

John B Rafferty

List of Publications by Year in descending order

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62
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3,007
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186265

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62
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62
docs citations

62
times ranked

3097
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Molecular basis of triclosan activity. <i>Nature</i> , 1999, 398, 383-384. | 27.8 | 473 |
| 2 | Three-dimensional crystal structures of <i>Escherichia coli</i> met repressor with and without corepressor. <i>Nature</i> , 1989, 341, 705-710. | 27.8 | 192 |
| 3 | Triclosan inhibits the growth of <i>Plasmodium falciparum</i> and <i>Toxoplasma gondii</i> by inhibition of Apicomplexan Fab I. <i>International Journal for Parasitology</i> , 2001, 31, 109-113. | 3.1 | 190 |
| 4 | Structural Studies of Fatty Acyl-(Acyl Carrier Protein) Thioesters Reveal a Hydrophobic Binding Cavity that Can Expand to Fit Longer Substrates. <i>Journal of Molecular Biology</i> , 2007, 365, 135-145. | 4.2 | 142 |
| 5 | Crystal structure of <i>E. coli</i> RuvA with bound DNA Holliday junction at 6 Å... resolution. <i>Nature Structural Biology</i> , 1998, 5, 441-446. | 9.7 | 135 |
| 6 | Cooperative tandem binding of met repressor of <i>Escherichia coli</i> . <i>Nature</i> , 1989, 341, 711-715. | 27.8 | 122 |
| 7 | X-Ray Crystallographic Studies on Butyryl-ACP Reveal Flexibility of the Structure around a Putative Acyl Chain Binding Site. <i>Structure</i> , 2002, 10, 825-835. | 3.3 | 114 |
| 8 | Common themes in redox chemistry emerge from the X-ray structure of oilseed rape (<i>Brassica napus</i>) enoyl acyl carrier protein reductase. <i>Structure</i> , 1995, 3, 927-938. | 3.3 | 110 |
| 9 | Structural insight into gene transcriptional regulation and effector binding by the Lrp/AsnC family. <i>Nucleic Acids Research</i> , 2006, 34, 1439-1449. | 14.5 | 106 |
| 10 | Crystallographic analysis of triclosan bound to enoyl reductase. <i>Journal of Molecular Biology</i> , 1999, 294, 527-535. | 4.2 | 90 |
| 11 | The X-ray structure of <i>Brassica napus</i> β^2 -keto acyl carrier protein reductase and its implications for substrate binding and catalysis. <i>Structure</i> , 2000, 8, 339-347. | 3.3 | 88 |
| 12 | Analysis of the Structure, Substrate Specificity, and Mechanism of Squash Glycerol-3-Phosphate (1)-Acyltransferase. <i>Structure</i> , 2001, 9, 347-353. | 3.3 | 82 |
| 13 | Structural and Functional Analysis of the Kid Toxin Protein from <i>E. coli</i> Plasmid R1. <i>Structure</i> , 2002, 10, 1425-1433. | 3.3 | 77 |
| 14 | A Novel Ligand-binding Domain Involved in Regulation of Amino Acid Metabolism in Prokaryotes. <i>Journal of Biological Chemistry</i> , 2002, 277, 37464-37468. | 3.4 | 72 |
| 15 | A study of the structure-activity relationship for diazaborine inhibition of <i>Escherichia coli</i> enoyl-ACP reductase. <i>Journal of Molecular Biology</i> , 2001, 309, 171-180. | 4.2 | 65 |
| 16 | The Structure of <i>Bacillus subtilis</i> RecU Holliday Junction Resolvase and Its Role in Substrate Selection and Sequence-Specific Cleavage. <i>Structure</i> , 2005, 13, 1341-1351. | 3.3 | 61 |
| 17 | The Crystal Structure of Diadenosine Tetraphosphate Hydrolase from <i>Caenorhabditis elegans</i> in Free and Binary Complex Forms. <i>Structure</i> , 2002, 10, 589-600. | 3.3 | 57 |
| 18 | Inhibitor Binding Studies on Enoyl Reductase Reveal Conformational Changes Related to Substrate Recognition. <i>Journal of Biological Chemistry</i> , 1999, 274, 30811-30817. | 3.4 | 55 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | The X-ray structure of Escherichia coli enoyl reductase with bound NAD + at 2.1 Å.. resolution 1 1 Edited by R. Huber. Journal of Molecular Biology, 1998, 284, 1529-1546. | 4.2 | 51 |
| 20 | Structural and functional characterization of NanU, a novel high-affinity sialic acid-inducible binding protein of oral and gut-dwelling Bacteroidetes species. Biochemical Journal, 2014, 458, 499-511. | 3.7 | 43 |
| 21 | The RuvABC resolvasome. FEBS Journal, 2002, 269, 5492-5501. | 0.2 | 41 |
| 22 | Studies of Toxoplasma gondii and Plasmodium falciparum enoyl acyl carrier protein reductase and implications for the development of antiparasitic agents. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 328-338. | 2.5 | 40 |
| 23 | The molecular basis of endolytic activity of a multidomain alginate lyase from Defluviitalea phaphyphila, a representative of a new lyase family, PL39. Journal of Biological Chemistry, 2019, 294, 18077-18091. | 3.4 | 37 |
| 24 | Direct observation of DNA threading in flap endonuclease complexes. Nature Structural and Molecular Biology, 2016, 23, 640-646. | 8.2 | 35 |
| 25 | The Virulence Factor PEB4 (Cj0596) and the Periplasmic Protein Cj1289 Are Two Structurally Related SurA-like Chaperones in the Human Pathogen Campylobacter jejuni. Journal of Biological Chemistry, 2011, 286, 21254-21265. | 3.4 | 33 |
| 26 | The CoupSTU and TarPQM Transporters in Rhodospseudomonas palustris: Redundant, Promiscuous Uptake Systems for Lignin-Derived Aromatic Substrates. PLoS ONE, 2013, 8, e59844. | 2.5 | 33 |
| 27 | Cloning, characterisation and crystallisation of a diadenosine 5'-P1,P4-tetraphosphate pyrophosphohydrolase from Caenorhabditis elegans. BBA - Proteins and Proteomics, 2001, 1550, 27-36. | 2.1 | 32 |
| 28 | Structural Basis of Synercid® (Quinupristin-Dalfopristin) Resistance in Gram-positive Bacterial Pathogens. Journal of Biological Chemistry, 2003, 278, 29963-29970. | 3.4 | 32 |
| 29 | Fatty Acid Biosynthesis in Plants – Metabolic Pathways, Structure and Organization. Advances in Photosynthesis and Respiration, 2009, , 11-34. | 1.0 | 27 |
| 30 | Expression, purification and crystallization of the Plasmodium falciparum enoyl reductase. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1246-1248. | 2.5 | 25 |
| 31 | The Structure of Escherichia coli RusA Endonuclease Reveals a New Holliday Junction DNA Binding Fold. Structure, 2003, 11, 1557-1567. | 3.3 | 24 |
| 32 | Structural similarities between Escherichia coli RuvA protein and other DNA-binding proteins and a mutational analysis of its binding to the holliday junction. Journal of Molecular Biology, 1998, 278, 105-116. | 4.2 | 23 |
| 33 | Molecular genetic analysis of enoyl-acyl carrier protein reductase inhibition by diazaborine. Molecular Microbiology, 1999, 31, 443-450. | 2.5 | 22 |
| 34 | Squash Glycerol-3-phosphate (1)-Acyltransferase. Journal of Biological Chemistry, 2002, 277, 43918-43923. | 3.4 | 22 |
| 35 | Insights into the mechanisms of homologous recombination from the structure of RuvA. Current Opinion in Structural Biology, 1997, 7, 798-803. | 5.7 | 20 |
| 36 | Structural basis for high-affinity adipate binding to AdpC (<sc>RPA</sc>4515), an orphan periplasmic-binding protein from the tripartite tricarboxylate transporter (<sc>TTT</sc>) family in <i>Rhodospseudomonas palustris</i>. FEBS Journal, 2017, 284, 4262-4277. | 4.7 | 20 |

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|----|--|------|-----------|
| 37 | Identification and structural analysis of the tripartite $\hat{\pm}$ -pore forming toxin of <i>Aeromonas hydrophila</i> . <i>Nature Communications</i> , 2019, 10, 2900. | 12.8 | 20 |
| 38 | RusA Holliday junction resolvase: DNA complex structureâ€™insights into selectivity and specificity. <i>Nucleic Acids Research</i> , 2006, 34, 5577-5584. | 14.5 | 19 |
| 39 | Crystallization of the NADH-specific Enoyl Acyl Carrier Protein Reductase from <i>Brassica napus</i> . <i>Journal of Molecular Biology</i> , 1994, 237, 240-242. | 4.2 | 16 |
| 40 | Non-cytotoxic variants of the Kid protein that retain their auto-regulatory activity. <i>Plasmid</i> , 2003, 50, 120-130. | 1.4 | 16 |
| 41 | Analysis of the Catalytic and Binding Residues of the Diadenosine Tetraphosphate Pyrophosphohydrolase from <i>Caenorhabditis elegans</i> by Site-directed Mutagenesis. <i>Journal of Biological Chemistry</i> , 2003, 278, 4435-4439. | 3.4 | 16 |
| 42 | The Stalk Region of the RecU Resolvase Is Essential for Holliday Junction Recognition and Distortion. <i>Journal of Molecular Biology</i> , 2011, 410, 39-49. | 4.2 | 14 |
| 43 | Crystallization of the met repressor from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1988, 200, 217-219. | 4.2 | 12 |
| 44 | Insights into the structure and assembly of the <i>Bacillus subtilis</i> clamp-loader complex and its interaction with the replicative helicase. <i>Nucleic Acids Research</i> , 2013, 41, 5115-5126. | 14.5 | 12 |
| 45 | Crystallization and preliminary X-ray crystallographic studies on acyl-(acyl carrier protein) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 330-332. | 2.5 | 11 |
| 46 | Crystallization and preliminary X-ray crystallographic studies on the parD-encoded protein Kid from <i>Escherichia coli</i> plasmid R1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 355-358. | 2.5 | 10 |
| 47 | Acyltransferases and their role in the biosynthesis of lipids - opportunities for new oils. <i>Journal of Plant Physiology</i> , 2001, 158, 505-513. | 3.5 | 9 |
| 48 | Structural Analysis of <i>Bacillus subtilis</i> SPP1 Phage Helicase Loader Protein G39P. <i>Journal of Biological Chemistry</i> , 2003, 278, 15304-15312. | 3.4 | 9 |
| 49 | Mutants of phage ϕ IL 67 RuvC with enhanced Holliday junction binding selectivity and resolution symmetry. <i>Molecular Microbiology</i> , 2013, 89, 1240-1258. | 2.5 | 9 |
| 50 | A New Mechanism for High-Affinity Uptake of C4-Dicarboxylates in Bacteria Revealed by the Structure of <i>Rhodospseudomonas palustris</i> MatC (RPA3494), a Periplasmic Binding Protein of the Tripartite Tricarboxylate Transporter (TTT) Family. <i>Journal of Molecular Biology</i> , 2019, 431, 351-367. | 4.2 | 7 |
| 51 | Characterisation of a tripartite $\hat{\pm}$ -pore forming toxin from <i>Serratia marcescens</i> . <i>Scientific Reports</i> , 2021, 11, 6447. | 3.3 | 7 |
| 52 | Crystallization of the NADP-dependent $\hat{2}$ -keto acyl-carrier protein reductase from <i>Brassica napus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 86-88. | 2.5 | 5 |
| 53 | Structural insights into dynamics of RecUâ€™HJ complex formation elucidates key role of NTR and stalk region toward formation of reactive state. <i>Nucleic Acids Research</i> , 2017, 45, 975-986. | 14.5 | 5 |
| 54 | Crystallization of the NADP-dependent $\hat{2}$ -keto acyl carrier protein reductase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 427-429. | 2.5 | 4 |

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|----|---|-----|-----------|
| 55 | Crystallization of <i>Escherichia coli</i> RuvA complexed with a synthetic Holliday junction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 263-265. | 2.5 | 4 |
| 56 | Rapid analysis of protein-nucleic acid complexes using MALDI TOF mass spectrometry and ion pair reverse phase liquid chromatography. <i>Journal of Proteomics</i> , 2004, 58, 39-48. | 2.4 | 4 |
| 57 | The structural basis for high-affinity uptake of lignin-derived aromatic compounds by proteobacterial TRAP transporters. <i>FEBS Journal</i> , 2022, 289, 436-456. | 4.7 | 3 |
| 58 | Crystallization and quaternary structure analysis of an Lrp-like regulatory protein from the hyperthermophile <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 886-888. | 2.5 | 2 |
| 59 | Crystallization of a complex of <i>Caenorhabditis elegans</i> diadenosine tetraphosphate hydrolase and a non-hydrolysable substrate analogue, AppCH2ppA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 526-528. | 2.5 | 1 |
| 60 | Crystallization of RusA Holliday junction resolvase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2262-2264. | 2.5 | 1 |
| 61 | Crystallization and preliminary X-ray analysis of the receiver domain of a putative response regulator, BPSLO128, from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 917-922. | 0.7 | 0 |
| 62 | Towards a Structural Understanding of Enzymes of Lipid Biosynthesis. , 1995, , 55-57. | | 0 |