

# Michele Cianci

## List of Publications by Year in descending order

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83  
papers

2,259  
citations

172457

29  
h-index

233421

45  
g-index

88  
all docs

88  
docs citations

88  
times ranked

3216  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular insights into the interaction between human nicotinamide phosphoribosyltransferase and Toll-like receptor 4. <i>Journal of Biological Chemistry</i> , 2022, 298, 101669.	3.4	10
2	Inhibition of Urease, a Ni-Enzyme: The Reactivity of a Key Thiol With Mono- and Di-Substituted Catechols Elucidated by Kinetic, Structural, and Theoretical Studies. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 6029-6035.	13.8	12
3	Inhibition of Urease, a Ni-Enzyme: The Reactivity of a Key Thiol With Mono- and Di-Substituted Catechols Elucidated by Kinetic, Structural, and Theoretical Studies. <i>Angewandte Chemie</i> , 2021, 133, 6094-6100.	2.0	3
4	Kinetic and structural analysis of the inactivation of urease by mixed-ligand phosphine halide Ag(I) complexes. <i>Journal of Inorganic Biochemistry</i> , 2021, 218, 111375.	3.5	10
5	Medicinal Au(III) compounds targeting urease as prospective antimicrobial agents: unveiling the structural basis for enzyme inhibition. <i>Dalton Transactions</i> , 2021, 50, 14444-14452.	3.3	10
6	Structure, dynamics, and function of SrnR, a transcription factor for nickel-dependent gene expression. <i>Metallomics</i> , 2021, 13, .	2.4	4
7	Interactions of tolcapone analogues as stabilizers of the amyloidogenic protein transthyretin. <i>Bioorganic Chemistry</i> , 2020, 103, 104144.	4.1	4
8	Functional Characterization of COG1713 (YqeK) as a Novel Diadenosine Tetraphosphate Hydrolase Family. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	11
9	Principles of lipid-enzyme interactions in the limbus region of the catalytic site of <i>Candida antarctica</i> Lipase B. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 358-363.	7.5	19
10	The Impact of pH on Catalytically Critical Protein Conformational Changes: The Case of the Urease, a Nickel Enzyme. <i>Chemistry - A European Journal</i> , 2019, 25, 12145-12158.	3.3	21
11	The Structure of the Elusive Urease-Urea Complex Unveils the Mechanism of a Paradigmatic Nickel-Dependent Enzyme. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 7415-7419.	13.8	66
12	The Structure of the Elusive Urease-Urea Complex Unveils the Mechanism of a Paradigmatic Nickel-Dependent Enzyme. <i>Angewandte Chemie</i> , 2019, 131, 7493-7497.	2.0	7
13	Insights into Urease Inhibition by N-(n-Butyl) Phosphoric Triamide through an Integrated Structural and Kinetic Approach. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2127-2138.	5.2	33
14	An NAD <sup>+</sup> Phosphorylase Toxin Triggers <i>Mycobacterium tuberculosis</i> Cell Death. <i>Molecular Cell</i> , 2019, 73, 1282-1291.e8.	9.7	58
15	Inhibition Mechanism of Urease by Au(III) Compounds Unveiled by X-ray Diffraction Analysis. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 564-570.	2.8	30
16	Choosing your (Friedel) mates wisely: grouping data sets to improve anomalous signal. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 200-210.	2.3	6
17	Long-wavelength Mesh&Collect native SAD phasing from microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 192-199.	2.3	8
18	The signal-to-noise ratio in SAD experiments. <i>Crystallography Reviews</i> , 2018, 24, 73-101.	1.5	5

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19	The structure of urease inactivated by Ag( <sup>i</sup> ): a new paradigm for enzyme inhibition by heavy metals. Dalton Transactions, 2018, 47, 8240-8247.	3.3	54
20	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
21	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
22	Inactivation of urease by catechol: Kinetics and structure. Journal of Inorganic Biochemistry, 2017, 166, 182-189.	3.5	57
23	P13, the EMBL macromolecular crystallography beamline at the low-emittance PETRA III ring for high- and low-energy phasing with variable beam focusing. Journal of Synchrotron Radiation, 2017, 24, 323-332.	2.4	155
24	Merging of synchrotron serial crystallographic data by a genetic algorithm. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1026-1035.	2.3	26
25	Data collection with a tailored X-ray beam size at 2.69 Å wavelength (4.6 keV): sulfur SAD phasing of Cdc23Nterm. Acta Crystallographica Section D: Structural Biology, 2016, 72, 403-412.	2.3	10
26	Inactivation of urease by 1,4-benzoquinone: chemistry at the protein surface. Dalton Transactions, 2016, 45, 5455-5459.	3.3	61
27	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
28	Evaluation of MRSAD phasing protocols. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s202-s202.	0.1	0
29	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
30	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
31	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
32	3-Sulfinopropionyl-coenzyme A (3SP-CoA) desulfinate from <i>Advenella mimigardefordensis</i> DPN7 <sup>T</sup> : crystal structure and function of a desulfinate with an acyl-CoA dehydrogenase fold. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1360-1372.	2.5	6
33	On the origin and variation of colors in lobster carapace. Physical Chemistry Chemical Physics, 2015, 17, 16723-16732.	2.8	35
34	Structural evidence for asymmetric ligand binding to transthyretin. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1582-1592.	2.5	21
35	Transthyretin Binding Heterogeneity and Anti-amyloidogenic Activity of Natural Polyphenols and Their Metabolites. Journal of Biological Chemistry, 2015, 290, 29769-29780.	3.4	42
36	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

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37	Cloning, purification, crystallization and 1.57 Å resolution X-ray data analysis of AmsI, the tyrosine phosphatase controlling amylovoran biosynthesis in the plant pathogen <i>Erwinia amylovora</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1693-1696.	0.8	4
38	Expression, purification, crystallization and preliminary X-ray analysis of glucose-1-phosphate uridylyltransferase (GalU) from <i>Erwinia amylovora</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1249-1251.	0.8	7
39	IRIDE: Interdisciplinary research infrastructure based on dual electron linacs and lasers. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2014, 740, 138-146.	1.6	9
40	Extensive counter-ion interactions seen at the surface of subtilisin in an aqueous medium. <i>RSC Advances</i> , 2014, 4, 36771-36776.	3.6	3
41	Fluoride inhibition of <i>Sporosarcina pasteurii</i> urease: structure and thermodynamics. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 1243-1261.	2.6	58
42	The crystal structure of <i>Sporosarcina pasteurii</i> urease in a complex with citrate provides new hints for inhibitor design. <i>Journal of Biological Inorganic Chemistry</i> , 2013, 18, 391-399.	2.6	49
43	Cloning, expression, purification, crystallization and preliminary X-ray analysis of <i>EaLsc</i> , a levansucrase from <i>Erwinia amylovora</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 570-573.	0.7	15
44	EMBL beamlines for macromolecular crystallography at PETRA-III. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s319-s319.	0.3	1
45	EMBL beamlines for macromolecular crystallography at PETRA-III. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s145-s145.	0.3	0
46	High angular resolution slope measuring deflectometry for the characterization of ultra-precise reflective x-ray optics. <i>Measurement Science and Technology</i> , 2012, 23, 074015.	2.6	9
47	Structural characterization of recombinant crustacyanin subunits from the lobster <i>Homarus americanus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 846-853.	0.7	16
48	Interaction of Counterions with Subtilisin in Acetonitrile: Insights from Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2012, 116, 5838-5848.	2.6	7
49	Protonation-state determination in proteins using high-resolution X-ray crystallography: effects of resolution and completeness. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 800-809.	2.5	39
50	EMBL beamlines for life-science applications at PETRA III. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, s148-s148.	0.3	0
51	Determining protonation states in proteins using high-resolution X-ray crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, s90-s90.	0.3	2
52	Holo-Ni <sup>2+</sup> - <i>Helicobacter pylori</i> NikR contains four square-planar nickel-binding sites at physiological pH. <i>Dalton Transactions</i> , 2011, 40, 7831.	3.3	28
53	Polarized X-ray Absorption Near-Edge Structure Spectroscopy of Neuroglobin and Myoglobin Single Crystals. <i>Journal of Physical Chemistry B</i> , 2010, 114, 13223-13231.	2.6	12
54	Crystallographic Analysis of Counterion Effects on Subtilisin Enzymatic Action in Acetonitrile. <i>Journal of the American Chemical Society</i> , 2010, 132, 2293-2300.	13.7	9

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55	Microfocus beamline for macromolecular crystallography MX2 @ PETRA III. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s118-s119.	0.3	1
56	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
57	The ligand environment of zinc stored in vesicles. Biochemical and Biophysical Research Communications, 2009, 380, 198-203.	2.1	79
58	EMBL macromolecular crystallography beamlines @ PETRA3 - Hamburg Germany. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s334-s334.	0.3	0
59	The interdependence of wavelength, redundancy and dose in sulfur SAD experiments. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1196-1209.	2.5	42
60	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
61	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
62	The determination of protonation states in proteins. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 906-922.	2.5	66
63	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
64	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
65	Synchrotron and Neutron Techniques in Biological Crystallography. ChemInform, 2005, 36, no.	0.0	0
66	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
67	Anomalous scattering in structural chemistry and biology. Crystallography Reviews, 2005, 11, 245-335.	1.5	44
68	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
69	Structural studies on human $\beta$ -thrombin. Acta Crystallographica Section A: Foundations and Advances, 2005, 61, c244-c244.	0.3	0
70	The structure and refinement of apocrustacyanin C2 to 1.3 Å resolution and the search for differences between this protein and the homologous apoproteins A1 and C1. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 493-498.	2.5	9
71	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
72	Synchrotron and neutron techniques in biological crystallography. Chemical Society Reviews, 2004, 33, 548.	38.1	30

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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	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
75	Unravelling the structural chemistry of the colouration mechanism in lobster shell. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2072-2082.	2.5	65
76	Time-resolved and static-ensemble structural chemistry of hydroxymethylbilane synthase. Faraday Discussions, 2003, 122, 131-144.	3.2	23
77	The molecular basis of the coloration mechanism in lobster shell: $\hat{\text{A}}^2$ -Crustacyanin at 3.2-Å resolution. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9795-9800.	7.1	177
78	The molecular basis of the coloration mechanism in lobster shell: $\hat{\text{I}}^2$ -crustacyanin at 3.2-Å resolution. Acta Crystallographica Section A: Foundations and Advances, 2002, 58, c121-c121.	0.3	1
79	Structure of lobster apocrustacyanin A1 using softer X-rays. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1219-1229.	2.5	38
80	Apocrustacyanin A1 from the lobster carotenoprotein $\hat{\text{I}}^2$ -crustacyanin: crystallization and initial X-ray analysis involving softer X-rays. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1064-1066.	2.5	4
81	Specific interaction of lipoate at the active site of rhodanese. BBA - Proteins and Proteomics, 2000, 1481, 103-108.	2.1	16
82	A combined anomalous scattering and direct methods approach to solve apocrustacyanin proteins (C1 and A1). Acta Crystallographica Section A: Foundations and Advances, 2000, 56, s61-s61.	0.3	0
83	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