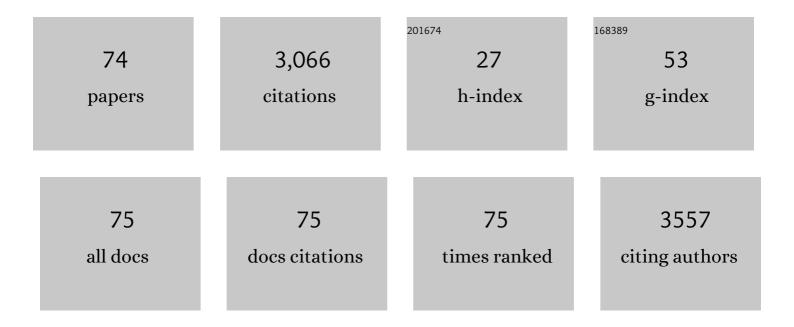
List of Publications by Year in descending order

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MANUL RANSAL

#	Article	IF	CITATIONS
1	RNA-mediated translation regulation in viral genomes: computational advances in the recognition of sequences and structures. Briefings in Bioinformatics, 2020, 21, 1151-1163.	6.5	5
2	Biomolecular Structures: Prediction, Identification and Analyses. , 2019, , 504-534.		2
3	Variation of gene expression in plants is influenced by gene architecture and structural properties of promoters. PLoS ONE, 2019, 14, e0212678.	2.5	29
4	Identification of putative promoters in 48 eukaryotic genomes on the basis of DNA free energy. Scientific Reports, 2018, 8, 4520.	3.3	35
5	Modulation of Gene Expression by Gene Architecture and Promoter Structure. , 2018, , .		1
6	Flexibility and structure of flanking DNA impact transcription factor affinity for its core motif. Nucleic Acids Research, 2018, 46, 11883-11897.	14.5	62
7	Toward a Universal Structural and Energetic Model for Prokaryotic Promoters. Biophysical Journal, 2018, 115, 1180-1189.	0.5	7
8	Dynamics of physiologically relevant noncanonical DNA structures: an overview from experimental and theoretical studies. Briefings in Functional Genomics, 2018, 18, 192-204.	2.7	2
9	Unveiling DNA structural features of promoters associated with various types of TSSs in prokaryotic transcriptomes and their role in gene expression. DNA Research, 2017, 24, dsw045.	3.4	16
10	RNAHelix: computational modeling of nucleic acid structures with Watson–Crick and non-canonical base pairs. Journal of Computer-Aided Molecular Design, 2017, 31, 219-235.	2.9	8
11	<scp>DNA</scp> structural features of eukaryotic <scp>TATA</scp> â€containing and <scp>TATA</scp> â€less promoters. FEBS Open Bio, 2017, 7, 324-334.	2.3	48
12	New insight into the architecture of oxyâ€anion pocket in unliganded conformation of <scp>GAT</scp> domains: A <scp>MD</scp> â€simulation study. Proteins: Structure, Function and Bioinformatics, 2016, 84, 360-373.	2.6	2
13	Data on diverse roles of helix perturbations in membrane proteins. Data in Brief, 2016, 9, 781-802.	1.0	2
14	Insights into the Structural Dynamics of Nucleocytoplasmic Transport of tRNA by Exportin-t. Biophysical Journal, 2016, 110, 1264-1279.	0.5	5
15	The role of sequence in altering the unfolding pathway of an RNA pseudoknot: a steered molecular dynamics study. Physical Chemistry Chemical Physics, 2016, 18, 28767-28780.	2.8	7
16	Genome-Wide Targets Regulated by the OsMADS1 Transcription Factor Reveals Its DNA Recognition Properties. Plant Physiology, 2016, 172, 372-388.	4.8	25
17	Helix perturbations in membrane proteins assist in inter-helical interactions and optimal helix positioning in the bilayer. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 2804-2817.	2.6	9
18	Structural features of DNA are conserved in the promoter region of orthologous genes across different strains of <i>Helicobacter pylori</i> . FEMS Microbiology Letters, 2016, 363, fnw207.	1.8	9

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19	Structural and functional analyses of PolyProline-II helices in globular proteins. Journal of Structural Biology, 2016, 196, 414-425.	2.8	21
20	Dissecting Ï€â€helices: sequence, structure and function. FEBS Journal, 2015, 282, 4415-4432.	4.7	32
21	DNA Structure and Promoter Engineering. , 2015, , 241-254.		10
22	Identification of local variations within secondary structures of proteins. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1077-1086.	2.5	22
23	Stacking interactions in RNA and DNA: Rollâ€slide energy hyperspace for ten unique dinucleotide steps. Biopolymers, 2015, 103, 134-147.	2.4	14
24	<i>MolBridge</i> : a program for identifying nonbonded interactions in small molecules and biomolecular structures. Journal of Applied Crystallography, 2014, 47, 1772-1776.	4.5	16
25	Role of DNA sequence based structural features of promoters in transcription initiation and gene expression. Current Opinion in Structural Biology, 2014, 25, 77-85.	5.7	81
26	Sequence dependent variations in RNA duplex are related to non-canonical hydrogen bond interactions in dinucleotide steps. BMC Research Notes, 2014, 7, 83.	1.4	12
27	Editorial overview: Theory and simulation: Tools for solving the insolvable. Current Opinion in Structural Biology, 2014, 25, iv-v.	5.7	9
28	Sequence and conformational preferences at termini of αâ€helices in membrane proteins: Role of the helix environment. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3420-3436.	2.6	5
29	Local Structural and Environmental Factors Define the Efficiency of an RNA Pseudoknot Involved in Programmed Ribosomal Frameshift Process. Journal of Physical Chemistry B, 2014, 118, 11905-11920.	2.6	9
30	DNA STRUCTURAL FEATURES AND ARCHITECTURE OF PROMOTER REGIONS PLAY A ROLE IN GENE RESPONSIVENESS OF <i>S. cerevisiae</i> . Journal of Bioinformatics and Computational Biology, 2013, 11, 1343001.	0.8	13
31	HELANAL-Plus: a web server for analysis of helix geometry in protein structures. Journal of Biomolecular Structure and Dynamics, 2012, 30, 773-783.	3.5	62
32	Characterization of structural and free energy properties of promoters associated with Primary and Operon TSS in Helicobacter pylori genome and their orthologs. Journal of Biosciences, 2012, 37, 423-431.	1.1	11
33	Nucleic acids in disease and disorder: Understanding the language of life emerging from the â€~ABC' of DNA. Journal of Biosciences, 2012, 37, 375-378.	1.1	0
34	Intrinsic structural variability of DNA allows multiple genomic encoding for nucleosomesComment on "Cracking the chromatin code: Precise rule of nucleosome positioning―by E.N. Trifonov. Physics of Life Reviews, 2011, 8, 67-68.	2.8	0
35	An ensemble of B-DNA dinucleotide geometries lead to characteristic nucleosomal DNA structure and provide plasticity required for gene expression. BMC Structural Biology, 2011, 11, 1.	2.3	44
36	PromBase: a web resource for various genomic features and predicted promoters in prokaryotic genomes. BMC Research Notes, 2011, 4, 257.	1.4	27

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37	DNA Free Energy-Based Promoter Prediction and Comparative Analysis of Arabidopsis and Rice Genomes Â. Plant Physiology, 2011, 156, 1300-1315.	4.8	43
38	High-quality annotation of promoter regions for 913 bacterial genomes. Bioinformatics, 2010, 26, 3043-3050.	4.1	45
39	Small local variations in B-form DNA lead to a large variety of global geometries which can accommodate most DNA-binding protein motifs. BMC Structural Biology, 2009, 9, 24.	2.3	28
40	Relative stability of DNA as a generic criterion for promoter prediction: whole genome annotation of microbial genomes with varying nucleotide base composition. Molecular BioSystems, 2009, 5, 1758.	2.9	37
41	Identification and annotation of promoter regions in microbial genome sequences on the basis of DNA stability. Journal of Biosciences, 2007, 32, 851-862.	1.1	31
42	Conformational specificity of non-canonical base pairs and higher order structures in nucleic acids: crystal structure database analysis. Journal of Computer-Aided Molecular Design, 2006, 20, 629-645.	2.9	54
43	Collagen Structure: The Madras Triple Helix and the Current Scenario. IUBMB Life, 2005, 57, 161-172.	3.4	160
44	A novel method for prokaryotic promoter prediction based on DNA stability. BMC Bioinformatics, 2005, 6, 1.	2.6	462
45	Structural properties of promoters: similarities and differences between prokaryotes and eukaryotes. Nucleic Acids Research, 2005, 33, 3165-3175.	14.5	117
46	Structural Insights into the Effect of Hydration and Ions on A-Tract DNA: A Molecular Dynamics Study. Biophysical Journal, 2003, 85, 1805-1816.	0.5	42
47	An assessment of three dinucleotide parameters to predict DNA curvature by quantitative comparison with experimental data. Nucleic Acids Research, 2003, 31, 2647-2658.	14.5	22
48	A Nanosecond Molecular Dynamics Study of Antiparallel d(G) <sub>7</sub> Quadruplex Structures: Effect of the Coordinated Cations. Journal of Biomolecular Structure and Dynamics, 2001, 18, 647-669.	3.5	14
49	G-Quadruplex Structure Can Be Stable with Only Some Coordination Sites Being Occupied by Cations:Â A Six-Nanosecond Molecular Dynamics Study. Journal of Physical Chemistry B, 2001, 105, 7572-7578.	2.6	52
50	A standard reference frame for the description of nucleic acid base-pair geometry 1 1Edited by P. E. Wright 2 2This is a document of the Nomenclature Committee of IUBMB (NC-IUBMB)/IUPAC-IUBMB Joint Commission on Biochemical Nomenclature (JCBN), whose members are R. Cammack (chairman), A. Bairoch, H.M. Berman, S. Boyce, C.R. Cantor, K. Elliott, D. Horton, M. Kanehisa, A. Kotyk, G.P. Moss, N. Sharon and K.F. Tipton Journal of Molecular Biology, 2001, 313, 229-237.	4.2	533
51	Modelling studies on neurodegenerative disease-causing triplet repeat sequences d(GGC/GCC)n and d(CAG/CTG)n. Journal of Biosciences, 2001, 26, 649-665.	1.1	7
52	The Madras triple helix: Origins and current status. Resonance, 2001, 6, 38-47.	0.3	2
53	HELANAL: A Program to Characterize Helix Geometry in Proteins. Journal of Biomolecular Structure and Dynamics, 2000, 17, 811-819.	3.5	157
54	Effect of Coordinated Ions on Structure and Flexibility of Parallel G-quadruplexes: A Molecular Dynamics Study. Journal of Biomolecular Structure and Dynamics, 2000, 17, 11-28.	3.5	16

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55	Symposia lectures. Journal of Biosciences, 1999, 24, 5-31.	1.1	Ο
56	Contributory presentations/posters. Journal of Biosciences, 1999, 24, 33-198.	1.1	0
57	C-HO hydrogen bonds in minor groove of A-tracts in DNA double helices. Journal of Molecular Biology, 1999, 294, 1149-1158.	4.2	72
58	Dissecting α-helices: Position-specific analysis of α-helices in globular proteins. Proteins: Structure, Function and Bioinformatics, 1998, 31, 460-476.	2.6	126
59	Molecular Dynamics Simulations on Parallel and Antiparallel C.G*G Triplexes. Journal of Biomolecular Structure and Dynamics, 1998, 16, 511-526.	3.5	1
60	Geometrical and Sequence Characteristics of α-Helices in Globular Proteins. Biophysical Journal, 1998, 75, 1935-1944.	0.5	102
61	Sequence-Independent Recombination Triple Helices: A Molecular Dynamics Study. Journal of Biomolecular Structure and Dynamics, 1997, 15, 333-345.	3.5	8
62	Structural Polymorphism in d(T) <sub>12</sub> .d(A) <sub>12</sub> *d(T) <sub>12</sub> Triple Helices. Journal of Biomolecular Structure and Dynamics, 1995, 13, 493-505.	3.5	14
63	Molecular Modeling Studies on Amphotericin B and its Complex with Phospholipid. Journal of Biomolecular Structure and Dynamics, 1995, 12, 957-970.	3.5	17
64	Conformational polymorphism in telomeric structures: Loop orientation and interloop pairing in d(G4TnG4). Biopolymers, 1994, 34, 1187-1211.	2.4	23
65	Conformational polymorphism in G-tetraplex structures: strand reversal by base flipover or sugar flipover. Nucleic Acids Research, 1993, 21, 1767-1774.	14.5	35
66	Groove Width and Depth of B-DNA Structures Depend on Local Variation in Slide. Journal of Biomolecular Structure and Dynamics, 1992, 10, 213-226.	3.5	39
67	DNA Polymorphism and Local Variation in Base-Pair Orientation: A Theoretical Rationale. Journal of Biomolecular Structure and Dynamics, 1991, 9, 127-142.	3.5	12
68	Local Variability and Base Sequence Effects in DNA Crystal Structures. Journal of Biomolecular Structure and Dynamics, 1990, 8, 539-572.	3.5	55
69	A Self-Consistent Formulation for Analysis and Generation of Non-Uniform DNA Structures. Journal of Biomolecular Structure and Dynamics, 1989, 6, 635-653.	3.5	45
70	Molecular mechanics studies on poly(purine) · poly(pyrimidine) sequences in DNA: Polymorphism and local variability. Biopolymers, 1989, 28, 531-548.	2.4	4
71	Energetics of Left and Right Handed Models of DNA. Journal of Biomolecular Structure and Dynamics, 1987, 4, 1027-1040.	3.5	2
72	Sequence-dependent molecular conformation of polynucleotides: right and left-handed helices. International Journal of Biological Macromolecules, 1981, 3, 2-8.	7.5	14

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73	Structure factor calculations of various DNA duplexes. International Journal of Quantum Chemistry, 1981, 20, 407-417.	2.0	6
74	ROLE OF NONâ€PLANAR PEPTIDE UNIT IN REGULAR POLYPEPTIDE HELICES:. International Journal of Peptide and Protein Research, 1981, 18, 374-382.	0.1	7