

Olwyn Byron

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

2,398
citations

218677

26
h-index

223800

46
g-index

74
all docs

74
docs citations

74
times ranked

3246
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Crystal structure of a PDZ domain. <i>Nature</i> , 1996, 382, 649-652. | 27.8 | 322 |
| 2 | A GRASP55-rab2 effector complex linking Golgi structure to membrane traffic. <i>Journal of Cell Biology</i> , 2001, 155, 877-884. | 5.2 | 202 |
| 3 | Calicivirus VP2 forms a portal-like assembly following receptor engagement. <i>Nature</i> , 2019, 565, 377-381. | 27.8 | 103 |
| 4 | SOMO (SOLution MOdeler). <i>Structure</i> , 2005, 13, 723-734. | 3.3 | 101 |
| 5 | Identification of Bacterial Target Proteins for the Salicylidene Acylhydrazide Class of Virulence-blocking Compounds. <i>Journal of Biological Chemistry</i> , 2011, 286, 29922-29931. | 3.4 | 94 |
| 6 | The PDZ Domain of Human Erythrocyte p55 Mediates Its Binding to the Cytoplasmic Carboxyl Terminus of Glycophorin C. <i>Journal of Biological Chemistry</i> , 1997, 272, 24191-24197. | 3.4 | 87 |
| 7 | A New Level of Architectural Complexity in the Human Pyruvate Dehydrogenase Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 19772-19780. | 3.4 | 74 |
| 8 | A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420. | 2.5 | 71 |
| 9 | Self-interaction of pneumolysin, the pore-forming protein toxin of <i>Streptococcus pneumoniae</i> . <i>Journal of Molecular Biology</i> , 1998, 284, 1223-1237. | 4.2 | 68 |
| 10 | Lectin-Like Bacteriocins from <i>Pseudomonas</i> spp. Utilise D-Rhamnose Containing Lipopolysaccharide as a Cellular Receptor. <i>PLoS Pathogens</i> , 2014, 10, e1003898. | 4.7 | 56 |
| 11 | Biochemical analysis of TssK, a core component of the bacterial Type VI secretion system, reveals distinct oligomeric states of TssK and identifies a TssK-TssFG subcomplex. <i>Biochemical Journal</i> , 2014, 461, 291-304. | 3.7 | 53 |
| 12 | The Role of Cholesterol in the Activity of Pneumolysin, a Bacterial Protein Toxin. <i>Biophysical Journal</i> , 2004, 86, 3141-3151. | 0.5 | 51 |
| 13 | The metabolic enzyme AdhE controls the virulence of <i>Escherichia coli</i> O157:H7. <i>Molecular Microbiology</i> , 2014, 93, 199-211. | 2.5 | 49 |
| 14 | Structural Analysis of the Protein/Lipid Complexes Associated with Pore Formation by the Bacterial Toxin Pneumolysin. <i>Journal of Biological Chemistry</i> , 2001, 276, 5714-5719. | 3.4 | 48 |
| 15 | The Solution Structure and Oligomerization Behavior of Two Bacterial Toxins: Pneumolysin and Perfringolysin O. <i>Biophysical Journal</i> , 2004, 87, 540-552. | 0.5 | 48 |
| 16 | Solution Structure of the Tn3 Resolvase-Crossover Site Synaptic Complex. <i>Molecular Cell</i> , 2004, 16, 127-137. | 9.7 | 44 |
| 17 | Human Homologue of the <i>Drosophila</i> Discs Large Tumor Suppressor Protein Forms an Oligomer in Solution. <i>Journal of Biological Chemistry</i> , 2000, 275, 13759-13770. | 3.4 | 43 |
| 18 | Molecular dissection of the CD2-C58 counter-receptor interface identifies CD2 Tyr86 and CD58 Lys34 residues as the functional hot spot. Edited by I. Wilson. <i>Journal of Molecular Biology</i> , 2001, 312, 711-720. | 4.2 | 42 |

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|----|--|------|-----------|
| 19 | Discovery, characterization and <i>in vivo</i> activity of pyocin SD2, a protein antibiotic from <i>Pseudomonas aeruginosa</i> . <i>Biochemical Journal</i> , 2016, 473, 2345-2358. | 3.7 | 42 |
| 20 | Studies on the structure and mechanism of a bacterial protein toxin by analytical ultracentrifugation and small-angle neutron scattering 1 Edited by M. F. Moody. <i>Journal of Molecular Biology</i> , 1999, 293, 1145-1160. | 4.2 | 41 |
| 21 | Aldehyde-alcohol dehydrogenase forms a high-order spiroosome architecture critical for its activity. <i>Nature Communications</i> , 2019, 10, 4527. | 12.8 | 39 |
| 22 | The Potassium Binding Protein Kbp Is a Cytoplasmic Potassium Sensor. <i>Structure</i> , 2016, 24, 741-749. | 3.3 | 38 |
| 23 | Hydrodynamic bead modeling of biological macromolecules. <i>Methods in Enzymology</i> , 2000, 321, 278-304. | 1.0 | 32 |
| 24 | 19Å... Solution Structure of the Filarial Nematode Immunomodulatory Protein, ES-62. <i>Biophysical Journal</i> , 2003, 84, 489-500. | 0.5 | 31 |
| 25 | Novel Size-Independent Modeling of the Dilute Solution Conformation of the Immunoglobulin IgG Fab ² Domain Using SOLPRO and ELLIPS. <i>Biophysical Journal</i> , 1999, 77, 2902-2910. | 0.5 | 29 |
| 26 | Structural basis for centromere maintenance by <i>Drosophila</i> CENP-A chaperone CAL 1. <i>EMBO Journal</i> , 2020, 39, e103234. | 7.8 | 29 |
| 27 | Characterisation of the low affinity interaction between rat cell adhesion molecules CD2 and CD48 by analytical ultracentrifugation. <i>European Biophysics Journal</i> , 1997, 25, 455-462. | 2.2 | 27 |
| 28 | The Stoichiometry of Trimeric SIV Glycoprotein Interaction with CD4 Differs from That of Anti-envelope Antibody Fab Fragments. <i>Journal of Biological Chemistry</i> , 2001, 276, 42667-42676. | 3.4 | 27 |
| 29 | Variation in the organization and subunit composition of the mammalian pyruvate dehydrogenase complex E2/E3BP core assembly. <i>Biochemical Journal</i> , 2011, 437, 565-574. | 3.7 | 27 |
| 30 | Neutron scattering: good news for biotechnology. <i>Current Opinion in Biotechnology</i> , 2000, 11, 72-80. | 6.6 | 26 |
| 31 | Structure of the bacterial plant-ferredoxin receptor FusA. <i>Nature Communications</i> , 2016, 7, 13308. | 12.8 | 26 |
| 32 | Low resolution solution structure of the apo form of Escherichia coli haemoglobin protease Hbp. <i>Journal of Molecular Biology</i> , 2002, 315, 1179-1187. | 4.2 | 25 |
| 33 | Structures of the Ultra-High-Affinity Protein-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. | 4.2 | 25 |
| 34 | Hydrodynamic and mass spectrometry analysis of nearly-intact human fibrinogen, chicken fibrinogen, and of a substantially monodisperse human fibrinogen fragment X. <i>Archives of Biochemistry and Biophysics</i> , 2010, 493, 157-168. | 3.0 | 23 |
| 35 | Structure of the atypical bacteriocin pectocin M ² implies a novel mechanism of protein uptake. <i>Molecular Microbiology</i> , 2014, 93, 234-246. | 2.5 | 23 |
| 36 | The Pyruvate Dehydrogenase Complex and Related Assemblies in Health and Disease. <i>Sub-Cellular Biochemistry</i> , 2017, 83, 523-550. | 2.4 | 23 |

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|----|---|-----|-----------|
| 37 | Computing translational diffusion and sedimentation coefficients: an evaluation of experimental data and programs. <i>European Biophysics Journal</i> , 2015, 44, 417-431. | 2.2 | 21 |
| 38 | Hydrodynamic Modeling: The Solution Conformation of Macromolecules and Their Complexes. <i>Methods in Cell Biology</i> , 2008, 84, 327-373. | 1.1 | 20 |
| 39 | Investigations into the molecular size and shape of tomato extensin. <i>Biochemical Journal</i> , 1996, 320, 577-583. | 3.7 | 18 |
| 40 | Low-Resolution Reconstruction of a Synthetic DNA Holliday Junction. <i>Biophysical Journal</i> , 2004, 86, 3060-3069. | 0.5 | 18 |
| 41 | Structural Characterisation of Tpx from <i>Yersinia pseudotuberculosis</i> Reveals Insights into the Binding of Salicylidene Acylhydrazide Compounds. <i>PLoS ONE</i> , 2012, 7, e32217. | 2.5 | 17 |
| 42 | Aldehyde-alcohol dehydrogenase undergoes structural transition to form extended spiroosomes for substrate channeling. <i>Communications Biology</i> , 2020, 3, 298. | 4.4 | 16 |
| 43 | Protein-protein interactions: a supra-structural phenomenon demanding trans-disciplinary biophysical approaches. <i>Current Opinion in Structural Biology</i> , 2015, 35, 76-86. | 5.7 | 15 |
| 44 | Merging In-Solution X-ray and Neutron Scattering Data Allows Fine Structural Analysis of Membrane-Protein Detergent Complexes. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 3910-3914. | 4.6 | 14 |
| 45 | The polyprotein and FAR lipid binding proteins of nematodes: shape and monomer/dimer states in ligand-free and bound forms. <i>European Biophysics Journal</i> , 2003, 32, 465-476. | 2.2 | 13 |
| 46 | Behavior of Tn3 Resolvase in Solution and Its Interaction with res. <i>Biophysical Journal</i> , 2005, 89, 1920-1931. | 0.5 | 12 |
| 47 | Biochemical and structural characterization of the apicoplast dihydrolipoamide dehydrogenase of <i>Plasmodium falciparum</i> . <i>Bioscience Reports</i> , 2015, 35, . | 2.4 | 12 |
| 48 | Identification and Characterization of Novel Compounds Blocking Shiga Toxin Expression in <i>Escherichia coli</i> O157:H7. <i>Frontiers in Microbiology</i> , 2016, 7, 1930. | 3.5 | 12 |
| 49 | Structural and biophysical analysis of nuclease protein antibiotics. <i>Biochemical Journal</i> , 2016, 473, 2799-2812. | 3.7 | 12 |
| 50 | Purification and Characterization of Pyruvate Kinase from <i>Schizosaccharomyces pombe</i> : Evidence for an Unusual Quaternary Structure. <i>Protein Expression and Purification</i> , 1998, 14, 247-253. | 1.3 | 11 |
| 51 | Characterization of a periplasmic nitrate reductase in complex with its biosynthetic chaperone. <i>FEBS Journal</i> , 2014, 281, 246-260. | 4.7 | 11 |
| 52 | Structure of protease-cleaved <i>Escherichia coli</i> α -2-macroglobulin reveals a putative mechanism of conformational activation for protease entrapment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1478-1486. | 2.5 | 11 |
| 53 | A global multi-technique approach to study low-resolution solution structures. <i>Journal of Applied Crystallography</i> , 2005, 38, 874-887. | 4.5 | 10 |
| 54 | Hydrodynamic Modeling and Its Application in AUC. <i>Methods in Enzymology</i> , 2015, 562, 81-108. | 1.0 | 9 |

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|----|--|-----|-----------|
| 55 | Structure-specific recognition protein-1 (SSRP1) is an elongated homodimer that binds histones. <i>Journal of Biological Chemistry</i> , 2018, 293, 10071-10083. | 3.4 | 9 |
| 56 | Contribution of inter-subunit interactions to the thermostability of <i>Pyrococcus furiosus</i> citrate synthase. <i>Extremophiles</i> , 2011, 15, 327-336. | 2.3 | 8 |
| 57 | DT diaphorase exists as a dimer-tetramer equilibrium in solution. <i>European Biophysics Journal</i> , 1997, 25, 423-430. | 2.2 | 5 |
| 58 | Oligomerisation and thermal stability of polyvalent integrin $\alpha 5 \beta 1$ ligands. <i>Biophysical Chemistry</i> , 2009, 142, 34-39. | 2.8 | 5 |
| 59 | Conformational spectra α probing protein conformational changes. <i>Biophysical Chemistry</i> , 1999, 80, 189-197. | 2.8 | 4 |
| 60 | Recombinant expression, purification, crystallization and preliminary X-ray diffraction analysis of the C-terminal DUF490963 α 1138 domain of TamB from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1272-1275. | 0.8 | 4 |
| 61 | Analytical ultracentrifugation (AUC): a seminal tool offering multiple solutions. <i>European Biophysics Journal</i> , 2018, 47, 693-696. | 2.2 | 4 |
| 62 | Physical characterization and ATPase activity of 14S dynein fractions from <i>Tetrahymena thermophila</i> . <i>Journal of Muscle Research and Cell Motility</i> , 1997, 18, 697-709. | 2.0 | 3 |
| 63 | FolX from <i>Pseudomonas aeruginosa</i> is octameric in both crystal and solution. <i>FEBS Letters</i> , 2012, 586, 1160-1165. | 2.8 | 3 |
| 64 | US-SOMO: Methods for Construction and Hydration of Macromolecular Hydrodynamic Models. , 2021, , 1-11. | | 3 |
| 65 | The structure of an orthorhombic crystal form of a 'forced reduced' thiol peroxidase reveals lattice formation aided by the presence of the affinity tag. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 522-526. | 0.7 | 2 |
| 66 | A preliminary investigation of the hydrodynamic properties of two novel monoclonal antibodies. <i>Biochemical Society Transactions</i> , 1990, 18, 1030-1031. | 3.4 | 1 |
| 67 | Structure and dimerization of translation initiation factor α IF5B in solution. <i>Biochemical and Biophysical Research Communications</i> , 2011, 416, 140-145. | 2.1 | 1 |
| 68 | High-resolution structure of the alcohol dehydrogenase domain of the bifunctional bacterial enzyme AdhE. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 414-421. | 0.8 | 1 |
| 69 | Estimation of the dissociation constant of the cell adhesion molecules srCD2 and srCD48 using analytical ultracentrifugation. <i>Biochemical Society Transactions</i> , 1995, 23, 435S-435S. | 3.4 | 0 |
| 70 | Structure and mechanism of the bacterial protein toxin, pneumolysin. <i>Biochemical Society Transactions</i> , 1999, 27, A55-A55. | 3.4 | 0 |
| 71 | Hydrodynamic bead modelling of the 2:1 p50 α β 3 complex. <i>Biophysical Chemistry</i> , 2004, 108, 259-271. | 2.8 | 0 |
| 72 | Introduction: Calculation of Hydrodynamic Parameters. , 2016, , 147-167. | | 0 |