

# Andrew J Fisher

## List of Publications by Year in descending order

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35  
papers

1,215  
citations

430874

18  
h-index

395702

33  
g-index

35  
all docs

35  
docs citations

35  
times ranked

1716  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures of human ADAR2 bound to dsRNA reveal base-flipping mechanism and basis for site selectivity. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 426-433.	8.2	154
2	A Sialyltransferase Mutant with Decreased Donor Hydrolysis and Reduced Sialidase Activities for Directly Sialylating Lewis <sup>x</sup> . <i>ACS Chemical Biology</i> , 2012, 7, 1232-1240.	3.4	135
3	Directed Evolution of a Selective and Sensitive Serotonin Sensor via Machine Learning. <i>Cell</i> , 2020, 183, 1986-2002.e26.	28.9	104
4	Crystal Structures of <i>Pasteurella multocida</i> Sialyltransferase Complexes with Acceptor and Donor Analogues Reveal Substrate Binding Sites and Catalytic Mechanism,. <i>Biochemistry</i> , 2007, 46, 6288-6298.	2.5	97
5	The Receptor-like Cytoplasmic Kinase BIK1 Localizes to the Nucleus and Regulates Defense Hormone Expression during Plant Innate Immunity. <i>Cell Host and Microbe</i> , 2018, 23, 485-497.e5.	11.0	92
6	Cytidine 5'-Monophosphate (CMP)-Induced Structural Changes in a Multifunctional Sialyltransferase from <i>Pasteurella multocida</i> ,. <i>Biochemistry</i> , 2006, 45, 2139-2148.	2.5	76
7	Crystal Structure of ATP Sulfurylase from <i>Penicillium chrysogenum</i> : Insights into the Allosteric Regulation of Sulfate Assimilation. <i>Biochemistry</i> , 2001, 40, 6795-6804.	2.5	68
8	Crystal Structure of Adenosine 5'-Phosphosulfate Kinase from <i>Penicillium chrysogenum</i> . <i>Biochemistry</i> , 2000, 39, 1613-1621.	2.5	49
9	Insight into the Radical Mechanism of Phycocyanobilin Ferredoxin Oxidoreductase (PcyA) Revealed by X-ray Crystallography and Biochemical Measurements. <i>Biochemistry</i> , 2007, 46, 1484-1494.	2.5	47
10	Recognition of duplex RNA by the deaminase domain of the RNA editing enzyme ADAR2. <i>Nucleic Acids Research</i> , 2015, 43, 1123-1132.	14.5	38
11	Structural Analysis of an Avr4 Effector Ortholog Offers Insight into Chitin Binding and Recognition by the Cf-4 Receptor. <i>Plant Cell</i> , 2016, 28, 1945-1965.	6.6	37
12	Structure of the <i>Cladosporium fulvum</i> Avr4 effector in complex with (GlcNAc) <sub>6</sub> reveals the ligand-binding mechanism and uncouples its intrinsic function from recognition by the Cf-4 resistance protein. <i>PLoS Pathogens</i> , 2018, 14, e1007263.	4.7	37
13	Asymmetric dimerization of adenosine deaminase acting on RNA facilitates substrate recognition. <i>Nucleic Acids Research</i> , 2020, 48, 7958-7972.	14.5	33
14	Controlling miRNA-like off-target effects of an siRNA with nucleobase modifications. <i>Organic and Biomolecular Chemistry</i> , 2017, 15, 10029-10036.	2.8	30
15	Click Modification of RNA at Adenosine: Structure and Reactivity of 7-Ethynyl- and 7-Triazolyl-8-aza-7-deazaadenosine in RNA. <i>ACS Chemical Biology</i> , 2014, 9, 1780-1787.	3.4	29
16	A Bump-Hole Approach for Directed RNA Editing. <i>Cell Chemical Biology</i> , 2019, 26, 269-277.e5.	5.2	28
17	Effects of Aicardi-Goutières syndrome mutations predicted from ADAR-RNA structures. <i>RNA Biology</i> , 2017, 14, 164-170.	3.1	22
18	Crystal structures of sialyltransferase from <i>Photobacterium damsela</i> . <i>FEBS Letters</i> , 2014, 588, 4720-4729.	2.8	21

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19	A far-red cyanobacteriochrome lineage specific for verdins. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27962-27970.	7.1	20
20	Structural basis for eukaryotic mRNA modification. Current Opinion in Structural Biology, 2018, 53, 59-68.	5.7	18
21	Rational Design of RNA Editing Guide Strands: Cytidine Analogs at the Orphan Position. Journal of the American Chemical Society, 2021, 143, 6865-6876.	13.7	12
22	Î±2â€“6-Neosialidase: A Sialyltransferase Mutant as a Sialyl Linkage-Specific Sialidase. ACS Chemical Biology, 2018, 13, 1228-1234.	3.4	11
23	Insight into the potential factors influencing the catalytic direction in cellobiose 2-epimerase by crystallization and mutagenesis. Acta Crystallographica Section D: Structural Biology, 2020, 76, 1104-1113.	2.3	11
24	Crystal Structures of <i>Mycobacterium tuberculosis</i> CysQ, with Substrate and Products Bound. Biochemistry, 2015, 54, 6830-6841.	2.5	9
25	<i>Enterococcus faecalis</i> Î±1â€“2-mannosidase (EfManâ€“): an efficient catalyst for glycoprotein N-glycan modification. FEBS Letters, 2020, 594, 439-451.	2.8	9
26	The Crystal Structure of Calmodulin Bound to the Cardiac Ryanodine Receptor (RyR2) at Residues Phe424â€“Val4271 Reveals a Fifth Calcium Binding Site. Biochemistry, 2021, 60, 1088-1096.	2.5	6
27	Catalytic Cycle of <i>Neisseria meningitidis</i> CMP-Sialic Acid Synthetase Illustrated by High-Resolution Protein Crystallography. Biochemistry, 2020, 59, 3157-3168.	2.5	5
28	Structural characterization of a nonhydrolyzing UDP-GlcNAc 2-epimerase from <i>Neisseria meningitidis</i> serogroup A. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 557-567.	0.8	4
29	Structures of <i>Bacteroides fragilis</i> uridine 5â€“diphosphate-N-acetylglucosamine (UDP-GlcNAc) acyltransferase (BflpxA). Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1068-1076.	2.5	3
30	Arabidopsis receptor-like cytoplasmic kinase BIK1: purification, crystallization and X-ray diffraction analysis. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 738-742.	0.8	3
31	Crystal structure of breast regression protein 39 (BRP39), a signaling glycoprotein expressed during mammary gland apoptosis, at 2.6Å... resolution. Journal of Structural Biology, 2021, 213, 107737.	2.8	3
32	Functional and Structural Analysis of the Toxin-Binding Site of the Cadherin G-Protein-Coupled Receptor, BT-R <sub>1</sub> , for Cry1A Toxins of <i>Bacillus thuringiensis</i> . Biochemistry, 2022, 61, 752-766.	2.5	3
33	Expression, purification and preliminary crystallographic analysis of <i>Mycobacterium tuberculosis</i> CysQ, a phosphatase involved in sulfur metabolism. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 750-753.	0.8	1
34	Induction of Positive Cooperativity by Amino Acid Replacements Within the C-Terminal Domain of <i>Penicillium chrysogenum</i> ATP Sulfurylase. Biochemical Society Transactions, 2000, 28, A320-A320.	3.4	0
35	Novel DNA and RNA inhibitors of metallo-Î²-lactamase. FASEB Journal, 2006, 20, .	0.5	0