

Philip W Fowler

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

55
papers

2,108
citations

26
h-index

45
g-index

66
ext. papers

2,772
ext. citations

7.7
avg, IF

4.56
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 55 | Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018 , 379, 1403-1415 | 59.2 | 243 |
| 54 | Crystal structure of a prokaryotic homologue of the mammalian oligopeptide-proton symporters, PepT1 and PepT2. <i>EMBO Journal</i> , 2011 , 30, 417-26 | 13 | 209 |
| 53 | Alternating access mechanism in the POT family of oligopeptide transporters. <i>EMBO Journal</i> , 2012 , 31, 3411-21 | 13 | 162 |
| 52 | Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020 , 9, | 8.9 | 122 |
| 51 | The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. <i>Clinical Infectious Diseases</i> , 2021 , 73, e699-e709 | 11.6 | 120 |
| 50 | Modelling biological complexity: a physical scientist's perspective. <i>Journal of the Royal Society Interface</i> , 2005 , 2, 267-80 | 4.1 | 83 |
| 49 | Helix-helix interactions in membrane proteins: coarse-grained simulations of glycoporphin a helix dimerization. <i>Biochemistry</i> , 2008 , 47, 10503-12 | 3.2 | 77 |
| 48 | Nothing to sneeze at: a dynamic and integrative computational model of an influenza A virion. <i>Structure</i> , 2015 , 23, 584-597 | 5.2 | 71 |
| 47 | Gating topology of the proton-coupled oligopeptide symporters. <i>Structure</i> , 2015 , 23, 290-301 | 5.2 | 67 |
| 46 | The selectivity of K ⁺ ion channels: testing the hypotheses. <i>Biophysical Journal</i> , 2008 , 95, 5062-72 | 2.9 | 59 |
| 45 | H bonding at the helix-bundle crossing controls gating in Kir potassium channels. <i>Neuron</i> , 2007 , 55, 602-14.9 | 14.9 | 59 |
| 44 | Membrane stiffness is modified by integral membrane proteins. <i>Soft Matter</i> , 2016 , 12, 7792-7803 | 3.6 | 55 |
| 43 | Flexible gates generate occluded intermediates in the transport cycle of LacY. <i>Journal of Molecular Biology</i> , 2014 , 426, 735-51 | 6.5 | 49 |
| 42 | Protein crowding and lipid complexity influence the nanoscale dynamic organization of ion channels in cell membranes. <i>Scientific Reports</i> , 2017 , 7, 16647 | 4.9 | 48 |
| 41 | The pore of voltage-gated potassium ion channels is strained when closed. <i>Nature Communications</i> , 2013 , 4, 1872 | 17.4 | 45 |
| 40 | Insights into how nucleotide-binding domains power ABC transport. <i>Structure</i> , 2009 , 17, 1213-22 | 5.2 | 38 |
| 39 | Alchembed: A Computational Method for Incorporating Multiple Proteins into Complex Lipid Geometries. <i>Journal of Chemical Theory and Computation</i> , 2015 , 11, 2743-2754 | 6.4 | 37 |

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| 38 | Roles of Interleaflet Coupling and Hydrophobic Mismatch in Lipid Membrane Phase-Separation Kinetics. <i>Journal of the American Chemical Society</i> , 2016 , 138, 11633-42 | 16.4 | 37 |
| 37 | Antibiotic resistance prediction for from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019 , 4, 191 | 4.8 | 34 |
| 36 | Energetics of Multi-Ion Conduction Pathways in Potassium Ion Channels. <i>Journal of Chemical Theory and Computation</i> , 2013 , 9, 5176-5189 | 6.4 | 31 |
| 35 | Monotopic enzymes and lipid bilayers: a comparative study. <i>Biochemistry</i> , 2007 , 46, 3108-15 | 3.2 | 31 |
| 34 | Validating a 14-Drug Microtiter Plate Containing Bedaquiline and Delamanid for Large-Scale Research Susceptibility Testing of Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62, | 5.9 | 31 |
| 33 | An observational cohort study on the incidence of SARS-CoV-2 infection and B.1.1.7 variant infection in healthcare workers by antibody and vaccination status. <i>Clinical Infectious Diseases</i> , 2021 , | 11.6 | 31 |
| 32 | Phylogenetically informative mutations in genes implicated in antibiotic resistance in Mycobacterium tuberculosis complex. <i>Genome Medicine</i> , 2020 , 12, 27 | 14.4 | 30 |
| 31 | Crystal Structures of the Extracellular Domain from PepT1 and PepT2 Provide Novel Insights into Mammalian Peptide Transport. <i>Structure</i> , 2015 , 23, 1889-1899 | 5.2 | 30 |
| 30 | Accurate Prediction of Ligand Affinities for a Proton-Dependent Oligopeptide Transporter. <i>Cell Chemical Biology</i> , 2016 , 23, 299-309 | 8.2 | 27 |
| 29 | Control of pH and PIP2 gating in heteromeric Kir4.1/Kir5.1 channels by H-Bonding at the helix-bundle crossing. <i>Channels</i> , 2007 , 1, 327-30 | 3 | 26 |
| 28 | Functional complementation and genetic deletion studies of KirBac channels: activatory mutations highlight gating-sensitive domains. <i>Journal of Biological Chemistry</i> , 2010 , 285, 40754-61 | 5.4 | 22 |
| 27 | Molecular modeling and simulation studies of ion channel structures, dynamics and mechanisms. <i>Methods in Cell Biology</i> , 2008 , 90, 233-65 | 1.8 | 22 |
| 26 | Grid-based steered thermodynamic integration accelerates the calculation of binding free energies. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2005 , 363, 1999-2015 | 3 | 22 |
| 25 | Membrane Compartmentalization Reducing the Mobility of Lipids and Proteins within a Model Plasma Membrane. <i>Journal of Physical Chemistry B</i> , 2016 , 120, 8873-81 | 3.4 | 22 |
| 24 | A computational protocol for the integration of the monotopic protein prostaglandin H2 synthase into a phospholipid bilayer. <i>Biophysical Journal</i> , 2006 , 91, 401-10 | 2.9 | 21 |
| 23 | Robust Prediction of Resistance to Trimethoprim in Staphylococcus aureus. <i>Cell Chemical Biology</i> , 2018 , 25, 339-349.e4 | 8.2 | 16 |
| 22 | NRas slows the rate at which a model lipid bilayer phase separates. <i>Faraday Discussions</i> , 2014 , 169, 209-236 | 3.6 | 16 |
| 21 | Rapid, Accurate, and Precise Calculation of Relative Binding Affinities for the SH2 Domain Using a Computational Grid. <i>Journal of Chemical Theory and Computation</i> , 2007 , 3, 1193-202 | 6.4 | 15 |

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| 20 | Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64, | 5.9 | 13 |
| 19 | GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2450-2460 | 8.3 | 11 |
| 18 | Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of Mycobacterium tuberculosis. <i>Microbiology (United Kingdom)</i> , 2018 , 164, 1522-1530 | 2.9 | 10 |
| 17 | Large scale molecular dynamics simulation of native and mutant dihydropteroate synthase-sulphanilamide complexes suggests the molecular basis for dihydropteroate synthase drug resistance. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2005 , 363, 2055-73 | 3 | 8 |
| 16 | State-dependent network connectivity determines gating in a K ⁺ channel. <i>Structure</i> , 2014 , 22, 1037-46 | 5.2 | 7 |
| 15 | Detailed Examination of a Single Conduction Event in a Potassium Channel. <i>Journal of Physical Chemistry Letters</i> , 2013 , 4, 3104-3109 | 6.4 | 6 |
| 14 | Cryo-EM structure and resistance landscape of M. tuberculosis MmpL3: An emergent therapeutic target. <i>Structure</i> , 2021 , 29, 1182-1191.e4 | 5.2 | 6 |
| 13 | Effect of the Southeast Asian Ovalocytosis Deletion on the Conformational Dynamics of Signal-Anchor Transmembrane Segment 1 of Red Cell Anion Exchanger 1 (AE1, Band 3, or SLC4A1). <i>Biochemistry</i> , 2017 , 56, 712-722 | 3.2 | 5 |
| 12 | Epidemiological cutoff values for a 96-well broth microdilution plate for high-throughput research antibiotic susceptibility testing of M. tuberculosis | | 5 |
| 11 | Author response: Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study 2020 , | | 4 |
| 10 | Prediction of pyrazinamide resistance in Mycobacterium tuberculosis using structure-based machine learning approaches | | 4 |
| 9 | How quickly can we predict trimethoprim resistance using alchemical free energy methods?. <i>Interface Focus</i> , 2020 , 10, 20190141 | 3.9 | 3 |
| 8 | Deciphering Bedaquiline and Clofazimine Resistance in Tuberculosis: An Evolutionary Medicine Approach | | 3 |
| 7 | The 2021 WHO catalogue of complex mutations associated with drug resistance: A genotypic analysis.. <i>Lancet Microbe, The</i> , 2022 , 3, e265-e273 | 22.2 | 3 |
| 6 | Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of Mycobacterium tuberculosis | | 2 |
| 5 | Scalable Pathogen Pipeline Platform (SP ³): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing 2019 , | | 1 |
| 4 | Insights into the structural nature of the transition state in the Kir channel gating pathway. <i>Channels</i> , 2014 , 8, 551-5 | 3 | 1 |
| 3 | Rapid turnaround multiplex sequencing of SARS-CoV-2: comparing tiling amplicon protocol performance | | 1 |

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| 2 | Validating a 14-drug microtitre plate containing bedaquiline and delamanid for large-scale research susceptibility testing of <i>Mycobacterium tuberculosis</i> | 1 |
| 1 | BashTheBug: a crowd of volunteers reproducibly and accurately measure the minimum inhibitory concentrations of 13 antitubercular drugs from photographs of 96-well broth microdilution plates | 1 |