

Vito Calderone

List of Publications by Year in descending order

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75
papers

2,858
citations

159358

30
h-index

174990

52
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79
all docs

79
docs citations

79
times ranked

3554
citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of Non-Lethal Selection on Spontaneous Revertants of Frameshift Mutations: The Escherichia coli Δ hisF Case. <i>Microorganisms</i> , 2022, 10, 692.	1.6	4
2	Identification and Characterization of an RRM-Containing, RNA Binding Protein in <i>Acinetobacter baumannii</i> . <i>Biomolecules</i> , 2022, 12, 922.	1.8	0
3	Revisiting paramagnetic relaxation enhancements in slowly rotating systems: how long is the long range?. <i>Magnetic Resonance</i> , 2021, 2, 25-31.	0.8	2
4	A High-Resolution View of the Coordination Environment in a Paramagnetic Metalloprotein from its Magnetic Properties. <i>Angewandte Chemie</i> , 2021, 133, 15087-15093.	1.6	5
5	A High-Resolution View of the Coordination Environment in a Paramagnetic Metalloprotein from its Magnetic Properties. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 14960-14966.	7.2	13
6	A fragment-based approach identifies an allosteric pocket that impacts malate dehydrogenase activity. <i>Communications Biology</i> , 2021, 4, 949.	2.0	2
7	SARS-CoV-2 M ^{pro} inhibition by a zinc ion: structural features and hints for drug design. <i>Chemical Communications</i> , 2021, 57, 7910-7913.	2.2	12
8	On the Mechanism of Bioinspired Formation of Inorganic Oxides: Structural Evidence of the Electrostatic Nature of the Interaction between a Mononuclear Inorganic Precursor and Lysozyme. <i>Biomolecules</i> , 2021, 11, 43.	1.8	4
9	On the complementarity of X-ray and NMR data. <i>Journal of Structural Biology: X</i> , 2020, 4, 100019.	0.7	7
10	Integrative Approaches in Structural Biology: A More Complete Picture from the Combination of Individual Techniques. <i>Biomolecules</i> , 2019, 9, 370.	1.8	19
11	Exploration of zinc-binding groups for the design of inhibitors for the oxytocinase subfamily of M1 aminopeptidases. <i>Bioorganic and Medicinal Chemistry</i> , 2019, 27, 115177.	1.4	4
12	In-house high-energy-remote SAD phasing using the magic triangle: how to tackle the P_1 low symmetry using multiple orientations of the same crystal of human IBA57 to increase the multiplicity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 317-324.	1.1	4
13	Reviewing the Crystal Structure of S100Z and Other Members of the S100 Family: Implications in Calcium-Regulated Quaternary Structure. <i>Methods in Molecular Biology</i> , 2019, 1929, 487-499.	0.4	5
14	Characterization of PEGylated Asparaginase: New Opportunities from NMR Analysis of Large PEGylated Therapeutics. <i>Chemistry - A European Journal</i> , 2019, 25, 1984-1991.	1.7	32
15	Metal centers in biomolecular solid-state NMR. <i>Journal of Structural Biology</i> , 2019, 206, 99-109.	1.3	10
16	Non-crystallographic symmetry in proteins: Jahn-Teller-like and Butterfly-like effects?. <i>Journal of Biological Inorganic Chemistry</i> , 2019, 24, 91-101.	1.1	2
17	When molecular replacement has no trivial solution: The importance of model editing in human S100Z X-ray structure solution. <i>Inorganica Chimica Acta</i> , 2018, 470, 402-406.	1.2	1
18	Interaction of Half Oxa-/Half cis -Platin Complex with Human Superoxide Dismutase and Induced Reduction of Neurotoxicity. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 1094-1098.	1.3	2

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19	IBA57 Recruits ISCA2 to Form a [2Fe-2S] Cluster-Mediated Complex. <i>Journal of the American Chemical Society</i> , 2018, 140, 14401-14412.	6.6	44
20	Solving the crystal structure of human calcium-free S100Z: the siege and conquer of one of the last S100 family strongholds. <i>Journal of Biological Inorganic Chemistry</i> , 2017, 22, 519-526.	1.1	2
21	Lipoyl-Homotaurine Derivative (ADM_12) Reverts Oxaliplatin-Induced Neuropathy and Reduces Cancer Cells Malignancy by Inhibiting Carbonic Anhydrase IX (CAIX). <i>Journal of Medicinal Chemistry</i> , 2017, 60, 9003-9011.	2.9	12
22	Simultaneous use of solution NMR and X-ray data in <i>REFMAC5</i> for joint refinement/detection of structural differences. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 958-967.	2.5	45
23	Human Ind1 expression causes over-expression of E. coli beta-lactamase ampicillin resistance protein. <i>Protein Expression and Purification</i> , 2014, 104, 26-33.	0.6	2
24	Structure of matrix metalloproteinase-3 with a platinum-based inhibitor. <i>Chemical Communications</i> , 2013, 49, 5492.	2.2	11
25	Molecular Determinants of a Selective Matrix Metalloprotease-12 Inhibitor: Insights from Crystallography and Thermodynamic Studies. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 1149-1159.	2.9	37
26	Unraveling Hidden Regulatory Sites in Structurally Homologous Metalloproteases. <i>Journal of Molecular Biology</i> , 2013, 425, 2330-2346.	2.0	52
27	Discovery of a New Class of Potent MMP Inhibitors by Structure-Based Optimization of the Arylsulfonamide Scaffold. <i>ACS Medicinal Chemistry Letters</i> , 2013, 4, 565-569.	1.3	18
28	Molecular view of an electron transfer process essential for iron-sulfur protein biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7136-7141.	3.3	63
29	An Electron-Transfer Path through an Extended Disulfide Relay System: The Case of the Redox Protein ALR. <i>Journal of the American Chemical Society</i> , 2012, 134, 1442-1445.	6.6	40
30	Interaction of Cisplatin with Human Superoxide Dismutase. <i>Journal of the American Chemical Society</i> , 2012, 134, 7009-7014.	6.6	65
31	The catalytic domain of MMP-1 studied through tagged lanthanides. <i>FEBS Letters</i> , 2012, 586, 557-567.	1.3	45
32	Structural characterization of human S100A16, a low-affinity calcium binder. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 243-256.	1.1	18
33	Structure of the extended-spectrum β -lactamase TEM-72 inhibited by citrate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 303-306.	0.7	14
34	Molecular recognition and substrate mimicry drive the electron-transfer process between MIA40 and ALR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4811-4816.	3.3	92
35	Structure-based approach to nanomolar, water soluble matrix metalloproteinases inhibitors (MMPi). <i>European Journal of Medicinal Chemistry</i> , 2010, 45, 5919-5925.	2.6	30
36	Crystal Structure of the Narrow-Spectrum OXA-46 Class D β -Lactamase: Relationship between Active-Site Lysine Carbamylation and Inhibition by Polycarboxylates. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 2167-2174.	1.4	31

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37	Entropic Contribution to the Linking Coefficient in Fragment Based Drug Design: A Case Study. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 4285-4289.	2.9	70
38	High-Resolution Crystal Structure of the Subclass B3 Metallo- β -Lactamase BJP-1: Rational Basis for Substrate Specificity and Interaction with Sulfonamides. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4343-4351.	1.4	46
39	Structural and dynamic aspects related to oligomerization of apo SOD1 and its mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6980-6985.	3.3	109
40	Crystal Structure of the OXA-48 β -Lactamase Reveals Mechanistic Diversity among Class D Carbapenemases. <i>Chemistry and Biology</i> , 2009, 16, 540-547.	6.2	144
41	Biotin-Tagged Probes for MMP Expression and Activation: Design, Synthesis, and Binding Properties. <i>Bioconjugate Chemistry</i> , 2009, 20, 719-727.	1.8	10
42	Structural Basis of Serine/Threonine Phosphatase Inhibition by the Archetypal Small Molecules Cantharidin and Norcantharidin. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 4838-4843.	2.9	62
43	Copper(I)-mediated protein-protein interactions result from suboptimal interaction surfaces. <i>Biochemical Journal</i> , 2009, 422, 37-42.	1.7	85
44	Evidence of Reciprocal Reorientation of the Catalytic and Hemopexin-Like Domains of Full-Length MMP-12. <i>Journal of the American Chemical Society</i> , 2008, 130, 7011-7021.	6.6	84
45	Exploring the Subtleties of Drug-Receptor Interactions: The Case of Matrix Metalloproteinases. <i>Journal of the American Chemical Society</i> , 2007, 129, 2466-2475.	6.6	72
46	A Structure-based Proposal for the Catalytic Mechanism of the Bacterial Acid Phosphatase AphA belonging to the DDDD Superfamily of Phosphohydrolases. <i>Journal of Molecular Biology</i> , 2006, 355, 708-721.	2.0	29
47	Synthesis of bicyclic molecular scaffolds (BTAA): An investigation towards new selective MMP-12 inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2006, 14, 7392-7403.	1.4	21
48	Structural Investigation of Cisplatin-Protein Interactions: Selective Platination of His19 in a Cuprozinc Superoxide Dismutase. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 1267-1269.	7.2	107
49	Snapshots of the Reaction Mechanism of Matrix Metalloproteinases. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 7952-7955.	7.2	98
50	A High-Affinity Carbohydrate-Containing Inhibitor of Matrix Metalloproteinases. <i>ChemMedChem</i> , 2006, 1, 598-601.	1.6	28
51	A hint for the function of human Sco1 from different structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8595-8600.	3.3	99
52	A prokaryotic superoxide dismutase paralog lacking two Cu ligands: From largely unstructured in solution to ordered in the crystal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7541-7546.	3.3	28
53	The crystal structure of yeast copper thionein: The solution of a long-lasting enigma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 51-56.	3.3	146
54	Conformational variability of matrix metalloproteinases: Beyond a single 3D structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5334-5339.	3.3	143

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55	From an Inactive Prokaryotic SOD Homologue to an Active Protein through Site-Directed Mutagenesis. <i>Journal of the American Chemical Society</i> , 2005, 127, 13287-13292.	6.6	11
56	Crystal Structure of Amine Oxidase from Bovine Serum. <i>Journal of Molecular Biology</i> , 2005, 346, 991-1004.	2.0	79
57	Practical aspects of the integration of different software in protein structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2150-2155.	2.5	3
58	The First Structure of a Bacterial Class B Acid Phosphatase Reveals Further Structural Heterogeneity Among Phosphatases of the Haloacid Dehalogenase Fold. <i>Journal of Molecular Biology</i> , 2004, 335, 761-773.	2.0	27
59	Crystal Structure of the Catalytic Domain of Human Matrix Metalloproteinase 10. <i>Journal of Molecular Biology</i> , 2004, 336, 707-716.	2.0	49
60	Title is missing!. <i>Angewandte Chemie</i> , 2003, 115, 2777-2780.	1.6	9
61	X-ray Structures of Binary and Ternary Enzyme-Product-Inhibitor Complexes of Matrix Metalloproteinases. <i>Angewandte Chemie - International Edition</i> , 2003, 42, 2673-2676.	7.2	41
62	Crystallization and preliminary X-ray data of amine oxidase from bovine serum. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 727-729.	2.5	8
63	Expression, purification, crystallization and preliminary X-ray characterization of the class B acid phosphatase (AphA) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1058-1060.	2.5	5
64	Crystal structure of the PsbQ protein of photosystem II from higher plants. <i>EMBO Reports</i> , 2003, 4, 900-905.	2.0	78
65	High-resolution Structures of Retinol-binding Protein in Complex with Retinol: pH-induced Protein Structural Changes in the Crystal State. <i>Journal of Molecular Biology</i> , 2003, 329, 841-850.	2.0	30
66	The Evolutionarily Conserved Trimeric Structure of CutA1 Proteins Suggests a Role in Signal Transduction. <i>Journal of Biological Chemistry</i> , 2003, 278, 45999-46006.	1.6	52
67	Ligand Binding and Structural Analysis of a Human Putative Cellular Retinol-binding Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 41970-41977.	1.6	80
68	Identification and Structural Analysis of a Zebrafish Apo and Holo Cellular Retinol-binding Protein. <i>Journal of Molecular Biology</i> , 2002, 321, 527-535.	2.0	17
69	Cloning of human 3-hydroxyanthranilic acid dioxygenase in <i>Escherichia coli</i> : characterisation of the purified enzyme and its in vitro inhibition by Zn ²⁺ . <i>BBA - Proteins and Proteomics</i> , 2002, 1596, 283-292.	2.1	16
70	Structure of chicken plasma retinol-binding protein. <i>BBA - Proteins and Proteomics</i> , 2001, 1550, 64-69.	2.1	21
71	Identification, retinoid binding, and x-ray analysis of a human retinol-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 3710-3715.	3.3	88
72	The structure of human aldose reductase bound to the inhibitor IDD384. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 536-540.	2.5	25

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73	The unusual amino acid triplet Asn-Ile-Cys is a glycosylation consensus site in human alpha-lactalbumin. <i>The Protein Journal</i> , 1997, 16, 747-753.	1.1	25
74	Amino acid sequence and crystal structure of buffalo α -lactalbumin. <i>FEBS Letters</i> , 1996, 394, 91-95.	1.3	26
75	Human milk proteins may interfere in ELISA measurements of bovine β -lactoglobulin in human milk. <i>Acta Paediatrica, International Journal of Paediatrics</i> , 1996, 85, 543-549.	0.7	26