

# David P Giedroc

## 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.

190  
papers

8,613  
citations

53  
h-index

83  
g-index

206  
ext. papers

9,878  
ext. citations

7  
avg, IF

6.24  
L-index

| #   | Paper  | IF   | Citations |
|-----|--|------|-----------|
| 190 | Zn-regulated GTPase metalloprotein activator 1 modulates vertebrate zinc homeostasis.. <i>Cell</i> , <b>2022</b>   | 56.2 | 5         |
| 189 | Protocol for using organic persulfides to measure the chemical reactivity of persulfide sensors. <i>STAR Protocols</i> , <b>2022</b> , 3, 101424   | 1.4  | 0         |
| 188 | SifR is an Rrf2-family quinone sensor associated with catechol iron uptake in <i>Streptococcus pneumoniae</i> D39. <i>Journal of Biological Chemistry</i> , <b>2022</b> , 102046   | 5.4  | 0         |
| 187 | Functional asymmetry and chemical reactivity of CsoR family persulfide sensors. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 12556-12576  | 20.1 | 3         |
| 186 | COG0523 proteins: a functionally diverse family of transition metal-regulated G3E P-loop GTP hydrolases from bacteria to man. <i>Metallomics</i> , <b>2021</b> , 13,   | 4.5  | 10        |
| 185 | Structural basis for persulfide-sensing specificity in a transcriptional regulator. <i>Nature Chemical Biology</i> , <b>2021</b> , 17, 65-70   | 11.7 | 9         |
| 184 | Molecular Evolution of Transition Metal Bioavailability at the Host-Pathogen Interface. <i>Trends in Microbiology</i> , <b>2021</b> , 29, 441-457  | 12.4 | 14        |
| 183 | Proteomics Profiling of -sulfurated Proteins in. <i>Bio-protocol</i> , <b>2021</b> , 11, e4000   | 0.9  | 0         |
| 182 | Metal Ion Homeostasis <b>2021</b> , 929-953  |      |           |
| 181 | H, C, N backbone resonance assignments of the apo and holo forms of the ABC transporter solute binding protein PiuA from <i>Streptococcus pneumoniae</i> . <i>Biomolecular NMR Assignments</i> , <b>2020</b> , 14, 233-238 | 0.7  | 2         |
| 180 | <i>Clostridioides difficile</i> Senses and Hijacks Host Heme for Incorporation into an Oxidative Stress Defense System. <i>Cell Host and Microbe</i> , <b>2020</b> , 28, 411-421.e6  | 23.4 | 23        |
| 179 | Iron Acquisition by Bacterial Pathogens: Beyond Tris-Catecholate Complexes. <i>ChemBioChem</i> , <b>2020</b> , 21, 1955-1967   | 3.8  | 8         |
| 178 | The Response of to Hydrogen Sulfide Reveals Two Independent Persulfide-Sensing Systems and a Connection to Biofilm Regulation. <i>MBio</i> , <b>2020</b> , 11,   | 7.8  | 13        |
| 177 | Cell-free biosensors for rapid detection of water contaminants. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1451-1459  | 41.5 | 75        |
| 176 | Multi-metal nutrient restriction and crosstalk in metallostasis systems in microbial pathogens. <i>Current Opinion in Microbiology</i> , <b>2020</b> , 55, 17-25   | 7.9  | 14        |
| 175 | Hydrogen Sulfide Signaling and Enzymology <b>2020</b> , 430-473  |      | 2         |
| 174 | Glucose-Induced Biofilm Accessory Protein A (GbaA) Is a Monothiol-Dependent Electrophile Sensor. <i>Biochemistry</i> , <b>2020</b> , 59, 2882-2895   | 3.2  | 4         |

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| 173 | HS and reactive sulfur signaling at the host-bacterial pathogen interface. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 13150-13168   | 5.4  | 14 |
| 172 | The Pneumococcal Iron Uptake Protein A (PiuA) Specifically Recognizes Tetradentate Febis- and Mono-Catechol Complexes. <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 5390-5410  | 6.5  | 3  |
| 171 | Structure of the Large Extracellular Loop of FtsX and Its Interaction with the Essential Peptidoglycan Hydrolase PcsB in <i>Streptococcus pneumoniae</i> . <i>MBio</i> , <b>2019</b> , 10,   | 7.8  | 20 |
| 170 | Mechanistic Insights into the Metal-Dependent Activation of Zn-Dependent Metallochaperones. <i>Inorganic Chemistry</i> , <b>2019</b> , 58, 13661-13672   | 5.1  | 20 |
| 169 | A Mn-sensing riboswitch activates expression of a Mn <sup>2+</sup> /Ca <sup>2+</sup> ATPase transporter in <i>Streptococcus</i> . <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 6885-6899  | 20.1 | 13 |
| 168 | Multi-metal Restriction by Calprotectin Impacts De Novo Flavin Biosynthesis in <i>Acinetobacter baumannii</i> . <i>Cell Chemical Biology</i> , <b>2019</b> , 26, 745-755.e7  | 8.2  | 35 |
| 167 | An <i>Acinetobacter baumannii</i> , Zinc-Regulated Peptidase Maintains Cell Wall Integrity during Immune-Mediated Nutrient Sequestration. <i>Cell Reports</i> , <b>2019</b> , 26, 2009-2018.e6   | 10.6 | 36 |
| 166 | Hydrogen Sulfide Sensing through Reactive Sulfur Species (RSS) and Nitroxyl (HNO) in <i>Enterococcus faecalis</i> . <i>ACS Chemical Biology</i> , <b>2018</b> , 13, 1610-1620  | 4.9  | 19 |
| 165 | Tuning site-specific dynamics to drive allosteric activation in a pneumococcal zinc uptake regulator. <i>ELife</i> , <b>2018</b> , 7,  | 8.9  | 18 |
| 164 | Metal-dependent allosteric activation and inhibition on the same molecular scaffold: the copper sensor CopY from. <i>Chemical Science</i> , <b>2018</b> , 9, 105-118   | 9.4  | 19 |
| 163 | Thioredoxin Profiling of Multiple Thioredoxin-Like Proteins in. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2385   | 5.7  | 13 |
| 162 | Functional Role of Solvent Entropy and Conformational Entropy of Metal Binding in a Dynamically Driven Allosteric System. <i>Journal of the American Chemical Society</i> , <b>2018</b> , 140, 9108-9119                                     | 16.4 | 17 |
| 161 | Perturbation of manganese metabolism disrupts cell division in <i>Streptococcus pneumoniae</i> . <i>Molecular Microbiology</i> , <b>2017</b> , 104, 334-348  | 4.1  | 33 |
| 160 | The zinc efflux activator SczA protects <i>Streptococcus pneumoniae</i> serotype 2 D39 from intracellular zinc toxicity. <i>Molecular Microbiology</i> , <b>2017</b> , 104, 636-651  | 4.1  | 19 |
| 159 | Sulfide-responsive transcriptional repressor SqrR functions as a master regulator of sulfide-dependent photosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 2355-2360 | 11.5 | 50 |
| 158 | Biological and Chemical Adaptation to Endogenous Hydrogen Peroxide Production in D39. <i>MSphere</i> , <b>2017</b> , 2,  | 5    | 32 |
| 157 | A new player in bacterial sulfide-inducible transcriptional regulation. <i>Molecular Microbiology</i> , <b>2017</b> , 105, 347-352   | 4.1  | 13 |
| 156 | Entropy redistribution controls allostery in a metalloregulatory protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 4424-4429  | 11.5 | 55 |

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| 155 | Metallochaperones and metalloregulation in bacteria. <i>Essays in Biochemistry</i> , <b>2017</b> , 61, 177-200   | 7.6  | 53 |
| 154 | Hydrogen Sulfide and Reactive Sulfur Species Impact Proteome S-Sulfhydration and Global Virulence Regulation in <i>Staphylococcus aureus</i> . <i>ACS Infectious Diseases</i> , <b>2017</b> , 3, 744-755   | 5.5  | 45 |
| 153 | Sulfide Homeostasis and Nitroxyl Intersect via Formation of Reactive Sulfur Species in. <i>MSphere</i> , <b>2017</b> , 2,  | 5    | 45 |
| 152 | The S2 Cu(i) site in CupA from <i>Streptococcus pneumoniae</i> is required for cellular copper resistance. <i>Metallomics</i> , <b>2016</b> , 8, 61-70   | 4.5  | 15 |
| 151 | <i>Staphylococcus aureus</i> sqr Encodes a Type II Sulfide:Quinone Oxidoreductase and Impacts Reactive Sulfur Speciation in Cells. <i>Biochemistry</i> , <b>2016</b> , 55, 6524-6534   | 3.2  | 28 |
| 150 | Crystal structure of <i>Clostridium difficile</i> toxin A. <i>Nature Microbiology</i> , <b>2016</b> , 1, 15002   | 26.6 | 62 |
| 149 | The Response of <i>Acinetobacter baumannii</i> to Zinc Starvation. <i>Cell Host and Microbe</i> , <b>2016</b> , 19, 826-36   | 23.4 | 79 |
| 148 | <sup>1</sup> H, <sup>13</sup> C, <sup>15</sup> N resonance assignments of the extracellular loop 1 domain (ECL1) of <i>Streptococcus pneumoniae</i> D39 FtsX, an essential cell division protein. <i>Biomolecular NMR Assignments</i> , <b>2016</b> , 10, 89-92 <sup>0.7</sup> |      | 2  |
| 147 | Functional Determinants of Metal Ion Transport and Selectivity in Paralogous Cation Diffusion Facilitator Transporters CzcD and MntE in <i>Streptococcus pneumoniae</i> . <i>Journal of Bacteriology</i> , <b>2016</b> , 198, 1066-76  | 3.5  | 37 |
| 146 | Bacterial Strategies to Maintain Zinc Metallostasis at the Host-Pathogen Interface. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 20858-20868  | 5.4  | 89 |
| 145 | <i>Staphylococcus aureus</i> CstB Is a Novel Multidomain Persulfide Dioxygenase-Sulfurtransferase Involved in Hydrogen Sulfide Detoxification. <i>Biochemistry</i> , <b>2015</b> , 54, 4542-54   | 3.2  | 40 |
| 144 | Electrostatic occlusion and quaternary structural ion pairing are key determinants of Cu(I)-mediated allostery in the copper-sensing operon repressor (CsoR). <i>Biochemistry</i> , <b>2015</b> , 54, 2463-72 <sup>3.2</sup>   |      | 13 |
| 143 | Conformational analysis and chemical reactivity of the multidomain sulfurtransferase, <i>Staphylococcus aureus</i> CstA. <i>Biochemistry</i> , <b>2015</b> , 54, 2385-98   | 3.2  | 22 |
| 142 | Cysteine sulfur chemistry in transcriptional regulators at the host-bacterial pathogen interface. <i>Biochemistry</i> , <b>2015</b> , 54, 3235-49  | 3.2  | 17 |
| 141 | SHAPE analysis of the RNA secondary structure of the Mouse Hepatitis Virus 5'Suntranslated region and N-terminal nsp1 coding sequences. <i>Virology</i> , <b>2015</b> , 475, 15-27   | 3.6  | 22 |
| 140 | Resolution of Stepwise Cooperativities of Copper Binding by the Homotetrameric Copper-Sensitive Operon Repressor (CsoR): Impact on Structure and Stability. <i>Angewandte Chemie</i> , <b>2015</b> , 127, 12986-12990 <sup>3.6</sup>   |      |    |
| 139 | Resolution of Stepwise Cooperativities of Copper Binding by the Homotetrameric Copper-Sensitive Operon Repressor (CsoR): Impact on Structure and Stability. <i>Angewandte Chemie - International Edition</i> , <b>2015</b> , 54, 12795-9                                       | 16.4 | 10 |
| 138 | Recent developments in copper and zinc homeostasis in bacterial pathogens. <i>Current Opinion in Chemical Biology</i> , <b>2014</b> , 19, 59-66  | 9.7  | 88 |

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| 137 | Copper transport and trafficking at the host-bacterial pathogen interface. <i>Accounts of Chemical Research</i> , <b>2014</b> , 47, 3605-13  | 24.3 | 71 |
| 136 | Conversion of S-phenylsulfonyleysteine residues to mixed disulfides at pH 4.0: utility in protein thiol blocking and in protein-S-nitrosothiol detection. <i>Organic and Biomolecular Chemistry</i> , <b>2014</b> , 12, 7942-36  | 3.9  | 12 |
| 135 | Backbone and stereospecific methyl side chain resonance assignments of the homodimeric zinc sensor AdcR (32 kDa) in the apo- and Zn(II)-bound states. <i>Biomolecular NMR Assignments</i> , <b>2014</b> , 8, 11-4  | 0.7  | 2  |
| 134 | Insights into Protein Allostery in the CsoR/RcnR Family of Transcriptional Repressors. <i>Chemistry Letters</i> , <b>2014</b> , 43, 20-25  | 1.7  | 36 |
| 133 | Cu(I)-mediated allosteric switching in a copper-sensing operon repressor (CsoR). <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 19204-17  | 5.4  | 43 |
| 132 | The CsoR-like sulfurtransferase repressor (CstR) is a persulfide sensor in <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , <b>2014</b> , 94, 1343-60  | 4.1  | 71 |
| 131 | <sup>1</sup> H, <sup>13</sup> C, <sup>15</sup> N resonance assignments of murine hepatitis virus nonstructural protein 3a. <i>Biomolecular NMR Assignments</i> , <b>2014</b> , 8, 15-7   | 0.7  | 1  |
| 130 | Solution NMR refinement of a metal ion bound protein using metal ion inclusive restrained molecular dynamics methods. <i>Journal of Biomolecular NMR</i> , <b>2013</b> , 56, 125-37  | 3    | 19 |
| 129 | <sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignments of NmtR, a Ni(II)/Co(II) metalloregulatory protein of <i>Mycobacterium tuberculosis</i> . <i>Biomolecular NMR Assignments</i> , <b>2013</b> , 7, 145-8                                      | 0.7  | 2  |
| 128 | Metal-Regulated Gene Expression <b>2013</b> , 35-49  |      |    |
| 127 | Physical characterization of the manganese-sensing pneumococcal surface antigen repressor from <i>Streptococcus pneumoniae</i> . <i>Biochemistry</i> , <b>2013</b> , 52, 7689-701  | 3.2  | 35 |
| 126 | Selenite and tellurite form mixed seleno- and tellurotrisulfides with CstR from <i>Staphylococcus aureus</i> . <i>Metallomics</i> , <b>2013</b> , 5, 335-42  | 4.5  | 17 |
| 125 | Allosteric inhibition of a zinc-sensing transcriptional repressor: insights into the arsenic repressor (ArsR) family. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 1143-57   | 6.5  | 29 |
| 124 | A new structural paradigm in copper resistance in <i>Streptococcus pneumoniae</i> . <i>Nature Chemical Biology</i> , <b>2013</b> , 9, 177-83   | 11.7 | 72 |
| 123 | Backbone resonance assignments of the homotetrameric (48 kD) copper sensor CsoR from <i>Geobacillus thermodenitrificans</i> in the apo- and Cu(I)-bound states: insights into copper-mediated allostery. <i>Biomolecular NMR Assignments</i> , <b>2013</b> , 7, 279-83 | 0.7  | 10 |
| 122 | Energetics of zinc-mediated interactions in the allosteric pathways of metal sensor proteins. <i>Journal of the American Chemical Society</i> , <b>2013</b> , 135, 30-3  | 16.4 | 18 |
| 121 | Solution structure of mouse hepatitis virus (MHV) nsp3a and determinants of the interaction with MHV nucleocapsid (N) protein. <i>Journal of Virology</i> , <b>2013</b> , 87, 3502-15  | 6.6  | 26 |
| 120 | Co-ordinate synthesis and protein localization in a bacterial organelle by the action of a penicillin-binding-protein. <i>Molecular Microbiology</i> , <b>2013</b> , 90, 1162-77   | 4.1  | 19 |

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| 119 | Manganese acquisition and homeostasis at the host-pathogen interface. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2013</b> , 3, 91   | 5.9  | 86  |
| 118 | Solution structure of Mycobacterium tuberculosis NmtR in the apo state: insights into Ni(II)-mediated allostery. <i>Biochemistry</i> , <b>2012</b> , 51, 2619-29  | 3.2  | 37  |
| 117 | Metal site occupancy and allosteric switching in bacterial metal sensor proteins. <i>Archives of Biochemistry and Biophysics</i> , <b>2012</b> , 519, 210-22  | 4.1  | 55  |
| 116 | Simulations of allosteric motions in the zinc sensor CzrA. <i>Journal of the American Chemical Society</i> , <b>2012</b> , 134, 3367-76   | 16.4 | 36  |
| 115 | Functional transcriptional regulatory sequence (TRS) RNA binding and helix destabilizing determinants of murine hepatitis virus (MHV) nucleocapsid (N) protein. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 7063-73 | 5.4  | 36  |
| 114 | Allosteric coupling between transition metal-binding sites in homooligomeric metal sensor proteins. <i>Methods in Molecular Biology</i> , <b>2012</b> , 796, 31-51  | 1.4  | 5   |
| 113 | Illuminating allostery in metal sensing transcriptional regulators. <i>Methods in Molecular Biology</i> , <b>2012</b> , 875, 165-92   | 1.4  | 6   |
| 112 | Zinc: DNA-Binding Proteins <b>2011</b> ,  |      | 1   |
| 111 | Crystal structure of the zinc-dependent MarR family transcriptional regulator AdcR in the Zn(II)-bound state. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 19614-7  | 16.4 | 49  |
| 110 | The solution structure of coronaviral stem-loop 2 (SL2) reveals a canonical CUYG tetraloop fold. <i>FEBS Letters</i> , <b>2011</b> , 585, 1049-53   | 3.8  | 23  |
| 109 | Metalloregulatory proteins: metal selectivity and allosteric switching. <i>Biophysical Chemistry</i> , <b>2011</b> , 156, 103-14  | 3.5  | 121 |
| 108 | Interplay between manganese and zinc homeostasis in the human pathogen <i>Streptococcus pneumoniae</i> . <i>Metallomics</i> , <b>2011</b> , 3, 38-41  | 4.5  | 81  |
| 107 | Mycobacterium tuberculosis NmtR harbors a nickel sensing site with parallels to <i>Escherichia coli</i> RcnR. <i>Biochemistry</i> , <b>2011</b> , 50, 7941-52   | 3.2  | 32  |
| 106 | Ratiometric pulse-chase amidination mass spectrometry as a probe of biomolecular complex formation. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 9092-9  | 7.8  | 18  |
| 105 | A conserved RNA pseudoknot in a putative molecular switch domain of the 3' untranslated region of coronaviruses is only marginally stable. <i>Rna</i> , <b>2011</b> , 17, 1747-59   | 5.8  | 26  |
| 104 | Mouse hepatitis virus stem-loop 4 functions as a spacer element required to drive subgenomic RNA synthesis. <i>Journal of Virology</i> , <b>2011</b> , 85, 9199-209   | 6.6  | 26  |
| 103 | Control of copper resistance and inorganic sulfur metabolism by paralogous regulators in <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 13522-31  | 5.4  | 75  |
| 102 | Predicting loop-helix tertiary structural contacts in RNA pseudoknots. <i>Rna</i> , <b>2010</b> , 16, 538-52  | 5.8  | 32  |

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|-----|---|------|-----|
| 101 | A Q63E Rhodobacter sphaeroides AppA BLUF domain mutant is locked in a pseudo-light-excited signaling state. <i>Biochemistry</i> , <b>2010</b> , 49, 10682-90  | 3.2  | 12  |
| 100 | The metalloregulatory zinc site in Streptococcus pneumoniae AdcR, a zinc-activated MarR family repressor. <i>Journal of Molecular Biology</i> , <b>2010</b> , 403, 197-216  | 6.5  | 71  |
| 99  | Elucidation of the functional metal binding profile of a Cd(II)/Pb(II) sensor CmtR(Sc) from Streptomyces coelicolor. <i>Biochemistry</i> , <b>2010</b> , 49, 6617-26  | 3.2  | 15  |
| 98  | The CRR1 nutritional copper sensor in Chlamydomonas contains two distinct metal-responsive domains. <i>Plant Cell</i> , <b>2010</b> , 22, 4098-113  | 11.6 | 68  |
| 97  | Ribosomal Frameshifting in Decoding Plant Viral RNAs. <i>Nucleic Acids and Molecular Biology</i> , <b>2010</b> , 193-220  |      | 11  |
| 96  | Mouse hepatitis virus stem-loop 2 adopts a uYNMG(U)a-like tetraloop structure that is highly functionally tolerant of base substitutions. <i>Journal of Virology</i> , <b>2009</b> , 83, 12084-93   | 6.6  | 31  |
| 95  | Solution structure of a paradigm ArsR family zinc sensor in the DNA-bound state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 18177-82   | 11.5 | 54  |
| 94  | Structure of Thermotoga maritima TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn <sup>2+</sup> -binding FCD domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 356-65 |      | 28  |
| 93  | Hydrogen peroxide sensing in Bacillus subtilis: it is all about the (metallo)regulator. <i>Molecular Microbiology</i> , <b>2009</b> , 73, 1-4   | 4.1  | 19  |
| 92  | Unnatural amino acid substitution as a probe of the allosteric coupling pathway in a mycobacterial Cu(I) sensor. <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 18044-5   | 16.4 | 50  |
| 91  | Energetics of allosteric negative coupling in the zinc sensor S. aureus CzrA. <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 17860-70   | 16.4 | 30  |
| 90  | Spectroscopic studies of the AppA BLUF domain from Rhodobacter sphaeroides: addressing movement of tryptophan 104 in the signaling state. <i>Biochemistry</i> , <b>2009</b> , 48, 9969-79   | 3.2  | 40  |
| 89  | Frameshifting RNA pseudoknots: structure and mechanism. <i>Virus Research</i> , <b>2009</b> , 139, 193-208  | 6.4  | 221 |
| 88  | Coronavirus N protein N-terminal domain (NTD) specifically binds the transcriptional regulatory sequence (TRS) and melts TRS-cTRS RNA duplexes. <i>Journal of Molecular Biology</i> , <b>2009</b> , 394, 544-57   | 6.5  | 99  |
| 87  | Coordination chemistry of bacterial metal transport and sensing. <i>Chemical Reviews</i> , <b>2009</b> , 109, 4644-81   | 68.1 | 450 |
| 86  | Molecular insights into the metal selectivity of the copper(I)-sensing repressor CsoR from Bacillus subtilis. <i>Biochemistry</i> , <b>2009</b> , 48, 3325-34   | 3.2  | 90  |
| 85  | Structural lability in stem-loop 1 drives a 5SUTR-3SUTR interaction in coronavirus replication. <i>Journal of Molecular Biology</i> , <b>2008</b> , 377, 790-803  | 6.5  | 69  |
| 84  | Simulating RNA folding kinetics on approximated energy landscapes. <i>Journal of Molecular Biology</i> , <b>2008</b> , 381, 1055-67   | 6.5  | 48  |

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| 83 | A Cu(I)-sensing ArsR family metal sensor protein with a relaxed metal selectivity profile. <i>Biochemistry</i> , <b>2008</b> , 47, 10564-75  | 3.2  | 41  |
| 82 | Copper sensing function of Drosophila metal-responsive transcription factor-1 is mediated by a tetranuclear Cu(I) cluster. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 3128-38   | 20.1 | 37  |
| 81 | Multiple metal binding domains enhance the Zn(II) selectivity of the divalent metal ion transporter AztA. <i>Biochemistry</i> , <b>2007</b> , 46, 11057-68   | 3.2  | 18  |
| 80 | CsoR is a novel Mycobacterium tuberculosis copper-sensing transcriptional regulator <b>2007</b> , 3, 60-8  |      | 250 |
| 79 | Resonance assignments of the metal sensor CzrA in the apo-, Zn <sup>2+</sup> - and DNA-bound (42 kDa) states. <i>Biomolecular NMR Assignments</i> , <b>2007</b> , 1, 99-101  | 0.7  | 13  |
| 78 | A U-turn motif-containing stem-loop in the coronavirus 5' untranslated region plays a functional role in replication. <i>Rna</i> , <b>2007</b> , 13, 763-80  | 5.8  | 56  |
| 77 | Metal sensor proteins: nature's metalloregulated allosteric switches. <i>Dalton Transactions</i> , <b>2007</b> , 3107-204.3  |      | 165 |
| 76 | Putative cis-acting stem-loops in the 5' untranslated region of the severe acute respiratory syndrome coronavirus can substitute for their mouse hepatitis virus counterparts. <i>Journal of Virology</i> , <b>2006</b> , 80, 10600-14 | 6.6  | 37  |
| 75 | The global structures of a wild-type and poorly functional plant luteoviral mRNA pseudoknot are essentially identical. <i>Rna</i> , <b>2006</b> , 12, 1959-69  | 5.8  | 29  |
| 74 | Structural insights into homo- and heterotropic allosteric coupling in the zinc sensor <i>S. aureus</i> CzrA from covalently fused dimers. <i>Journal of the American Chemical Society</i> , <b>2006</b> , 128, 1937-47                | 16.4 | 17  |
| 73 | Pairwise coupling analysis of helical junction hydrogen bonding interactions in luteoviral RNA pseudoknots. <i>Biochemistry</i> , <b>2006</b> , 45, 11162-71   | 3.2  | 10  |
| 72 | Individual metal ligands play distinct functional roles in the zinc sensor <i>Staphylococcus aureus</i> CzrA. <i>Journal of Molecular Biology</i> , <b>2006</b> , 356, 1124-36   | 6.5  | 53  |
| 71 | Kinetics of metal binding by the toxic metal-sensing transcriptional repressor <i>Staphylococcus aureus</i> pI258 CadC. <i>Journal of Inorganic Biochemistry</i> , <b>2006</b> , 100, 1024-34  | 4.2  | 18  |
| 70 | Dissecting non-canonical interactions in frameshift-stimulating mRNA pseudoknots. <i>Journal of Biomolecular NMR</i> , <b>2006</b> , 35, 209-23  | 3    | 14  |
| 69 | Stem-loop 1 in the 5' SUTR of the SARS coronavirus can substitute for its counterpart in mouse hepatitis virus. <i>Advances in Experimental Medicine and Biology</i> , <b>2006</b> , 581, 105-8  | 3.6  | 8   |
| 68 | A previously unrecognized UNR stem-loop structure in the coronavirus 5' untranslated region plays a functional role in replication. <i>Advances in Experimental Medicine and Biology</i> , <b>2006</b> , 581, 25-30                    | 3.6  | 4   |
| 67 | Structural and functional characterization of <i>Mycobacterium tuberculosis</i> CmtR, a PblI/CdII-sensing SmtB/ArsR metalloregulatory repressor. <i>Biochemistry</i> , <b>2005</b> , 44, 8976-88                                       | 3.2  | 53  |
| 66 | A zinc(II)/lead(II)/cadmium(II)-inducible operon from the <i>Cyanobacterium anabaena</i> is regulated by AztR, an alpha3N ArsR/SmtB metalloregulator. <i>Biochemistry</i> , <b>2005</b> , 44, 8673-83                                  | 3.2  | 53  |



|    |  |      |     |
|----|--|------|-----|
| 65 | Structural determinants of metal selectivity in prokaryotic metal-responsive transcriptional regulators. <i>BioMetals</i> , <b>2005</b> , 18, 413-28   | 3.4  | 115 |
| 64 | A loop 2 cytidine-stem 1 minor groove interaction as a positive determinant for pseudoknot-stimulated -1 ribosomal frameshifting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 12694-9                                      | 11.5 | 78  |
| 63 | A novel cysteine cluster in human metal-responsive transcription factor 1 is required for heavy metal-induced transcriptional activation in vivo. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 4515-22  | 5.4  | 44  |
| 62 | Dual functions of single-stranded DNA-binding protein in helicase loading at the bacteriophage T4 DNA replication fork. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 19035-45   | 5.4  | 35  |
| 61 | A novel cyanobacterial SmtB/ArsR family repressor regulates the expression of a CPx-ATPase and a metallothionein in response to both Cu(I)/Ag(I) and Zn(II)/Cd(II). <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 17810-8  | 5.4  | 43  |
| 60 | Ratiometric pulsed alkylation mass spectrometry as a probe of thiolate reactivity in different metalloderivatives of <i>Staphylococcus aureus</i> pl258 CadC. <i>Biochemistry</i> , <b>2004</b> , 43, 3824-34  | 3.2  | 31  |
| 59 | Metal Specificity of Metallosensors <b>2004</b> , 1-16   |      | 1   |
| 58 | The SmtB/ArsR family of metalloregulatory transcriptional repressors: Structural insights into prokaryotic metal resistance. <i>FEMS Microbiology Reviews</i> , <b>2003</b> , 27, 131-43   | 15.1 | 293 |
| 57 | Detection of scalar couplings involving 2SHydroxyl protons across hydrogen bonds in a frameshifting mRNA pseudoknot. <i>Journal of the American Chemical Society</i> , <b>2003</b> , 125, 4676-7   | 16.4 | 37  |
| 56 | A metal-ligand-mediated intersubunit allosteric switch in related SmtB/ArsR zinc sensor proteins. <i>Journal of Molecular Biology</i> , <b>2003</b> , 333, 683-95  | 6.5  | 107 |
| 55 | Structural elements of metal selectivity in metal sensor proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 3713-8  | 11.5 | 105 |
| 54 | Characterization of a metalloregulatory bismuth(III) site in <i>Staphylococcus aureus</i> pl258 CadC repressor. <i>Journal of Biological Inorganic Chemistry</i> , <b>2002</b> , 7, 551-9  | 3.7  | 29  |
| 53 | A nickel-cobalt-sensing ArsR-SmtB family repressor. Contributions of cytosol and effector binding sites to metal selectivity. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 38441-8  | 5.4  | 124 |
| 52 | Structural characterization of distinct alpha3N and alpha5 metal sites in the cyanobacterial zinc sensor SmtB. <i>Biochemistry</i> , <b>2002</b> , 41, 9765-75   | 3.2  | 53  |
| 51 | Allosteric negative regulation of smt O/P binding of the zinc sensor, SmtB, by metal ions: a coupled equilibrium analysis. <i>Biochemistry</i> , <b>2002</b> , 41, 9776-86   | 3.2  | 54  |
| 50 | Thermodynamic analysis of conserved loop-stem interactions in P1-P2 frameshifting RNA pseudoknots from plant Luteoviridae. <i>Biochemistry</i> , <b>2002</b> , 41, 10665-74  | 3.2  | 33  |
| 49 | Elucidation of primary (alpha(3)N) and vestigial (alpha(5)) heavy metal-binding sites in <i>Staphylococcus aureus</i> pl258 CadC: evolutionary implications for metal ion selectivity of ArsR/SmtB metal sensor proteins. <i>Journal of Molecular Biology</i> , <b>2002</b> , 319, 685-701 | 6.5  | 96  |
| 48 | Solution structure of a luteoviral P1-P2 frameshifting mRNA pseudoknot. <i>Journal of Molecular Biology</i> , <b>2002</b> , 322, 621-33  | 6.5  | 73  |

|    |   |     |     |
|----|---|-----|-----|
| 47 | Conformational heterogeneity in the C-terminal zinc fingers of human MTF-1: an NMR and zinc-binding study. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 42322-32   | 5.4 | 29  |
| 46 | Metal response element (MRE)-binding transcription factor-1 (MTF-1): structure, function, and regulation. <i>Antioxidants and Redox Signaling</i> , <b>2001</b> , 3, 577-96   | 8.4 | 129 |
| 45 | Spectroscopic properties of the metalloregulatory Cd(II) and Pb(II) sites of <i>S. aureus</i> pI258 CadC. <i>Biochemistry</i> , <b>2001</b> , 40, 4426-36   | 3.2 | 83  |
| 44 | Ratiometric pulsed alkylation/mass spectrometry of the cysteine pairs in individual zinc fingers of MRE-binding transcription factor-1 (MTF-1) as a probe of zinc chelate stability. <i>Biochemistry</i> , <b>2001</b> , 40, 15164-75 | 3.2 | 51  |
| 43 | Spectroscopic characterization of Co(II)-, Ni(II)-, and Cd(II)-substituted wild-type and non-native retroviral-type zinc finger peptides. <i>Journal of Biological Inorganic Chemistry</i> , <b>2000</b> , 5, 93-101                  | 3.7 | 59  |
| 42 | Contribution of the intercalated adenosine at the helical junction to the stability of the gag-pro frameshifting pseudoknot from mouse mammary tumor virus. <i>Rna</i> , <b>2000</b> , 6, 409-21                                      | 5.8 | 36  |
| 41 | Mutations in the N-terminal cooperativity domain of gene 32 protein alter properties of the T4 DNA replication and recombination systems. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 31496-504                       | 5.4 | 10  |
| 40 | Energetics of a strongly pH dependent RNA tertiary structure in a frameshifting pseudoknot. <i>Journal of Molecular Biology</i> , <b>2000</b> , 296, 659-71   | 6.5 | 77  |
| 39 | Structure, stability and function of RNA pseudoknots involved in stimulating ribosomal frameshifting. <i>Journal of Molecular Biology</i> , <b>2000</b> , 298, 167-85   | 6.5 | 189 |
| 38 | The zinc metalloregulatory protein <i>Synechococcus</i> PCC7942 SmtB binds a single zinc ion per monomer with high affinity in a tetrahedral coordination geometry. <i>Biochemistry</i> , <b>2000</b> , 39, 11818-29                  | 3.2 | 109 |
| 37 | Thermodynamics of stabilization of RNA pseudoknots by cobalt(III) hexaammine. <i>Biopolymers</i> , <b>1999</b> , 50, 443-58   | 2.2 | 16  |
| 36 | MRE-Binding transcription factor-1: weak zinc-binding finger domains 5 and 6 modulate the structure, affinity, and specificity of the metal-response element complex. <i>Biochemistry</i> , <b>1999</b> , 38, 12913-25                | 3.2 | 96  |
| 35 | Equilibrium unfolding pathway of an H-type RNA pseudoknot which promotes programmed -1 ribosomal frameshifting. <i>Journal of Molecular Biology</i> , <b>1999</b> , 289, 1283-99  | 6.5 | 32  |
| 34 | Solution structure and backbone dynamics of Mason-Pfizer monkey virus (MPMV) nucleocapsid protein. <i>Protein Science</i> , <b>1998</b> , 7, 2265-80  | 6.3 | 29  |
| 33 | Structural and functional heterogeneity among the zinc fingers of human MRE-binding transcription factor-1. <i>Biochemistry</i> , <b>1998</b> , 37, 11152-61  | 3.2 | 71  |
| 32 | Equilibrium unfolding (folding) pathway of a model H-type pseudoknotted RNA: the role of magnesium ions in stability. <i>Biochemistry</i> , <b>1998</b> , 37, 16116-29  | 3.2 | 42  |
| 31 | Mutational analysis of domain II beta of bacteriophage Mu transposase: domains II alpha and II beta belong to different catalytic complementation groups. <i>Journal of Molecular Biology</i> , <b>1998</b> , 275, 221-32             | 6.5 | 22  |
| 30 | Non-nearest neighbor effects on the thermodynamics of unfolding of a model mRNA pseudoknot. <i>Journal of Molecular Biology</i> , <b>1998</b> , 279, 545-64   | 6.5 | 46  |

|    |   |      |     |
|----|---|------|-----|
| 29 | The RNA molecule CsrB binds to the global regulatory protein CsrA and antagonizes its activity in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 17502-10                                | 5.4  | 326 |
| 28 | Zinc site redesign in T4 gene 32 protein: structure and stability of cobalt(II) complexes formed by wild-type and metal ligand substitution mutants. <i>Biochemistry</i> , <b>1997</b> , 36, 730-42                             | 3.2  | 34  |
| 27 | Base-pairings within the RNA pseudoknot associated with the simian retrovirus-1 gag-pro frameshift site. <i>Journal of Molecular Biology</i> , <b>1997</b> , 270, 464-70  | 6.5  | 43  |
| 26 | Structure of the autoregulatory pseudoknot within the gene 32 messenger RNA of bacteriophages T2 and T6: a model for a possible family of structurally related RNA pseudoknots. <i>Biochemistry</i> , <b>1996</b> , 35, 4187-98 | 3.2  | 56  |
| 25 | The N-terminal B-domain of T4 gene 32 protein modulates the lifetime of cooperatively bound Gp32-ss nucleic acid complexes. <i>Biochemistry</i> , <b>1996</b> , 35, 14395-404   | 3.2  | 6   |
| 24 | Thermodynamics of folding of the RNA pseudoknot of the T4 gene 32 autoregulatory messenger RNA. <i>Biochemistry</i> , <b>1996</b> , 35, 4176-86   | 3.2  | 35  |
| 23 | Characterization of a cooperativity domain mutant Lys3 --> Ala (K3A) T4 gene 32 protein. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 27623-9  | 5.4  | 13  |
| 22 | Interaction of retroviral nucleocapsid proteins with transfer RNAPhe: a lead ribozyme and 1H NMR study. <i>Nucleic Acids Research</i> , <b>1996</b> , 24, 3568-75   | 20.1 | 14  |
| 21 | X-ray and Visible Absorption Spectroscopy of Wild-Type and Mutant T4 Gene 32 Proteins: His64, not His81, Is the Non-Thiolate Zinc Ligand. <i>Journal of the American Chemical Society</i> , <b>1995</b> , 117, 9437-9440        | 16.4 | 15  |
| 20 | Recombinant HIV-1 nucleocapsid protein accelerates HIV-1 reverse transcriptase catalyzed DNA strand transfer reactions and modulates RNase H activity. <i>Biochemistry</i> , <b>1994</b> , 33, 13817-23                         | 3.2  | 167 |
| 19 | Effects of substitution of proposed Zn(II) ligand His81 or His64 in phage T4 gene 32 protein: spectroscopic evidence for a novel zinc coordination complex. <i>Biochemistry</i> , <b>1994</b> , 33, 8139-48                     | 3.2  | 8   |
| 18 | Energetics of arginine-4 substitution mutants in the N-terminal cooperativity domain of T4 gene 32 protein. <i>Biochemistry</i> , <b>1993</b> , 32, 11235-46  | 3.2  | 22  |
| 17 | Retroviral nucleocapsid proteins possess potent nucleic acid strand renaturation activity. <i>Protein Science</i> , <b>1993</b> , 2, 231-43   | 6.3  | 77  |
| 16 | Zn(II) coordination domain mutants of T4 gene 32 protein. <i>Biochemistry</i> , <b>1992</b> , 31, 765-74  | 3.2  | 29  |
| 15 | Site-specific 1,N6-ethenoadenylated single-stranded oligonucleotides as structural probes for the T4 gene 32 protein-ssDNA complex. <i>Biochemistry</i> , <b>1991</b> , 30, 8230-42   | 3.2  | 18  |
| 14 | NMR spectroscopy of 113Cd(II)-substituted gene 32 protein. <i>Biochemistry</i> , <b>1989</b> , 28, 2410-8   | 3.2  | 34  |
| 13 | 1H NMR studies of T4 gene 32 protein: effects of zinc removal and reconstitution. <i>Biochemistry</i> , <b>1989</b> , 28, 8828-32   | 3.2  | 20  |
| 12 | Thermal denaturation of T4 gene 32 protein: effects of zinc removal and substitution. <i>Biochemistry</i> , <b>1988</b> , 27, 5240-5  | 3.2  | 30  |

|    |   |      |     |
|----|---|------|-----|
| 11 | Calcium effects on calmodulin lysine reactivities. <i>Archives of Biochemistry and Biophysics</i> , <b>1987</b> , 252, 136-44   | 4.4  | 27  |
| 10 | The function of zinc in gene 32 protein from T4. <i>Biochemistry</i> , <b>1987</b> , 26, 5251-9   | 3.2  | 54  |
| 9  | Gene 32 protein, the single-stranded DNA binding protein from bacteriophage T4, is a zinc metalloprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1986</b> , 83, 8452-6 | 11.5 | 137 |
| 8  | Zinc metalloproteins involved in replication and transcription. <i>Journal of Inorganic Biochemistry</i> , <b>1986</b> , 28, 155-69   | 4.2  | 20  |
| 7  | Structural and functional differences between the two intrinsic zinc ions of Escherichia coli RNA polymerase. <i>Biochemistry</i> , <b>1986</b> , 25, 4969-78   | 3.2  | 38  |
| 6  | Functional properties of covalent beta-endorphin peptide/calmodulin complexes. Chlorpromazine binding and phosphodiesterase activation. <i>Biochemistry</i> , <b>1985</b> , 24, 1203-11                                     | 3.2  | 32  |
| 5  | Mechanism-based inhibitors of dopamine beta-hydroxylase: inhibition by 2-bromo-3-(p-hydroxyphenyl)-1-propene. <i>Biochemistry</i> , <b>1984</b> , 23, 3590-8  | 3.2  | 21  |
| 4  | Identification of beta-endorphin residues 14-25 as a region involved in the inhibition of calmodulin-stimulated phosphodiesterase activity. <i>Biochemistry</i> , <b>1983</b> , 22, 5584-91                                 | 3.2  | 37  |
| 3  | des-(1-13) human beta-endorphin interacts with calmodulin. <i>Peptides</i> , <b>1983</b> , 4, 191-4   | 3.8  | 12  |
| 2  | Structural determinants of persulfide-sensing specificity in a dithiol-based transcriptional regulator  |      | 2   |
| 1  | Rapid, Low-Cost Detection of Water Contaminants Using Regulated In Vitro Transcription  |      | 17  |