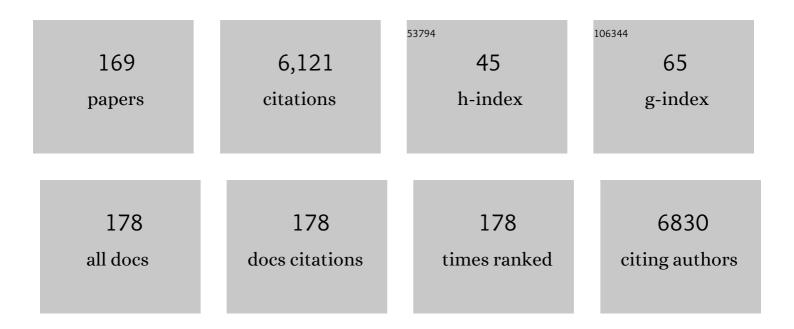
Marcelo A Marti

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	H2S and NO cooperatively regulate vascular tone by activating a neuroendocrine HNO–TRPA1–CGRP signalling pathway. Nature Communications, 2014, 5, 4381.	12.8	324
2	The Catalytic Mechanism of Peptidylglycine α-Hydroxylating Monooxygenase Investigated by Computer Simulation. Journal of the American Chemical Society, 2006, 128, 12817-12828.	13.7	137
3	A DFT-Based QM-MM Approach Designed for the Treatment of Large Molecular Systems:Â Application to Chorismate Mutase. Journal of Physical Chemistry B, 2003, 107, 13728-13736.	2.6	116
4	Aromatic–Aromatic Interactions in Proteins: Beyond the Dimer. Journal of Chemical Information and Modeling, 2011, 51, 1623-1633.	5.4	115
5	Evidence for a ferryl intermediate in a heme-based dioxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17371-17376.	7.1	113
6	Multiple-Steering QMâ^'MM Calculation of the Free Energy Profile in Chorismate Mutase. Journal of the American Chemical Society, 2005, 127, 6940-6941.	13.7	112
7	Theoretical Study of the Truncated Hemoglobin HbN:Â Exploring the Molecular Basis of the NO Detoxification Mechanism. Journal of the American Chemical Society, 2005, 127, 4433-4444.	13.7	111
8	pH-Dependent Conformational Changes in Proteins and Their Effect on Experimental pKas: The Case of Nitrophorin 4. PLoS Computational Biology, 2012, 8, e1002761.	3.2	110
9	Discrimination of Nitroxyl and Nitric Oxide by Water-Soluble Mn(III) Porphyrins. Journal of the American Chemical Society, 2005, 127, 4680-4684.	13.7	109
10	Ligand-induced dynamical regulation of NO conversion in Mycobacterium tuberculosis truncated hemoglobin-N. Proteins: Structure, Function and Bioinformatics, 2006, 64, 457-464.	2.6	95
11	Heme Protein Oxygen Affinity Regulation Exerted by Proximal Effects. Journal of the American Chemical Society, 2006, 128, 12455-12461.	13.7	91
12	Dioxygen affinity in heme proteins investigated by computer simulation. Journal of Inorganic Biochemistry, 2006, 100, 761-770.	3.5	89
13	Nitroxyl (azanone) trapping by metalloporphyrins. Coordination Chemistry Reviews, 2011, 255, 2764-2784.	18.8	84
14	Fast Nitroxyl Trapping by Ferric Porphyrins. Journal of the American Chemical Society, 2003, 125, 15272-15273.	13.7	82
15	The Structural Biology of Galectin-Ligand Recognition: Current Advances in Modeling Tools, Protein Engineering, and Inhibitor Design. Frontiers in Chemistry, 2019, 7, 823.	3.6	80
16	Free Energy Calculations with Non-Equilibrium Methods: Applications of the Jarzynski Relationship. Theoretical Chemistry Accounts, 2006, 116, 338-346.	1.4	79
17	Nitric Oxide Is Reduced to HNO by Proton-Coupled Nucleophilic Attack by Ascorbate, Tyrosine, and Other Alcohols. A New Route to HNO in Biological Media?. Journal of the American Chemical Society, 2015, 137, 4720-4727.	13.7	79
18	Modeling heme proteins using atomistic simulations. Physical Chemistry Chemical Physics, 2006, 8, 5611-5628.	2.8	77

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19	Time-Resolved Electrochemical Quantification of Azanone (HNO) at Low Nanomolar Level. Analytical Chemistry, 2013, 85, 10262-10269.	6.5	73
20	Trapping and Characterization of a Reaction Intermediate in Carbapenem Hydrolysis by <i>B. cereus</i> Metallo-l²-lactamase. Journal of the American Chemical Society, 2008, 130, 15852-15863.	13.7	72
21	The NtrY/X twoâ€component system of <i>Brucella</i> spp. acts as a redox sensor and regulates the expression of nitrogen respiration enzymes. Molecular Microbiology, 2012, 85, 39-50.	2.5	72
22	Complete Reaction Mechanism of Indoleamine 2,3-Dioxygenase as Revealed by QM/MM Simulations. Journal of Physical Chemistry B, 2012, 116, 1401-1413.	2.6	68
23	Molecular Dynamics in Mixed Solvents Reveals Protein–Ligand Interactions, Improves Docking, and Allows Accurate Binding Free Energy Predictions. Journal of Chemical Information and Modeling, 2017, 57, 846-863.	5.4	68
24	Molecular Basis for the Electric Field Modulation of Cytochrome <i>c</i> Structure and Function. Journal of the American Chemical Society, 2009, 131, 16248-16256.	13.7	66
25	Inhibitory effect of quercetin on matrix metalloproteinase 9 activity Molecular mechanism and structure–activity relationship of the flavonoid–enzyme interaction. European Journal of Pharmacology, 2010, 644, 138-145.	3.5	65
26	Nitric Oxide Interaction with Cytochromecâ€~ and Its Relevance to Guanylate Cyclase. Why Does the Iron Histidine Bond Break?. Journal of the American Chemical Society, 2005, 127, 7721-7728.	13.7	64
27	Molecular Basis of Coupled Protein and Electron Transfer Dynamics of Cytochrome c in Biomimetic Complexes. Journal of the American Chemical Society, 2010, 132, 5769-5778.	13.7	64
28	A Surface Effect Allows HNO/NO Discrimination by a Cobalt Porphyrin Bound to Gold. Inorganic Chemistry, 2010, 49, 6955-6966.	4.0	63
29	A Microscopic Study of the Deoxyhemoglobin-Catalyzed Generation of Nitric Oxide from Nitrite Anion. Biochemistry, 2008, 47, 9793-9802.	2.5	62
30	Role of Pre-A Motif in Nitric Oxide Scavenging by Truncated Hemoglobin, HbN, of Mycobacterium tuberculosis. Journal of Biological Chemistry, 2009, 284, 14457-14468.	3.4	59
31	CG2AA: backmapping protein coarse-grained structures. Bioinformatics, 2016, 32, 1235-1237.	4.1	59
32	Reactions of HNO with Metal Porphyrins: Underscoring the Biological Relevance of HNO. Accounts of Chemical Research, 2014, 47, 2907-2916.	15.6	56
33	Whole Genome Sequencing Reveals a De Novo SHANK3 Mutation in Familial Autism Spectrum Disorder. PLoS ONE, 2015, 10, e0116358.	2.5	55
34	Exploring the molecular basis of heme coordination in human neuroglobin. Proteins: Structure, Function and Bioinformatics, 2008, 71, 695-705.	2.6	54
35	The first step of the dioxygenation reaction carried out by tryptophan dioxygenase and indoleamine 2,3-dioxygenase as revealed by quantum mechanical/molecular mechanical studies. Journal of Biological Inorganic Chemistry, 2010, 15, 811-823.	2.6	53
36	Target-Pathogen: a structural bioinformatic approach to prioritize drug targets in pathogens. Nucleic Acids Research, 2018, 46, D413-D418.	14.5	53

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37	Heme-oxygenase-1 implications in cell morphology and the adhesive behavior of prostate cancer cells. Oncotarget, 2014, 5, 4087-4102.	1.8	53
38	Structural and Molecular Basis of the Peroxynitrite-mediated Nitration and Inactivation of Trypanosoma cruzi Iron-Superoxide Dismutases (Fe-SODs) A and B. Journal of Biological Chemistry, 2014, 289, 12760-12778.	3.4	51
39	An integrative, multi-omics approach towards the prioritization of Klebsiella pneumoniae drug targets. Scientific Reports, 2018, 8, 10755.	3.3	50
40	Dynamical Characterization of the Heme NO Oxygen Binding (HNOX) Domain. Insight into Soluble Guanylate Cyclase Allosteric Transition. Biochemistry, 2008, 47, 9416-9427.	2.5	49
41	Role of Heme Distortion on Oxygen Affinity in Heme Proteins: The Protoglobin Case. Journal of Physical Chemistry B, 2010, 114, 8536-8543.	2.6	49
42	Exploring the molecular basis of human manganese superoxide dismutase inactivation mediated by tyrosine 34 nitration. Archives of Biochemistry and Biophysics, 2011, 507, 304-309.	3.0	48
43	Physiological concentrations of melatonin inhibit the nitridergic pathway in the Syrian hamster retina. Journal of Pineal Research, 2002, 33, 31-36.	7.4	47
44	Structural determinants of ligand migration in <i>Mycobacterium tuberculosis</i> truncated hemoglobin O. Proteins: Structure, Function and Bioinformatics, 2008, 73, 372-379.	2.6	47
45	Solvent structure improves docking prediction in lectin–carbohydrate complexes. Glycobiology, 2013, 23, 241-258.	2.5	47
46	WATCLUST: a tool for improving the design of drugs based on protein-water interactions. Bioinformatics, 2015, 31, 3697-3699.	4.1	47
47	Systemic Type I IFN Inflammation in Human ISG15 Deficiency Leads to Necrotizing Skin Lesions. Cell Reports, 2020, 31, 107633.	6.4	47
48	Dynamical Regulation of Ligand Migration by a Gate-Opening Molecular Switch in Truncated Hemoglobin-N fromMycobacterium tuberculosis. Journal of the American Chemical Society, 2007, 129, 6782-6788.	13.7	46
49	Insights on Glucocorticoid Receptor Activity Modulation through the Binding of Rigid Steroids. PLoS ONE, 2010, 5, e13279.	2.5	44
50	High pressure reveals structural determinants for globin hexacoordination: Neuroglobin and myoglobin cases. Proteins: Structure, Function and Bioinformatics, 2009, 75, 885-894.	2.6	43
51	Molecular Basis for the Substrate Stereoselectivity in Tryptophan Dioxygenase. Biochemistry, 2011, 50, 10910-10918.	2.5	42
52	AutoDock Bias: improving binding mode prediction and virtual screening using known protein–ligand interactions. Bioinformatics, 2019, 35, 3836-3838.	4.1	42
53	HNO Is Produced by the Reaction of NO with Thiols. Journal of the American Chemical Society, 2017, 139, 14483-14487.	13.7	41
54	Modulation of the NO trans effect in heme proteins: implications for the activation of soluble guanylate cyclase. Journal of Biological Inorganic Chemistry, 2003, 8, 595-600.	2.6	39

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55	QMâ^'MM Study of Nitrite Reduction by Nitrite Reductase ofPseudomonas aeruginosa. Journal of Physical Chemistry B, 2004, 108, 18073-18080.	2.6	39
56	Comparing and combining implicit ligand sampling with multiple steered molecular dynamics to study ligand migration processes in heme proteins. Journal of Computational Chemistry, 2011, 32, 2219-2231.	3.3	39
57	Protein Topology Determines Cysteine Oxidation Fate: The Case of Sulfenyl Amide Formation among Protein Families. PLoS Computational Biology, 2015, 11, e1004051.	3.2	39
58	Bond or Cage Effect:  How Nitrophorins Transport and Release Nitric Oxide. Journal of the American Chemical Society, 2008, 130, 1611-1618.	13.7	38
59	Aromatic clusters in protein–protein and protein–drug complexes. Journal of Cheminformatics, 2020, 12, 30.	6.1	38
60	pH-Dependent Mechanism of Nitric Oxide Release in Nitrophorins 2 and 4. Journal of Physical Chemistry B, 2009, 113, 1192-1201.	2.6	37
61	Small ligand–globin interactions: Reviewing lessons derived from computer simulation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1722-1738.	2.3	37
62	Redox Potential Determines the Reaction Mechanism of HNO Donors with Mn and Fe Porphyrins: Defining the Better Traps. Inorganic Chemistry, 2014, 53, 7351-7360.	4.0	37
63	Mechanism of the Reaction of Human Manganese Superoxide Dismutase with Peroxynitrite: Nitration of Critical Tyrosine 34. Biochemistry, 2016, 55, 3403-3417.	2.5	37
64	Thermal Fluctuations Determine the Electronâ€Transfer Rates of Cytochrome c in Electrostatic and Covalent Complexes. ChemPhysChem, 2010, 11, 1225-1235.	2.1	36
65	Unraveling the molecular basis for ligand binding in truncated hemoglobins: The trHbO <i>Bacillus subtilis</i> case. Proteins: Structure, Function and Bioinformatics, 2010, 78, 962-970.	2.6	36
66	Discussing Endogenous NO•/HNO Interconversion Aided by Phenolic Drugs and Vitamins. Inorganic Chemistry, 2015, 54, 9342-9350.	4.0	36
67	Evolutionary and Functional Relationships in the Truncated Hemoglobin Family. PLoS Computational Biology, 2016, 12, e1004701.	3.2	36
68	HNO trapping and assisted decomposition of nitroxyl donors by ferric hemes. Polyhedron, 2007, 26, 4673-4679.	2.2	35
69	Mechanism of Product Release in NO Detoxification from <i>Mycobacterium tuberculosis</i> Truncated Hemoglobin N. Journal of the American Chemical Society, 2008, 130, 1688-1693.	13.7	35
70	Substrate stereoâ€specificity in tryptophan dioxygenase and indoleamine 2,3â€dioxygenase. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2961-2972.	2.6	35
71	TuberQ: a Mycobacterium tuberculosis protein druggability database. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau035-bau035.	3.0	35
72	Oxygen affinity controlled by dynamical distal conformations: The soybean leghemoglobin and the Paramecium caudatum hemoglobin cases. Proteins: Structure, Function and Bioinformatics, 2007, 68, 480-487.	2.6	33

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73	Carbohydrate-Binding Proteins: Dissecting Ligand Structures through Solvent Environment Occupancy. Journal of Physical Chemistry B, 2009, 113, 8717-8724.	2.6	33
74	Computer simulation and SERR detection of cytochrome c dynamics at SAM-coated electrodes. Electrochimica Acta, 2009, 54, 4963-4970.	5.2	32
75	Characterization of the Galectin-1 Carbohydrate Recognition Domain in Terms of Solvent Occupancy. Journal of Physical Chemistry B, 2007, 111, 7360-7366.	2.6	31
76	Ligand Migration in Methanosarcina acetivorans Protoglobin: Effects of Ligand Binding and Dimeric Assembly. Journal of Physical Chemistry B, 2011, 115, 13771-13780.	2.6	31
77	Molecular basis of intramolecular electron transfer in proteins during radical-mediated oxidations: Computer simulation studies in model tyrosine–cysteine peptides in solution. Archives of Biochemistry and Biophysics, 2012, 525, 82-91.	3.0	31
78	Protein dynamics and ligand migration interplay as studied by computer simulation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1054-1064.	2.3	30
79	Molecular Dynamics Simulations Provide Atomistic Insight into Hydrogen Exchange Mass Spectrometry Experiments. Journal of Chemical Theory and Computation, 2013, 9, 658-669.	5.3	30
80	Heme oxygenase-1 in the forefront of a multi-molecular network that governs cell–cell contacts and filopodia-induced zippering in prostate cancer. Cell Death and Disease, 2016, 7, e2570-e2570.	6.3	30
81	An optimized methodology for whole genome sequencing of RNA respiratory viruses from nasopharyngeal aspirates. PLoS ONE, 2018, 13, e0199714.	2.5	30
82	Hydrophobic Effect Drives Oxygen Uptake in Myoglobin via Histidine E7. Journal of Biological Chemistry, 2013, 288, 6754-6762.	3.4	28
83	QM/MM study of the C—C coupling reaction mechanism of CYP121, an essential Cytochrome p450 of <i>Mycobacterium tuberculosis</i> . Proteins: Structure, Function and Bioinformatics, 2014, 82, 1004-1021.	2.6	28
84	The hemoglobins of the subâ€Antarctic fish <i>Cottoperca gobio</i> , a phyletically basal species – oxygenâ€binding equilibria, kinetics and molecular dynamics. FEBS Journal, 2009, 276, 2266-2277.	4.7	27
85	Nitric Oxide Reactivity with Globins as Investigated Through Computer Simulation. Methods in Enzymology, 2008, 437, 477-498.	1.0	26
86	Structural Model for p75NTR–TrkA Intracellular Domain Interaction: A Combined FRET and Bioinformatics Study. Journal of Molecular Biology, 2011, 414, 681-698.	4.2	26
87	Role of PheE15 Gate in Ligand Entry and Nitric Oxide Detoxification Function of Mycobacterium tuberculosis Truncated Hemoglobin N. PLoS ONE, 2012, 7, e49291.	2.5	26
88	Underlying Thermodynamics of pH-Dependent Allostery. Journal of Physical Chemistry B, 2014, 118, 12818-12826.	2.6	26
89	Solvents to Fragments to Drugs: MD Applications in Drug Design. Molecules, 2018, 23, 3269.	3.8	25
90	Environment effects on chemical reactivity of heme proteins. International Journal of Quantum Chemistry, 2002, 90, 1505-1514.	2.0	23

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91	An Integrated Computational Analysis of the Structure, Dynamics, and Ligand Binding Interactions of the Human Galectin Network. Journal of Chemical Information and Modeling, 2011, 51, 1918-1930.	5.4	23
92	Role of the Distal Hydrogen-Bonding Network in Regulating Oxygen Affinity in the Truncated Hemoglobin III fromCampylobacter jejuni. Biochemistry, 2011, 50, 3946-3956.	2.5	23
93	Structural basis for ligand recognition in a mushroom lectin: solvent structure as specificity predictor. Carbohydrate Research, 2011, 346, 939-948.	2.3	23
94	Ligand Migration in the Apolar Tunnel of Cerebratulus lacteus Mini-Hemoglobin. Journal of Biological Chemistry, 2011, 286, 5347-5358.	3.4	23
95	Molecular Mechanism of Myoglobin Autoxidation: Insights from Computer Simulations. Journal of Physical Chemistry B, 2015, 119, 1802-1813.	2.6	23
96	Tertiary and quaternary structural basis of oxygen affinity in human hemoglobin as revealed by multiscale simulations. Scientific Reports, 2017, 7, 10926.	3.3	23
97	High-throughput splicing assays identify missense and silent splice-disruptive POU1F1 variants underlying pituitary hormone deficiency. American Journal of Human Genetics, 2021, 108, 1526-1539.	6.2	23
98	Exploring the Molecular Basis of Action of the Passive Antiglucocorticoid 21-Hydroxy-6,19-epoxyprogesterone. Journal of Medicinal Chemistry, 2008, 51, 1352-1360.	6.4	22
99	Two distinct heme distal site states define Cerebratulus lacteus mini-hemoglobin oxygen affinity. Proteins: Structure, Function and Bioinformatics, 2005, 62, 641-648.	2.6	21
100	The peculiar heme pocket of the 2/2 hemoglobin of cold-adapted Pseudoalteromonas haloplanktis TAC125. Journal of Biological Inorganic Chemistry, 2011, 16, 299-311.	2.6	21
101	Structural Study of a Flexible Active Site Loop in Human Indoleamine 2,3-Dioxygenase and Its Functional Implications. Biochemistry, 2016, 55, 2785-2793.	2.5	21
102	A whole genome bioinformatic approach to determine potential latent phase specific targets in Mycobacterium tuberculosis. Tuberculosis, 2016, 97, 181-192.	1.9	21
103	Cosolvent-Based Protein Pharmacophore for Ligand Enrichment in Virtual Screening. Journal of Chemical Information and Modeling, 2019, 59, 3572-3583.	5.4	21
104	Engineered chimeras reveal the structural basis of hexacoordination in globins: A case study of neuroglobin and myoglobin. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 169-177.	2.4	20
105	Allelic differences in a vacuolar invertase affect Arabidopsis growth at early plant development. Journal of Experimental Botany, 2016, 67, 4091-4103.	4.8	20
106	Germline and somatic mutations in cortical malformations: Molecular defects in Argentinean patients with neuronal migration disorders. PLoS ONE, 2017, 12, e0185103.	2.5	20
107	Molecular Basis for the pH Dependent Structural Transition of Nitrophorin 4. Journal of Physical Chemistry B, 2009, 113, 2135-2142.	2.6	19
108	A protective protein matrix improves the discrimination of nitroxyl from nitric oxide by MnIII protoporphyrinate IX in aerobic media. Journal of Inorganic Biochemistry, 2011, 105, 1044-1049.	3.5	19

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109	CDK2 and PKA Mediated-Sequential Phosphorylation Is Critical for p19INK4d Function in the DNA Damage Response. PLoS ONE, 2012, 7, e35638.	2.5	19
110	Using crystallographic water properties for the analysis and prediction of lectin-carbohydrate complex structures. Glycobiology, 2015, 25, 181-196.	2.5	19
111	Linking the Structure and Thermal Stability of β-Galactoside-Binding Protein Galectin-1 to Ligand Binding and Dimerization Equilibria. Biochemistry, 2010, 49, 7652-7658.	2.5	18
112	Structural Insights into the HWE Histidine Kinase Family: The Brucella Blue Light-Activated Histidine Kinase Domain. Journal of Molecular Biology, 2016, 428, 1165-1179.	4.2	18
113	Genetics and genomic medicine in Argentina. Molecular Genetics & Genomic Medicine, 2018, 6, 481-491.	1.2	17
114	Next generation sequencing panel based on single molecule molecular inversion probes for detecting genetic variants in children with hypopituitarism. Molecular Genetics & Genomic Medicine, 2018, 6, 514-525.	1.2	17
115	Gordon Holmes Syndrome Caused by RNF216 Novel Mutation in 2 Argentinean Siblings. Movement Disorders Clinical Practice, 2019, 6, 259-262.	1.5	17
116	Proximal effects in the modulation of nitric oxide synthase reactivity: a QM-MM study. Journal of Biological Inorganic Chemistry, 2005, 10, 595-604.	2.6	16
117	Hemisuccinate of 21â€Hydroxyâ€6,19â€Epoxyprogesterone: A Tissueâ€Specific Modulator of the Clucocorticoid Receptor. ChemMedChem, 2008, 3, 1869-1877.	3.2	16
118	From Genome to Drugs: New Approaches in Antimicrobial Discovery. Frontiers in Pharmacology, 2021, 12, 647060.	3.5	16
119	Probing the Chemotaxis Periplasmic Sensor Domains from Geobacter sulfurreducens by Combined Resonance Raman and Molecular Dynamic Approaches: NO and CO Sensing. Journal of Physical Chemistry B, 2010, 114, 11251-11260.	2.6	15
120	Mechanistic Insight into the Enzymatic Reduction of Truncated Hemoglobin N of Mycobacterium tuberculosis. Journal of Biological Chemistry, 2014, 289, 21573-21583.	3.4	15
121	A quantitative model for oxygen uptake and release in a family of hemeproteins. Bioinformatics, 2016, 32, 1805-1813.	4.1	15
122	Kinase Activation by Small Conformational Changes. Journal of Chemical Information and Modeling, 2020, 60, 821-832.	5.4	15
123	Clamping, bending, and twisting inter-domain motions in the misfold-recognizing portion of UDP-glucose: Glycoprotein glucosyltransferase. Structure, 2021, 29, 357-370.e9.	3.3	15
124	A Remote Secondary Binding Pocket Promotes Heteromultivalent Targeting of DC-SIGN. Journal of the American Chemical Society, 2021, 143, 18977-18988.	13.7	15
125	Protonation of histidine 55 affects the oxygen access to heme in the alpha chain of the hemoglobin from the Antarctic fish <i>Trematomus bernacchii</i> . IUBMB Life, 2011, 63, 175-182.	3.4	14
126	Improving Efficiency in SMD Simulations Through a Hybrid Differential Relaxation Algorithm. Journal of Chemical Theory and Computation, 2014, 10, 4609-4617.	5.3	14

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127	Tyrosine oxidation and nitration in transmembrane peptides is connected to lipid peroxidation. Archives of Biochemistry and Biophysics, 2017, 622, 9-25.	3.0	14
128	Rapid Whole-Cell Assay of Antitubercular Drugs Using Second-Generation Fluoromycobacteriophages. Antimicrobial Agents and Chemotherapy, 2016, 60, 3253-3256.	3.2	13
129	Electron transfer dynamics of Rhodothermus marinus caa3 cytochrome c domains on biomimetic films. Physical Chemistry Chemical Physics, 2011, 13, 18088.	2.8	12
130	Draft Genome Sequence of Bizionia argentinensis, Isolated from Antarctic Surface Water. Journal of Bacteriology, 2011, 193, 6797-6798.	2.2	12
131	Structure and function of crocodilian hemoglobins and allosteric regulation by chloride, ATP, and CO ₂ . American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2020, 318, R657-R667.	1.8	12
132	p38Î ³ Activation Triggers Dynamical Changes in Allosteric Docking Sites. Biochemistry, 2011, 50, 1384-1395.	2.5	11
133	Multiscale approach to the activation and phosphotransfer mechanism of CpxA histidine kinase reveals a tight coupling between conformational and chemical steps. Biochemical and Biophysical Research Communications, 2018, 498, 305-312.	2.1	11
134	Ligand uptake in Mycobacterium tuberculosis truncated hemoglobins is controlled by both internal tunnels and active site water molecules. F1000Research, 2015, 4, 22.	1.6	11
135	Quaternary structure effects on the hexacoordination equilibrium in rice hemoglobin rHb1: Insights from molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2013, 81, 863-873.	2.6	10
136	Coarse-Grained Simulations of Heme Proteins: Validation and Study of Large Conformational Transitions. Journal of Chemical Theory and Computation, 2016, 12, 3390-3397.	5.3	10
137	Single nucleotide polymorphisms may explain the contrasting phenotypes of two variants of a multidrug-resistant Mycobacterium tuberculosis strain. Tuberculosis, 2017, 103, 28-36.	1.9	10
138	VarQ: A Tool for the Structural and Functional Analysis of Human Protein Variants. Frontiers in Genetics, 2018, 9, 620.	2.3	10
139	The key role of water in the dioxygenase function of Escherichia coli flavohemoglobin. Journal of Inorganic Biochemistry, 2013, 119, 75-84.	3.5	9
140	Theoretical Insights into the Reaction and Inhibition Mechanism of Metal-Independent Retaining Glycosyltransferase Responsible for Mycothiol Biosynthesis. Journal of Physical Chemistry B, 2017, 121, 471-478.	2.6	9
141	Biased Docking for Protein–Ligand Pose Prediction. Methods in Molecular Biology, 2021, 2266, 39-72.	0.9	9
142	Thyroid Hormone Interactions with DMPC Bilayers. A Molecular Dynamics Study. Journal of Physical Chemistry B, 2009, 113, 13357-13364.	2.6	8
143	Azanone (HNO) interaction with Hemeproteins and metalloporphyrins. Advances in Inorganic Chemistry, 2012, , 97-139.	1.0	8
144	Evaluation of nitroxyl donors' effect on mycobacteria. Tuberculosis, 2018, 109, 35-40.	1.9	8

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145	Structural and mechanistic comparison of the Cyclopropane Mycolic Acid Synthases (CMAS) protein family of Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2018, 498, 288-295.	2.1	8
146	An efficient use of X-ray information, homology modeling, molecular dynamics and knowledge-based docking techniques to predict protein–monosaccharide complexes. Glycobiology, 2019, 29, 124-136.	2.5	8
147	Conformational and Reaction Dynamic Coupling in Histidine Kinases: Insights from Hybrid QM/MM Simulations. Journal of Chemical Information and Modeling, 2020, 60, 833-842.	5.4	8
148	Ligand uptake in Mycobacterium tuberculosis truncated hemoglobins is controlled by both internal tunnels and active site water molecules. F1000Research, 2015, 4, 22.	1.6	8
149	Mycobacterium tuberculosis DosS binds H2S through its Fe3+ heme iron to regulate the DosR dormancy regulon. Redox Biology, 2022, 52, 102316.	9.0	8
150	The Underlying Mechanism of HNO Production by the Myoglobin-Mediated Oxidation of Hydroxylamine. Inorganic Chemistry, 2020, 59, 7939-7952.	4.0	7
151	Spastic ataxia with eye-of-the-tiger-like sign in 4 siblings due to novel compound heterozygous AFG3L2 mutation. Parkinsonism and Related Disorders, 2020, 73, 52-54.	2.2	7
152	Pulmonary Alveolar Proteinosis and Multiple Infectious Diseases in a Child with Autosomal Recessive Complete IRF8 Deficiency. Journal of Clinical Immunology, 2022, 42, 975-985.	3.8	7
153	Biological activity and ligand binding mode to the progesterone receptor of A-homo analogues of progesterone. Bioorganic and Medicinal Chemistry, 2011, 19, 1683-1691.	3.0	6
154	Efficient Calculation of Enzyme Reaction Free Energy Profiles Using a Hybrid Differential Relaxation Algorithm. Advances in Protein Chemistry and Structural Biology, 2015, 100, 33-65.	2.3	5
155	Binding of the substrate UDP-glucuronic acid induces conformational changes in the xanthan gum glucuronosyltransferase. Protein Engineering, Design and Selection, 2016, 29, 197-207.	2.1	5
156	LigQ : A Webserver to Select and Prepare Ligands for Virtual Screening. Journal of Chemical Information and Modeling, 2017, 57, 1741-1746.	5.4	5
157	Stabilization and detection of nitroxyl by iron and cobalt porphyrins in solution and on surfaces. Journal of Porphyrins and Phthalocyanines, 2010, 14, 1012-1018.	0.8	4
158	1H, 15N and 13C chemical shift assignments of the BA42 protein of the psychrophilic bacteria Bizionia argentinensis sp. nov. Biomolecular NMR Assignments, 2012, 6, 181-183.	0.8	3
159	The allosteric modulation of thyroxine-binding globulin affinity is entropy driven. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 3570-3577.	2.4	3
160	Oculocutaneous albinism type 1B associated with a functionally significant tyrosinase gene polymorphism detected with Whole Exome Sequencing. Ophthalmic Genetics, 2021, 42, 291-295.	1.2	3
161	Reaction of Amines with NO at room temperature and atmospheric pressure: is nitroxyl a reaction intermediate?. Pure and Applied Chemistry, 2020, 92, 2005-2014.	1.9	3
162	MotSASi: Functional short linear motifs (SLiMs) prediction based on genomic single nucleotide variants and structural data. Biochimie, 2022, 197, 59-73.	2.6	3

#	Article	IF	CITATIONS
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