Philip W Fowler

List of Publications by Year
in descending order

52 papers	3,232 citations	185998 28 h-index	197535 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. Clinical Infectious Diseases, 2022, 74, 1208-1219.	2.9	64
2	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. Lancet Microbe, The, 2022, 3, e265-e273.	3.4	114
3	ReadItAndKeep: rapid decontamination of SARS-CoV-2 sequencing reads. Bioinformatics, 2022, 38, 3291-3293.	1.8	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. ELife, 2022, 11, .	2.8	7
5	Cryo-EM structure and resistance landscape of M.Âtuberculosis MmpL3: An emergent therapeutic target. Structure, 2021, 29, 1182-1191.e4.	1.6	25
6	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.	2.9	235
7	How quickly can we predict trimethoprim resistance using alchemical free energy methods?. Interface Focus, 2020, 10, 20190141.	1.5	4
8	Phylogenetically informative mutations in genes implicated in antibiotic resistance in Mycobacterium tuberculosis complex. Genome Medicine, 2020, 12, 27.	3.6	58
9	GenomegaMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. Molecular Biology and Evolution, 2020, 37, 2450-2460.	3.5	25
10	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in Escherichia coli. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	33
11	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. ELife, 2020, 9, .	2.8	196
12	Predicting Resistance Is (Not) Futile. ACS Central Science, 2019, 5, 1312-1314.	5.3	5
13	Scalable Pathogen Pipeline Platform (SP^3): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing. , 2019, , .		1
14	Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191.	0.9	103
15	Robust Prediction of Resistance to Trimethoprim in Staphylococcus aureus. Cell Chemical Biology, 2018, 25, 339-349.e4.	2.5	32
16	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. New England Journal of Medicine, 2018, 379, 1403-1415.	13.9	405
17	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, .	1.4	62
18	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.	0.7	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). Biochemistry, 2017, 56, 712-722.	1.2	6
20	Protein crowding and lipid complexity influence the nanoscale dynamic organization of ion channels in cell membranes. Scientific Reports, 2017, 7, 16647.	1.6	68
21	Accurate Prediction of Ligand Affinities for a Proton-Dependent Oligopeptide Transporter. Cell Chemical Biology, 2016, 23, 299-309.	2.5	34
22	Membrane Compartmentalization Reducing the Mobility of Lipids and Proteins within a Model Plasma Membrane. Journal of Physical Chemistry B, 2016, 120, 8873-8881.	1.2	24
23	Membrane stiffness is modified by integral membrane proteins. Soft Matter, 2016, 12, 7792-7803.	1.2	90
24	Roles of Interleaflet Coupling and Hydrophobic Mismatch in Lipid Membrane Phase-Separation Kinetics. Journal of the American Chemical Society, 2016, 138, 11633-11642.	6.6	51
25	The Effect of Proteins and Lipids on Membrane Stiffness. Biophysical Journal, 2016, 110, 243a.	0.2	0
26	Crystal Structures of the Extracellular Domain from PepT1 and PepT2 Provide Novel Insights into Mammalian Peptide Transport. Structure, 2015, 23, 1889-1899.	1.6	40
27	Gating Topology of the Proton-Coupled Oligopeptide Symporters. Structure, 2015, 23, 290-301.	1.6	98
28	Nothing to Sneeze At: A Dynamic and Integrative Computational Model of an Influenza A Virion. Structure, 2015, 23, 584-597.	1.6	90
29	Alchembed: A Computational Method for Incorporating Multiple Proteins into Complex Lipid Geometries. Journal of Chemical Theory and Computation, 2015, 11, 2743-2754.	2.3	42
30	NRas slows the rate at which a model lipid bilayer phase separates. Faraday Discussions, 2014, 169, 209-223.	1.6	19
31	Insights into the structural nature of the transition state in the Kir channel gating pathway. Channels, 2014, 8, 551-555.	1.5	3
32	Flexible Gates Generate Occluded Intermediates in the Transport Cycle of LacY. Journal of Molecular Biology, 2014, 426, 735-751.	2.0	70
33	State-Dependent Network Connectivity Determines Gating in a K+ Channel. Structure, 2014, 22, 1037-1046.	1.6	8
34	Energetics of Multi-Ion Conduction Pathways in Potassium Ion Channels. Journal of Chemical Theory and Computation, 2013, 9, 5176-5189.	2.3	41
35	The pore of voltage-gated potassium ion channels is strained when closed. Nature Communications, 2013, 4, 1872.	5.8	52
36	Detailed Examination of a Single Conduction Event in a Potassium Channel. Journal of Physical Chemistry Letters, 2013, 4, 3104-3109.	2.1	8

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37	Alternating access mechanism in the POT family of oligopeptide transporters. EMBO Journal, 2012, 31, 3411-3421.	3.5	226
38	Crystal structure of a prokaryotic homologue of the mammalian oligopeptide-proton symporters, PepT1 and PepT2. EMBO Journal, 2011, 30, 417-426.	3.5	269
39	Functional Complementation and Genetic Deletion Studies of KirBac Channels. Journal of Biological Chemistry, 2010, 285, 40754-40761.	1.6	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.	1.6	40
42	Chapter 12 Molecular Modeling and Simulation Studies of Ion Channel Structures, Dynamics and Mechanisms. Methods in Cell Biology, 2008, 90, 233-265.	0.5	24
43	The Selectivity of K+ Ion Channels: Testing the Hypotheses. Biophysical Journal, 2008, 95, 5062-5072.	0.2	63
44	Helixâ^'Helix Interactions in Membrane Proteins: Coarse-Grained Simulations of Glycophorin A Helix Dimerization. Biochemistry, 2008, 47, 10503-10512.	1.2	82
45	Control of pH and PIP₂Gating in Heteromeric Kir4.1/Kir5.1 Channels by H-Bonding at the Helix-Bundle Crossing. Channels, 2007, 1, 327-330.	1.5	30
46	H Bonding at the Helix-Bundle Crossing Controls Gating in Kir Potassium Channels. Neuron, 2007, 55, 602-614.	3.8	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.	2.3	16
48	Monotopic Enzymes and Lipid Bilayers:Â A Comparative Studyâ€. Biochemistry, 2007, 46, 3108-3115.	1.2	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.	0.2	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.	1.6	23
51	Large scale molecular dynamics simulation of native and mutant dihydropteroate synthaseâ€“sulphanilamide complexes suggests the molecular basis for dihydropteroate synthase drug resistance. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2005, 363, 2055-2073.	1.6	9
52	Modelling biological complexity: a physical scientist's perspective. Journal of the Royal Society Interface, 2005, 2, 267-280.	1.5	104