

# Edward D Lowe

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

4,298  
citations

147726

31  
h-index

155592

55  
g-index

61  
all docs

61  
docs citations

61  
times ranked

6372  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Heterotypic interactions drive antibody synergy against a malaria vaccine candidate. <i>Nature Communications</i> , 2022, 13, 933.   | 5.8  | 23        |
| 2  | Toxin import through the antibiotic efflux channel TolC. <i>Nature Communications</i> , 2021, 12, 4625.  | 5.8  | 11        |
| 3  | 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        |
| 4  | Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. <i>Structure</i> , 2021, 29, 1014-1028.e8.   | 1.6  | 9         |
| 5  | Structural Basis of Teneurin-Latrophilin Interaction in Repulsive Guidance of Migrating Neurons. <i>Cell</i> , 2020, 180, 323-339.e19.   | 13.5 | 91        |
| 6  | 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        |
| 7  | 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         |
| 8  | Pyocin S5 Import into <i>Pseudomonas aeruginosa</i> Reveals a Generic Mode of Bacteriocin Transport. <i>MBio</i> , 2020, 11, .   | 1.8  | 42        |
| 9  | Crystal structure of the catalytic C $\alpha$ lobe of the HECT $\alpha$ -type ubiquitin ligase E6AP. <i>Protein Science</i> , 2020, 29, 1550-1554.   | 3.1  | 12        |
| 10 | Structures of Teneurin adhesion receptors reveal an ancient fold for cell-cell interaction. <i>Nature Communications</i> , 2018, 9, 1079.  | 5.8  | 68        |
| 11 | 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        |
| 12 | Investigation of the mycobacterial enzyme HsaD as a potential novel target for anti $\alpha$ -tubercular agents using a fragment $\alpha$ -based drug design approach. <i>British Journal of Pharmacology</i> , 2017, 174, 2209-2224.                | 2.7  | 19        |
| 13 | The N-Terminal Region of Fibrillin-1 Mediates a Bipartite Interaction with LTBP1. <i>Structure</i> , 2017, 25, 1208-1221.e5.   | 1.6  | 15        |
| 14 | 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        |
| 15 | Structures of mammalian ER $\alpha$ -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        |
| 16 | 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       |
| 17 | Structures of the Ultra-High-Affinity Protein $\alpha$ -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        |
| 18 | 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        |

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|----|---|-----|-----------|
| 19 | Structural basis for ligand and innate immunity factor uptake by the trypanosome haptoglobin-haemoglobin receptor. <i>ELife</i> , 2014, 3, e05553.  | 2.8 | 49        |
| 20 | <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        |
| 21 | 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        |
| 22 | 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        |
| 23 | Structure of arylamine N-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         |
| 24 | Fragment-based approaches for anti-tuberculosis drug discovery. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s349-s349.  | 0.3 | 0         |
| 25 | Structural and functional characterization of Rpn12 identifies residues required for Rpn10 proteasome incorporation. <i>Biochemical Journal</i> , 2012, 448, 55-65.   | 1.7 | 23        |
| 26 | 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        |
| 27 | 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        |
| 28 | Bilirubin oxidase from <i>Myrothecium verrucaria</i> : X-ray determination of the complete crystal structure and a rational surface modification for enhanced electrocatalytic O <sub>2</sub> reduction. <i>Dalton Transactions</i> , 2011, 40, 6668.                                 | 1.6 | 128       |
| 29 | Activation of nitrofurazone by azoreductases: multiple activities in one enzyme. <i>Scientific Reports</i> , 2011, 1, 63.   | 1.6 | 30        |
| 30 | 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       |
| 31 | 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        |
| 32 | 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        |
| 33 | 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        |
| 34 | 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        |
| 35 | A Novel Mechanism for Azoreduction. <i>Journal of Molecular Biology</i> , 2010, 400, 24-37.   | 2.0 | 48        |
| 36 | A novel mechanism for azoreduction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s137-s137.  | 0.3 | 0         |

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|----|--|-----|-----------|
| 37 | Identification and structural analysis of type I collagen sites in complex with fibronectin fragments. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4195-4200.                              | 3.3 | 77        |
| 38 | Structure and Interdomain Interactions of a Hybrid Domain: A Disulphide-Rich Module of the Fibrillin/LTBP Superfamily of Matrix Proteins. Structure, 2009, 17, 759-768.  | 1.6 | 44        |
| 39 | The structure of an integrin/talin complex reveals the basis of inside-out signal transduction. EMBO Journal, 2009, 28, 3623-3632.   | 3.5 | 287       |
| 40 | Selective small molecule inhibitors of the potential breast cancer marker, human arylamine N-acetyltransferase 1, and its murine homologue, mouse arylamine N-acetyltransferase 2. Bioorganic and Medicinal Chemistry, 2009, 17, 905-918.  | 1.4 | 75        |
| 41 | Structure of HsaD, a steroid-degrading hydrolase, from <i>Mycobacterium tuberculosis</i> . Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 2-7.   | 0.7 | 31        |
| 42 | The structure of P-TEFb (CDK9/cyclin T1), its complex with flavopiridol and regulation by phosphorylation. EMBO Journal, 2008, 27, 1907-1918.  | 3.5 | 295       |
| 43 | Structural Analysis of the Interactions Between Paxillin LD Motifs and $\hat{\pm}$ -Parvin. Structure, 2008, 16, 1521-1531.  | 1.6 | 32        |
| 44 | Structure of Daidzin, a Naturally Occurring Anti-Alcohol-Addiction Agent, in Complex with Human Mitochondrial Aldehyde Dehydrogenase. Journal of Medicinal Chemistry, 2008, 51, 4482-4487.   | 2.9 | 73        |
| 45 | Divergence of Cofactor Recognition across Evolution: Coenzyme A Binding in a Prokaryotic Arylamine N-Acetyltransferase. Journal of Molecular Biology, 2008, 375, 178-191.  | 2.0 | 56        |
| 46 | An Integrin Phosphorylation Switch. Journal of Biological Chemistry, 2008, 283, 5420-5426.   | 1.6 | 98        |
| 47 | Molecular Cloning, Characterisation and Ligand-bound Structure of an Azoreductase from <i>Pseudomonas aeruginosa</i> . Journal of Molecular Biology, 2007, 373, 1213-1228.   | 2.0 | 66        |
| 48 | Structures of the Dsk2 UBL and UBA domains and their complex. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 177-188.   | 2.5 | 69        |
| 49 | The structure of cyclin E1/CDK2: implications for CDK2 activation and CDK2-independent roles. EMBO Journal, 2005, 24, 452-463.   | 3.5 | 128       |
| 50 | Mechanism of Lys48-linked polyubiquitin chain recognition by the Mud1 UBA domain. EMBO Journal, 2005, 24, 3178-3189.   | 3.5 | 87        |
| 51 | The Crystal Structure of Human CDK7 and Its Protein Recognition Properties. Structure, 2004, 12, 2067-2079.  | 1.6 | 124       |
| 52 | Can child care assistance in welfare and employment programs support the employment of low-income families?. Journal of Policy Analysis and Management, 2004, 23, 723-743.   | 1.1 | 49        |
| 53 | Crystallization and preliminary crystallographic analysis of BbCRASP-1, a complement regulator-acquiring surface protein of <i>Borrelia burgdorferi</i> . Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 929-932. | 2.5 | 9         |
| 54 | The crystal structure of the human polo-like kinase-1 polo box domain and its phospho-peptide complex. EMBO Journal, 2003, 22, 5757-5768.  | 3.5 | 209       |

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|----|--|-----|-----------|
| 55 | Crystal Structure of the Potassium Channel KirBac1.1 in the Closed State. <i>Science</i> , 2003, 300, 1922-1926.   | 6.0 | 763       |
| 56 | Specificity Determinants of Recruitment Peptides Bound to Phospho-CDK2/Cyclin A. <i>Biochemistry</i> , 2002, 41, 15625-15634.  | 1.2 | 152       |
| 57 | The structural basis for substrate recognition and control by protein kinases1. <i>FEBS Letters</i> , 1998, 430, 1-11.   | 1.3 | 185       |
| 58 | Globalization, Childhood, and Psychological Anthropology. , 0, , 315-336.  |     | 10        |
| 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         |