

Shan-Ho Chou

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.

129
papers

3,002
citations

29
h-index

50
g-index

135
ext. papers

3,597
ext. citations

6.6
avg, IF

5.14
L-index

#	Paper	IF	Citations
129	The RNA Chaperone Protein Hfq Regulates the Characteristic Sporulation and Insecticidal Activity of .. <i>Frontiers in Microbiology</i> , 2022 , 13, 884528	5.7	
128	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	8.5	1
127	Bacterial quorum sensing quenching activity of leucyl aminopeptidase acts by interacting with autoinducer synthase.. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 6179-6190	6.8	0
126	Ways to control harmful biofilms: prevention, inhibition, and eradication. <i>Critical Reviews in Microbiology</i> , 2021 , 47, 57-78	7.8	9
125	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	5.7	7
124	Which Is Stronger? A Continuing Battle Between Cry Toxins and Insects. <i>Frontiers in Microbiology</i> , 2021 , 12, 665101	5.7	4
123	<i>Lysobacter enzymogenes</i> antagonizes soilborne bacteria using the type IV secretion system. <i>Environmental Microbiology</i> , 2021 , 23, 4673-4688	5.2	2
122	Antifungal weapons of <i>Lysobacter</i> , a mighty biocontrol agent. <i>Environmental Microbiology</i> , 2021 , 23, 5704-5715	5.2	4
121	A non-flagellated, predatory soil bacterium reprograms a chemosensory system to control antifungal antibiotic production via cyclic di-GMP signalling. <i>Environmental Microbiology</i> , 2021 , 23, 878-892	5.2	6
120	The Multiple Regulatory Relationship Between RNA-Chaperone Hfq and the Second Messenger c-di-GMP. <i>Frontiers in Microbiology</i> , 2021 , 12, 689619	5.7	1
119	Clp is a "busy" transcription factor in the bacterial warrior,. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3564-3572	6.8	2
118	Sequence conservation, domain architectures, and phylogenetic distribution of the HD-GYP type c-di-GMP phosphodiesterases.. <i>Journal of Bacteriology</i> , 2021 , jb0056121	3.5	2
117	6S-1 RNA Contributes to Sporulation and Parasporal Crystal Formation in. <i>Frontiers in Microbiology</i> , 2020 , 11, 604458	5.7	5
116	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	6.8	3
115	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,	5.9	5
114	A decade of research on the second messenger c-di-AMP. <i>FEMS Microbiology Reviews</i> , 2020 , 44, 701-724	15.1	32
113	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,	4.1	3

112	Cyclic di-GMP in Streptomyces: A New Conformation, New Binding Mode, New Receptor, and a New Mechanism to Control Cell Development. <i>Molecular Cell</i> , 2020 , 77, 443-445	17.6	3
111	Cyclic di-AMP, a second messenger of primary importance: tertiary structures and binding mechanisms. <i>Nucleic Acids Research</i> , 2020 , 48, 2807-2829	20.1	29
110	Knockout of Diguanylate Cyclase Genes in <i>Lysobacter enzymogenes</i> to Improve Production of Antifungal Factor and Increase Its Application in Seed Coating. <i>Current Microbiology</i> , 2020 , 77, 1006-1015	5.4	4
109	Cyclic di-GMP-Dependent Regulation of Antibiotic Biosynthesis in <i>Lysobacter</i> 2020 , 329-336		1
108	Noncanonical Cyclic di-GMP Binding Modes 2020 , 125-134		
107	Cyclic di-GMP Signaling in the Phytopathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> 2020 , 427-442		
106	A YajQ-LysR-like, cyclic 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	5.7	8
105	2-Methylcitrate cycle: a well-regulated controller of <i>Bacillus</i> sporulation. <i>Environmental Microbiology</i> , 2020 , 22, 1125-1140	5.2	6
104	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	7.6	10
103	ClpP mediates antagonistic interaction of <i>Lysobacter enzymogenes</i> with a crop fungal pathogen. <i>Biological Control</i> , 2020 , 140, 104125	3.8	4
102	Structural Conservation and Diversity of PilZ-Related Domains. <i>Journal of Bacteriology</i> , 2020 , 202,	3.5	11
101	A c-di-AMP riboswitch controlling operon transcription regulates the potassium transporter system in. <i>Communications Biology</i> , 2019 , 2, 151	6.7	17
100	Spermidine plays a significant role in stabilizing a master transcription factor Clp to promote antifungal activity in <i>Lysobacter enzymogenes</i> . <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 1811-1822	5.7	3
99	Insights into the distinct cooperation between the transcription factor Clp and Le DSF signaling in the regulation of antifungal factors in <i>Lysobacter enzymogenes</i> OH11. <i>Biological Control</i> , 2018 , 120, 52-58	3.8	5
98	Sigma factor RpoN employs a dual transcriptional regulation for controlling twitching motility and biofilm formation in <i>Lysobacter enzymogenes</i> OH11. <i>Current Genetics</i> , 2018 , 64, 515-527	2.9	3
97	c-di-GMP Regulates Various Phenotypes and Insecticidal Activity of Gram-Positive. <i>Frontiers in Microbiology</i> , 2018 , 9, 45	5.7	24
96	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	4.7	
95	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	20.1	29

94	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	5.7	10
93	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	11.5	18
92	Regulation of Inducible Potassium Transporter KdpFABC by the KdpD/KdpE Two-Component System in. <i>Frontiers in Microbiology</i> , 2017 , 8, 570	5.7	25
91	Transcriptome Landscape of. <i>Frontiers in Microbiology</i> , 2017 , 8, 2505	5.7	26
90	Nucleotide binding by the widespread high-affinity cyclic di-GMP receptor MshEN domain. <i>Nature Communications</i> , 2016 , 7, 12481	17.4	83
89	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	4.9	47
88	Diversity of Cyclic Di-GMP-Binding Proteins and Mechanisms. <i>Journal of Bacteriology</i> , 2016 , 198, 32-46	3.5	159
87	A TonB-dependent receptor regulates antifungal HSAF biosynthesis in <i>Lysobacter</i> . <i>Scientific Reports</i> , 2016 , 6, 26881	4.9	14
86	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	4.9	17
85	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	4.9	25
84	Direct Regulation of Extracellular Chitinase Production by the Transcription Factor LeClp in <i>Lysobacter</i> enzymogenes OH11. <i>Phytopathology</i> , 2016 , 106, 971-7	3.8	15
83	Functional and genomic insights into the pathogenesis of <i>Burkholderia</i> species to rice. <i>Environmental Microbiology</i> , 2016 , 18, 780-90	5.2	18
82	Backbone resonance assignments of the 54kDa dimeric C-terminal domain of murine STING in complex with DMXAA. <i>Biomolecular NMR Assignments</i> , 2015 , 9, 271-4	0.7	3
81	Structural Insights into the Distinct Binding Mode of Cyclic Di-AMP with SaCpaA_RCK. <i>Biochemistry</i> , 2015 , 54, 4936-51	3.2	36
80	Complete Genome Sequence of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strain 17 from Taiwan. <i>Genome Announcements</i> , 2015 , 3,		15
79	Structure and dynamics of polymyxin-resistance-associated response regulator PmrA in complex with promoter DNA. <i>Nature Communications</i> , 2015 , 6, 8838	17.4	27
78	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, 4080-93	20.1	14
77	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, 171263		1

76	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, 326-30	1.1	4
75	A cyclic GMP-dependent signalling pathway regulates bacterial phytopathogenesis. <i>EMBO Journal</i> , 2013 , 32, 2430-8	13	40
74	A cyclic GMP-dependent signalling pathway regulates bacterial phytopathogenesis. <i>EMBO Journal</i> , 2013 , 32, 2779-2781	13	1
73	Novel c-di-GMP recognition modes of the mouse innate immune adaptor protein STING. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 352-66		29
72	Novel c-di-GMP recognition modes of the mouse innate immune adaptor protein STING. Corrigendum. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 1191-1191		
71	Crystallization and preliminary X-ray diffraction characterization of the XccFimX(EAL)-c-di-GMP and XccFimX(EAL)-c-di-GMP-XccPilZ complexes from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 301-5		5
70	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, 1380-92		35
69	Crystallization studies of the murine c-di-GMP sensor protein STING. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 906-10		9
68	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, 1247-50		2
67	Functional divergence of FimX in PilZ binding and type IV pilus regulation. <i>Journal of Bacteriology</i> , 2012 , 194, 5922-31	3.5	20
66	A novel tetrameric PilZ domain structure from xanthomonads. <i>PLoS ONE</i> , 2011 , 6, e22036	3.7	18
65	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		45
64	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, 152-7	4.7	2
63	Lipid bilayer-assisted release of an enediyne antibiotic from neocarzinostatin chromoprotein. <i>Biochemistry</i> , 2010 , 49, 7722-32	3.2	1
62	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, 646-62	6.5	150
61	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, 636-42		24
60	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, 282-8	4.2	32
59	<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, 1042-8	4.2	30

58	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, 1056-9		4
57	Unique GTP-binding pocket and allostery of uridylate kinase from a gram-negative phytopathogenic bacterium. <i>Journal of Molecular Biology</i> , 2009 , 385, 1113-26	6.5	8
56	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, 951-66	6.5	26
55	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, 189-99	6.5	11
54	The first crystal structure of gluconolactonase important in the glucose secondary metabolic pathways. <i>Journal of Molecular Biology</i> , 2008 , 384, 604-14	6.5	25
53	Crystal structure of DFA0005 complexed with alpha-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, 362-71	4.2	
52	The crystallization of apo-form UMP kinase from <i>Xanthomonas campestris</i> is significantly improved in a strong magnetic field. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 438-42		3
51	XC5848, an ORFan protein from <i>Xanthomonas campestris</i> , adopts a novel variant of Sm-like motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 1006-10	4.2	3
50	The crystal structure of XC1258 from <i>Xanthomonas campestris</i> : a putative procaryotic Nit protein with an arsenic adduct in the active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 665-71	4.2	11
49	A model for enediyne antibiotic transport/release. <i>FASEB Journal</i> , 2007 , 21, A628	0.9	
48	A new model for ligand release. Role of side chain in gating the enediyne antibiotic. <i>Journal of Biological Chemistry</i> , 2006 , 281, 16025-33	5.4	11
47	Structure of XC6422 from <i>Xanthomonas campestris</i> at 1.6 Å resolution: a small serine alpha/beta-hydrolase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 498-503		3
46	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		1
45	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, 239-42	4.2	10
44	Crystal structure of a putative acyl-CoA thioesterase from <i>Xanthomonas campestris</i> (XC229) adopts a tetrameric hotdog fold of epsilon-gamma mode. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 823-6	4.2	2
43	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, 783-6	4.2	7
42	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, 1046-50	4.2	3
41	The crystal structure of XC847 from <i>Xanthomonas campestris</i> : a 3R5R oligoribonuclease of DnaQ fold family with a novel opposingly shifted helix. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 1036-40	4.2	18

40	Preparation of amino-acid-type selective isotope labeling of protein expressed in <i>Pichia pastoris</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 279-87	4.2	33
39	DNA aptamers as potential anti-HIV agents. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 231-4	10.3	63
38	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, 167-72	3	10
37	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, 697-9		2
36	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, 703-5		1
35	Cloning, purification, crystallization and preliminary X-ray crystallographic analysis of XC847, a 3R5R oligoribonuclease from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 902-5		19
34	Stable and unique DNA duplex motifs. <i>Nucleic Acids Symposium Series</i> , 2005 , 11-2		
33	The nature of actinomycin D binding to d(AACCAXYG) sequence motifs. <i>Nucleic Acids Research</i> , 2004 , 32, 271-7	20.1	19
32	Sheared-type G(anti).C(syn) base-pair: a unique d(GXC) loop closure motif. <i>Journal of Molecular Biology</i> , 2003 , 329, 351-61	6.5	6
31	Binding of actinomycin D to single-stranded DNA of sequence motifs d(TGTCT(n)G) and d(TGT(n)GTCT). <i>Biophysical Journal</i> , 2003 , 84, 432-9	2.9	17
30	Solution structure of the ActD-5RCCGTT3GTGG-3R complex: drug interaction with tandem G.T mismatches and hairpin loop backbone. <i>Nucleic Acids Research</i> , 2003 , 31, 2622-9	20.1	16
29	Unusual DNA duplex and hairpin motifs. <i>Nucleic Acids Research</i> , 2003 , 31, 2461-74	20.1	71
28	Unique actinomycin D binding to self-complementary d(CXYGGCCYXR R) sequences: duplex disruption and binding to a nominally base-paired hairpin. <i>Nucleic Acids Research</i> , 2003 , 31, 4238-46	20.1	11
27	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, 6625-30	11.5	27
26	The solution structure of [d(CGC)r(amamam)d(TTTGCG)] ₂ . <i>Journal of Biomolecular NMR</i> , 2001 , 21, 209-20		3
25	Novel cross-strand three-purine stack of the highly conserved 5RGA/AAG-5R internal loop at the 3R end termini of Parvovirus genomes. <i>Journal of Biomolecular NMR</i> , 2001 , 21, 307-19	3	2
24	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	3	14
23	Zipper-like Watson-Crick base-pairs. <i>Journal of Molecular Biology</i> , 2001 , 312, 753-68	6.5	14

22	Solution structure of a DNA double helix incorporating four consecutive non-Watson-Crick base-pairs. <i>Journal of Molecular Biology</i> , 2001 , 312, 769-81	6.5	12
21	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, 139-52	6.5	15
20	Elucidation of the solution structure of cardiotoxin analogue V from the Taiwan cobra (<i>Naja naja atra</i>)--identification of structural features important for the lethal action of snake venom cardiotoxins. <i>Protein Science</i> , 2000 , 9, 637-46	6.3	36
19	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	3	13
18	NMR studies of DNA structures containing sheared purine-purine and purine-pyrimidine base pairs. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000 , 17 Suppl 1, 303-13	3.6	4
17	Structural studies of symmetric DNA undecamers containing non-symmetrical sheared (PuGAPu):(PyGAPy) motifs. <i>Journal of Biomolecular NMR</i> , 1999 , 14, 157-67	3	13
16	Cross-strand purine-pyrimidine stack and sheared purine-pyrimidine pairing in the human HIV-1 reverse transcriptase inhibitors. <i>Journal of Molecular Biology</i> , 1999 , 285, 41-8	6.5	27
15	Stable sheared A.C pair in DNA hairpins. <i>Journal of Molecular Biology</i> , 1999 , 287, 301-13	6.5	25
14	Stable formation of a pyrimidine-rich loop hairpin in a cruciform promoter. <i>Journal of Molecular Biology</i> , 1999 , 292, 309-20	6.5	21
13	Systematic NMR Assignments of DNA Exchangeable Protons. <i>Journal of the Chinese Chemical Society</i> , 1999 , 46, 699-706	1.5	10
12	Sheared purine x purine pairing in biology. <i>Journal of Molecular Biology</i> , 1997 , 267, 1055-67	6.5	64
11	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. <i>Journal of Molecular Biology</i> , 1997 , 273, 840-56	6.5	59
10	On the relative ability of centromeric GNA triplets to form hairpins versus self-paired duplexes. <i>Journal of Molecular Biology</i> , 1996 , 259, 445-57	6.5	34
9	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	6.5	66
8	Structure of a single-cytidine hairpin loop formed by the DNA triplet GCA. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 1012-7	17.6	53
7	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, 623-37	6.5	32
6	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, 467-79	6.5	36
5	The unusual structure of the human centromere (GGA) ₂ motif. Unpaired guanosine residues stacked between sheared G.A pairs. <i>Journal of Molecular Biology</i> , 1994 , 244, 259-68	6.5	53

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|---|--|-----|-----|
| 4 | Base pairing geometry in GA mismatches depends entirely on the neighboring sequence. <i>Journal of Molecular Biology</i> , 1992 , 228, 1037-41 | 6.5 | 78 |
| 3 | Solution structure of [d(ATGAGCGAATA)] ₂ . Adjacent G:A mismatches stabilized by cross-strand base-stacking and BII phosphate groups. <i>Journal of Molecular Biology</i> , 1992 , 228, 138-55 | 6.5 | 92 |
| 2 | 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. <i>Journal of Molecular Biology</i> , 1983 , 171, 319-36 | 6.5 | 540 |
| 1 | Mycobacterial CarD defines a novel mechanism of response to starvation stress | | 1 |