Philip W Fowler

List of Publications by Year in Descending Order

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	The 2021 WHO catalogue of complex mutations associated with drug resistance: A genotypic analysis.. *Lancet Microbe, The*, **2022**, 3, e265-e273	22.2	3
54	Cryo-EM structure and resistance landscape of M. tuberculosis MmpL3: An emergent therapeutic target. *Structure*, **2021**, 29, 1182-1191.e4	5.2	6
53	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. *Clinical Infectious Diseases*, **2021**,	11.6	31
52	The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. *Clinical Infectious Diseases*, **2021**, 73, e699-e709	11.6	120
51	Phylogenetically informative mutations in genes implicated in antibiotic resistance in Mycobacterium tuberculosis complex. *Genome Medicine*, **2020**, 12, 27	14.4	30
50	GenomegaMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. *Molecular Biology and Evolution*, **2020**, 37, 2450-2460	8.3	11
49	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in. *Antimicrobial Agents and Chemotherapy*, **2020**, 64,	5.9	13
48	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. *ELife*, **2020**, 9,	8.9	122
47	Author response: Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study **2020**,		4
46	How quickly can we predict trimethoprim resistance using alchemical free energy methods?. *Interface Focus*, **2020**, 10, 20190141	3.9	3
45	Scalable Pathogen Pipeline Platform (SP^3): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing **2019**,		1
44	Antibiotic resistance prediction for from genome sequence data with Mykrobe. *Wellcome Open Research*, **2019**, 4, 191	4.8	34
43	Robust Prediction of Resistance to Trimethoprim in Staphylococcus aureus. *Cell Chemical Biology*, **2018**, 25, 339-349.e4	8.2	16
42	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of Mycobacterium tuberculosis. *Microbiology (United Kingdom)*, **2018**, 164, 1522-1530	2.9	10
41	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. *New England Journal of Medicine*, **2018**, 379, 1403-1415	59.2	243
40	Validating a 14-Drug Microtiter Plate Containing Bedaquiline and Delamanid for Large-Scale Research Susceptibility Testing of Mycobacterium tuberculosis. *Antimicrobial Agents and Chemotherapy*, **2018**, 62,	5.9	31
39	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). *Biochemistry*, **2017**, 56, 712-722	3.2	5

38	Protein crowding and lipid complexity influence the nanoscale dynamic organization of ion channels in cell membranes. *Scientific Reports*, **2017**, 7, 16647	4.9	48
37	Membrane stiffness is modified by integral membrane proteins. *Soft Matter*, **2016**, 12, 7792-7803	3.6	55
36	Roles of Interleaflet Coupling and Hydrophobic Mismatch in Lipid Membrane Phase-Separation Kinetics. *Journal of the American Chemical Society*, **2016**, 138, 11633-42	16.4	37
35	Accurate Prediction of Ligand Affinities for a Proton-Dependent Oligopeptide Transporter. *Cell Chemical Biology*, **2016**, 23, 299-309	8.2	27
34	Membrane Compartmentalization Reducing the Mobility of Lipids and Proteins within a Model Plasma Membrane. *Journal of Physical Chemistry B*, **2016**, 120, 8873-81	3.4	22
33	Nothing to sneeze at: a dynamic and integrative computational model of an influenza A virion. *Structure*, **2015**, 23, 584-597	5.2	71
32	Alchembed: A Computational Method for Incorporating Multiple Proteins into Complex Lipid Geometries. *Journal of Chemical Theory and Computation*, **2015**, 11, 2743-2754	6.4	37
31	Crystal Structures of the Extracellular Domain from PepT1 and PepT2 Provide Novel Insights into Mammalian Peptide Transport. *Structure*, **2015**, 23, 1889-1899	5.2	30
30	Gating topology of the proton-coupled oligopeptide symporters. *Structure*, **2015**, 23, 290-301	5.2	67
29	Flexible gates generate occluded intermediates in the transport cycle of LacY. *Journal of Molecular Biology*, **2014**, 426, 735-51	6.5	49
28	State-dependent network connectivity determines gating in a K+ channel. *Structure*, **2014**, 22, 1037-46	5.2	7
27	NRas slows the rate at which a model lipid bilayer phase separates. *Faraday Discussions*, **2014**, 169, 209-223	3.6	16
26	Insights into the structural nature of the transition state in the Kir channel gating pathway. *Channels*, **2014**, 8, 551-5	3	1
25	Energetics of Multi-Ion Conduction Pathways in Potassium Ion Channels. *Journal of Chemical Theory and Computation*, **2013**, 9, 5176-5189	6.4	31
24	The pore of voltage-gated potassium ion channels is strained when closed. *Nature Communications*, **2013**, 4, 1872	17.4	45
23	Detailed Examination of a Single Conduction Event in a Potassium Channel. *Journal of Physical Chemistry Letters*, **2013**, 4, 3104-3109	6.4	6
22	Alternating access mechanism in the POT family of oligopeptide transporters. *EMBO Journal*, **2012**, 31, 3411-21	13	162
21	Crystal structure of a prokaryotic homologue of the mammalian oligopeptide-proton symporters, PepT1 and PepT2. *EMBO Journal*, **2011**, 30, 417-26	13	209

20	Functional complementation and genetic deletion studies of KirBac channels: activatory mutations highlight gating-sensitive domains. *Journal of Biological Chemistry*, **2010**, 285, 40754-61	5.4	22
19	Insights into how nucleotide-binding domains power ABC transport. *Structure*, **2009**, 17, 1213-22	5.2	38
18	Molecular modeling and simulation studies of ion channel structures, dynamics and mechanisms. *Methods in Cell Biology*, **2008**, 90, 233-65	1.8	22
17	The selectivity of K+ ion channels: testing the hypotheses. *Biophysical Journal*, **2008**, 95, 5062-72	2.9	59
16	Helix-helix interactions in membrane proteins: coarse-grained simulations of glycophorin a helix dimerization. *Biochemistry*, **2008**, 47, 10503-12	3.2	77
15	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, 1193-202	6.4	15
14	Monotopic enzymes and lipid bilayers: a comparative study. *Biochemistry*, **2007**, 46, 3108-15	3.2	31
13	Control of pH and PIP2 gating in heteromeric Kir4.1/Kir5.1 channels by H-Bonding at the helix-bundle crossing. *Channels*, **2007**, 1, 327-30	3	26
12	H bonding at the helix-bundle crossing controls gating in Kir potassium channels. *Neuron*, **2007**, 55, 602-14	13.9	59
11	A computational protocol for the integration of the monotopic protein prostaglandin H2 synthase into a phospholipid bilayer. *Biophysical Journal*, **2006**, 91, 401-10	2.9	21
10	Modelling biological complexity: a physical scientist's perspective. *Journal of the Royal Society Interface*, **2005**, 2, 267-80	4.1	83
9	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	22
8	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, 2055-73	3	8
7	Rapid turnaround multiplex sequencing of SARS-CoV-2: comparing tiling amplicon protocol performance		1
6	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of Mycobacterium tuberculosis		2
5	Validating a 14-drug microtitre plate containing bedaquiline and delamanid for large-scale research susceptibility testing of Mycobacterium tuberculosis		1
4	Prediction of pyrazinamide resistance in Mycobacterium tuberculosis using structure-based machine learning approaches		4
3	Deciphering Bedaquiline and Clofazimine Resistance in Tuberculosis: An Evolutionary Medicine Approach		3