

Catherine Venien-Bryan

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

2,351
citations

201385

27
h-index

214527

47
g-index

66
all docs

66
docs citations

66
times ranked

3351
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Structural and functional characterization of a human potassium channel, Kir2.1. <i>Biophysical Journal</i> , 2022, 121, 176a. | 0.2 | 0 |
| 2 | 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. | 1.8 | 0 |
| 3 | 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. | 1.9 | 1 |
| 4 | MicroRNA Biophysically Modulates Cardiac Action Potential by Direct Binding to Ion Channel. <i>Circulation</i> , 2021, 143, 1597-1613. | 1.6 | 33 |
| 5 | Unexpected Gating Behaviour of an Engineered Potassium Channel Kir. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 691901. | 1.6 | 3 |
| 6 | Biochemistry, structure, and cellular internalization of a four nanobody-bearing Fc dimer. <i>Protein Science</i> , 2021, 30, 1946-1957. | 3.1 | 2 |
| 7 | New Structural insights into Kir channel gating from molecular simulations, HDX-MS and functional studies. <i>Scientific Reports</i> , 2020, 10, 8392. | 1.6 | 10 |
| 8 | 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. | 2.5 | 18 |
| 9 | Gating Mechanism of a Potassium Channel, Experimental and Theoretical Studies. <i>Biophysical Journal</i> , 2019, 116, 208a. | 0.2 | 0 |
| 10 | 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. | 0.4 | 56 |
| 11 | Utilization of interferometric light microscopy for the rapid analysis of virus abundance in a river. <i>Research in Microbiology</i> , 2017, 168, 413-418. | 1.0 | 22 |
| 12 | The CRACAM Robot: Two-Dimensional Crystallization of Membrane Protein. <i>Methods in Molecular Biology</i> , 2017, 1635, 303-316. | 0.4 | 0 |
| 13 | The FANCD2-FANCI complex is recruited to DNA interstrand crosslinks before monoubiquitination of FANCD2. <i>Nature Communications</i> , 2016, 7, 12124. | 5.8 | 69 |
| 14 | 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. | 3.1 | 42 |
| 15 | Mapping of the epitopes of poliovirus type 2 in complex with antibodies. <i>Molecular Immunology</i> , 2015, 67, 233-239. | 1.0 | 8 |
| 16 | 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. | 1.6 | 10 |
| 17 | Structural studies of virus-antibody immune complexes (poliovirus type I): Characterization of the epitopes in 3D. <i>Molecular Immunology</i> , 2015, 63, 279-286. | 1.0 | 11 |
| 18 | Control of KirBac3.1 Potassium Channel Gating at the Interface between Cytoplasmic Domains. <i>Journal of Biological Chemistry</i> , 2014, 289, 143-151. | 1.6 | 20 |

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|----|--|------|-----------|
| 19 | Global structural changes of an ion channel during its gating are followed by ion mobility mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17170-17175. | 3.3 | 63 |
| 20 | Growth of Large and Highly Ordered 2D Crystals of a K ⁺ Channel, Structural Role of Lipidic Environment. Biophysical Journal, 2013, 105, 398-408. | 0.2 | 8 |
| 21 | Monolayer Two-Dimensional Crystallization of Membrane Proteins. Methods in Molecular Biology, 2013, 955, 59-71. | 0.4 | 0 |
| 22 | Tetrameric structure of SUR2B revealed by electron microscopy of oriented single particles. FEBS Journal, 2013, 280, 1051-1063. | 2.2 | 9 |
| 23 | Comparison of the Structure of a Bacterial Potassium Channel in Both 2D and 3D Crystals. Biophysical Journal, 2012, 102, 536a. | 0.2 | 0 |
| 24 | Structure of a KirBac potassium channel with an open bundle crossing indicates a mechanism of channel gating. Nature Structural and Molecular Biology, 2012, 19, 158-163. | 3.6 | 92 |
| 25 | Mouse TSPO in a lipid environment interacting with a functionalized monolayer. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 2791-2800. | 1.4 | 19 |
| 26 | Generation of protein lattices by fusing proteins with matching rotational symmetry. Nature Nanotechnology, 2011, 6, 558-562. | 15.6 | 214 |
| 27 | Evidence for the Assembly of a Bacterial Tripartite Multidrug Pump with a Stoichiometry of 3:6:3. Journal of Biological Chemistry, 2011, 286, 26900-26912. | 1.6 | 49 |
| 28 | Regulation of Flagellum Number by FliA and FlgM and Role in Biofilm Formation by Rhodobacter sphaeroides. Journal of Bacteriology, 2011, 193, 4010-4014. | 1.0 | 32 |
| 29 | Conformational Changes During the Gating of a Potassium Channel Revealed by Structural Mass Spectrometry. Structure, 2010, 18, 839-846. | 1.6 | 76 |
| 30 | Separating speed and ability to displace roadblocks during DNA translocation by FtsK. EMBO Journal, 2010, 29, 1423-1433. | 3.5 | 34 |
| 31 | The 3-dimensional structure of a hepatitis C virus p7 ion channel by electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12712-12716. | 3.3 | 139 |
| 32 | The Structure of Phosphorylase Kinase Holoenzyme at 9.9 Å... Resolution and Location of the Catalytic Subunit and the Substrate Glycogen Phosphorylase. Structure, 2009, 17, 117-127. | 1.6 | 28 |
| 33 | Protein structure determination by electron cryo-microscopy. Current Opinion in Pharmacology, 2009, 9, 636-642. | 1.7 | 34 |
| 34 | The HupR Receiver Domain Crystal Structure in its Nonphospho and Inhibitory Phospho States. Journal of Molecular Biology, 2009, 385, 51-64. | 2.0 | 15 |
| 35 | Phosphotyrosine-dependent in vitro reconstitution of recombinant LAT-nucleated multiprotein signalling complexes on liposomes. Molecular Membrane Biology, 2009, 26, 159-170. | 2.0 | 13 |
| 36 | The Structure Of Phosphorylase Kinase Holoenzyme At Subnanometer Resolution, Location Of The Catalytic Subunit And The Substrate Glycogen Phosphorylase. Biophysical Journal, 2009, 96, 413a. | 0.2 | 0 |

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|----|--|-----|-----------|
| 37 | Calcineurin Bâ€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. | 1.5 | 11 |
| 38 | 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. | 1.1 | 25 |
| 39 | Synthesis of a hemifluorinated amphiphile designed for self-assembly and two-dimensional crystallization of membrane protein. <i>Tetrahedron Letters</i> , 2008, 49, 2247-2250. | 0.7 | 15 |
| 40 | 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. | 1.0 | 12 |
| 41 | Direct Visualization of KirBac3.1 Potassium Channel Gating by Atomic Force Microscopy. <i>Journal of Molecular Biology</i> , 2007, 374, 500-505. | 2.0 | 28 |
| 42 | Binding of pulmonary surfactant proteins to carbon nanotubes; potential for damage to lung immune defense mechanisms. <i>Carbon</i> , 2007, 45, 607-617. | 5.4 | 100 |
| 43 | Studies of the ATPase activity of the ABC protein SUR1. <i>FEBS Journal</i> , 2007, 274, 3532-3544. | 2.2 | 62 |
| 44 | Role of Aromatic Localization in the Gating Process of a Potassium Channel. <i>Biophysical Journal</i> , 2006, 90, L01-L03. | 0.2 | 35 |
| 45 | Structural and Functional Studies of the Response Regulator HupR. <i>Journal of Molecular Biology</i> , 2006, 359, 276-288. | 2.0 | 15 |
| 46 | Two Different Conformational States of the KirBac3.1 Potassium Channel Revealed by Electron Crystallography. <i>Structure</i> , 2005, 13, 1463-1472. | 1.6 | 100 |
| 47 | Structural Analysis of the Anaphase-Promoting Complex Reveals Multiple Active Sites and Insights into Polyubiquitylation. <i>Molecular Cell</i> , 2005, 20, 855-866. | 4.5 | 81 |
| 48 | An unusual soluble $\hat{1}^2$ -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. | 1.0 | 53 |
| 49 | Modeling of an Ion Channel in Its Open Conformation. <i>Biophysical Journal</i> , 2005, 89, L01-L03. | 0.2 | 35 |
| 50 | 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. | 2.0 | 12 |
| 51 | Structural Changes of the Prion Protein in Lipid Membranes Leading to Aggregation and Fibrillizationâ€. <i>Biochemistry</i> , 2003, 42, 3295-3304. | 1.2 | 165 |
| 52 | Two-Dimensional Crystallization of a Histidine-Tagged Protein on Monolayers of Fluidity-Enhanced Ni ²⁺ -Chelating Lipids. <i>Langmuir</i> , 2002, 18, 9502-9512. | 1.6 | 27 |
| 53 | Three-Dimensional Structure of Phosphorylase Kinase at 22 Å... Resolution and Its Complex with Glycogen Phosphorylase b. <i>Structure</i> , 2002, 10, 33-41. | 1.6 | 23 |
| 54 | Two-dimensional crystallization of a membrane protein on a detergent-resistant lipid monolayer 1 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 308, 639-647. | 2.0 | 68 |

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|----|---|-----|-----------|
| 55 | Functional and structural differences between the prion protein from two alleles prnpa and prnpb of mouse. FEBS Journal, 2000, 267, 2452-2459. | 0.2 | 19 |
| 56 | Copper Refolding of Prion Protein. Biochemical and Biophysical Research Communications, 2000, 276, 1217-1224. | 1.0 | 56 |
| 57 | Projection structure of a transcriptional regulator, HupR, determined by electron cryo-microscopy. Journal of Molecular Biology, 2000, 296, 863-871. | 2.0 | 11 |
| 58 | Synchrotron Radiation Diffraction from Two-Dimensional Protein Crystals at the Air/Water Interface. Biophysical Journal, 2000, 79, 496-500. | 0.2 | 35 |
| 59 | Surface-Induced Polymerization of Actin. Biophysical Journal, 1999, 76, 1580-1590. | 0.2 | 43 |
| 60 | Oligomeric structure of the repressor of the bacteriophage Mu early operon. FEBS Journal, 1998, 252, 408-415. | 0.2 | 9 |
| 61 | Characterization of the Growth of 2D Protein Crystals on a Lipid Monolayer by Ellipsometry and Rigidity Measurements Coupled to Electron Microscopy. Biophysical Journal, 1998, 74, 2649-2657. | 0.2 | 76 |
| 62 | Structural study of the response regulator HupR from Rhodobacter capsulatus. electron microscopy of two-dimensional crystals on a nickel-chelating lipid. Journal of Molecular Biology, 1997, 274, 687-692. | 2.0 | 52 |
| 63 | Effect of the C-terminal proline repeats on ordered packing of squid rhodopsin and its mobility in membranes. FEBS Letters, 1995, 359, 45-49. | 1.3 | 16 |