

# Duilio Cascio

## List of Publications by Year in descending order

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58  
papers

5,114  
citations

126907

33  
h-index

138484

58  
g-index

65  
all docs

65  
docs citations

65  
times ranked

7346  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the toxic core of $\beta$ -synuclein from invisible crystals. <i>Nature</i> , 2015, 525, 486-490.	27.8	528
2	Accurate design of megadalton-scale two-component icosahedral protein complexes. <i>Science</i> , 2016, 353, 389-394.	12.6	466
3	Molecular basis for amyloid- $\beta$ polymorphism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16938-16943.	7.1	383
4	Atomic structures of low-complexity protein segments reveal kinked $\beta$ sheets that assemble networks. <i>Science</i> , 2018, 359, 698-701.	12.6	376
5	Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , 2016, 13, 177-183.	19.0	274
6	Crystal Structures of Spin Labeled T4 Lysozyme Mutants: Implications for the Interpretation of EPR Spectra in Terms of Structure. <i>Biochemistry</i> , 2000, 39, 8396-8405.	2.5	242
7	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.	8.2	183
8	Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. <i>Nature Methods</i> , 2017, 14, 399-402.	19.0	158
9	Structure of <i>Tetrahymena</i> telomerase reveals previously unknown subunits, functions, and interactions. <i>Science</i> , 2015, 350, aab4070.	12.6	134
10	Computational design of self-assembling cyclic protein homo-oligomers. <i>Nature Chemistry</i> , 2017, 9, 353-360.	13.6	130
11	Structure and Proposed Activity of a Member of the VapBC Family of Toxin-Antitoxin Systems. <i>Journal of Biological Chemistry</i> , 2009, 284, 276-283.	3.4	118
12	Uncovering the Mechanism of Aggregation of Human Transthyretin. <i>Journal of Biological Chemistry</i> , 2015, 290, 28932-28943.	3.4	117
13	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> , 2006, 281, 21577-21581.	3.4	107
14	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.	7.1	104
15	De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , 2016, 539, 43-47.	27.8	98
16	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.	7.1	95
17	Atomic structures of fibrillar segments of hIAPP suggest tightly mated $\beta$ -sheets are important for cytotoxicity. <i>ELife</i> , 2017, 6, .	6.0	95
18	Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , 1987, 329, 354-356.	27.8	91

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19	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.	8.2	89
20	Toxicity of Eosinophil MBP Is Repressed by Intracellular Crystallization and Promoted by Extracellular Aggregation. <i>Molecular Cell</i> , 2015, 57, 1011-1021.	9.7	88
21	Sub-Ångström cryo-EM structure of a prion protofibril reveals a polar clasp. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 131-134.	8.2	87
22	CryoEM structure of the low-complexity domain of hnRNPA2 and its conversion to pathogenic amyloid. <i>Nature Communications</i> , 2020, 11, 4090.	12.8	81
23	Structure-based inhibitors of amyloid beta core suggest a common interface with tau. <i>ELife</i> , 2019, 8, .	6.0	81
24	NarL Dimerization? Suggestive Evidence from a New Crystal Form,. <i>Biochemistry</i> , 1998, 37, 3665-3676.	2.5	70
25	Crystal structure of activated tobacco rubisco complexed with the reaction intermediate analogue 2â€œcarboxyâ€œarabinitol 1, 5â€œbisphosphate. <i>Protein Science</i> , 1993, 2, 1136-1146.	7.6	61
26	Structure-based inhibitors halt prion-like seeding by Alzheimerâ€™s diseaseâ€œand tauopathyâ€œderived brain tissue samples. <i>Journal of Biological Chemistry</i> , 2019, 294, 16451-16464.	3.4	51
27	Common fibrillar spines of amyloid-Î² and human islet amyloid polypeptide revealed by microelectron diffraction and structure-based inhibitors. <i>Journal of Biological Chemistry</i> , 2018, 293, 2888-2902.	3.4	50
28	Inhibition by small-molecule ligands of formation of amyloid fibrils of an immunoglobulin light chain variable domain. <i>ELife</i> , 2015, 4, e10935.	6.0	48
29	Structure of amyloid-Î² (20-34) with Alzheimerâ€™s-associated isomerization at Asp23 reveals a distinct protofilament interface. <i>Nature Communications</i> , 2019, 10, 3357.	12.8	45
30	Centrosymmetric bilayers in the 0.75 Å resolution structure of a designed alpha-helical peptide, D, Lâ€œAlphaâ€œ1. <i>Protein Science</i> , 1999, 8, 1410-1422.	7.6	43
31	An ancestral nuclear protein assembly: Crystal structure of theMethanopyrus kandlerihistone. <i>Protein Science</i> , 2001, 10, 2002-2007.	7.6	43
32	Characterization of Reactive Organometallic Species via MicroED. <i>ACS Central Science</i> , 2019, 5, 1507-1513.	11.3	39
33	Structural basis of 7SK RNA 5â€œ-Î³-phosphate methylation and retention by MePCE. <i>Nature Chemical Biology</i> , 2019, 15, 132-140.	8.0	38
34	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.	7.1	38
35	Formation of Amyloid Fibers by Monomeric Light Chain Variable Domains. <i>Journal of Biological Chemistry</i> , 2014, 289, 27513-27525.	3.4	37
36	Packed protein bilayers in the 0.90 Å resolution structure of a designed alpha helical bundle. <i>Protein Science</i> , 1999, 8, 1400-1409.	7.6	34

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37	Serial femtosecond crystallography on in vivo-grown crystals drives elucidation of mosquito Cyt1Aa bioactivation cascade. <i>Nature Communications</i> , 2020, 11, 1153.	12.8	31
38	Prospecting for natural products by genome mining and microcrystal electron diffraction. <i>Nature Chemical Biology</i> , 2021, 17, 872-877.	8.0	31
39	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, 64-69.	7.6	24
40	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.	2.1	23
41	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.	4.7	22
42	Protein structural biology using cell-free platform from wheat germ. <i>Advanced Structural and Chemical Imaging</i> , 2018, 4, 13.	4.0	21
43	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.	3.4	21
44	Structural mapping of the C <sub>1</sub> and B <sub>1</sub> ATPases of <i>Plasmodium falciparum</i> : Targeting protein folding and secretion for antimalarial drug design. <i>Protein Science</i> , 2015, 24, 1508-1520.	7.6	20
45	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.	2.5	20
46	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.	7.6	20
47	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> , 2015, 456, 403-409.	2.1	18
48	Crystal Structure of Bicc1 SAM Polymer and Mapping of Interactions between the Ciliothy-Associated Proteins Bicc1, ANKS3, and ANKS6. <i>Structure</i> , 2018, 26, 209-224.e6.	3.3	18
49	Cooperative DNA binding by proteins through DNA shape complementarity. <i>Nucleic Acids Research</i> , 2019, 47, 8874-8887.	14.5	16
50	Homochiral and racemic MicroED structures of a peptide repeat from the ice-nucleation protein InaZ. <i>IUCr</i> , 2019, 6, 197-205.	2.2	16
51	Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , 2017, 74, 472-481.	2.0	12
52	Isolation and X-ray Crystal Structure of an Electrogenenerated TEMPO <sup>3-</sup> Charge-Transfer Complex. <i>Organic Letters</i> , 2021, 23, 454-458.	4.6	12
53	X-ray grade crystals of a designed $\pm$ helical coiled coil. <i>Protein Science</i> , 1992, 1, 956-957.	7.6	11
54	Low-cost and portable UV holographic microscope for high-contrast protein crystal imaging. <i>APL Photonics</i> , 2019, 4, 030804.	5.7	11

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55	Multiple serine transposase dimers assemble the transposon-end synaptic complex during IS607-family transposition. <i>ELife</i> , 2018, 7, .	6.0	9
56	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> , 2016, 72, 863-869.	0.8	5
57	Structure of the methanofuran/methanopterin-biosynthetic enzyme MJ1099 from <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1472-1479.	0.8	2
58	Crystal Structure and Bioinformatics Inferred Function of Protein A2617 from <i>Methylobium petroleiphilum</i> . <i>FASEB Journal</i> , 2016, 30, 601.9.	0.5	0