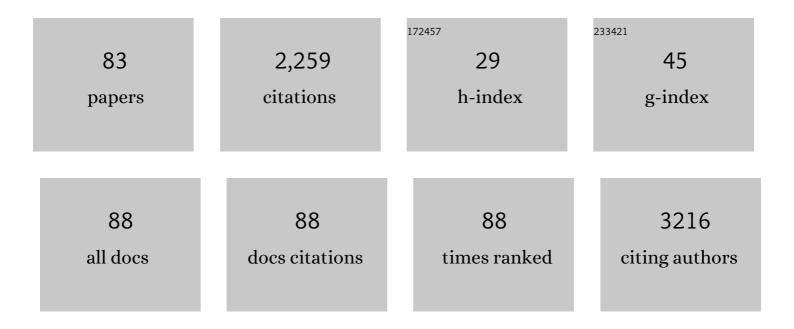
Michele Cianci

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The molecular basis of the coloration mechanism in lobster shell: Â-Crustacyanin at 3.2-A resolution. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9795-9800.	7.1	177
2	P13, the EMBL macromolecular crystallography beamline at the low-emittance PETRA III ring forÂhigh- and low-energy phasing with variable beam focusing. Journal of Synchrotron Radiation, 2017, 24, 323-332.	2.4	155
3	Open and closed states of Candida antarctica lipase B: protonation and the mechanism of interfacial activation. Journal of Lipid Research, 2015, 56, 2348-2358.	4.2	125
4	Crystal Structure of Peach Pru p 3, the Prototypic Member of the Family of Plant Non-specific Lipid Transfer Protein Pan-allergens. Journal of Molecular Biology, 2006, 356, 684-694.	4.2	122
5	The ligand environment of zinc stored in vesicles. Biochemical and Biophysical Research Communications, 2009, 380, 198-203.	2.1	79
6	The determination of protonation states in proteins. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 906-922.	2.5	66
7	The Structure of the Elusive Urease–Urea Complex Unveils the Mechanism of a Paradigmatic Nickelâ€Dependent Enzyme. Angewandte Chemie - International Edition, 2019, 58, 7415-7419.	13.8	66
8	Unravelling the structural chemistry of the colouration mechanism in lobster shell. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2072-2082.	2.5	65
9	X-ray structure analysis of a metalloprotein with enhanced active-site resolution using in situ x-ray absorption near edge structure spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6211-6216.	7.1	64
10	Inactivation of urease by 1,4-benzoquinone: chemistry at the protein surface. Dalton Transactions, 2016, 45, 5455-5459.	3.3	61
11	Fluoride inhibition of Sporosarcina pasteurii urease: structure and thermodynamics. Journal of Biological Inorganic Chemistry, 2014, 19, 1243-1261.	2.6	58
12	An NAD+ Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. Molecular Cell, 2019, 73, 1282-1291.e8.	9.7	58
13	Inactivation of urease by catechol: Kinetics and structure. Journal of Inorganic Biochemistry, 2017, 166, 182-189.	3.5	57
14	The crystal structure of Erwinia amylovora levansucrase provides a snapshot of the products of sucrose hydrolysis trapped into the active site. Journal of Structural Biology, 2015, 191, 290-298.	2.8	56
15	The structure of urease inactivated by Ag(<scp>i</scp>): a new paradigm for enzyme inhibition by heavy metals. Dalton Transactions, 2018, 47, 8240-8247.	3.3	54
16	Urease Inhibition in the Presence of <i>N</i> -(<i>n</i> Butyl)thiophosphoric Triamide, a Suicide Substrate: Structure and Kinetics. Biochemistry, 2017, 56, 5391-5404.	2.5	53
17	The crystal structure of Sporosarcina pasteurii urease in a complex with citrate provides new hints for inhibitor design. Journal of Biological Inorganic Chemistry, 2013, 18, 391-399.	2.6	49
18	Anomalous scattering in structural chemistry and biology¶. Crystallography Reviews, 2005, 11, 245-335.	1.5	44

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19	The interdependence of wavelength, redundancy and dose in sulfur SAD experiments. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1196-1209.	2.5	42
20	Transthyretin Binding Heterogeneity and Anti-amyloidogenic Activity of Natural Polyphenols and Their Metabolites. Journal of Biological Chemistry, 2015, 290, 29769-29780.	3.4	42
21	Kinetic and structural studies reveal a unique binding mode of sulfite to the nickel center in urease. Journal of Inorganic Biochemistry, 2016, 154, 42-49.	3.5	42
22	A high-throughput structural biology/proteomics beamline at the SRS on a new multipole wiggler. Journal of Synchrotron Radiation, 2005, 12, 455-466.	2.4	39
23	Protonation-state determination in proteins using high-resolution X-ray crystallography: effects of resolution and completeness. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 800-809.	2.5	39
24	Structure of lobster apocrustacyanin A1using softer X-rays. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1219-1229.	2.5	38
25	S-SWAT (softer single-wavelength anomalous technique): potential in high-throughput protein crystallography. Acta Crystallographica Section A: Foundations and Advances, 2003, 59, 327-334.	0.3	38
26	On the origin and variation of colors in lobster carapace. Physical Chemistry Chemical Physics, 2015, 17, 16723-16732.	2.8	35
27	Insights into Urease Inhibition by <i>N</i> -(<i>n</i> Butyl) Phosphoric Triamide through an Integrated Structural and Kinetic Approach. Journal of Agricultural and Food Chemistry, 2019, 67, 2127-2138.	5.2	33
28	Synchrotron and neutron techniques in biological crystallography. Chemical Society Reviews, 2004, 33, 548.	38.1	30
29	Inhibition Mechanism of Urease by Au(III) Compounds Unveiled by X-ray Diffraction Analysis. ACS Medicinal Chemistry Letters, 2019, 10, 564-570.	2.8	30
30	Holo-Ni2+Helicobacter pylori NikR contains four square-planar nickel-binding sites at physiological pH. Dalton Transactions, 2011, 40, 7831.	3.3	28
31	Merging of synchrotron serial crystallographic data by a genetic algorithm. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1026-1035.	2.3	26
32	NH2-terminal Sequence Truncation Decreases the Stability of Bovine Rhodanese, Minimally Perturbs Its Crystal Structure, and Enhances Interaction with GroEL under Native Conditions. Journal of Biological Chemistry, 1999, 274, 13938-13947.	3.4	25
33	Time-resolved and static-ensemble structural chemistry of hydroxymethylbilane synthase. Faraday Discussions, 2003, 122, 131-144.	3.2	23
34	Structural evidence for asymmetric ligand binding to transthyretin. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1582-1592.	2.5	21
35	The Impact of pH on Catalytically Critical Protein Conformational Changes: The Case of the Urease, a Nickel Enzyme. Chemistry - A European Journal, 2019, 25, 12145-12158.	3.3	21
36	Study of sulphation of Candoglia marble by means of micro X-ray diffraction experiments. Applied Physics A: Materials Science and Processing, 2006, 83, 689-694.	2.3	19

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37	Principles of lipid–enzyme interactions in the limbus region of the catalytic site of Candida antarctica Lipase B. International Journal of Biological Macromolecules, 2020, 158, 358-363.	7.5	19
38	Specific interaction of lipoate at the active site of rhodanese. BBA - Proteins and Proteomics, 2000, 1481, 103-108.	2.1	16
39	Structural characterization of recombinant crustacyanin subunits from the lobster <i>Homarus americanus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 846-853.	0.7	16
40	Cloning, expression, purification, crystallization and preliminary X-ray analysis of <i>Ea</i> Lsc, a levansucrase from <i>Erwinia amylovora</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 570-573.	0.7	15
41	Glucose-1-phosphate uridylyltransferase from Erwinia amylovora : Activity, structure and substrate specificity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1348-1357.	2.3	13
42	Polarized X-ray Absorption Near-Edge Structure Spectroscopy of Neuroglobin and Myoglobin Single Crystals. Journal of Physical Chemistry B, 2010, 114, 13223-13231.	2.6	12
43	Inhibition of Urease, a Niâ€Enzyme: The Reactivity of a Key Thiol With Mono―and Diâ€Substituted Catechols Elucidated by Kinetic, Structural, and Theoretical Studies. Angewandte Chemie - International Edition, 2021, 60, 6029-6035.	13.8	12
44	Functional Characterization of COG1713 (YqeK) as a Novel Diadenosine Tetraphosphate Hydrolase Family. Journal of Bacteriology, 2020, 202, .	2.2	11
45	Data collection with a tailored X-ray beam size at 2.69â€Ã wavelength (4.6â€keV): sulfur SAD phasing of Cdc23Nterm. Acta Crystallographica Section D: Structural Biology, 2016, 72, 403-412.	2.3	10
46	Kinetic and structural analysis of the inactivation of urease by mixed-ligand phosphine halide Ag(I) complexes. Journal of Inorganic Biochemistry, 2021, 218, 111375.	3.5	10
47	Medicinal Au(<scp>i</scp>) compounds targeting urease as prospective antimicrobial agents: unveiling the structural basis for enzyme inhibition. Dalton Transactions, 2021, 50, 14444-14452.	3.3	10
48	Molecular insights into the interaction between human nicotinamide phosphoribosyltransferase and Toll-like receptor 4. Journal of Biological Chemistry, 2022, 298, 101669.	3.4	10
49	The structure and refinement of apocrustacyanin C2to 1.3â€Ã resolution and the search for differences between this protein and the homologous apoproteins A1and C1. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 493-498.	2.5	9
50	Crystallographic Analysis of Counterion Effects on Subtilisin Enzymatic Action in Acetonitrile. Journal of the American Chemical Society, 2010, 132, 2293-2300.	13.7	9
51	High angular resolution slope measuring deflectometry for the characterization of ultra-precise reflective x-ray optics. Measurement Science and Technology, 2012, 23, 074015.	2.6	9
52	IRIDE: Interdisciplinary research infrastructure based on dual electron linacs and lasers. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2014, 740, 138-146.	1.6	9
53	Long-wavelength <i>Mesh&Collect</i> native SAD phasing from microcrystals. Acta Crystallographica Section D: Structural Biology, 2019, 75, 192-199.	2.3	8
54	The role of wavelength and source in the search for sulfur-atom positions evaluated in two case studies: lysozyme at room temperature and cryo apocrustacyanin A1. Journal of Applied Crystallography, 2004, 37, 555-564.	4.5	7

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55	Interaction of Counterions with Subtilisin in Acetonitrile: Insights from Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2012, 116, 5838-5848.	2.6	7
56	Expression, purification, crystallization and preliminary X-ray analysis of glucose-1-phosphate uridylyltransferase (GalU) from <i>Erwinia amylovora</i> . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1249-1251.	0.8	7
57	The Structure of the Elusive Urease–Urea Complex Unveils the Mechanism of a Paradigmatic Nickelâ€Dependent Enzyme. Angewandte Chemie, 2019, 131, 7493-7497.	2.0	7
58	3-Sulfinopropionyl-coenzyme A (3SP-CoA) desulfinase from <i>Advenella mimigardefordensis</i> DPN7 ^T : crystal structure and function of a desulfinase with an acyl-CoA dehydrogenase fold. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1360-1372.	2.5	6
59	Choosing your (Friedel) mates wisely: grouping data sets to improve anomalous signal. Acta Crystallographica Section D: Structural Biology, 2019, 75, 200-210.	2.3	6
60	The signal-to-noise ratio in SAD experiments. Crystallography Reviews, 2018, 24, 73-101.	1.5	5
61	Apocrustacyanin A1 from the lobster carotenoprotein α-crustacyanin: crystallization and initial X-ray analysis involving softer X-rays. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1064-1066.	2.5	4
62	Cloning, purification, crystallization and 1.57â€Ã resolution X-ray data analysis of AmsI, the tyrosine phosphatase controlling amylovoran biosynthesis in the plant pathogenErwinia amylovora. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1693-1696.	0.8	4
63	Interactions of tolcapone analogues as stabilizers of the amyloidogenic protein transthyretin. Bioorganic Chemistry, 2020, 103, 104144.	4.1	4
64	Structure, dynamics, and function of SrnR, a transcription factor for nickel-dependent gene expression. Metallomics, 2021, 13, .	2.4	4
65	The interdependence of wavelength, redundancy and dose on a sulfur SAD experiment. Acta Crystallographica Section A: Foundations and Advances, 2008, 64, C29-C30.	0.3	3
66	Extensive counter-ion interactions seen at the surface of subtilisin in an aqueous medium. RSC Advances, 2014, 4, 36771-36776.	3.6	3
67	Inhibition of Urease, a Niâ€Enzyme: The Reactivity of a Key Thiol With Mono―and Diâ€Substituted Catechols Elucidated by Kinetic, Structural, and Theoretical Studies. Angewandte Chemie, 2021, 133, 6094-6100.	2.0	3
68	Determining protonation states in proteins using high-resolution X-ray crystallography. Acta Crystallographica Section A: Foundations and Advances, 2012, 68, s90-s90.	0.3	2
69	EMBL beamlines for macromolecular crystallography at PETRAÂIII. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s319-s319.	0.3	1
70	The molecular basis of the coloration mechanism in lobster shell: β-crustacyanin at 3.2â€Ã resolution. Acta Crystallographica Section A: Foundations and Advances, 2002, 58, c121-c121.	0.3	1
71	Microfocus beamline for macromolecular crystallography MX2 @ PETRA III. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s118-s119.	0.3	1
72	The allergenic non-specific lipid transfer protein from peach: structural studies. Acta Crystallographica Section A: Foundations and Advances, 2005, 61, c252-c252.	0.3	1

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73	How to pick the best low-hanging fruit in medically important target genomes. Acta Crystallographica Section A: Foundations and Advances, 2004, 60, s138-s138.	0.3	0
74	Synchrotron and Neutron Techniques in Biological Crystallography. ChemInform, 2005, 36, no.	0.0	0
75	EMBL P13 beamline and derivative laboratory at PETRA III @DESY: phasing of biological macromolecules with softer X-rays and heavy atom derivatives. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s187-s187.	0.1	0
76	A combined anomalous scattering and direct methods approach to solve apocrustacyanin proteins (C1and A1). Acta Crystallographica Section A: Foundations and Advances, 2000, 56, s61-s61.	0.3	0
77	Structural studies on human α-thrombin. Acta Crystallographica Section A: Foundations and Advances, 2005, 61, c244-c244.	0.3	0
78	EMBL macromolecular crystallography beamlines @ PETRA3 - Hamburg Germany. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s334-s334.	0.3	0
79	EMBL MX1 beamline for macromolecular crystallography at PETRA III @ DESY, Hamburg, Germany. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s117-s117.	0.3	0
80	EMBL beamlines for life-science applications at PETRA III. Acta Crystallographica Section A: Foundations and Advances, 2012, 68, s148-s148.	0.3	0
81	EMBL beamlines for macromolecular crystallography at PETRAÂIII. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s145-s145.	0.3	0
82	Evaluation of MRSAD phasing protocols. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s202-s202.	0.1	0
83	P13 and P14, the EMBL beamlines for macromolecular crystallography at PETRAIII. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s194-s194.	0.1	0