

# John B Rafferty

## List of Publications by Year in descending order

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62  
papers

3,007  
citations

186265

28  
h-index

161849

54  
g-index

62  
all docs

62  
docs citations

62  
times ranked

3097  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Characterisation of a tripartite $\hat{\pm}$ -pore forming toxin from <i>Serratia marcescens</i> . <i>Scientific Reports</i> , 2021, 11, 6447.	3.3	7
3	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
4	The molecular basis of endolytic activity of a multidomain alginate lyase from <i>Defluviitalea phaphyphila</i> , a representative of a new lyase family, PL39. <i>Journal of Biological Chemistry</i> , 2019, 294, 18077-18091.	3.4	37
5	A New Mechanism for High-Affinity Uptake of C4-Dicarboxylates in Bacteria Revealed by the Structure of <i>Rhodopseudomonas 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
6	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> <i>Rhodopseudomonas palustris</i> FEBS Journal, 2017, 284, 4262-4277.	4.7	20
7	Structural insights into dynamics of RecU-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
8	Direct observation of DNA threading in flap endonuclease complexes. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 640-646.	8.2	35
9	Structural and functional characterization of NanU, a novel high-affinity sialic acid-inducible binding protein of oral and gut-dwelling <i>Bacteroidetes</i> species. <i>Biochemical Journal</i> , 2014, 458, 499-511.	3.7	43
10	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
11	Mutants of phage $\phi$ IL 67 RuvC with enhanced Holliday junction binding selectivity and resolution symmetry. <i>Molecular Microbiology</i> , 2013, 89, 1240-1258.	2.5	9
12	The CouPSTU and TarPQM Transporters in <i>Rhodopseudomonas palustris</i> : Redundant, Promiscuous Uptake Systems for Lignin-Derived Aromatic Substrates. <i>PLoS ONE</i> , 2013, 8, e59844.	2.5	33
13	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
14	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
15	The Virulence Factor PEB4 (Cj0596) and the Periplasmic Protein Cj1289 Are Two Structurally Related SurA-like Chaperones in the Human Pathogen <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 21254-21265.	3.4	33
16	Fatty Acid Biosynthesis in Plants – Metabolic Pathways, Structure and Organization. <i>Advances in Photosynthesis and Respiration</i> , 2009, , 11-34.	1.0	27
17	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
18	Studies of <i>Toxoplasma gondii</i> and <i>Plasmodium falciparum</i> enoyl acyl carrier protein reductase and implications for the development of antiparasitic agents. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 328-338.	2.5	40

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19	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
20	RusA Holliday junction resolvase: DNA complex structure insights into selectivity and specificity. <i>Nucleic Acids Research</i> , 2006, 34, 5577-5584.	14.5	19
21	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
22	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
23	The Structure of <i>Escherichia coli</i> RusA Endonuclease Reveals a New Holliday Junction DNA Binding Fold. <i>Structure</i> , 2003, 11, 1557-1567.	3.3	24
24	Non-cytotoxic variants of the Kid protein that retain their auto-regulatory activity. <i>Plasmid</i> , 2003, 50, 120-130.	1.4	16
25	Expression, purification and crystallization of the <i>Plasmodium falciparum</i> enoyl reductase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1246-1248.	2.5	25
26	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
27	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
28	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
29	Structural Basis of Synercid® (Quinupristin-Dalfopristin) Resistance in Gram-positive Bacterial Pathogens. <i>Journal of Biological Chemistry</i> , 2003, 278, 29963-29970.	3.4	32
30	Squash Glycerol-3-phosphate (1)-Acyltransferase. <i>Journal of Biological Chemistry</i> , 2002, 277, 43918-43923.	3.4	22
31	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
32	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
33	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
34	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
35	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
36	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

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37	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
38	The RuvABC resolvasome. <i>FEBS Journal</i> , 2002, 269, 5492-5501.	0.2	41
39	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
40	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
41	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
42	Cloning, characterisation and crystallisation of a diadenosine 5'-P1,P4-tetraphosphate pyrophosphohydrolase from <i>Caenorhabditis elegans</i> . <i>BBA - Proteins and Proteomics</i> , 2001, 1550, 27-36.	2.1	32
43	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
44	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
45	Crystallization of the NADP-dependent $\beta^2$ -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
46	The X-ray structure of <i>Brassica napus</i> $\beta^2$ -keto acyl carrier protein reductase and its implications for substrate binding and catalysis. <i>Structure</i> , 2000, 8, 339-347.	3.3	88
47	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
48	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
49	Molecular genetic analysis of enoyl-acyl carrier protein reductase inhibition by diazaborine. <i>Molecular Microbiology</i> , 1999, 31, 443-450.	2.5	22
50	Molecular basis of triclosan activity. <i>Nature</i> , 1999, 398, 383-384.	27.8	473
51	Crystallographic analysis of triclosan bound to enoyl reductase. <i>Journal of Molecular Biology</i> , 1999, 294, 527-535.	4.2	90
52	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
53	Crystallization of the NADP-dependent $\beta^2$ -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
54	Structural similarities between <i>Escherichia coli</i> RuvA protein and other DNA-binding proteins and a mutational analysis of its binding to the holliday junction. <i>Journal of Molecular Biology</i> , 1998, 278, 105-116.	4.2	23

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55	The X-ray structure of Escherichia coli enoyl reductase with bound NAD + at 2.1 Å... resolution 1 Edited by R. Huber. Journal of Molecular Biology, 1998, 284, 1529-1546.	4.2	51
56	Insights into the mechanisms of homologous recombination from the structure of RuvA. Current Opinion in Structural Biology, 1997, 7, 798-803.	5.7	20
57	Common themes in redox chemistry emerge from the X-ray structure of oilseed rape (Brassica napus) enoyl acyl carrier protein reductase. Structure, 1995, 3, 927-938.	3.3	110
58	Towards a Structural Understanding of Enzymes of Lipid Biosynthesis. , 1995, , 55-57.		0
59	Crystallization of the NADH-specific Enoyl Acyl Carrier Protein Reductase from Brassica napus. Journal of Molecular Biology, 1994, 237, 240-242.	4.2	16
60	Three-dimensional crystal structures of Escherichia coli met repressor with and without corepressor. Nature, 1989, 341, 705-710.	27.8	192
61	Cooperative tandem binding of met repressor of Escherichia coli. Nature, 1989, 341, 711-715.	27.8	122
62	Crystallization of the met repressor from Escherichia coli. Journal of Molecular Biology, 1988, 200, 217-219.	4.2	12