

Philip W Fowler

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

3,232
citations

186265

28
h-index

197818

49
g-index

66
all docs

66
docs citations

66
times ranked

4735
citing authors

#	ARTICLE	IF	CITATIONS
1	An Observational Cohort Study on the Incidence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection and B.1.1.7 Variant Infection in Healthcare Workers by Antibody and Vaccination Status. <i>Clinical Infectious Diseases</i> , 2022, 74, 1208-1219.	5.8	64
2	The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
3	ReadItAndKeep: rapid decontamination of SARS-CoV-2 sequencing reads. <i>Bioinformatics</i> , 2022, 38, 3291-3293.	4.1	5
4	A crowd of BashTheBug volunteers reproducibly and accurately measure the minimum inhibitory concentrations of 13 antitubercular drugs from photographs of 96-well broth microdilution plates. <i>ELife</i> , 2022, 11, .	6.0	7
5	Cryo-EM structure and resistance landscape of <i>M.Âtuberculosis</i> MmpL3: An emergent therapeutic target. <i>Structure</i> , 2021, 29, 1182-1191.e4.	3.3	25
6	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.	5.8	235
7	How quickly can we predict trimethoprim resistance using alchemical free energy methods?. <i>Interface Focus</i> , 2020, 10, 20190141.	3.0	4
8	Phylogenetically informative mutations in genes implicated in antibiotic resistance in <i>Mycobacterium tuberculosis</i> complex. <i>Genome Medicine</i> , 2020, 12, 27.	8.2	58
9	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460.	8.9	25
10	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	33
11	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020, 9, .	6.0	196
12	Predicting Resistance Is (Not) Futile. <i>ACS Central Science</i> , 2019, 5, 1312-1314.	11.3	5
13	Scalable Pathogen Pipeline Platform (SP ³): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing. , 2019, , .		1
14	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	1.8	103
15	Robust Prediction of Resistance to Trimethoprim in <i>Staphylococcus aureus</i> . <i>Cell Chemical Biology</i> , 2018, 25, 339-349.e4.	5.2	32
16	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	27.0	405
17	Validating a 14-Drug Microtiter Plate Containing Bedaquiline and Delamanid for Large-Scale Research Susceptibility Testing of <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	62
18	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of <i>Mycobacterium tuberculosis</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 1522-1530.	1.8	21

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19	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.	2.5	6
20	Protein crowding and lipid complexity influence the nanoscale dynamic organization of ion channels in cell membranes. <i>Scientific Reports</i> , 2017, 7, 16647.	3.3	68
21	Accurate Prediction of Ligand Affinities for a Proton-Dependent Oligopeptide Transporter. <i>Cell Chemical Biology</i> , 2016, 23, 299-309.	5.2	34
22	Membrane Compartmentalization Reducing the Mobility of Lipids and Proteins within a Model Plasma Membrane. <i>Journal of Physical Chemistry B</i> , 2016, 120, 8873-8881.	2.6	24
23	Membrane stiffness is modified by integral membrane proteins. <i>Soft Matter</i> , 2016, 12, 7792-7803.	2.7	90
24	Roles of Interleaflet Coupling and Hydrophobic Mismatch in Lipid Membrane Phase-Separation Kinetics. <i>Journal of the American Chemical Society</i> , 2016, 138, 11633-11642.	13.7	51
25	The Effect of Proteins and Lipids on Membrane Stiffness. <i>Biophysical Journal</i> , 2016, 110, 243a.	0.5	0
26	Crystal Structures of the Extracellular Domain from PepT1 and PepT2 Provide Novel Insights into Mammalian Peptide Transport. <i>Structure</i> , 2015, 23, 1889-1899.	3.3	40
27	Gating Topology of the Proton-Coupled Oligopeptide Symporters. <i>Structure</i> , 2015, 23, 290-301.	3.3	98
28	Nothing to Sneeze At: A Dynamic and Integrative Computational Model of an Influenza A Virion. <i>Structure</i> , 2015, 23, 584-597.	3.3	90
29	Alchembed: A Computational Method for Incorporating Multiple Proteins into Complex Lipid Geometries. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 2743-2754.	5.3	42
30	NRas slows the rate at which a model lipid bilayer phase separates. <i>Faraday Discussions</i> , 2014, 169, 209-223.	3.2	19
31	Insights into the structural nature of the transition state in the Kir channel gating pathway. <i>Channels</i> , 2014, 8, 551-555.	2.8	3
32	Flexible Gates Generate Occluded Intermediates in the Transport Cycle of LacY. <i>Journal of Molecular Biology</i> , 2014, 426, 735-751.	4.2	70
33	State-Dependent Network Connectivity Determines Gating in a K ⁺ Channel. <i>Structure</i> , 2014, 22, 1037-1046.	3.3	8
34	Energetics of Multi-Ion Conduction Pathways in Potassium Ion Channels. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 5176-5189.	5.3	41
35	The pore of voltage-gated potassium ion channels is strained when closed. <i>Nature Communications</i> , 2013, 4, 1872.	12.8	52
36	Detailed Examination of a Single Conduction Event in a Potassium Channel. <i>Journal of Physical Chemistry Letters</i> , 2013, 4, 3104-3109.	4.6	8

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37	Alternating access mechanism in the POT family of oligopeptide transporters. EMBO Journal, 2012, 31, 3411-3421.	7.8	226
38	Crystal structure of a prokaryotic homologue of the mammalian oligopeptide-proton symporters, PepT1 and PepT2. EMBO Journal, 2011, 30, 417-426.	7.8	269
39	Functional Complementation and Genetic Deletion Studies of KirBac Channels. Journal of Biological Chemistry, 2010, 285, 40754-40761.	3.4	22
40	A Novel Rate Theory Approach To Transport In Ion Channels. , 2009, , .		1
41	Insights into How Nucleotide-Binding Domains Power ABC Transport. Structure, 2009, 17, 1213-1222.	3.3	40
42	Chapter 12 Molecular Modeling and Simulation Studies of Ion Channel Structures, Dynamics and Mechanisms. Methods in Cell Biology, 2008, 90, 233-265.	1.1	24
43	The Selectivity of K ⁺ Ion Channels: Testing the Hypotheses. Biophysical Journal, 2008, 95, 5062-5072.	0.5	63
44	Helix~Helix Interactions in Membrane Proteins: Coarse-Grained Simulations of Glycophorin A Helix Dimerization. Biochemistry, 2008, 47, 10503-10512.	2.5	82
45	Control of pH and PIP ₂ Gating in Heteromeric Kir4.1/Kir5.1 Channels by H-Bonding at the Helix-Bundle Crossing. Channels, 2007, 1, 327-330.	2.8	30
46	H Bonding at the Helix-Bundle Crossing Controls Gating in Kir Potassium Channels. Neuron, 2007, 55, 602-614.	8.1	63
47	Rapid, Accurate, and Precise Calculation of Relative Binding Affinities for the SH2 Domain Using a Computational Grid. Journal of Chemical Theory and Computation, 2007, 3, 1193-1202.	5.3	16
48	Monotopic Enzymes and Lipid Bilayers: A Comparative Study. Biochemistry, 2007, 46, 3108-3115.	2.5	36
49	A Computational Protocol for the Integration of the Monotopic Protein Prostaglandin H2 Synthase into a Phospholipid Bilayer. Biophysical Journal, 2006, 91, 401-410.	0.5	21
50	Grid-based steered thermodynamic integration accelerates the calculation of binding free energies. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2005, 363, 1999-2015.	3.4	23
51	Large scale molecular dynamics simulation of native and mutant dihydropteroate synthase~sulphanilamide complexes suggests the molecular basis for dihydropteroate synthase drug resistance. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2005, 363, 2055-2073.	3.4	9
52	Modelling biological complexity: a physical scientist's perspective. Journal of the Royal Society Interface, 2005, 2, 267-280.	3.4	104