

# Connie Darmanin

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

1,111  
citations

331670

21  
h-index

395702

33  
g-index

47  
all docs

47  
docs citations

47  
times ranked

1478  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Stability, flow alignment and a phase transition of the lipidic cubic phase during continuous flow injection. <i>Journal of Colloid and Interface Science</i> , 2022, 611, 588-598.               | 9.4  | 3         |
| 2  | Preferred orientation and its effects on intensity-correlation measurements. <i>IUCr</i> , 2022, 9, 231-242.  | 2.2  | 2         |
| 3  | Observations of phase changes in monoolein during high viscous injection. <i>Journal of Synchrotron Radiation</i> , 2022, 29, 602-614.  | 2.4  | 5         |
| 4  | Time-Resolved Crystallography. <i>Crystals</i> , 2022, 12, 561.   | 2.2  | 0         |
| 5  | Lysozyme conformational changes with ionic liquids: Spectroscopic, small angle x-ray scattering and crystallographic study. <i>Journal of Colloid and Interface Science</i> , 2021, 585, 433-443. | 9.4  | 24        |
| 6  | Analysis of Multi-Hit Crystals in Serial Synchrotron Crystallography Experiments Using High-Viscosity Injectors. <i>Crystals</i> , 2021, 11, 49.  | 2.2  | 5         |
| 7  | MyD88 TIR domain higher-order assembly interactions revealed by microcrystal electron diffraction and serial femtosecond crystallography. <i>Nature Communications</i> , 2021, 12, 2578.          | 12.8 | 55        |
| 8  | Data reduction for serial crystallography using a robust peak finder. <i>Journal of Applied Crystallography</i> , 2021, 54, 1360-1378.  | 4.5  | 10        |
| 9  | Fluctuation X-ray diffraction reveals three-dimensional nanostructure and disorder in self-assembled lipid phases. <i>Communications Materials</i> , 2020, 1, .                                   | 6.9  | 13        |
| 10 | Mixing and jetting analysis using continuous flow microfluidic sample delivery devices. <i>RSC Advances</i> , 2020, 10, 15694-15701.  | 3.6  | 16        |
| 11 | Lipidico Injection Protocol for Serial Crystallography Measurements at the Australian Synchrotron. <i>Journal of Visualized Experiments</i> , 2020, , .   | 0.3  | 2         |
| 12 | Evaluation of serial crystallographic structure determination within megahertz pulse trains. <i>Structural Dynamics</i> , 2019, 6, 064702.  | 2.3  | 26        |
| 13 | Ptychographic imaging of NaD1 induced yeast cell death. <i>Biomedical Optics Express</i> , 2019, 10, 4964.  | 2.9  | 8         |
| 14 | Microfluidic mixing and jetting devices based on SU8 and glass for time-resolved molecular imaging experiments. , 2019, , .   |      | 1         |
| 15 | Crystallization: A Novel Acoustomicrofluidic Nebulization Technique Yielding New Crystallization Morphologies ( <i>Adv. Mater.</i> 3/2018). <i>Advanced Materials</i> , 2018, 30, 1870018.        | 21.0 | 0         |
| 16 | A Novel Acoustomicrofluidic Nebulization Technique Yielding New Crystallization Morphologies. <i>Advanced Materials</i> , 2018, 30, 1602040.  | 21.0 | 15        |
| 17 | Megahertz serial crystallography. <i>Nature Communications</i> , 2018, 9, 4025.   | 12.8 | 147       |
| 18 | The Influence of Photoelectron Escape in Radiation Damage Simulations of Protein Micro-Crystallography. <i>Crystals</i> , 2018, 8, 267.   | 2.2  | 7         |

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|----|---|------|-----------|
| 19 | A peak-finding algorithm based on robust statistical analysis in serial crystallography. <i>Journal of Applied Crystallography</i> , 2017, 50, 1705-1715.   | 4.5  | 9         |
| 20 | Measurements of Long-range Electronic Correlations During Femtosecond Diffraction Experiments Performed on Nanocrystals of Buckminsterfullerene. <i>Journal of Visualized Experiments</i> , 2017, , .   | 0.3  | 3         |
| 21 | Nanoscale mapping of the three-dimensional deformation field within commercial nanodiamonds. <i>International Journal of Nanotechnology</i> , 2017, 14, 251.  | 0.2  | 3         |
| 22 | X-ray laser-induced electron dynamics observed by femtosecond diffraction from nanocrystals of Buckminsterfullerene. <i>Science Advances</i> , 2016, 2, e1601186.   | 10.3 | 20        |
| 23 | Effect of Lipidic Cubic Phase Structure on Functionality of the Dopamine 2L Receptor: Implications for in Meso Crystallization. <i>Crystal Growth and Design</i> , 2016, 16, 5014-5022.   | 3.0  | 12        |
| 24 | Protein crystal screening and characterization for serial femtosecond nanocrystallography. <i>Scientific Reports</i> , 2016, 6, 25345.  | 3.3  | 22        |
| 25 | Uptake of the butyrate receptors, GPR41 and GPR43, in lipidic bicontinuous cubic phases suitable for in meso crystallization. <i>Journal of Colloid and Interface Science</i> , 2015, 441, 78-84.   | 9.4  | 8         |
| 26 | In Meso Crystallization: Compatibility of Different Lipid Bicontinuous Cubic Mesophases with the Cubic Crystallization Screen in Aqueous Solution. <i>Crystal Growth and Design</i> , 2014, 14, 1771-1781.  | 3.0  | 29        |
| 27 | High-throughput analysis of the structural evolution of the monoolein cubic phase in situ under crystallogenesis conditions. <i>Soft Matter</i> , 2012, 8, 2310.  | 2.7  | 35        |
| 28 | Effect of lipid architecture on cubic phase susceptibility to crystallisation screens. <i>Soft Matter</i> , 2012, 8, 6884.  | 2.7  | 30        |
| 29 | High-Throughput Production and Structural Characterization of Libraries of Self-Assembly Lipidic Cubic Phase Materials. <i>ACS Combinatorial Science</i> , 2012, 14, 247-252.   | 3.8  | 42        |
| 30 | Enhanced uptake of an integral membrane protein, the dopamine D2L receptor, by cubic nanostructured lipidnanoparticles doped with Ni(chelated EDTA amphiphiles). <i>Soft Matter</i> , 2011, 7, 567-578.   | 2.7  | 29        |
| 31 | Hematin Hematin Self-Association States Involved in the Formation and Reactivity of the Malaria Parasite Pigment, Hemozoin. <i>Biochemistry</i> , 2010, 49, 6804-6811.  | 2.5  | 57        |
| 32 | Incorporation of the dopamine D2L receptor and bacteriorhodopsin within bicontinuous cubic lipid phases. 1. Relevance to in meso crystallization of integral membrane proteins in monoolein systems. <i>Soft Matter</i> , 2010, 6, 4828.                    | 2.7  | 41        |
| 33 | Incorporation of the dopamine D2L receptor and bacteriorhodopsin within bicontinuous cubic lipid phases. 2. Relevance to in meso crystallization of integral membrane proteins in novel lipid systems. <i>Soft Matter</i> , 2010, 6, 4838.                  | 2.7  | 34        |
| 34 | Characterisation of an autoreactive conformational epitope on GAD65 recognised by the human monoclonal antibody b78 using a combination of phage display, in vitro mutagenesis and molecular modelling. <i>Journal of Autoimmunity</i> , 2006, 26, 172-181. | 6.5  | 11        |
| 35 | Discovery of Potential Sorbitol Dehydrogenase Inhibitors from Virtual Screening. <i>Medicinal Chemistry</i> , 2006, 2, 239-242.   | 1.5  | 0         |
| 36 | Structure of the tetrameric form of human L-Xylulose reductase: Probing the inhibitor-binding site with molecular modeling and site-directed mutagenesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 424-432.                      | 2.6  | 17        |

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|----|--|-----|-----------|
| 37 | Structure of Aldehyde Reductase Holoenzyme in Complex with the Potent Aldose Reductase Inhibitor Fidarestat: Implications for Inhibitor Binding and Selectivity. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 5536-5542.  | 6.4 | 70        |
| 38 | Sorbitol Dehydrogenase: Structure, Function and Ligand Design. <i>Current Medicinal Chemistry</i> , 2004, 11, 465-476.   | 2.4 | 69        |
| 39 | Ultrahigh resolution drug design. II. Atomic resolution structures of human aldose reductase holoenzyme complexed with fidarestat and minalrestat: Implications for the binding of cyclic imide inhibitors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 805-813. | 2.6 | 83        |
| 40 | Crystal structure of human L-xylulose reductase holoenzyme: Probing the role of Asn107 with site-directed mutagenesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 724-732.  | 2.6 | 22        |
| 41 | Probing the ultra-high resolution structure of aldose reductase with molecular modelling and noncovalent mass spectrometry. <i>Bioorganic and Medicinal Chemistry</i> , 2004, 12, 3797-3806.   | 3.0 | 19        |
| 42 | High-Resolution Structures of Human Aldose Reductase Holoenzyme in Complex with Stereoisomers of the Potent Inhibitor Fidarestat: Stereospecific Interaction between the Enzyme and a Cyclic Imide Type Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 4530-4537.          | 6.4 | 29        |
| 43 | Expression, purification and preliminary crystallographic analysis of human sorbitol dehydrogenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 558-560.   | 2.5 | 2         |
| 44 | Structure-based design of inhibitors of human l-xylulose reductase modelled into the active site of the enzyme. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2003, 13, 1469-1474.   | 2.2 | 3         |
| 45 | Structure of human aldose reductase holoenzyme in complex with Statil: An approach to structure-based inhibitor design of the enzyme. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 50, 230-238.   | 2.6 | 25        |
| 46 | Modelling studies of the active site of human sorbitol dehydrogenase: an approach to structure-based inhibitor design of the enzyme. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2001, 11, 3133-3136.  | 2.2 | 24        |
| 47 | Modelling studies on the binding of substrate and inhibitor to the active site of human sorbitol dehydrogenase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2000, 10, 1101-1104.   | 2.2 | 24        |