

# Anne Grove

## List of Publications by Year in descending order

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100  
papers

2,922  
citations

172457

29  
h-index

206112

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g-index

103  
all docs

103  
docs citations

103  
times ranked

2755  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | Yeast Crf1p: An activator in need is an activator indeed. Computational and Structural Biotechnology Journal, 2022, 20, 107-116.  | 4.1 | 2         |
| 2  | Extracytoplasmic Function Sigma Factors Governing Production of the Primary Siderophores in Pathogenic Burkholderia Species. Frontiers in Microbiology, 2022, 13, 851011.                       | 3.5 | 7         |
| 3  | Impaired purine homeostasis plays a primary role in trimethoprim-mediated induction of virulence genes in Burkholderia thailandensis. Molecular Microbiology, 2021, 115, 610-622.               | 2.5 | 3         |
| 4  | Similar solutions to a common challenge: regulation of genes encoding Ralstonia solanacearum xanthine dehydrogenase. FEMS Microbiology Letters, 2021, 368, .                                    | 1.8 | 2         |
| 5  | Transcriptome RNA Sequencing Data Set of Differential Gene Expression in Escherichia coli BW25113 Wild-Type and slyA Mutant Strains. Microbiology Resource Announcements, 2021, 10, .           | 0.6 | 1         |
| 6  | Identification of a MarR Subfamily That Regulates Arsenic Resistance Genes. Applied and Environmental Microbiology, 2021, 87, e0158821.   | 3.1 | 7         |
| 7  | Do Global Regulators Hold the Key to Production of Bacterial Secondary Metabolites?. Antibiotics, 2019, 8, 160.   | 3.7 | 12        |
| 8  | The Link between Purine Metabolism and Production of Antibiotics in Streptomyces. Antibiotics, 2019, 8, 76.   | 3.7 | 22        |
| 9  | Redox Sensing by PecS from the Plant Pathogen Pectobacterium atrosepticum and Its Effect on Gene Expression and the Conformation of PecS-Bound Promoter DNA. Biochemistry, 2019, 58, 2564-2575. | 2.5 | 5         |
| 10 | An EmrB multidrug efflux pump in Burkholderia thailandensis with unexpected roles in antibiotic resistance. Journal of Biological Chemistry, 2019, 294, 1891-1903.                              | 3.4 | 10        |
| 11 | A role for Vibrio vulnificus PecS during hypoxia. Scientific Reports, 2019, 9, 2797.  | 3.3 | 4         |
| 12 | MarR Family Transcription Factors from <i>Burkholderia</i> Species: Hidden Clues to Control of Virulence-Associated Genes. Microbiology and Molecular Biology Reviews, 2019, 83, .              | 6.6 | 32        |
| 13 | Control of RNA polymerase II-transcribed genes by direct binding of TOR kinase. Current Genetics, 2018, 64, 131-135.  | 1.7 | 8         |
| 14 | Gene Regulation by Redox-Sensitive Burkholderia thailandensis OhrR and Its Role in Bacterial Killing of Caenorhabditis elegans. Infection and Immunity, 2018, 86, .                             | 2.2 | 10        |
| 15 | Redox-Sensitive MarR Homologue BifR from <i>Burkholderia thailandensis</i> Regulates Biofilm Formation. Biochemistry, 2017, 56, 2315-2327.  | 2.5 | 15        |
| 16 | Yeast HMO1: Linker Histone Reinvented. Microbiology and Molecular Biology Reviews, 2017, 81, .  | 6.6 | 34        |
| 17 | Control of DNA end resection by yeast Hmo1p affects efficiency of DNA end-joining. DNA Repair, 2017, 53, 15-23.   | 2.8 | 3         |
| 18 | Global Awakening of Cryptic Biosynthetic Gene Clusters in <i>Burkholderia thailandensis</i> . ACS Chemical Biology, 2017, 12, 3012-3021.  | 3.4 | 35        |

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|----|---|------|-----------|
| 19 | 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        |
| 20 | 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         |
| 21 | Regulation of Metabolic Pathways by MarR Family Transcription Factors. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 366-371.   | 4.1  | 61        |
| 22 | DNA damage regulates direct association of TOR kinase with the RNA polymerase II-transcribed <i>HMO1</i> gene. <i>Molecular Biology of the Cell</i> , 2017, 28, 2449-2459.  | 2.1  | 15        |
| 23 | 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       |
| 24 | 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        |
| 25 | <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        |
| 26 | 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        |
| 27 | The high mobility group protein HMO1 functions as a linker histone in yeast. <i>Epigenetics and Chromatin</i> , 2016, 9, 13.  | 3.9  | 22        |
| 28 | 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         |
| 29 | 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        |
| 30 | The regulatory role of <i>Streptomyces coelicolor</i> TamR in central metabolism. <i>Biochemical Journal</i> , 2015, 466, 347-358.  | 3.7  | 6         |
| 31 | A recommended workflow for DNase I footprinting using a capillary electrophoresis genetic analyzer. <i>Analytical Biochemistry</i> , 2015, 481, 1-3.  | 2.4  | 11        |
| 32 | A moonlighting function of <i>Mycobacterium smegmatis</i> Ku in zinc homeostasis?. <i>Protein Science</i> , 2015, 24, 253-263.  | 7.6  | 4         |
| 33 | Determining the Role of Metal Binding in Protein Cage Assembly. <i>Methods in Molecular Biology</i> , 2015, 1252, 91-100.   | 0.9  | 10        |
| 34 | 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        |
| 35 | MarR family transcription factors. <i>Current Biology</i> , 2013, 23, R142-R143.  | 3.9  | 127       |
| 36 | <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        |

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|----|---|------|-----------|
| 37 | 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        |
| 38 | <i>Mycobacterium smegmatis</i> Ku binds DNA without free ends. <i>Biochemical Journal</i> , 2013, 456, 275-282.   | 3.7  | 11        |
| 39 | The transcriptional regulator <i>TamR</i> from <i>S. treptomyces coelicolor</i> controls a key step in central metabolism during oxidative stress. <i>Molecular Microbiology</i> , 2013, 87, 1151-1166. | 2.5  | 26        |
| 40 | 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        |
| 41 | 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        |
| 42 | Interaction of <i>Saccharomyces cerevisiae</i> HMO2 Domains with Distorted DNA. <i>Biochemistry</i> , 2012, 51, 1825-1835.  | 2.5  | 10        |
| 43 | 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        |
| 44 | Expression of yeast high mobility group protein HMO1 is regulated by TOR signaling. <i>Gene</i> , 2011, 489, 55-62.   | 2.2  | 24        |
| 45 | MarR homologs with urate binding signature. <i>Protein Science</i> , 2011, 20, 621-629.   | 7.6  | 24        |
| 46 | Functional evolution of bacterial histone-like HU proteins. <i>Current Issues in Molecular Biology</i> , 2011, 13, 1-12.  | 2.4  | 80        |
| 47 | A tale of two functions: enzymatic activity and translational repression by carboxyltransferase. <i>Nucleic Acids Research</i> , 2010, 38, 1217-1227.   | 14.5 | 37        |
| 48 | 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       |
| 49 | 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        |
| 50 | 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        |
| 51 | Urate Is a Ligand for the Transcriptional Regulator PecS. <i>Journal of Molecular Biology</i> , 2010, 402, 539-551.   | 4.2  | 30        |
| 52 | Urate-responsive MarR homologs from <i>Burkholderia</i> . <i>Molecular BioSystems</i> , 2010, 6, 2133.  | 2.9  | 19        |
| 53 | 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        |
| 54 | A functional type I topoisomerase from <i>Pseudomonas aeruginosa</i> . <i>BMC Molecular Biology</i> , 2009, 10, 23.   | 3.0  | 6         |

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|----|--|------|-----------|
| 55 | <i>Mycobacterium smegmatis</i> histone-like protein Hlp is nucleoid associated. FEMS Microbiology Letters, 2009, 291, 232-240.   | 1.8  | 24        |
| 56 | Mechanism for Attenuation of DNA Binding by MarR Family Transcriptional Regulators by Small Molecule Ligands. Journal of Molecular Biology, 2009, 390, 1019-1029.  | 4.2  | 31        |
| 57 | Coordination of Ribosomal Protein and Ribosomal RNA Gene Expression in Response to TOR Signaling. Current Genomics, 2009, 10, 198-205.   | 1.6  | 65        |
| 58 | The C-Terminal Domain of HU-Related Histone-like Protein Hlp from <i>Mycobacterium smegmatis</i> Mediates DNA End-Joining. Biochemistry, 2008, 47, 8744-8753.  | 2.5  | 28        |
| 59 | DNA protection by histone-like protein HU from the hyperthermophilic eubacterium <i>Thermotoga maritima</i> . Nucleic Acids Research, 2008, 36, 3956-3968.   | 14.5 | 38        |
| 60 | The N-terminal Extensions of <i>Deinococcus radiodurans</i> Dps-1 Mediate DNA Major Groove Interactions as well as Assembly of the Dodecamer. Journal of Biological Chemistry, 2007, 282, 11921-11930.                     | 3.4  | 32        |
| 61 | DNA inhibits catalysis by the carboxyltransferase subunit of acetyl-CoA carboxylase: Implications for active site communication. Protein Science, 2007, 17, 34-42.   | 7.6  | 14        |
| 62 | Characterization of Yeast High Mobility Group Protein HMO2. FASEB Journal, 2007, 21, A283.   | 0.5  | 0         |
| 63 | <i>Pseudomonas aeruginosa</i> encodes a functional type IB topoisomerase. FASEB Journal, 2007, 21, A659.   | 0.5  | 0         |
| 64 | The <i>Deinococcus radiodurans</i> -Encoded HU Protein Has Two DNA-Binding Domains. Biochemistry, 2006, 45, 1723-1733.   | 2.5  | 22        |
| 65 | Interactions between N- and C-Terminal Domains of the <i>Saccharomyces cerevisiae</i> High-Mobility Group Protein HMO1 Are Required for DNA Bending. Biochemistry, 2006, 45, 3635-3645.                                    | 2.5  | 30        |
| 66 | The Crystal Structure of the Transcriptional Regulator HucR from <i>Deinococcus radiodurans</i> Reveals a Repressor Preconfigured for DNA Binding. Journal of Molecular Biology, 2006, 360, 168-177.                       | 4.2  | 50        |
| 67 | Crystal Structure of Dps-1, a Functionally Distinct Dps Protein from <i>Deinococcus radiodurans</i> . Journal of Molecular Biology, 2006, 361, 105-114.  | 4.2  | 43        |
| 68 | 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. Nucleic Acids Research, 2006, 34, 5585-5593. | 14.5 | 4         |
| 69 | Ligand-responsive transcriptional regulation by members of the MarR family of winged helix proteins. Current Issues in Molecular Biology, 2006, 8, 51-62.  | 2.4  | 211       |
| 70 | Surface salt bridges modulate the DNA site size of bacterial histone-like HU proteins. Biochemical Journal, 2005, 390, 49-55.  | 3.7  | 25        |
| 71 | Differential DNA Binding and Protection by Dimeric and Dodecameric forms of the Ferritin Homolog Dps from <i>Deinococcus radiodurans</i> . Journal of Molecular Biology, 2005, 347, 495-508.                               | 4.2  | 64        |
| 72 | Negative Cooperativity of Uric Acid Binding to the Transcriptional Regulator HucR from <i>Deinococcus radiodurans</i> . Journal of Molecular Biology, 2005, 350, 617-630.  | 4.2  | 42        |

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|----|---|-----|-----------|
| 73 | 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        |
| 74 | 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       |
| 75 | 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        |
| 76 | Fluoroquinolone-dependent DNA Supercoiling by <i>Vaccinia</i> Topoisomerase I. <i>Journal of Molecular Biology</i> , 2004, 342, 479-487.  | 4.2 | 9         |
| 77 | 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        |
| 78 | Surface Salt Bridges Modulate DNA Wrapping by the Type II DNA-Binding Protein TF1. <i>Biochemistry</i> , 2003, 42, 8739-8747.   | 2.5 | 14        |
| 79 | 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        |
| 80 | 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        |
| 81 | 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         |
| 82 | High-affinity DNA binding of HU protein from the hyperthermophile <i>Thermotoga maritima</i> . Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 2001, 311, 491-502.   | 4.2 | 33        |
| 83 | Mechanisms for the enhanced thermal stability of a mutant of transcription factor 1 as explained by <sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C NMR chemical shifts and secondary structure analysis. <i>BBA - Proteins and Proteomics</i> , 2000, 1478, 113-124. | 2.1 | 1         |
| 84 | The RNA polymerase III-recruiting factor TFIIIB induces a DNA bend between the TATA box and the transcriptional start site. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 285, 1429-1440.   | 4.2 | 30        |
| 85 | Affinity, stability and polarity of binding of the TATA binding protein governed by flexure at the TATA box. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 282, 731-739.  | 4.2 | 51        |
| 86 | 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        |
| 87 | 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        |
| 88 | Localizing flexibility within the target site of DNA-bending proteins. <i>Techniques in Protein Chemistry</i> , 1997, 8, 585-592.   | 0.3 | 1         |
| 89 | 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        |
| 90 | 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        |

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|-----|---|------|-----------|
| 91  | Structure of the Bacillus subtilis Phage SPO1-Encoded Type II DNA-binding Protein TF1 in Solution. Journal of Molecular Biology, 1996, 263, 259-268.  | 4.2  | 28        |
| 92  | Chemical synthesis and characterization of peptides and oligomeric proteins designed to form transmembrane ion channels. International Journal of Peptide and Protein Research, 1994, 43, 597-607.        | 0.1  | 28        |
| 93  | Reconstitution of Channel Proteins from Excitable Cells in Lipid Bilayers: Authentic and Designed Proteins. Methods in Neurosciences, 1994, , 361-380.  | 0.5  | 3         |
| 94  | Design Principles and Chemical Synthesis of Oligomeric Channel Proteins. Advances in Chemistry Series, 1994, , 329-354.   | 0.6  | 0         |
| 95  | Design of a functional calcium channel protein: Inferences about an ion channel-forming motif derived from the primary structure of voltage-gated calcium channels. Protein Science, 1993, 2, 1918-1930.  | 7.6  | 27        |
| 96  | Template-assembled synthetic proteins designed to adopt a globular, four-helix bundle conformation form ionic channels in lipid bilayers. Journal of the American Chemical Society, 1993, 115, 5919-5924. | 13.7 | 102       |
| 97  | [34] Synthetic peptides and proteins as models for pore-forming structure of channel proteins. Methods in Enzymology, 1992, 207, 510-525.   | 1.0  | 31        |
| 98  | Channel Proteins: From Anatomy to Design. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1992, , 249-268.  | 0.2  | 1         |
| 99  | A molecular blueprint for the pore-forming structure of voltage-gated calcium channels.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 6418-6422.            | 7.1  | 73        |
| 100 | Locus-specific detection of HLA-DQ and -DR antigens by antibodies against synthetic N-terminal octapeptides of the I <sup>2</sup> chain. FEBS Letters, 1985, 189, 329-337.                                | 2.8  | 5         |