Aaron J Oakley

List of Publications by Year
in descending order

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91
papers

4,357
citations

100601
38
h-index

129628
63
g-index

99
all docs

99
docs citations

99
times ranked

5879
citing authors

#	Article	IF	Citations
1	Proposed mechanism for monomethylarsonate reductase activity of human omega-class glutathione transferase GSTO1-1. Biochemical and Biophysical Research Communications, 2022, 590, 7-13.	1.0	1
2	Mechanistic behavior and subtle key events during DNA clamp opening and closing in T4 bacteriophage. International Journal of Biological Macromolecules, 2022, 208, 11-19.	3.6	54
3	Molecular interactions of <scp>STAC</scp> proteins with skeletal muscle dihydropyridine receptor and excitationâ€contraction coupling. Protein Science, 2022, 31, e4311.	3.1	2
4	Mechanism of transcription modulation by the transcription-repair coupling factor. Nucleic Acids Research, 2022, 50, 5688-5712.	6.5	6
5	RNA polymerases from low G+C gram-positive bacteria. Transcription, 2021, 12, 1-11.	1.7	3
6	Multiple classes and isoforms of the RNA polymerase recycling motor protein HelD. MicrobiologyOpen, 2021, 10, e1251.	1.2	1
7	Atomistic Insights into Photoprotein Formation: Computational Prediction of the Properties of Coelenterazine and Oxygen Binding in Obelin. Journal of Computational Chemistry, 2020, 41, 587-603.	1.5	5
8	Molecular basis for RNA polymerase-dependent transcription complex recycling by the helicase-like motor protein HelD. Nature Communications, 2020, 11, 6420.	5.8	29
9	Development of Benzenesulfonamide Derivatives as Potent Glutathione Transferase Omega-1 Inhibitors. Journal of Medicinal Chemistry, 2020, 63, 2894-2914.	2.9	12
10	A structural view of bacterial DNA replication. Protein Science, 2019, 28, 990-1004.	3.1	32
11	Reviewing Hit Discovery Literature for Difficult Targets: Glutathione Transferase Omega-1 as an Example. Journal of Medicinal Chemistry, 2018, 61, 7448-7470.	2.9	14
12	Crystal structures and biochemical characterization of DNA sliding clamps from three Gram-negative bacterial pathogens. Journal of Structural Biology, 2018, 204, 396-405.	1.3	6
13	Rational Design of a 310 -Helical PIP-Box Mimetic Targeting PCNA, the Human Sliding Clamp. Chemistry - A European Journal, 2018, 24, 11238-11238.	1.7	0
14	Fragment-Based Discovery of Inhibitors of the Bacterial DnaG-SSB Interaction. Antibiotics, 2018, 7, 14.	1.5	14
15	Identification of a novel tetrameric structure for human apolipoprotein-D. Journal of Structural Biology, 2018, 203, 205-218.	1.3	12
16	Rational Design of a 3₁₀â€Helical PIPâ€Box Mimetic Targeting PCNA, the Human Sliding Clamp. Chemistry - A European Journal, 2018, 24, 11325-11331.	1.7	16
17	Hotspots of age-related protein degradation: the importance of neighboring residues for the formation of non-disulfide crosslinks derived from cysteine. Biochemical Journal, 2017, 474, 2475-2487.	1.7	15
18	Structural and biophysical analyses of the skeletal dihydropyridine receptor Î² subunit Î²1a reveal critical roles of domain interactions for stability. Journal of Biological Chemistry, 2017, 292, 8401-8411.	1.6	7

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19	GSTO1-1 plays a pro-inflammatory role in models of inflammation, colitis and obesity. Scientific Reports, 2017, 7, 17832.	1.6	47
20	Dynamics of Open DNA Sliding Clamps. PLoS ONE, 2016, 11, e0154899.	1.1	19
21	Bacterial Sliding Clamp Inhibitors that Mimic the Sequential Binding Mechanism of Endogenous Linear Motifs. Journal of Medicinal Chemistry, 2015, 58, 4693-4702.	2.9	28
22	Replisome speed determines the efficiency of the Tusâˆ’Ter replication termination barrier. Nature, 2015, 525, 394-398.	13.7	42
23	Structure and function of a spectrin-like regulator of bacterial cytokinesis. Nature Communications, 2014, 5, 5421.	5.8	41
24	Intramolecular binding mode of the C-terminus of<i>Escherichia coli</i>single-stranded DNA binding protein determined by nuclear magnetic resonance spectroscopy. Nucleic Acids Research, 2014, 42, 2750-2757.	6.5	36
25	Structural and Binding Studies of the Cav1.1 Î²1A Subunit. Biophysical Journal, 2014, 106, 446a.	0.2	0
26	Efficient synthesis and antioxidant activity of coelenterazine analogues. Tetrahedron Letters, 2014, 55, 6212-6215.	0.7	19
27	Discovery of Lead Compounds Targeting the Bacterial Sliding Clamp Using a Fragment-Based Approach. Journal of Medicinal Chemistry, 2014, 57, 2799-2806.	2.9	49
28	DNA Replication Is the Target for the Antibacterial Effects of Nonsteroidal Anti-Inflammatory Drugs. Chemistry and Biology, 2014, 21, 481-487.	6.2	102
29	Structural and Thermodynamic Dissection of Linear Motif Recognition by the <i>E. coli</i> Sliding Clamp. Journal of Medicinal Chemistry, 2013, 56, 8665-8673.	2.9	23
30	Proofreading exonuclease on a tether: the complex between the E. coli DNA polymerase III subunits Î±, Îµ, Î¸ and Î² reveals a highly flexible arrangement of the proofreading domain. Nucleic Acids Research, 2013, 41, 5354-5367.	6.5	34
31	Structural Insights into Omega-Class Glutathione Transferases: A Snapshot of Enzyme Reduction and Identification of a Non-Catalytic Ligandin Site. PLoS ONE, 2013, 8, e60324.	1.1	36
32	Fragment-Based Screening by Protein Crystallography: Successes and Pitfalls. International Journal of Molecular Sciences, 2012, 13, 12857-12879.	1.8	50
33	Selective reduction of hydroperoxyeicosatetraenoic acids to their hydroxy derivatives by apolipoprotein D: implications for lipid antioxidant activity and Alzheimer's disease. Biochemical Journal, 2012, 442, 713-721.	1.7	62
34	Time to Face the Fats: What Can Mass Spectrometry Reveal about the Structure of Lipids and Their Interactions with Proteins?. Journal of the American Society for Mass Spectrometry, 2012, 23, 1441-1449.	1.2	24
35	Structural Insights into the Dehydroascorbate Reductase Activity of Human Omega-Class Glutathione Transferases. Journal of Molecular Biology, 2012, 420, 190-203.	2.0	60
36	Molecular Dynamics Analysis of Apolipoprotein-D - Lipid Hydroperoxide Interactions: Mechanism for Selective Oxidation of Met-93. PLoS ONE, 2012, 7, e34057.	1.1	24

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37	Binding Inhibitors of the Bacterial Sliding Clamp by Design. Journal of Medicinal Chemistry, 2011, 54, 4831-4838.	2.9	38
38	Glutathione transferases: a structural perspective. Drug Metabolism Reviews, 2011, 43, 138-151.	1.5	298
39	Novel Folding and Stability Defects Cause a Deficiency of Human Glutathione Transferase Omega 1. Journal of Biological Chemistry, 2011, 286, 4271-4279.	1.6	24
40	Identification and characterisation of new inhibitors for the human hematopoietic prostaglandin D 2 synthase. European Journal of Medicinal Chemistry, 2010, 45, 447-454.	2.6	15
41	Structural basis for cofactor-independent dioxygenation of <i>N</i> -heteroaromatic compounds at the Î±/Î²-hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 657-662.	3.3	77
42	Structural and Functional Basis of Resistance to Neuraminidase Inhibitors of Influenza B Viruses. Journal of Medicinal Chemistry, 2010, 53, 6421-6431.	2.9	75
43	Identification and Characterization of Î³-Glutamylamine Cyclotransferase, an Enzyme Responsible for Î³-Glutamyl-Ïµ-lysine Catabolism. Journal of Biological Chemistry, 2010, 285, 9642-9648.	1.6	33
44	The structure of Aspergillus niger phytase PhyA in complex with a phytate mimetic. Biochemical and Biophysical Research Communications, 2010, 397, 745-749.	1.0	42
45	Sodium translocation by the iminoglycinuria associated imino transporter (SLC6A20). Molecular Membrane Biology, 2009, 26, 333-346.	2.0	21
46	Malonate-bound structure of the glycerophosphodiesterase from<i>Enterobacter aerogenes</i>(GpdQ) and characterization of the native Fe²⁺metal-ion preference. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 681-685.	0.7	24
47	S-(4-Nitrophenacyl)glutathione is a specific substrate for glutathione transferase omega 1-1. Analytical Biochemistry, 2008, 374, 25-30.	1.1	44
48	The Anti-cancer Drug Chlorambucil as a Substrate for the Human Polymorphic Enzyme Glutathione Transferase P1-1: Kinetic Properties and Crystallographic Characterisation of Allelic Variants. Journal of Molecular Biology, 2008, 380, 131-144.	2.0	49
49	The Identification and Structural Characterization of C7orf24 as Î³-Glutamyl Cyclotransferase. Journal of Biological Chemistry, 2008, 283, 22031-22042.	1.6	110
50	Polymorphism of glutathione transferase Omega 1 in a population exposed to a high environmental arsenic burden. Pharmacogenetics and Genomics, 2008, 18, 1-10.	0.7	40
51	Anisotropic atomic motions in high-resolution protein crystallography molecular dynamics simulations. Physical Biology, 2007, 4, 79-90.	0.8	14
52	Crystallization and diffraction data of 1H-3-hydroxy-4-oxoquinoline 2,4-dioxygenase: a cofactor-free oxygenase of the Î±/Î²-hydrolase family. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 378-381.	0.7	8
53	Magneto-Optic Spectroscopy of a Protein Tetramer Binding Two Exciton-Coupled Chlorophylls. Journal of the American Chemical Society, 2006, 128, 3649-3658.	6.6	63
54	A Molecular Mousetrap Determines Polarity of Termination of DNA Replication in E. coli. Cell, 2006, 125, 1309-1319.	13.5	114

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55	Mechanism and Putative Structure of B0-like Neutral Amino Acid Transporters. Journal of Membrane Biology, 2006, 213, 111-118.	1.0	23
56	A molecular mousetrap determines polarity of replication fork arrest at Tusâ€•<i>Ter</i> sites in <i>E. coli</i>. FASEB Journal, 2006, 20, A911.	0.2	0
57	Three-dimensional structure of (1,4)-Î²-d-mannan mannanohydrolase from tomato fruit. Protein Science, 2005, 14, 1233-1241.	3.1	60
58	Glutathione transferases: new functions. Current Opinion in Structural Biology, 2005, 15, 716-723.	2.6	181
59	Purification, crystallization and preliminary crystallographic analysis of DehIVa, a dehalogenase fromBurkholderia cepaciaMBA4. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 271-273.	0.7	2
60	Comparison of negative and positive ion electrospray ionization mass spectra of calmodulin and its complex with trifluoperazine. Rapid Communications in Mass Spectrometry, 2005, 19, 2123-2130.	0.7	19
61	T Cell Determinants Incorporating Î²-Amino Acid Residues Are Protease Resistant and Remain Immunogenic In Vivo. Journal of Immunology, 2005, 175, 3810-3818.	0.4	56
62	Crystal and Solution Structures of the Helicase-binding Domain of Escherichia coli Primase. Journal of Biological Chemistry, 2005, 280, 11495-11504.	1.6	62
63	Identification, characterization and structure of a new Delta class glutathione transferase isoenzyme. Biochemical Journal, 2005, 388, 763-771.	1.7	82
64	Targeting the JNK MAPK cascade for inhibition: basic science and therapeutic potential. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1697, 89-101.	1.1	231
65	Crystal Structure of Haloalkane Dehalogenase LinB from Sphingomonas paucimobilis UT26 at 0.95 Å… Resolution:â€‰ Dynamics of Catalytic Residues,. Biochemistry, 2004, 43, 870-878.	1.2	82
66	Expression, purification, crystallization, and NMR studies of the helicase interaction domain of Escherichia coli DnaG primase. Protein Expression and Purification, 2004, 33, 304-310.	0.6	11
67	The 2.2 Å… Crystal Structure of a Pocilloporin Pigment Reveals a Nonplanar Chromophore Conformation. Structure, 2003, 11, 275-284.	1.6	127
68	Characterization of a family 11 xylanase fromBacillus subtillisB230 used for paper bleaching. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 627-636.	2.5	33
69	Flexibility revealed by the 1.85â€…Å… crystal structure of the Î² sliding-clamp subunit ofEscherichia coliDNA polymerase III. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1192-1199.	2.5	64
70	Haloalkane Dehalogenase LinB fromSphingomonas paucimobilisUT26:Â X-ray Crystallographic Studies of Dehalogenation of Brominated Substratesâ€‚â€¡. Biochemistry, 2003, 42, 10104-10112.	1.2	43
71	The 2.0-Å… Crystal Structure of eqFP611, a Far Red Fluorescent Protein from the Sea Anemone Entacmaea quadricolor. Journal of Biological Chemistry, 2003, 278, 44626-44631.	1.6	158
72	Thermodynamic Description of the Effect of the Mutation Y49F on Human Glutathione Transferase P1-1 in Binding with Glutathione and the Inhibitor S-Hexylglutathione. Journal of Biological Chemistry, 2003, 278, 46938-46948.	1.6	20

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73	Exploring the Structure and Activity of Haloalkane Dehalogenase from Sphingomonas paucimobilis UT26: Evidence for Product- and Water-Mediated Inhibition,. Biochemistry, 2002, 41, 4847-4855.	1.2	49
74	Crystallization of two glutathione S-transferases from an unusual gene family. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 870-872.	2.5	4
75	Effects of i-propanol on the structural dynamics ofThermomyces lanuginosalipase revealed by tryptophan fluorescence. Protein Science, 2001, 10, 339-351.	3.1	37
76	The crystal structures of glutathione Sâ€transferases isozymes 1â€“3 and 1â€“4 from <i>Anopheles dirus</i> species B. Protein Science, 2001, 10, 2176-2185.	3.1	73
77	Macromolecular Crystallography As A Tool For Investigating Drug, Enzyme And Receptor Interactions. Clinical and Experimental Pharmacology and Physiology, 2000, 27, 145-151.	0.9	9
78	Structures of thermolabile mutants of human glutathione transferase P1-1 1 1Edited by R. Huber. Journal of Molecular Biology, 2000, 302, 295-302.	2.0	17
79	Valine 10 May Act as a Driver for Product Release from the Active Site of Human Glutathione Transferase P1-1â€,â€¡. Biochemistry, 2000, 39, 15961-15970.	1.2	3
80	Structure and function of the bacterial mechanosensitive channel of large conductance. Protein Science, 1999, 8, 1915-1921.	3.1	48
81	The ligandin (non-substrate) binding site of human pi class glutathione transferase is located in the electrophile binding site (H-site). Journal of Molecular Biology, 1999, 291, 913-926.	2.0	121
82	Human theta class glutathione transferase: the crystal structure reveals a sulfate-binding pocket within a buried active site. Structure, 1998, 6, 309-322.	1.6	147
83	Preliminary X-ray crystallographic studies of a newly defined human theta-class glutathione transferase. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 148-150.	2.5	4
84	Evidence for an Induced-Fit Mechanism Operating in Pi Class Glutathione Transferases,. Biochemistry, 1998, 37, 9912-9917.	1.2	56
85	Solution Structure of Glutathione Bound to Human Glutathione Transferase P1-1:Â Comparison of NMR Measurements with the Crystal Structureâ€. Biochemistry, 1998, 37, 3020-3027.	1.2	28
86	Mutations of gly to ala in human glutathione transferase P1-1 affect helix 2 (G-site) and induce positive cooperativity in the binding of glutathione 1 1Edited by R. Huber. Journal of Molecular Biology, 1998, 284, 1717-1725.	2.0	29
87	The Three-Dimensional Structure of the Human Pi Class Glutathione Transferase P1-1 in Complex with the Inhibitor Ethacrynic Acid and Its Glutathione Conjugate,. Biochemistry, 1997, 36, 576-585.	1.2	125
88	Multifunctional Role of Tyr 108 in the Catalytic Mechanism of Human Glutathione Transferase P1-1. Crystallographic and Kinetic Studies on the Y108F Mutant Enzymeâ€,â€¡. Biochemistry, 1997, 36, 6207-6217.	1.2	65
89	The structures of human glutathione transferase P1-1 in complex with glutathione and various inhibitors at high resolution. Journal of Molecular Biology, 1997, 274, 84-100.	2.0	172
90	The glutathione conjugate of ethacrynic acid can bind to human pi class glutathione transferase P1-1 in two different modes. FEBS Letters, 1997, 419, 32-36.	1.3	49

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91	Structural Flexibility Modulates the Activity of Human Glutathione Transferase P1-1. Journal of Biological Chemistry, 1996, 271, 16193-16198.	1.6	49