Stable and Unique DNA Duplex Motifs. <i>Nucleic Acids Symposium Series</i> , 2005, 49, 11-12.	0.3	0
98	The nature of actinomycin D binding to d(AACCXYG) sequence motifs. <i>Nucleic Acids Research</i> , 2004, 32, 271-277.	6.5	48
99	Sheared-type Ganti A -Csyn Base-pair: A Unique d(GXC) Loop Closure Motif. <i>Journal of Molecular Biology</i> , 2003, 329, 351-361.	2.0	7
100	Binding of Actinomycin D to Single-Stranded DNA of Sequence Motifs d(TGTCTnG) and d(TGTnGTCT). <i>Biophysical Journal</i> , 2003, 84, 432-439.	0.2	20
101	Solution structure of the ActD-5'-CCGTT3GTGG-3' complex: drug interaction with tandem Gmiddle dotT mismatches and hairpin loop backbone. <i>Nucleic Acids Research</i> , 2003, 31, 2622-2629.	6.5	19
102	Unusual DNA duplex and hairpin motifs. <i>Nucleic Acids Research</i> , 2003, 31, 2461-2474.	6.5	87
103	Unique actinomycin D binding to self-complementary d(CXYGGCCY'X'G) sequences: duplex disruption and binding to a nominally base-paired hairpin. <i>Nucleic Acids Research</i> , 2003, 31, 4238-4246.	6.5	11
104	Looped out and perpendicular: Deformation of Watson-Crick base pair associated with actinomycin D binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6625-6630.	3.3	31
105	Zipper-like Watson-Crick base-pairs 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2001, 312, 753-768.	2.0	14
106	Solution structure of a DNA double helix incorporating four consecutive non-Watson-Crick base-pairs 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2001, 312, 769-781.	2.0	12
107	Quadruple intercalated G-6 stack: a possible motif in the fold-back structure of the <i>Drosophila</i> centromeric dodeca-satellite?. <i>Journal of Molecular Biology</i> , 2001, 314, 139-152.	2.0	15
108	The solution structure of [d(CGC)r(amamam)d(TTTGCC)] ₂ . <i>Journal of Biomolecular NMR</i> , 2001, 21, 209-220.	1.6	3

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109	Novel cross-strand three-purine stack of the highly conserved 5'-GA/AAG-5' internal loop at the 3'-end termini of Parvovirus genomes. <i>Journal of Biomolecular NMR</i> , 2001, 21, 307-319.	1.6	2
110	Enhanced loop DNA folding induced by thymine-CH ₃ group contact and perpendicular guanine-thymine interaction. <i>Journal of Biomolecular NMR</i> , 2001, 19, 33-48.	1.6	16
111	Natural abundance heteronuclear NMR studies of the T3 mini-loop hairpin in the terminal repeat of the adenoassociated virus 2. <i>Journal of Biomolecular NMR</i> , 2000, 17, 1-16.	1.6	15
112	NMR Studies of DNA Structures Containing Sheared Purine-Purine and Purine-Pyrimidine Base Pairs. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000, 17, 303-313.	2.0	4
113	Elucidation of the solution structure of cardiotoxin analogue V from the Taiwan cobra (<i>Naja naja</i>) Tj ETQq1. <i>Overexpression of cardiotoxins</i> . <i>Protein Science</i> , 2000, 9, 637-646.	3.1	41
114	Structural studies of symmetric DNA undecamers containing non-symmetrical sheared (PuGAPu):(PyGAPy) motifs. <i>Journal of Biomolecular NMR</i> , 1999, 14, 157-167.	1.6	14
115	Cross-strand purine-pyrimidine stack and sheared purine-pyrimidine pairing in the human HIV-1 reverse transcriptase inhibitors. Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1999, 285, 41-48.	2.0	28
116	Stable sheared A-C pair in DNA hairpins. Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1999, 287, 301-313.	2.0	25
117	Stable formation of a pyrimidine-rich loop hairpin in a cruciform promoter. Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1999, 292, 309-320.	2.0	21
118	Systematic NMR Assignments of DNA Exchangeable Protons. <i>Journal of the Chinese Chemical Society</i> , 1999, 46, 699-706.	0.8	11
119	Sheared purine-purine pairing in biology. <i>Journal of Molecular Biology</i> , 1997, 267, 1055-1067.	2.0	66
120	Centromeric pyrimidine strands fold into an intercalated motif by forming a double hairpin with a Novel T:G:G:T tetrad: solution structure of the d(TCCCGTTTCCA) dimer. Edited by I Tinoco. <i>Journal of Molecular Biology</i> , 1997, 273, 840-856.	2.0	74
121	On the Relative Ability of Centromeric GNA Triplets to Form Hairpins versus Self-paired Duplexes. <i>Journal of Molecular Biology</i> , 1996, 259, 445-457.	2.0	36
122	Hairpin Loops Consisting of Single Adenine Residues Closed by Sheared A-A and G-G Pairs Formed by the DNA Triplets AAA and GAG: Solution Structure of the d(GTACAAAGTAC) Hairpin. <i>Journal of Molecular Biology</i> , 1996, 264, 981-1001.	2.0	67
123	Structure of a single-cytidine hairpin loop formed by the DNA triplet GCA. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 1012-1017.	3.6	54
124	The Structure of a Novel DNA Duplex Formed by Human Centromere d(TGGAA) Repeats with Possible Implications for Chromosome Attachment during Mitosis. <i>Journal of Molecular Biology</i> , 1995, 254, 623-637.	2.0	33
125	DNA Sequence GCGAATGAGC Containing the Human Centromere Core Sequence GAAT Forms a Self-complementary Duplex with Sheared G-A Pairs in Solution. <i>Journal of Molecular Biology</i> , 1994, 241, 467-479.	2.0	41
126	The Unusual Structure of the Human Centromere (GGA) ₂ Motif. <i>Journal of Molecular Biology</i> , 1994, 244, 259-268.	2.0	58

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127	Base pairing geometry in GA mismatches depends entirely on the neighboring sequence. Journal of Molecular Biology, 1992, 228, 1037-1041.	2.0	89
128	Solution structure of [d(ATGAGCGAATA)] ₂ . Journal of Molecular Biology, 1992, 228, 138-155.	2.0	100
129	Assignment of the non-exchangeable proton resonances of d(C-G-C-G-A-A-T-T-C-G-C-G) using two-dimensional nuclear magnetic resonance methods. Journal of Molecular Biology, 1983, 171, 319-336.	2.0	617