

Edward D Lowe

List of Publications by Year in descending order

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59
papers

4,298
citations

147566

31
h-index

155451

55
g-index

61
all docs

61
docs citations

61
times ranked

6372
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure of the Potassium Channel KirBac1.1 in the Closed State. <i>Science</i> , 2003, 300, 1922-1926.	6.0	763
2	The structure of P-TEFb (CDK9/cyclin T1), its complex with flavopiridol and regulation by phosphorylation. <i>EMBO Journal</i> , 2008, 27, 1907-1918.	3.5	295
3	The structure of an integrin/talin complex reveals the basis of inside-out signal transduction. <i>EMBO Journal</i> , 2009, 28, 3623-3632.	3.5	287
4	The crystal structure of the human polo-like kinase-1 polo box domain and its phospho-peptide complex. <i>EMBO Journal</i> , 2003, 22, 5757-5768.	3.5	209
5	The structural basis for substrate recognition and control by protein kinases I. <i>FEBS Letters</i> , 1998, 430, 1-11.	1.3	185
6	Specificity Determinants of Recruitment Peptides Bound to Phospho-CDK2/Cyclin A. <i>Biochemistry</i> , 2002, 41, 15625-15634.	1.2	152
7	Structural Conservation Despite Huge Sequence Diversity Allows EPCR Binding by the PfEMP1 Family Implicated in Severe Childhood Malaria. <i>Cell Host and Microbe</i> , 2015, 17, 118-129.	5.1	141
8	The structure of cyclin E1/CDK2: implications for CDK2 activation and CDK2-independent roles. <i>EMBO Journal</i> , 2005, 24, 452-463.	3.5	128
9	Bilirubin oxidase from <i>Myrothecium verrucaria</i> : X-ray determination of the complete crystal structure and a rational surface modification for enhanced electrocatalytic O ₂ reduction. <i>Dalton Transactions</i> , 2011, 40, 6668.	1.6	128
10	The Crystal Structure of Human CDK7 and Its Protein Recognition Properties. <i>Structure</i> , 2004, 12, 2067-2079.	1.6	124
11	How the biotin-streptavidin interaction was made even stronger: investigation via crystallography and a chimaeric tetramer. <i>Biochemical Journal</i> , 2011, 435, 55-63.	1.7	112
12	An Integrin Phosphorylation Switch. <i>Journal of Biological Chemistry</i> , 2008, 283, 5420-5426.	1.6	98
13	Structural Basis of Teneurin-Latrophilin Interaction in Repulsive Guidance of Migrating Neurons. <i>Cell</i> , 2020, 180, 323-339.e19.	13.5	91
14	Characterization of a Carbon-Carbon Hydrolase from <i>Mycobacterium tuberculosis</i> Involved in Cholesterol Metabolism. <i>Journal of Biological Chemistry</i> , 2010, 285, 434-443.	1.6	89
15	Mechanism of Lys48-linked polyubiquitin chain recognition by the Mud1 UBA domain. <i>EMBO Journal</i> , 2005, 24, 3178-3189.	3.5	87
16	Identification and structural analysis of type I collagen sites in complex with fibronectin fragments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4195-4200.	3.3	77
17	Selective small molecule inhibitors of the potential breast cancer marker, human arylamine N-acetyltransferase 1, and its murine homologue, mouse arylamine N-acetyltransferase 2. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 905-918.	1.4	75
18	Structure of Daidzin, a Naturally Occurring Anti-Alcohol-Addiction Agent, in Complex with Human Mitochondrial Aldehyde Dehydrogenase. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 4482-4487.	2.9	73

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19	Structures of the Dsk2 UBL and UBA domains and their complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 177-188.	2.5	69
20	Structures of Teneurin adhesion receptors reveal an ancient fold for cell-cell interaction. <i>Nature Communications</i> , 2018, 9, 1079.	5.8	68
21	Molecular Cloning, Characterisation and Ligand-bound Structure of an Azoreductase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2007, 373, 1213-1228.	2.0	66
22	Structures of mammalian ER α -glucosidase II capture the binding modes of broad-spectrum iminosugar antivirals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4630-8.	3.3	65
23	Structure of Rpn10 and Its Interactions with Polyubiquitin Chains and the Proteasome Subunit Rpn12*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33992-34003.	1.6	61
24	Divergence of Cofactor Recognition across Evolution: Coenzyme A Binding in a Prokaryotic Arylamine N-Acetyltransferase. <i>Journal of Molecular Biology</i> , 2008, 375, 178-191.	2.0	56
25	Identification of NAD(P)H Quinone Oxidoreductase Activity in Azoreductases from <i>P. aeruginosa</i> : Azoreductases and NAD(P)H Quinone Oxidoreductases Belong to the Same FMN-Dependent Superfamily of Enzymes. <i>PLoS ONE</i> , 2014, 9, e98551.	1.1	55
26	<i>Caenorhabditis elegans</i> centriolar protein SAS-6 forms a spiral that is consistent with imparting a ninefold symmetry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11373-11378.	3.3	54
27	Can child care assistance in welfare and employment programs support the employment of low-income families?. <i>Journal of Policy Analysis and Management</i> , 2004, 23, 723-743.	1.1	49
28	Structural basis for ligand and innate immunity factor uptake by the trypanosome haptoglobin-haemoglobin receptor. <i>ELife</i> , 2014, 3, e05553.	2.8	49
29	A Novel Mechanism for Azoreduction. <i>Journal of Molecular Biology</i> , 2010, 400, 24-37.	2.0	48
30	Structure and Interdomain Interactions of a Hybrid Domain: A Disulphide-Rich Module of the Fibrillin/LTBP Superfamily of Matrix Proteins. <i>Structure</i> , 2009, 17, 759-768.	1.6	44
31	Pyocin S5 Import into <i>Pseudomonas aeruginosa</i> Reveals a Generic Mode of Bacteriocin Transport. <i>MBio</i> , 2020, 11, .	1.8	42
32	Structural Analysis of the Interactions Between Paxillin LD Motifs and α -Parvin. <i>Structure</i> , 2008, 16, 1521-1531.	1.6	32
33	Structure of HsaD, a steroid-degrading hydrolase, from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 2-7.	0.7	31
34	Activation of nitrofurazone by azoreductases: multiple activities in one enzyme. <i>Scientific Reports</i> , 2011, 1, 63.	1.6	30
35	Development of tools to automate quantitative analysis of radiation damage in SAXS experiments. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 63-72.	1.0	28
36	Piperidinols That Show Anti-Tubercular Activity as Inhibitors of Arylamine N-Acetyltransferase: An Essential Enzyme for Mycobacterial Survival Inside Macrophages. <i>PLoS ONE</i> , 2012, 7, e52790.	1.1	27

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37	Structures of the Ultra-High-Affinity Proteinâ€‘Protein Complexes of Pyocins S2 and AP41 and Their Cognate Immunity Proteins from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2015, 427, 2852-2866.	2.0	25
38	Probing the architecture of the <i>Mycobacterium marinum</i> arylamine N-acetyltransferase active site. <i>Protein and Cell</i> , 2010, 1, 384-392.	4.8	24
39	Structure of arylamine N-acetyltransferase from <i>Mycobacterium tuberculosis</i> determined by cross-seeding with the homologous protein from <i>M. marinum</i> : triumph over adversity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1433-1446.	2.5	24
40	High-Throughput PIXE as an Essential Quantitative Assay for Accurate Metalloprotein Structural Analysis: Development and Application. <i>Journal of the American Chemical Society</i> , 2020, 142, 185-197.	6.6	24
41	Role of tyrosine 131 in the active site of paAzoR1, an azoreductase with specificity for the inflammatory bowel disease prodrug balsalazide. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 2-7.	0.7	23
42	Structural and functional characterization of Rpn12 identifies residues required for Rpn10 proteasome incorporation. <i>Biochemical Journal</i> , 2012, 448, 55-65.	1.7	23
43	Heterotypic interactions drive antibody synergy against a malaria vaccine candidate. <i>Nature Communications</i> , 2022, 13, 933.	5.8	23
44	Investigation of the mycobacterial enzyme HsaD as a potential novel target for anti-tubercular agents using a fragment-based drug design approach. <i>British Journal of Pharmacology</i> , 2017, 174, 2209-2224.	2.7	19
45	Structural basis for duplex RNA recognition and cleavage by <i>Archaeoglobus fulgidus</i> C3PO. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 380-386.	3.6	16
46	The N-Terminal Region of Fibrillin-1 Mediates a Bipartite Interaction with LTBP1. <i>Structure</i> , 2017, 25, 1208-1221.e5.	1.6	15
47	Cloning, expression, purification, crystallization and X-ray analysis of inositol monophosphatase from <i>Mus musculus</i> and <i>Homo sapiens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1149-1152.	0.7	14
48	Reconstitution and Structural Analysis of a HECT Ligase-Ubiquitin Complex via an Activity-Based Probe. <i>ACS Chemical Biology</i> , 2021, 16, 1615-1621.	1.6	13
49	Crystal structure of the catalytic C-lobe of the HECT-type ubiquitin ligase E6AP. <i>Protein Science</i> , 2020, 29, 1550-1554.	3.1	12
50	Pathological macromolecular crystallographic data affected by twinning, partial-disorder and exhibiting multiple lattices for testing of data processing and refinement tools. <i>Scientific Reports</i> , 2018, 8, 14876.	1.6	11
51	Toxin import through the antibiotic efflux channel TolC. <i>Nature Communications</i> , 2021, 12, 4625.	5.8	11
52	Globalization, Childhood, and Psychological Anthropology. , 0, , 315-336.		10
53	Crystallization and preliminary crystallographic analysis of BbCRASP-1, a complement regulator-acquiring surface protein of <i>Borrelia burgdorferi</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 929-932.	2.5	9
54	Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. <i>Structure</i> , 2021, 29, 1014-1028.e8.	1.6	9

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55	Structure of arylamineN-acetyltransferase from <i>M. tuberculosis</i> : triumph over adversity. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s83-s83.	0.3	2
56	Are shared models always cultural models? A study of the cultural model of affect and emotion in Chuuk. <i>Journal of Cultural Cognitive Science</i> , 2020, 4, 31-43.	0.5	2
57	A novel mechanism for azoreduction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s137-s137.	0.3	0
58	Fragment-based approaches for anti-tuberculosis drug discovery. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s349-s349.	0.3	0
59	Gardens in a postsuburb: Community garden governance and ethos in Orange County. <i>Journal of Agriculture, Food Systems, and Community Development</i> , 0, , 1-18.	2.4	0