

# Catherine Venien-Bryan

## List of Publications by Year in descending order

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63  
papers

2,351  
citations

201674

27  
h-index

214800

47  
g-index

66  
all docs

66  
docs citations

66  
times ranked

3351  
citing authors

#	ARTICLE	IF	CITATIONS
1	Generation of protein lattices by fusing proteins with matching rotational symmetry. <i>Nature Nanotechnology</i> , 2011, 6, 558-562.	31.5	214
2	Structural Changes of the Prion Protein in Lipid Membranes Leading to Aggregation and Fibrillization. <i>Biochemistry</i> , 2003, 42, 3295-3304.	2.5	165
3	The 3-dimensional structure of a hepatitis C virus p7 ion channel by electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12712-12716.	7.1	139
4	Two Different Conformational States of the KirBac3.1 Potassium Channel Revealed by Electron Crystallography. <i>Structure</i> , 2005, 13, 1463-1472.	3.3	100
5	Binding of pulmonary surfactant proteins to carbon nanotubes; potential for damage to lung immune defense mechanisms. <i>Carbon</i> , 2007, 45, 607-617.	10.3	100
6	Structure of a KirBac potassium channel with an open bundle crossing indicates a mechanism of channel gating. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 158-163.	8.2	92
7	Structural Analysis of the Anaphase-Promoting Complex Reveals Multiple Active Sites and Insights into Polyubiquitylation. <i>Molecular Cell</i> , 2005, 20, 855-866.	9.7	81
8	Characterization of the Growth of 2D Protein Crystals on a Lipid Monolayer by Ellipsometry and Rigidity Measurements Coupled to Electron Microscopy. <i>Biophysical Journal</i> , 1998, 74, 2649-2657.	0.5	76
9	Conformational Changes During the Gating of a Potassium Channel Revealed by Structural Mass Spectrometry. <i>Structure</i> , 2010, 18, 839-846.	3.3	76
10	The FANCD2-FANCI complex is recruited to DNA interstrand crosslinks before monoubiquitination of FANCD2. <i>Nature Communications</i> , 2016, 7, 12124.	12.8	69
11	Two-dimensional crystallization of a membrane protein on a detergent-resistant lipid monolayer 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 308, 639-647.	4.2	68
12	Global structural changes of an ion channel during its gating are followed by ion mobility mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17170-17175.	7.1	63
13	Studies of the ATPase activity of the ABC protein SUR1. <i>FEBS Journal</i> , 2007, 274, 3532-3544.	4.7	62
14	Copper Refolding of Prion Protein. <i>Biochemical and Biophysical Research Communications</i> , 2000, 276, 1217-1224.	2.1	56
15	Cryo-electron microscopy and X-ray crystallography: complementary approaches to structural biology and drug discovery. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 174-183.	0.8	56
16	An unusual soluble $\beta$ -turn-rich conformation of prion is involved in fibril formation and toxic to neuronal cells. <i>Biochemical and Biophysical Research Communications</i> , 2005, 328, 292-305.	2.1	53
17	Structural study of the response regulator HupR from <i>Rhodobacter capsulatus</i> . electron microscopy of two-dimensional crystals on a nickel-chelating lipid. <i>Journal of Molecular Biology</i> , 1997, 274, 687-692.	4.2	52
18	Evidence for the Assembly of a Bacterial Tripartite Multidrug Pump with a Stoichiometry of 3:6:3. <i>Journal of Biological Chemistry</i> , 2011, 286, 26900-26912.	3.4	49

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19	Surface-Induced Polymerization of Actin. <i>Biophysical Journal</i> , 1999, 76, 1580-1590.	0.5	43
20	Top-down mass spectrometry of intact membrane protein complexes reveals oligomeric state and sequence information in a single experiment. <i>Protein Science</i> , 2015, 24, 1292-1300.	7.6	42
21	Synchrotron Radiation Diffraction from Two-Dimensional Protein Crystals at the Air/Water Interface. <i>Biophysical Journal</i> , 2000, 79, 496-500.	0.5	35
22	Modeling of an Ion Channel in Its Open Conformation. <i>Biophysical Journal</i> , 2005, 89, L01-L03.	0.5	35
23	Role of Aromatic Localization in the Gating Process of a Potassium Channel. <i>Biophysical Journal</i> , 2006, 90, L01-L03.	0.5	35
24	Protein structure determination by electron cryo-microscopy. <i>Current Opinion in Pharmacology</i> , 2009, 9, 636-642.	3.5	34
25	Separating speed and ability to displace roadblocks during DNA translocation by FtsK. <i>EMBO Journal</i> , 2010, 29, 1423-1433.	7.8	34
26	MicroRNA Biophysically Modulates Cardiac Action Potential by Direct Binding to Ion Channel. <i>Circulation</i> , 2021, 143, 1597-1613.	1.6	33
27	Regulation of Flagellum Number by FlhA and FlgM and Role in Biofilm Formation by <i>Rhodospirillum rubrum</i> . <i>Journal of Bacteriology</i> , 2011, 193, 4010-4014.	2.2	32
28	Direct Visualization of KirBac3.1 Potassium Channel Gating by Atomic Force Microscopy. <i>Journal of Molecular Biology</i> , 2007, 374, 500-505.	4.2	28
29	The Structure of Phosphorylase Kinase Holoenzyme at 9.9 Å... Resolution and Location of the Catalytic Subunit and the Substrate Glycogen Phosphorylase. <i>Structure</i> , 2009, 17, 117-127.	3.3	28
30	Two-Dimensional Crystallization of a Histidine-Tagged Protein on Monolayers of Fluidity-Enhanced Ni <sup>2+</sup> -Chelating Lipids. <i>Langmuir</i> , 2002, 18, 9502-9512.	3.5	27
31	Globular and pre-fibrillar prion aggregates are toxic to neuronal cells and perturb their electrophysiology. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 873-881.	2.3	25
32	Three-Dimensional Structure of Phosphorylase Kinase at 22 Å... Resolution and Its Complex with Glycogen Phosphorylase b. <i>Structure</i> , 2002, 10, 33-41.	3.3	23
33	Utilization of interferometric light microscopy for the rapid analysis of virus abundance in a river. <i>Research in Microbiology</i> , 2017, 168, 413-418.	2.1	22
34	Control of KirBac3.1 Potassium Channel Gating at the Interface between Cytoplasmic Domains. <i>Journal of Biological Chemistry</i> , 2014, 289, 143-151.	3.4	20
35	Functional and structural differences between the prion protein from two alleles prnpa and prnpb of mouse. <i>FEBS Journal</i> , 2000, 267, 2452-2459.	0.2	19
36	Mouse TSPO in a lipid environment interacting with a functionalized monolayer. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 2791-2800.	2.6	19

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37	A New Strategy for Atomic Flexible Fitting in Cryo-EM Maps by Molecular Dynamics with Excited Normal Modes (MDeNM-EMfit). <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2419-2423.	5.4	18
38	Effect of the C-terminal proline repeats on ordered packing of squid rhodopsin and its mobility in membranes. <i>FEBS Letters</i> , 1995, 359, 45-49.	2.8	16
39	Structural and Functional Studies of the Response Regulator HupR. <i>Journal of Molecular Biology</i> , 2006, 359, 276-288.	4.2	15
40	Synthesis of a hemifluorinated amphiphile designed for self-assembly and two-dimensional crystallization of membrane protein. <i>Tetrahedron Letters</i> , 2008, 49, 2247-2250.	1.4	15
41	The HupR Receiver Domain Crystal Structure in its Nonphospho and Inhibitory Phospho States. <i>Journal of Molecular Biology</i> , 2009, 385, 51-64.	4.2	15
42	Phosphotyrosine-dependent in vitro reconstitution of recombinant LAT-nucleated multiprotein signalling complexes on liposomes. <i>Molecular Membrane Biology</i> , 2009, 26, 159-170.	2.0	13
43	A Soluble VE-cadherin Fragment Forms 2D Arrays of Dimers upon Binding to a Lipid Monolayer. <i>Journal of Molecular Biology</i> , 2004, 337, 881-892.	4.2	12
44	Isolation, characterization and complete nucleotide sequence of a novel temperate bacteriophage Min1, isolated from the nematode pathogen <i>Microbacterium nematophilum</i> . <i>Research in Microbiology</i> , 2007, 158, 582-590.	2.1	12
45	Projection structure of a transcriptional regulator, HupR, determined by electron cryo-microscopy. <i>Journal of Molecular Biology</i> , 2000, 296, 863-871.	4.2	11
46	Calcineurin B-like domains in the large regulatory $\hat{1}\pm/\hat{1}^2$ subunits of phosphorylase kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1597-1606.	2.6	11
47	Structural studies of virus-antibody immune complexes (poliovirus type I): Characterization of the epitopes in 3D. <i>Molecular Immunology</i> , 2015, 63, 279-286.	2.2	11
48	Structural and Functional Highlights of Vacuolar Soluble Protein 1 from Pathogen <i>Trypanosoma brucei brucei</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 30498-30513.	3.4	10
49	New Structural insights into Kir channel gating from molecular simulations, HDX-MS and functional studies. <i>Scientific Reports</i> , 2020, 10, 8392.	3.3	10
50	Oligomeric structure of the repressor of the bacteriophage Mu early operon. <i>FEBS Journal</i> , 1998, 252, 408-415.	0.2	9
51	Tetrameric structure of SUR2B revealed by electron microscopy of oriented single particles. <i>FEBS Journal</i> , 2013, 280, 1051-1063.	4.7	9
52	Growth of Large and Highly Ordered 2D Crystals of a K <sup>+</sup> Channel, Structural Role of Lipidic Environment. <i>Biophysical Journal</i> , 2013, 105, 398-408.	0.5	8
53	Mapping of the epitopes of poliovirus type 2 in complex with antibodies. <i>Molecular Immunology</i> , 2015, 67, 233-239.	2.2	8
54	Unexpected Gating Behaviour of an Engineered Potassium Channel Kir. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 691901.	3.5	3

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55	Biochemistry, structure, and cellular internalization of a four nanobody-bearing Fc dimer. <i>Protein Science</i> , 2021, 30, 1946-1957.	7.6	2
56	Structural modeling of a novel membrane-bound globin-coupled sensor in <i>Geobacter sulfurreducens</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1874-1888.	4.1	1
57	The Structure Of Phosphorylase Kinase Holoenzyme At Subnanometer Resolution, Location Of The Catalytic Subunit And The Substrate Glycogen Phosphorylase. <i>Biophysical Journal</i> , 2009, 96, 413a.	0.5	0
58	Comparison of the Structure of a Bacterial Potassium Channel in Both 2D and 3D Crystals. <i>Biophysical Journal</i> , 2012, 102, 536a.	0.5	0
59	Monolayer Two-Dimensional Crystallization of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2013, 955, 59-71.	0.9	0
60	The CRACAM Robot: Two-Dimensional Crystallization of Membrane Protein. <i>Methods in Molecular Biology</i> , 2017, 1635, 303-316.	0.9	0
61	Gating Mechanism of a Potassium Channel, Experimental and Theoretical Studies. <i>Biophysical Journal</i> , 2019, 116, 208a.	0.5	0
62	Structural and functional characterization of a human potassium channel, Kir2.1. <i>Biophysical Journal</i> , 2022, 121, 176a.	0.5	0
63	Integrative Study of the Structural and Dynamical Properties of a KirBac3.1 Mutant: Functional Implication of a Highly Conserved Tryptophan in the Transmembrane Domain. <i>International Journal of Molecular Sciences</i> , 2022, 23, 335.	4.1	0