

# Duilio Cascio

## List of Publications by Citations

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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	Structure of the toxic core of $\beta$ synuclein from invisible crystals. <i>Nature</i> , <b>2015</b> , 525, 486-90	50.4	393
60	Accurate design of megadalton-scale two-component icosahedral protein complexes. <i>Science</i> , <b>2016</b> , 353, 389-94	33.3	322
59	Molecular basis for amyloid-beta polymorphism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 16938-43	11.5	306
58	Crystal structures of spin labeled T4 lysozyme mutants: implications for the interpretation of EPR spectra in terms of structure. <i>Biochemistry</i> , <b>2000</b> , 39, 8396-405	3.2	231
57	Atomic structures of low-complexity protein segments reveal kinked $\beta$ sheets that assemble networks. <i>Science</i> , <b>2018</b> , 359, 698-701	33.3	220
56	Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , <b>2016</b> , 13, 177-83	81.6	184
55	Atomic structures of TDP-43 LCD segments and insights into reversible or pathogenic aggregation. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 463-471	17.6	116
54	Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. <i>Nature Methods</i> , <b>2017</b> , 14, 399-402	21.6	109
53	Structure and proposed activity of a member of the VapBC family of toxin-antitoxin systems. VapBC-5 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 276-283	5.4	108
52	Structure of <i>Tetrahymena</i> telomerase reveals previously unknown subunits, functions, and interactions. <i>Science</i> , <b>2015</b> , 350, aab4070	33.3	105
51	The crystal structure of the primary $\text{Ca}^{2+}$ sensor of the $\text{Na}^{+}/\text{Ca}^{2+}$ exchanger reveals a novel $\text{Ca}^{2+}$ binding motif. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 21577-21581	5.4	88
50	Uncovering the Mechanism of Aggregation of Human Transthyretin. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 28932-43	5.4	85
49	Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , <b>1987</b> , 329, 354-6	50.4	83
48	Computational design of self-assembling cyclic protein homo-oligomers. <i>Nature Chemistry</i> , <b>2017</b> , 9, 353-360	36.6	78
47	Origins of stereoselectivity in evolved ketoreductases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E7065-72	11.5	76
46	Atomic structures of fibrillar segments of hIAPP suggest tightly mated $\beta$ sheets are important for cytotoxicity. <i>ELife</i> , <b>2017</b> , 6,	8.9	76
45	De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , <b>2016</b> , 539, 43-47	50.4	73

44	NarL dimerization? Suggestive evidence from a new crystal form. <i>Biochemistry</i> , <b>1998</b> , 37, 3665-76	3.2	67
43	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> , <b>2016</b> , 113, 11232-11236	11.5	66
42	Atomic-level evidence for packing and positional amyloid polymorphism by segment from TDP-43 RRM2. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 311-319	17.6	63
41	Toxicity of eosinophil MBP is repressed by intracellular crystallization and promoted by extracellular aggregation. <i>Molecular Cell</i> , <b>2015</b> , 57, 1011-1021	17.6	62
40	Sub-Å cryo-EM structure of a prion protofibril reveals a polar clasp. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 131-134	17.6	56
39	Crystal structure of activated tobacco rubisco complexed with the reaction-intermediate analogue 2-carboxy-arabinitol 1,5-bisphosphate. <i>Protein Science</i> , <b>1993</b> , 2, 1136-46	6.3	54
38	Centrosymmetric bilayers in the 0.75 Å resolution structure of a designed alpha-helical peptide, D,L-Alpha-1. <i>Protein Science</i> , <b>1999</b> , 8, 1410-22	6.3	41
37	An ancestral nuclear protein assembly: crystal structure of the <i>Methanopyrus kandleri</i> histone. <i>Protein Science</i> , <b>2001</b> , 10, 2002-7	6.3	38
36	Inhibition by small-molecule ligands of formation of amyloid fibrils of an immunoglobulin light chain variable domain. <i>ELife</i> , <b>2015</b> , 4, e10935	8.9	36
35	CryoEM structure of the low-complexity domain of hnRNPA2 and its conversion to pathogenic amyloid. <i>Nature Communications</i> , <b>2020</b> , 11, 4090	17.4	36
34	Packed protein bilayers in the 0.90 Å resolution structure of a designed alpha helical bundle. <i>Protein Science</i> , <b>1999</b> , 8, 1400-9	6.3	34
33	Structure-based inhibitors of amyloid beta core suggest a common interface with tau. <i>ELife</i> , <b>2019</b> , 8,	8.9	34
32	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> , <b>2018</b> , 293, 28882-2902	5.4	31
31	Structure of amyloid-β(20-34) with Alzheimer's-associated isomerization at Asp23 reveals a distinct protofilament interface. <i>Nature Communications</i> , <b>2019</b> , 10, 3357	17.4	25
30	Formation of amyloid fibers by monomeric light chain variable domains. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 27513-25	5.4	25
29	Structure-based inhibitors halt prion-like seeding by Alzheimer's disease and tauopathy-derived brain tissue samples. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 16451-16464	5.4	23
28	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> , <b>1994</b> , 3, 64-9	6.3	22
27	Crystal structure of Mdm12 and combinatorial reconstitution of Mdm12/Mmm1 ERMES complexes for structural studies. <i>Biochemical and Biophysical Research Communications</i> , <b>2017</b> , 488, 129-135	3.4	21

26	Characterization of Reactive Organometallic Species via MicroED. <i>ACS Central Science</i> , <b>2019</b> , 5, 1507-1513	36.8	20
25	Structure of a putative ClpS N-end rule adaptor protein from the malaria pathogen <i>Plasmodium falciparum</i> . <i>Protein Science</i> , <b>2016</b> , 25, 689-701	6.3	18
24	Structural mapping of the ClpB ATPases of <i>Plasmodium falciparum</i> : Targeting protein folding and secretion for antimalarial drug design. <i>Protein Science</i> , <b>2015</b> , 24, 1508-20	6.3	16
23	Crystal structure and solution characterization of the thioredoxin-2 from <i>Plasmodium falciparum</i> , a constituent of an essential parasitic protein export complex. <i>Biochemical and Biophysical Research Communications</i> , <b>2015</b> , 456, 403-9	3.4	15
22	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> , <b>2016</b> , 11, e0167763	3.7	15
21	Structural basis of 7SK RNA 5' triphosphate methylation and retention by MePCE. <i>Nature Chemical Biology</i> , <b>2019</b> , 15, 132-140	11.7	14
20	Structure and mechanism of TagA, a novel membrane-associated glycosyltransferase that produces wall teichoic acids in pathogenic bacteria. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007723	7.6	13
19	Serial femtosecond crystallography on in vivo-grown crystals drives elucidation of mosquitocidal Cyt1Aa bioactivation cascade. <i>Nature Communications</i> , <b>2020</b> , 11, 1153	17.4	11
18	X-ray grade crystals of a designed alpha-helical coiled coil. <i>Protein Science</i> , <b>1992</b> , 1, 956-7	6.3	11
17	Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , <b>2017</b> , 74, 472-481	2.4	10
16	Crystal Structure of Bicc1 SAM Polymer and Mapping of Interactions between the Ciliopathy-Associated Proteins Bicc1, ANKS3, and ANKS6. <i>Structure</i> , <b>2018</b> , 26, 209-224.e6	5.2	9
15	Prospecting for natural products by genome mining and microcrystal electron diffraction. <i>Nature Chemical Biology</i> , <b>2021</b> , 17, 872-877	11.7	9
14	Protein structural biology using cell-free platform from wheat germ. <i>Advanced Structural and Chemical Imaging</i> , <b>2018</b> , 4, 13	3.9	9
13	Homochiral and racemic MicroED structures of a peptide repeat from the ice-nucleation protein InaZ. <i>IUCrJ</i> , <b>2019</b> , 6, 197-205	4.7	8
12	Cooperative DNA binding by proteins through DNA shape complementarity. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 8874-8887	20.1	8
11	Low-cost and portable UV holographic microscope for high-contrast protein crystal imaging. <i>APL Photonics</i> , <b>2019</b> , 4, 030804	5.2	6
10	Inhibition of amyloid formation of the Nucleoprotein of SARS-CoV-2 <b>2021</b> ,		6
9	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> , <b>2020</b> , 295, 10662-10676	5.4	5

8	Isolation and X-ray Crystal Structure of an Electrogenerated TEMPO-N Charge-Transfer Complex. <i>Organic Letters</i> , <b>2021</b> , 23, 454-458	6.2	4
7	Structure of the methanofuran/methanopterin-biosynthetic enzyme MJ1099 from <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1472-9	1.1	2
6	Multiple serine transposase dimers assemble the transposon-end synaptic complex during IS-family transposition. <i>ELife</i> , <b>2018</b> , 7,	8.9	2
5	Homochiral and racemic MicroED structures of a peptide from the ice nucleation protein InaZ		2
4	Crystal structure of the toxin MsmeG_6760, the structural homolog of <i>Mycobacterium tuberculosis</i> Rv2035, a novel type II toxin involved in the hypoxic response. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2016</b> , 72, 863-869	1.1	2
3	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
2	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> , <b>2022</b> , 119, e2119952119	11.5	0
1	Crystal Structure and Bioinformatics Inferred Function of Protein A2617 from <i>Methylobium petroleiphilum</i> . <i>FASEB Journal</i> , <b>2016</b> , 30, 601.9	0.9	