

Duilio Cascio

List of Publications by Year in Descending Order

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

61
papers

3,604
citations

30
h-index

60
g-index

65
ext. papers

4,510
ext. citations

11.9
avg, IF

4.98
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 61 | Cryo-EM structure of RNA-induced tau fibrils reveals a small C-terminal core that may nucleate fibril formation.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2119952119 | 11.5 | 0 |
| 60 | Prospecting for natural products by genome mining and microcrystal electron diffraction. <i>Nature Chemical Biology</i> , 2021 , 17, 872-877 | 11.7 | 9 |
| 59 | Inhibition of amyloid formation of the Nucleoprotein of SARS-CoV-2 2021 , | | 6 |
| 58 | Isolation and X-ray Crystal Structure of an Electrogenated TEMPO-N Charge-Transfer Complex. <i>Organic Letters</i> , 2021 , 23, 454-458 | 6.2 | 4 |
| 57 | Crystal structure of a conformational antibody that binds tau oligomers and inhibits pathological seeding by extracts from donors with Alzheimer's disease. <i>Journal of Biological Chemistry</i> , 2020 , 295, 10662-10676 | 5.4 | 5 |
| 56 | Serial femtosecond crystallography on in vivo-grown crystals drives elucidation of mosquitoicidal Cyt1Aa bioactivation cascade. <i>Nature Communications</i> , 2020 , 11, 1153 | 17.4 | 11 |
| 55 | CryoEM structure of the low-complexity domain of hnRNPA2 and its conversion to pathogenic amyloid. <i>Nature Communications</i> , 2020 , 11, 4090 | 17.4 | 36 |
| 54 | Characterization of Reactive Organometallic Species via MicroED. <i>ACS Central Science</i> , 2019 , 5, 1507-1518 | 16.8 | 20 |
| 53 | Structure and mechanism of TagA, a novel membrane-associated glycosyltransferase that produces wall teichoic acids in pathogenic bacteria. <i>PLoS Pathogens</i> , 2019 , 15, e1007723 | 7.6 | 13 |
| 52 | Structure of amyloid- β (20-34) with Alzheimer's-associated isomerization at Asp23 reveals a distinct protofilament interface. <i>Nature Communications</i> , 2019 , 10, 3357 | 17.4 | 25 |
| 51 | Structure-based inhibitors halt prion-like seeding by Alzheimer's disease-and tauopathy-derived brain tissue samples. <i>Journal of Biological Chemistry</i> , 2019 , 294, 16451-16464 | 5.4 | 23 |
| 50 | Homochiral and racemic MicroED structures of a peptide repeat from the ice-nucleation protein InaZ. <i>IUCrJ</i> , 2019 , 6, 197-205 | 4.7 | 8 |
| 49 | Structure-based inhibitors of amyloid beta core suggest a common interface with tau. <i>ELife</i> , 2019 , 8, | 8.9 | 34 |
| 48 | Low-cost and portable UV holographic microscope for high-contrast protein crystal imaging. <i>APL Photonics</i> , 2019 , 4, 030804 | 5.2 | 6 |
| 47 | Cooperative DNA binding by proteins through DNA shape complementarity. <i>Nucleic Acids Research</i> , 2019 , 47, 8874-8887 | 20.1 | 8 |
| 46 | Structural basis of 7SK RNA 5'ppp-phosphate methylation and retention by MePCE. <i>Nature Chemical Biology</i> , 2019 , 15, 132-140 | 11.7 | 14 |
| 45 | Atomic structures of low-complexity protein segments reveal kinked β -sheets that assemble networks. <i>Science</i> , 2018 , 359, 698-701 | 33.3 | 220 |

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| 44 | Common fibrillar spines of amyloid- β and human islet amyloid polypeptide revealed by microelectron diffraction and structure-based inhibitors. <i>Journal of Biological Chemistry</i> , 2018 , 293, 2888-2902 | 5.4 | 31 |
| 43 | Sub-angstrom cryo-EM structure of a prion protofibril reveals a polar clasp. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 131-134 | 17.6 | 56 |
| 42 | Crystal Structure of Bicc1 SAM Polymer and Mapping of Interactions between the Ciliopathy-Associated Proteins Bicc1, ANKS3, and ANKS6. <i>Structure</i> , 2018 , 26, 209-224.e6 | 5.2 | 9 |
| 41 | Atomic-level evidence for packing and positional amyloid polymorphism by segment from TDP-43 RRM2. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 311-319 | 17.6 | 63 |
| 40 | Multiple serine transposase dimers assemble the transposon-end synaptic complex during IS-family transposition. <i>ELife</i> , 2018 , 7, | 8.9 | 2 |
| 39 | Protein structural biology using cell-free platform from wheat germ. <i>Advanced Structural and Chemical Imaging</i> , 2018 , 4, 13 | 3.9 | 9 |
| 38 | Atomic structures of TDP-43 LCD segments and insights into reversible or pathogenic aggregation. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 463-471 | 17.6 | 116 |
| 37 | Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. <i>Nature Methods</i> , 2017 , 14, 399-402 | 21.6 | 109 |
| 36 | Crystal structure of Mdm12 and combinatorial reconstitution of Mdm12/Mmm1 ERMES complexes for structural studies. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 488, 129-135 | 3.4 | 21 |
| 35 | Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , 2017 , 74, 472-481 | 2.4 | 10 |
| 34 | Computational design of self-assembling cyclic protein homo-oligomers. <i>Nature Chemistry</i> , 2017 , 9, 353-366 | 16.6 | 78 |
| 33 | Atomic structures of fibrillar segments of hIAPP suggest tightly mated β sheets are important for cytotoxicity. <i>ELife</i> , 2017 , 6, | 8.9 | 76 |
| 32 | Ab initio structure determination from prion nanocrystals at atomic resolution by MicroED. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 11232-11236 | 11.5 | 66 |
| 31 | Accurate design of megadalton-scale two-component icosahedral protein complexes. <i>Science</i> , 2016 , 353, 389-94 | 33.3 | 322 |
| 30 | Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , 2016 , 13, 177-81 | 81.6 | 184 |
| 29 | Crystal Structure and Bioinformatics Inferred Function of Protein A2617 from <i>Methylobium petroleophilum</i> . <i>FASEB Journal</i> , 2016 , 30, 601.9 | 0.9 | |
| 28 | Crystal Structure of the <i>Streptomyces coelicolor</i> Sortase E1 Transpeptidase Provides Insight into the Binding Mode of the Novel Class E Sorting Signal. <i>PLoS ONE</i> , 2016 , 11, e0167763 | 3.7 | 15 |
| 27 | Structure of a putative ClpS N-end rule adaptor protein from the malaria pathogen <i>Plasmodium falciparum</i> . <i>Protein Science</i> , 2016 , 25, 689-701 | 6.3 | 18 |

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|----|--|------|-----|
| 26 | Crystal structure of the toxin Msmeg_6760, the structural homolog of Mycobacterium tuberculosis Rv2035, a novel type II toxin involved in the hypoxic response. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 863-869 | 1.1 | 2 |
| 25 | De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , 2016 , 539, 43-47 | 50.4 | 73 |
| 24 | Toxicity of eosinophil MBP is repressed by intracellular crystallization and promoted by extracellular aggregation. <i>Molecular Cell</i> , 2015 , 57, 1011-1021 | 17.6 | 62 |
| 23 | Uncovering the Mechanism of Aggregation of Human Transthyretin. <i>Journal of Biological Chemistry</i> , 2015 , 290, 28932-43 | 5.4 | 85 |
| 22 | Structure of Tetrahymena telomerase reveals previously unknown subunits, functions, and interactions. <i>Science</i> , 2015 , 350, aab4070 | 33.3 | 105 |
| 21 | Structure of the toxic core of Bynuclein from invisible crystals. <i>Nature</i> , 2015 , 525, 486-90 | 50.4 | 393 |
| 20 | Crystal structure and solution characterization of the thioredoxin-2 from Plasmodium falciparum, a constituent of an essential parasitic protein export complex. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 456, 403-9 | 3.4 | 15 |
| 19 | Structural mapping of the ClpB ATPases of Plasmodium falciparum: Targeting protein folding and secretion for antimalarial drug design. <i>Protein Science</i> , 2015 , 24, 1508-20 | 6.3 | 16 |
| 18 | Origins of stereoselectivity in evolved ketoreductases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E7065-72 | 11.5 | 76 |
| 17 | Inhibition by small-molecule ligands of formation of amyloid fibrils of an immunoglobulin light chain variable domain. <i>ELife</i> , 2015 , 4, e10935 | 8.9 | 36 |
| 16 | Formation of amyloid fibers by monomeric light chain variable domains. <i>Journal of Biological Chemistry</i> , 2014 , 289, 27513-25 | 5.4 | 25 |
| 15 | Structure of the methanofuran/methanopterin-biosynthetic enzyme MJ1099 from Methanocaldococcus jannaschii. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1472-9 | 1.1 | 2 |
| 14 | Molecular basis for amyloid-beta polymorphism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 16938-43 | 11.5 | 306 |
| 13 | Structure and proposed activity of a member of the VapBC family of toxin-antitoxin systems. VapBC-5 from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , 2009 , 284, 276-283 | 5.4 | 108 |
| 12 | The crystal structure of the primary Ca ²⁺ sensor of the Na ⁺ /Ca ²⁺ exchanger reveals a novel Ca ²⁺ binding motif. <i>Journal of Biological Chemistry</i> , 2006 , 281, 21577-21581 | 5.4 | 88 |
| 11 | An ancestral nuclear protein assembly: crystal structure of the Methanopyrus kandleri histone. <i>Protein Science</i> , 2001 , 10, 2002-7 | 6.3 | 38 |
| 10 | Crystal structures of spin labeled T4 lysozyme mutants: implications for the interpretation of EPR spectra in terms of structure. <i>Biochemistry</i> , 2000 , 39, 8396-405 | 3.2 | 231 |
| 9 | Packed protein bilayers in the 0.90 Å resolution structure of a designed alpha helical bundle. <i>Protein Science</i> , 1999 , 8, 1400-9 | 6.3 | 34 |

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|---|--|------|----|
| 8 | Centrosymmetric bilayers in the 0.75 Å resolution structure of a designed alpha-helical peptide, D,L-Alpha-1. <i>Protein Science</i> , 1999 , 8, 1410-22 | 6.3 | 41 |
| 7 | NarL dimerization? Suggestive evidence from a new crystal form. <i>Biochemistry</i> , 1998 , 37, 3665-76 | 3.2 | 67 |
| 6 | Crystal structure of the unactivated ribulose 1,5-bisphosphate carboxylase/oxygenase complexed with a transition state analog, 2-carboxy-D-arabinitol 1,5-bisphosphate. <i>Protein Science</i> , 1994 , 3, 64-9 | 6.3 | 22 |
| 5 | Crystal structure of activated tobacco rubisco complexed with the reaction-intermediate analogue 2-carboxy-arabinitol 1,5-bisphosphate. <i>Protein Science</i> , 1993 , 2, 1136-46 | 6.3 | 54 |
| 4 | X-ray grade crystals of a designed alpha-helical coiled coil. <i>Protein Science</i> , 1992 , 1, 956-7 | 6.3 | 11 |
| 3 | Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , 1987 , 329, 354-6 | 50.4 | 83 |
| 2 | The cryoEM structure of the fibril-forming low-complexity domain of hnRNPA2 reveals distinct differences from pathogenic amyloid and shows how mutation converts it to the pathogenic form | | 1 |
| 1 | Homochiral and racemic MicroED structures of a peptide from the ice nucleation protein InaZ | | 2 |