

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	Functional and Structural Analysis of the Toxin-Binding Site of the Cadherin G-Protein-Coupled Receptor, BT-R ₁ , for Cry1A Toxins of <i>Bacillus thuringiensis</i> . <i>Biochemistry</i> , 2022, 61, 752-766.	2.5	3
2	The Crystal Structure of Calmodulin Bound to the Cardiac Ryanodine Receptor (RyR2) at Residues Phe4246-Val4271 Reveals a Fifth Calcium Binding Site. <i>Biochemistry</i> , 2021, 60, 1088-1096.	2.5	6
3	Rational Design of RNA Editing Guide Strands: Cytidine Analogs at the Orphan Position. <i>Journal of the American Chemical Society</i> , 2021, 143, 6865-6876.	13.7	12
4	Crystal structure of breast regression protein 39 (BRP39), a signaling glycoprotein expressed during mammary gland apoptosis, at 2.6 Å resolution. <i>Journal of Structural Biology</i> , 2021, 213, 107737.	2.8	3
5	Catalytic Cycle of <i>Neisseria meningitidis</i> CMP-Sialic Acid Synthetase Illustrated by High-Resolution Protein Crystallography. <i>Biochemistry</i> , 2020, 59, 3157-3168.	2.5	5
6	<i>Enterococcus faecalis</i> Î±1-mannosidase (EfMan1): an efficient catalyst for glycoprotein N-glycan modification. <i>FEBS Letters</i> , 2020, 594, 439-451.	2.8	9
7	Structural characterization of a nonhydrolyzing UDP-GlcNAc 2-epimerase from <i>Neisseria meningitidis</i> serogroup A. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 557-567.	0.8	4
8	A far-red cyanobacteriochrome lineage specific for verdins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27962-27970.	7.1	20
9	Directed Evolution of a Selective and Sensitive Serotonin Sensor via Machine Learning. <i>Cell</i> , 2020, 183, 1986-2002.e26.	28.9	104
10	Insight into the potential factors influencing the catalytic direction in cellobiose 2-epimerase by crystallization and mutagenesis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1104-1113.	2.3	11
11	Asymmetric dimerization of adenosine deaminase acting on RNA facilitates substrate recognition. <i>Nucleic Acids Research</i> , 2020, 48, 7958-7972.	14.5	33
12	A Bump-Hole Approach for Directed RNA Editing. <i>Cell Chemical Biology</i> , 2019, 26, 269-277.e5.	5.2	28
13	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
14	Î±6-Neosialidase: A Sialyltransferase Mutant as a Sialyl Linkage-Specific Sialidase. <i>ACS Chemical Biology</i> , 2018, 13, 1228-1234.	3.4	11
15	Structure of the <i>Cladosporium fulvum</i> Avr4 effector in complex with (GlcNAc) ₆ 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
16	Structural basis for eukaryotic mRNA modification. <i>Current Opinion in Structural Biology</i> , 2018, 53, 59-68.	5.7	18
17	Effects of Aicardi-Goutières syndrome mutations predicted from ADAR-RNA structures. <i>RNA Biology</i> , 2017, 14, 164-170.	3.1	22
18	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

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19	Arabidopsis receptor-like cytoplasmic kinase BIK1: purification, crystallization and X-ray diffraction analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 738-742.	0.8	3
20	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
21	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
22	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
23	Structures of <i>Bacteroides fragilis</i> uridine 5'-diphosphate-N-acetylglucosamine (UDP-GlcNAc) acyltransferase (BflpxA). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1068-1076.	2.5	3
24	Crystal Structures of <i>Mycobacterium tuberculosis</i> CysQ, with Substrate and Products Bound. <i>Biochemistry</i> , 2015, 54, 6830-6841.	2.5	9
25	Crystal structures of sialyltransferase from <i>Photobacterium damsela</i> . <i>FEBS Letters</i> , 2014, 588, 4720-4729.	2.8	21
26	Expression, purification and preliminary crystallographic analysis of <i>Mycobacterium tuberculosis</i> CysQ, a phosphatase involved in sulfur metabolism. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 750-753.	0.8	1
27	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
28	A Sialyltransferase Mutant with Decreased Donor Hydrolysis and Reduced Sialidase Activities for Directly Sialylating Lewis ^x . <i>ACS Chemical Biology</i> , 2012, 7, 1232-1240.	3.4	135
29	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
30	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
31	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
32	Novel DNA and RNA inhibitors of metallo- β -lactamase. <i>FASEB Journal</i> , 2006, 20, .	0.5	0
33	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
34	Induction of Positive Cooperativity by Amino Acid Replacements Within the C-Terminal Domain of <i>Penicillium chrysogenum</i> ATP Sulfurylase. <i>Biochemical Society Transactions</i> , 2000, 28, A320-A320.	3.4	0
35	Crystal Structure of Adenosine 5'-Phosphosulfate Kinase from <i>Penicillium chrysogenum</i> . <i>Biochemistry</i> , 2000, 39, 1613-1621.	2.5	49