

Olwyn Byron

List of Publications by Year in descending order

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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	US-SOMO: Methods for Construction and Hydration of Macromolecular Hydrodynamic Models. , 2021, , 1-11.		3
2	Aldehyde-alcohol dehydrogenase undergoes structural transition to form extended spiroosomes for substrate channeling. Communications Biology, 2020, 3, 298.	4.4	16
3	Structural basis for centromere maintenance by <i>Drosophila</i> CENP-A chaperone CAL1. EMBO Journal, 2020, 39, e103234.	7.8	29
4	High-resolution structure of the alcohol dehydrogenase domain of the bifunctional bacterial enzyme AdhE. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 414-421.	0.8	1
5	Aldehyde-alcohol dehydrogenase forms a high-order spiroosome architecture critical for its activity. Nature Communications, 2019, 10, 4527.	12.8	39
6	Calicivirus VP2 forms a portal-like assembly following receptor engagement. Nature, 2019, 565, 377-381.	27.8	103
7	Analytical ultracentrifugation (AUC): a seminal tool offering multiple solutions. European Biophysics Journal, 2018, 47, 693-696.	2.2	4
8	Structure-specific recognition protein-1 (SSRP1) is an elongated homodimer that binds histones. Journal of Biological Chemistry, 2018, 293, 10071-10083.	3.4	9
9	Merging In-Solution X-ray and Neutron Scattering Data Allows Fine Structural Analysis of Membrane-Protein Detergent Complexes. Journal of Physical Chemistry Letters, 2018, 9, 3910-3914.	4.6	14
10	The Pyruvate Dehydrogenase Complex and Related Assemblies in Health and Disease. Sub-Cellular Biochemistry, 2017, 83, 523-550.	2.4	23
11	Identification and Characterization of Novel Compounds Blocking Shiga Toxin Expression in Escherichia coli O157:H7. Frontiers in Microbiology, 2016, 7, 1930.	3.5	12
12	Introduction: Calculation of Hydrodynamic Parameters. , 2016, , 147-167.		0
13	The Potassium Binding Protein Kbp Is a Cytoplasmic Potassium Sensor. Structure, 2016, 24, 741-749.	3.3	38
14	Discovery, characterization and <i>in vivo</i> activity of pyocin SD2, a protein antibiotic from <i>Pseudomonas aeruginosa</i> . Biochemical Journal, 2016, 473, 2345-2358.	3.7	42
15	Structural and biophysical analysis of nuclease protein antibiotics. Biochemical Journal, 2016, 473, 2799-2812.	3.7	12
16	Structure of the bacterial plant-ferredoxin receptor FusA. Nature Communications, 2016, 7, 13308.	12.8	26
17	Hydrodynamic Modeling and Its Application in AUC. Methods in Enzymology, 2015, 562, 81-108.	1.0	9
18	Protein-protein interactions: a supra-structural phenomenon demanding trans-disciplinary biophysical approaches. Current Opinion in Structural Biology, 2015, 35, 76-86.	5.7	15

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19	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
20	Biochemical and structural characterization of the apicoplast dihydrolipoamide dehydrogenase of <i>Plasmodium falciparum</i> . <i>Bioscience Reports</i> , 2015, 35, .	2.4	12
21	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
22	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
23	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
24	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
25	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
26	The metabolic enzyme <i>AdhE</i> controls the virulence of <i>Escherichia coli</i> O157:H7. <i>Molecular Microbiology</i> , 2014, 93, 199-211.	2.5	49
27	Recombinant expression, purification, crystallization and preliminary X-ray diffraction analysis of the C-terminal DUF490963-1138 domain of TamB from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1272-1275.	0.8	4
28	Characterization of a periplasmic nitrate reductase in complex with its biosynthetic chaperone. <i>FEBS Journal</i> , 2014, 281, 246-260.	4.7	11
29	Structure of the atypical bacteriocin pectocin <i>M</i> ₂ implies a novel mechanism of protein uptake. <i>Molecular Microbiology</i> , 2014, 93, 234-246.	2.5	23
30	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
31	FolX from <i>Pseudomonas aeruginosa</i> is octameric in both crystal and solution. <i>FEBS Letters</i> , 2012, 586, 1160-1165.	2.8	3
32	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
33	Structure and dimerization of translation initiation factor aIF5B in solution. <i>Biochemical and Biophysical Research Communications</i> , 2011, 416, 140-145.	2.1	1
34	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
35	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
36	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

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37	Hydrodynamic and mass spectrometry analysis of nearly-intact human fibrinogen, chicken fibrinogen, and of a substantially monodisperse human fibrinogen fragment X. Archives of Biochemistry and Biophysics, 2010, 493, 157-168.	3.0	23
38	Oligomerisation and thermal stability of polyvalent integrin $\alpha 5 \beta 1$ ligands. Biophysical Chemistry, 2009, 142, 34-39.	2.8	5
39	Hydrodynamic Modeling: The Solution Conformation of Macromolecules and Their Complexes. Methods in Cell Biology, 2008, 84, 327-373.	1.1	20
40	A New Level of Architectural Complexity in the Human Pyruvate Dehydrogenase Complex. Journal of Biological Chemistry, 2006, 281, 19772-19780.	3.4	74
41	SOMO (SOLution MOdeler). Structure, 2005, 13, 723-734.	3.3	101
42	A global multi-technique approach to study low-resolution solution structures. Journal of Applied Crystallography, 2005, 38, 874-887.	4.5	10
43	Behavior of Tn3 Resolvase in Solution and Its Interaction with res. Biophysical Journal, 2005, 89, 1920-1931.	0.5	12
44	Hydrodynamic bead modelling of the 2:1 p50 α β complex. Biophysical Chemistry, 2004, 108, 259-271.	2.8	0
45	The Solution Structure and Oligomerization Behavior of Two Bacterial Toxins: Pneumolysin and Perfringolysin O. Biophysical Journal, 2004, 87, 540-552.	0.5	48
46	Solution Structure of the Tn3 Resolvase-Crossover Site Synaptic Complex. Molecular Cell, 2004, 16, 127-137.	9.7	44
47	Low-Resolution Reconstruction of a Synthetic DNA Holliday Junction. Biophysical Journal, 2004, 86, 3060-3069.	0.5	18
48	The Role of Cholesterol in the Activity of Pneumolysin, a Bacterial Protein Toxin. Biophysical Journal, 2004, 86, 3141-3151.	0.5	51
49	The polyprotein and FAR lipid binding proteins of nematodes: shape and monomer/dimer states in ligand-free and bound forms. European Biophysics Journal, 2003, 32, 465-476.	2.2	13
50	19Å... Solution Structure of the Filarial Nematode Immunomodulatory Protein, ES-62. Biophysical Journal, 2003, 84, 489-500.	0.5	31
51	Low resolution solution structure of the apo form of Escherichia coli haemoglobin protease Hbp. Journal of Molecular Biology, 2002, 315, 1179-1187.	4.2	25
52	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. Journal of Molecular Biology, 2001, 312, 711-720.	4.2	42
53	Structural Analysis of the Protein/Lipid Complexes Associated with Pore Formation by the Bacterial Toxin Pneumolysin. Journal of Biological Chemistry, 2001, 276, 5714-5719.	3.4	48
54	The Stoichiometry of Trimeric SIV Glycoprotein Interaction with CD4 Differs from That of Anti-envelope Antibody Fab Fragments. Journal of Biological Chemistry, 2001, 276, 42667-42676.	3.4	27

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55	A GRASP55-rab2 effector complex linking Golgi structure to membrane traffic. <i>Journal of Cell Biology</i> , 2001, 155, 877-884.	5.2	202
56	Neutron scattering: good news for biotechnology. <i>Current Opinion in Biotechnology</i> , 2000, 11, 72-80.	6.6	26
57	Human Homologue of the Drosophila Discs Large Tumor Suppressor Protein Forms an Oligomer in Solution. <i>Journal of Biological Chemistry</i> , 2000, 275, 13759-13770.	3.4	43
58	Hydrodynamic bead modeling of biological macromolecules. <i>Methods in Enzymology</i> , 2000, 321, 278-304.	1.0	32
59	Conformational spectra α^2 probing protein conformational changes. <i>Biophysical Chemistry</i> , 1999, 80, 189-197.	2.8	4
60	Novel Size-Independent Modeling of the Dilute Solution Conformation of the Immunoglobulin IgG Fab α^2 Domain Using SOLPRO and ELLIPS. <i>Biophysical Journal</i> , 1999, 77, 2902-2910.	0.5	29
61	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
62	Structure and mechanism of the bacterial protein toxin, pneumolysin. <i>Biochemical Society Transactions</i> , 1999, 27, A55-A55.	3.4	0
63	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
64	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
65	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
66	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
67	DT diaphorase exists as a dimer-tetramer equilibrium in solution. <i>European Biophysics Journal</i> , 1997, 25, 423-430.	2.2	5
68	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
69	Investigations into the molecular size and shape of tomato extensin. <i>Biochemical Journal</i> , 1996, 320, 577-583.	3.7	18
70	Crystal structure of a PDZ domain. <i>Nature</i> , 1996, 382, 649-652.	27.8	322
71	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
72	A preliminary investigation of the hydrodynamic properties of two novel monoclonal antibodies. <i>Biochemical Society Transactions</i> , 1990, 18, 1030-1031.	3.4	1