

# Anne Grove

## List of Publications by Year in descending order

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100  
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2,922  
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172457

29  
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206112

48  
g-index

103  
all docs

103  
docs citations

103  
times ranked

2755  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ligand-responsive transcriptional regulation by members of the MarR family of winged helix proteins. <i>Current Issues in Molecular Biology</i> , 2006, 8, 51-62.	2.4	211
2	Molecular Mechanisms of Ligand-Mediated Attenuation of DNA Binding by MarR Family Transcriptional Regulators. <i>Journal of Molecular Cell Biology</i> , 2010, 2, 243-254.	3.3	163
3	MarR family transcription factors. <i>Current Biology</i> , 2013, 23, R142-R143.	3.9	127
4	MarR family transcription factors: dynamic variations on a common scaffold. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017, 52, 595-613.	5.2	123
5	Template-assembled synthetic proteins designed to adopt a globular, four-helix bundle conformation form ionic channels in lipid bilayers. <i>Journal of the American Chemical Society</i> , 1993, 115, 5919-5924.	13.7	102
6	HucR, a Novel Uric Acid-responsive Member of the MarR Family of Transcriptional Regulators from <i>Deinococcus radiodurans</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 51442-51450.	3.4	101
7	Localized DNA Flexibility Contributes to Target Site Selection by DNA-bending Proteins. <i>Journal of Molecular Biology</i> , 1996, 260, 120-125.	4.2	95
8	Functional evolution of bacterial histone-like HU proteins. <i>Current Issues in Molecular Biology</i> , 2011, 13, 1-12.	2.4	80
9	A molecular blueprint for the pore-forming structure of voltage-gated calcium channels.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 6418-6422.	7.1	73
10	Coordination of Ribosomal Protein and Ribosomal RNA Gene Expression in Response to TOR Signaling. <i>Current Genomics</i> , 2009, 10, 198-205.	1.6	65
11	Differential DNA Binding and Protection by Dimeric and Dodecameric forms of the Ferritin Homolog Dps from <i>Deinococcus radiodurans</i> . <i>Journal of Molecular Biology</i> , 2005, 347, 495-508.	4.2	64
12	Regulation of Metabolic Pathways by MarR Family Transcription Factors. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 366-371.	4.1	61
13	The <i>Saccharomyces cerevisiae</i> High Mobility Group Box Protein HMO1 Contains Two Functional DNA Binding Domains. <i>Journal of Biological Chemistry</i> , 2004, 279, 55234-55240.	3.4	54
14	Affinity, stability and polarity of binding of the TATA binding protein governed by flexure at the TATA box 1 1Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 282, 731-739.	4.2	51
15	The Crystal Structure of the Transcriptional Regulator HucR from <i>Deinococcus radiodurans</i> Reveals a Repressor Preconfigured for DNA Binding. <i>Journal of Molecular Biology</i> , 2006, 360, 168-177.	4.2	50
16	Crystal Structure of Dps-1, a Functionally Distinct Dps Protein from <i>Deinococcus radiodurans</i> . <i>Journal of Molecular Biology</i> , 2006, 361, 105-114.	4.2	43
17	Negative Cooperativity of Uric Acid Binding to the Transcriptional Regulator HucR from <i>Deinococcus radiodurans</i> . <i>Journal of Molecular Biology</i> , 2005, 350, 617-630.	4.2	42
18	Histone-like Protein HU from <i>Deinococcus radiodurans</i> Binds Preferentially to Four-way DNA Junctions. <i>Journal of Molecular Biology</i> , 2004, 337, 561-571.	4.2	38

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19	DNA protection by histone-like protein HU from the hyperthermophilic eubacterium <i>Thermotoga maritima</i> . <i>Nucleic Acids Research</i> , 2008, 36, 3956-3968.	14.5	38
20	Substrate specificity of <i>Helicobacter pylori</i> histone-like HU protein is determined by insufficient stabilization of DNA flexure points. <i>Biochemical Journal</i> , 2004, 383, 343-351.	3.7	37
21	A tale of two functions: enzymatic activity and translational repression by carboxyltransferase. <i>Nucleic Acids Research</i> , 2010, 38, 1217-1227.	14.5	37
22	On the Connection Between Inherent DNA Flexure and Preferred Binding of Hydroxymethyluracil-containing DNA by the Type II DNA-binding Protein TF1. <i>Journal of Molecular Biology</i> , 1996, 260, 196-206.	4.2	36
23	Global Awakening of Cryptic Biosynthetic Gene Clusters in <i>Burkholderia thailandensis</i> . <i>ACS Chemical Biology</i> , 2017, 12, 3012-3021.	3.4	35
24	Yeast HMO1: Linker Histone Reinvented. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	6.6	34
25	High-affinity DNA binding of HU protein from the hyperthermophile <i>Thermotoga maritima</i> 1 Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 2001, 311, 491-502.	4.2	33
26	The Role of Surface-Exposed Lysines in Wrapping DNA about the Bacterial Histone-Like Protein HU. <i>Biochemistry</i> , 2002, 41, 7597-7603.	2.5	33
27	The N-terminal Extensions of <i>Deinococcus radiodurans</i> Dps-1 Mediate DNA Major Groove Interactions as well as Assembly of the Dodecamer. <i>Journal of Biological Chemistry</i> , 2007, 282, 11921-11930.	3.4	32
28	Ligand-Binding Pocket Bridges DNA-Binding and Dimerization Domains of the Urate-Responsive MarR Homologue MftR from <i>Burkholderia thailandensis</i> . <i>Biochemistry</i> , 2014, 53, 4368-4380.	2.5	32
29	MarR Family Transcription Factors from <i>Burkholderia</i> Species: Hidden Clues to Control of Virulence-Associated Genes. <i>Microbiology and Molecular Biology Reviews</i> , 2019, 83, .	6.6	32
30	[34] Synthetic peptides and proteins as models for pore-forming structure of channel proteins. <i>Methods in Enzymology</i> , 1992, 207, 510-525.	1.0	31
31	Mechanism for Attenuation of DNA Binding by MarR Family Transcriptional Regulators by Small Molecule Ligands. <i>Journal of Molecular Biology</i> , 2009, 390, 1019-1029.	4.2	31
32	The RNA polymerase III-recruiting factor TFIIIB induces a DNA bend between the TATA box and the transcriptional start site 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 285, 1429-1440.	4.2	30
33	Interactions between N- and C-Terminal Domains of the <i>Saccharomyces cerevisiae</i> High-Mobility Group Protein HMO1 Are Required for DNA Bending. <i>Biochemistry</i> , 2006, 45, 3635-3645.	2.5	30
34	Urate Is a Ligand for the Transcriptional Regulator PecS. <i>Journal of Molecular Biology</i> , 2010, 402, 539-551.	4.2	30
35	Structure of the <i>Bacillus subtilis</i> Phage SPO1-Encoded Type II DNA-binding Protein TF1 in Solution. <i>Journal of Molecular Biology</i> , 1996, 263, 259-268.	4.2	28
36	The C-Terminal Domain of HU-Related Histone-like Protein Hlp from <i>Mycobacterium smegmatis</i> Mediates DNA End-Joining. <i>Biochemistry</i> , 2008, 47, 8744-8753.	2.5	28

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37	Chemical synthesis and characterization of peptides and oligomeric proteins designed to form transmembrane ion channels. <i>International Journal of Peptide and Protein Research</i> , 1994, 43, 597-607.	0.1	28
38	Design of a functional calcium channel protein: Inferences about an ion channel-forming motif derived from the primary structure of voltage-gated calcium channels. <i>Protein Science</i> , 1993, 2, 1918-1930.	7.6	27
39	Functional comparison of <i>Deinococcus radiodurans</i> Dps proteins suggests distinct <i>in vivo</i> roles. <i>Biochemical Journal</i> , 2012, 447, 381-391.	3.7	26
40	C-terminal low-complexity sequence repeats of <i>Mycobacterium smegmatis</i> Ku modulate DNA binding. <i>Bioscience Reports</i> , 2013, 33, 175-84.	2.4	26
41	The transcriptional regulator <i>TamR</i> from <i>Streptomyces coelicolor</i> controls a key step in central metabolism during oxidative stress. <i>Molecular Microbiology</i> , 2013, 87, 1151-1166.	2.5	26
42	Surface salt bridges modulate the DNA site size of bacterial histone-like HU proteins. <i>Biochemical Journal</i> , 2005, 390, 49-55.	3.7	25
43	The C-Terminal Domain of Yeast High Mobility Group Protein HMO1 Mediates Lateral Protein Accretion and In-Phase DNA Bending. <i>Biochemistry</i> , 2010, 49, 4051-4059.	2.5	25
44	<i>Mycobacterium smegmatis</i> histone-like protein Hlp is nucleoid associated. <i>FEMS Microbiology Letters</i> , 2009, 291, 232-240.	1.8	24
45	Expression of yeast high mobility group protein HMO1 is regulated by TOR signaling. <i>Gene</i> , 2011, 489, 55-62.	2.2	24
46	MarR homologs with urate-binding signature. <i>Protein Science</i> , 2011, 20, 621-629.	7.6	24
47	Transcription Factor IIIB: The Architecture of Its DNA Complex, and Its Roles in Initiation of Transcription by RNA Polymerase III. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1998, 63, 121-131.	1.1	24
48	Yeast high mobility group protein HMO1 stabilizes chromatin and is evicted during repair of DNA double strand breaks. <i>Nucleic Acids Research</i> , 2015, 43, 5759-5770.	14.5	23
49	The <i>Deinococcus radiodurans</i> -Encoded HU Protein Has Two DNA-Binding Domains. <i>Biochemistry</i> , 2006, 45, 1723-1733.	2.5	22
50	The high mobility group protein HMO1 functions as a linker histone in yeast. <i>Epigenetics and Chromatin</i> , 2016, 9, 13.	3.9	22
51	The Link between Purine Metabolism and Production of Antibiotics in <i>Streptomyces</i> . <i>Antibiotics</i> , 2019, 8, 76.	3.7	22
52	Twin Hydroxymethyluracil-A Base Pair Steps Define the Binding Site for the DNA-bending Protein TF1. <i>Journal of Biological Chemistry</i> , 1997, 272, 13084-13087.	3.4	21
53	Urate-responsive MarR homologs from <i>Burkholderia</i> . <i>Molecular BioSystems</i> , 2010, 6, 2133.	2.9	19
54	Thermodynamics of the DNA Structural Selectivity of the Pol I DNA Polymerases from <i>Escherichia coli</i> and <i>Thermus aquaticus</i> . <i>Biophysical Journal</i> , 2010, 98, 3015-3024.	0.5	18

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55	Metal Binding at the <i>Deinococcus radiodurans</i> Dps-1 N-Terminal Metal Site Controls Dodecameric Assembly and DNA Binding. <i>Biochemistry</i> , 2012, 51, 6679-6689.	2.5	18
56	<i>Streptomyces coelicolor</i> Encodes a Urate-Responsive Transcriptional Regulator with Homology to PecS from Plant Pathogens. <i>Journal of Bacteriology</i> , 2013, 195, 4954-4965.	2.2	18
57	Histidine switch controlling pH-dependent protein folding and DNA binding in a transcription factor at the core of synthetic network devices. <i>Molecular BioSystems</i> , 2016, 12, 2417-2426.	2.9	18
58	The yeast high mobility group protein HMO2, a subunit of the chromatin-remodeling complex INO80, binds DNA ends. <i>Nucleic Acids Research</i> , 2009, 37, 6389-6399.	14.5	17
59	pH-Dependent DNA Distortion and Repression of Gene Expression by <i>Pectobacterium atrosepticum</i> PecS. <i>ACS Chemical Biology</i> , 2016, 11, 2049-2056.	3.4	16
60	<i>Streptomyces coelicolor</i> XdhR is a direct target of (p)ppGpp that controls expression of genes encoding xanthine dehydrogenase to promote purine salvage. <i>Molecular Microbiology</i> , 2016, 100, 701-718.	2.5	16
61	Redox-Sensitive MarR Homologue BifR from <i>Burkholderia thailandensis</i> Regulates Biofilm Formation. <i>Biochemistry</i> , 2017, 56, 2315-2327.	2.5	15
62	DNA damage regulates direct association of TOR kinase with the RNA polymerase II-transcribed HMO1 gene. <i>Molecular Biology of the Cell</i> , 2017, 28, 2449-2459.	2.1	15
63	Surface Salt Bridges Modulate DNA Wrapping by the Type II DNA-Binding Protein TF1. <i>Biochemistry</i> , 2003, 42, 8739-8747.	2.5	14
64	DNA inhibits catalysis by the carboxyltransferase subunit of acetyl-CoA carboxylase: Implications for active site communication. <i>Protein Science</i> , 2007, 17, 34-42.	7.6	14
65	On the stoichiometry of <i>Deinococcus radiodurans</i> Dps binding to duplex DNA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 713-721.	2.6	14
66	Marking the start site of RNA polymerase III transcription: the role of constraint, compaction and continuity of the transcribed DNA strand. <i>EMBO Journal</i> , 2002, 21, 704-714.	7.8	13
67	Do Global Regulators Hold the Key to Production of Bacterial Secondary Metabolites?. <i>Antibiotics</i> , 2019, 8, 160.	3.7	12
68	<i>Mycobacterium smegmatis</i> Ku binds DNA without free ends. <i>Biochemical Journal</i> , 2013, 456, 275-282.	3.7	11
69	A recommended workflow for DNase I footprinting using a capillary electrophoresis genetic analyzer. <i>Analytical Biochemistry</i> , 2015, 481, 1-3.	2.4	11
70	Interaction of <i>Saccharomyces cerevisiae</i> HMO2 Domains with Distorted DNA. <i>Biochemistry</i> , 2012, 51, 1825-1835.	2.5	10
71	The Stringent Response Induced by Phosphate Limitation Promotes Purine Salvage in <i>Agrobacterium fabrum</i> . <i>Biochemistry</i> , 2017, 56, 5831-5843.	2.5	10
72	Gene Regulation by Redox-Sensitive <i>Burkholderia thailandensis</i> OhrR and Its Role in Bacterial Killing of <i>Caenorhabditis elegans</i> . <i>Infection and Immunity</i> , 2018, 86, .	2.2	10

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73	An EmrB multidrug efflux pump in <i>Burkholderia thailandensis</i> with unexpected roles in antibiotic resistance. <i>Journal of Biological Chemistry</i> , 2019, 294, 1891-1903.	3.4	10
74	Determining the Role of Metal Binding in Protein Cage Assembly. <i>Methods in Molecular Biology</i> , 2015, 1252, 91-100.	0.9	10
75	Fluoroquinolone-dependent DNA Supercoiling by <i>Vaccinia</i> Topoisomerase I. <i>Journal of Molecular Biology</i> , 2004, 342, 479-487.	4.2	9
76	Control of RNA polymerase II-transcribed genes by direct binding of TOR kinase. <i>Current Genetics</i> , 2018, 64, 131-135.	1.7	8
77	Identification of a MarR Subfamily That Regulates Arsenic Resistance Genes. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0158821.	3.1	7
78	Extracytoplasmic Function Sigma Factors Governing Production of the Primary Siderophores in Pathogenic <i>Burkholderia</i> Species. <i>Frontiers in Microbiology</i> , 2022, 13, 851011.	3.5	7
79	Effects of DNA strand breaks on transcription by RNA polymerase III: insights into the role of TFIIIB and the polarity of promoter opening. <i>EMBO Journal</i> , 2002, 21, 5508-5515.	7.8	6
80	A functional type I topoisomerase from <i>Pseudomonas aeruginosa</i> . <i>BMC Molecular Biology</i> , 2009, 10, 23.	3.0	6
81	The regulatory role of <i>Streptomyces coelicolor</i> TamR in central metabolism. <i>Biochemical Journal</i> , 2015, 466, 347-358.	3.7	6
82	Locus-specific detection of HLA-DQ and -DR antigens by antibodies against synthetic N-terminal octapeptides of the I <sup>2</sup> chain. <i>FEBS Letters</i> , 1985, 189, 329-337.	2.8	5
83	Redox Sensing by PecS from the Plant Pathogen <i>Pectobacterium atrosepticum</i> and Its Effect on Gene Expression and the Conformation of PecS-Bound Promoter DNA. <i>Biochemistry</i> , 2019, 58, 2564-2575.	2.5	5
84	The <i>Saccharomyces cerevisiae</i> RNA polymerase III recruitment factor subunits Brf1 and Bdp1 impose a strict sequence preference for the downstream half of the TATA box. <i>Nucleic Acids Research</i> , 2006, 34, 5585-5593.	14.5	4
85	A moonlighting function of <i>Mycobacterium smegmatis</i> Ku in zinc homeostasis?. <i>Protein Science</i> , 2015, 24, 253-263.	7.6	4
86	A role for <i>Vibrio vulnificus</i> PecS during hypoxia. <i>Scientific Reports</i> , 2019, 9, 2797.	3.3	4
87	Control of DNA end resection by yeast Hmo1p affects efficiency of DNA end-joining. <i>DNA Repair</i> , 2017, 53, 15-23.	2.8	3
88	Cationic ionic liquid surfactant-polyacrylamide gel electrophoresis for enhanced separation of acidic and basic proteins with single-step ribonuclease b glycoforms separation. <i>Journal of Chromatography A</i> , 2017, 1515, 245-251.	3.7	3
89	Impaired purine homeostasis plays a primary role in trimethoprim-mediated induction of virulence genes in <i>Burkholderia thailandensis</i> . <i>Molecular Microbiology</i> , 2021, 115, 610-622.	2.5	3
90	Reconstitution of Channel Proteins from Excitable Cells in Lipid Bilayers: Authentic and Designed Proteins. <i>Methods in Neurosciences</i> , 1994, , 361-380.	0.5	3

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91	Similar solutions to a common challenge: regulation of genes encoding <i>Ralstonia solanacearum</i> xanthine dehydrogenase. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	2
92	Yeast Crf1p: An activator in need is an activator indeed. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 107-116.	4.1	2
93	Localizing flexibility within the target site of DNA-bending proteins. <i>Techniques in Protein Chemistry</i> , 1997, 8, 585-592.	0.3	1
94	Mechanisms for the enhanced thermal stability of a mutant of transcription factor 1 as explained by 1H, 15N and 13C NMR chemical shifts and secondary structure analysis. <i>BBA - Proteins and Proteomics</i> , 2000, 1478, 113-124.	2.1	1
95	Transcriptome RNA Sequencing Data Set of Differential Gene Expression in <i>Escherichia coli</i> BW25113 Wild-Type and <i>slyA</i> Mutant Strains. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
96	Channel Proteins: From Anatomy to Design. <i>Jerusalem Symposia on Quantum Chemistry and Biochemistry</i> , 1992, , 249-268.	0.2	1
97	Determination of (p)ppGpp Levels During Stringent Response in <i>Streptomyces coelicolor</i> by Thin Layer Chromatography. <i>Bio-protocol</i> , 2016, 6, .	0.4	1
98	Characterization of Yeast High Mobility Group Protein HMO2. <i>FASEB Journal</i> , 2007, 21, A283.	0.5	0
99	<i>Pseudomonas aeruginosa</i> encodes a functional type IB topoisomerase. <i>FASEB Journal</i> , 2007, 21, A659.	0.5	0
100	Design Principles and Chemical Synthesis of Oligomeric Channel Proteins. <i>Advances in Chemistry Series</i> , 1994, , 329-354.	0.6	0