

Marco Nardini

List of Publications by Year in descending order

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105
papers

5,044
citations

101543

36
h-index

98798

67
g-index

107
all docs

107
docs citations

107
times ranked

6188
citing authors

#	ARTICLE	IF	CITATIONS
1	Truncated (2/2) hemoglobin: Unconventional structures and functional roles in vivo and in human pathogenesis. <i>Molecular Aspects of Medicine</i> , 2022, 84, 101049.	6.4	5
2	The coexistence of cold activity and thermal stability in an Antarctic GH42 α -galactosidase relies on its hexameric quaternary arrangement. <i>FEBS Journal</i> , 2021, 288, 546-565.	4.7	31
3	Structural determinants for NF- κ B subunit organization and NF- κ B/DNA association in plants. <i>Plant Journal</i> , 2021, 105, 49-61.	5.7	36
4	Producing natural vanilla extract from green vanilla beans using a β -glucosidase from <i>Alicyclobacillus acidiphilus</i> . <i>Journal of Biotechnology</i> , 2021, 329, 21-28.	3.8	11
5	The activity and stability of a cold-active acylaminoacyl peptidase rely on its dimerization by domain swapping. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 263-274.	7.5	5
6	The USR domain of USF1 mediates NF- κ B interactions and cooperative DNA binding. <i>International Journal of Biological Macromolecules</i> , 2021, 193, 401-413.	7.5	0
7	Structural and Functional Characterization of the Globin-Coupled Sensors of <i>Azotobacter vinelandii</i> and <i>Bordetella pertussis</i> . <i>Antioxidants and Redox Signaling</i> , 2020, 32, 378-395.	5.4	4
8	The structural bases for agonist diversity in an <i>Arabidopsis thaliana</i> glutamate receptor-like channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 752-760.	7.1	70
9	Structural and functional properties of Antarctic fish cytoglobins-1: Cold-reactivity in multi-ligand reactions. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2132-2144.	4.1	10
10	Structural Basis of Inhibition of the Pioneer Transcription Factor NF- κ B by Suramin. <i>Cells</i> , 2020, 9, 2370.	4.1	8
11	Mycobacterial and Human Nitrobindins: Structure and Function. <i>Antioxidants and Redox Signaling</i> , 2020, 33, 229-246.	5.4	17
12	Saturn-Shaped Ice Burst Pattern and Fast Basal Binding of an Ice-Binding Protein from an Antarctic Bacterial Consortium. <i>Langmuir</i> , 2019, 35, 7337-7346.	3.5	12
13	The phosphorylatable Ser320 of NF- κ B is involved in DNA binding of the NF- κ B trimer. <i>FASEB Journal</i> , 2019, 33, 4790-4801.	0.5	4
14	Structure of a bacterial ice binding protein with two faces of interaction with ice. <i>FEBS Journal</i> , 2018, 285, 1653-1666.	4.7	21
15	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	2.6	11
16	Identification of <i>Plasmodium berghei</i> Oocyst Rupture Protein 2 (ORP2) domains involved in sporozoite egress from the oocyst. <i>International Journal for Parasitology</i> , 2018, 48, 1127-1136.	3.1	12
17	Fusicoccin Activates KAT1 Channels by Stabilizing their Interaction with 14-3-3- Proteins. <i>Plant Cell</i> , 2017, 29, tpc.00375.2017.	6.6	34
18	Crystal Structure of the <i>Arabidopsis thaliana</i> L1L/NF-YC3 Histone-fold Dimer Reveals Specificities of the LEC1 Family of NF- κ B Subunits in Plants. <i>Molecular Plant</i> , 2017, 10, 645-648.	8.3	48

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19	Structural determinants for NF-Y/DNA interaction at the CCAAT box. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 571-580.	1.9	47
20	The N-terminal pre- α region of <i>Mycobacterium tuberculosis</i> 2HbN promotes NO-dioxygenase activity. <i>FEBS Journal</i> , 2016, 283, 305-322.	4.7	10
21	Structure-Function Relationships in L-Amino Acid Deaminase, a Flavoprotein Belonging to a Novel Class of Biotechnologically Relevant Enzymes. <i>Journal of Biological Chemistry</i> , 2016, 291, 10457-10475.	3.4	46
22	A bacterial acyl aminoacyl peptidase couples flexibility and stability as a result of cold adaptation. <i>FEBS Journal</i> , 2016, 283, 4310-4324.	4.7	19
23	A redox signalling globin is essential for reproduction in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2015, 6, 8782.	12.8	42
24	Structural flexibility of the heme cavity in the cold-adapted truncated hemoglobin from the Antarctic marine bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>FEBS Journal</i> , 2015, 282, 2948-2965.	4.7	24
25	Structural Biology of Bacterial Haemophores. <i>Advances in Microbial Physiology</i> , 2015, 67, 127-176.	2.4	11
26	Structural Bases for the Regulation of CO Binding in the Archaeal Protoglobin from <i>Methanosarcina acetivorans</i> . <i>PLoS ONE</i> , 2015, 10, e0125959.	2.5	3
27	Sequence- and Structure-Based Immunoreactive Epitope Discovery for <i>Burkholderia pseudomallei</i> Flagellin. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003917.	3.0	40
28	Crystal structure of LptH, the periplasmic component of the lipopolysaccharide transport machinery from <i>Pseudomonas aeruginosa</i> . <i>FEBS Journal</i> , 2015, 282, 1980-1997.	4.7	31
29	Synchrotron Radiation and Bio-crystallography. , 2015, , 615-639.		0
30	Aminoacetone oxidase from <i>Streptococcus oligofermentans</i> belongs to a new three-domain family of bacterial flavoproteins. <i>Biochemical Journal</i> , 2014, 464, 387-399.	3.7	13
31	Crystal structures of two <i>Bacillus</i> carboxylesterases with different enantioselectivities. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 567-575.	2.3	20
32	Interactions of ataxin-3 with its molecular partners in the protein machinery that sorts protein aggregates to the aggresome. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 51, 58-64.	2.8	18
33	Cyclic dinucleotides bind the C-linker of HCN4 to control channel cAMP responsiveness. <i>Nature Chemical Biology</i> , 2014, 10, 457-462.	8.0	50
34	A conserved loop in polynucleotide phosphorylase (PNPase) essential for both RNA and ADP/phosphate binding. <i>Biochimie</i> , 2014, 97, 49-59.	2.6	12
35	Functional and structural roles of the N-terminal extension in <i>Methanosarcina acetivorans</i> protoglobin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1813-1823.	2.3	11
36	The Diversity of 2/2 (Truncated) Globins. <i>Advances in Microbial Physiology</i> , 2013, 63, 49-78.	2.4	38

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37	Protoglobin. <i>Advances in Microbial Physiology</i> , 2013, 63, 79-96.	2.4	25
38	Non-covalent and covalent modifications modulate the reactivity of monomeric mammalian globins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1750-1756.	2.3	27
39	Reductive nitrosylation of <i>Methanosarcina acetivorans</i> protoglobin: A comparative study. <i>Biochemical and Biophysical Research Communications</i> , 2013, 430, 1301-1305.	2.1	16
40	Structural, Kinetic, and Pharmacodynamic Mechanisms of α -Amino Acid Oxidase Inhibition by Small Molecules. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 3710-3724.	6.4	31
41	The H2A/H2B-like histone-fold domain proteins at the crossroad between chromatin and different DNA metabolisms. <i>Transcription</i> , 2013, 4, 114-119.	3.1	23
42	Sequence-Specific Transcription Factor NF-Y Displays Histone-like DNA Binding and H2B-like Ubiquitination. <i>Cell</i> , 2013, 152, 132-143.	28.9	249
43	Characterization of human DAAO variants potentially related to an increased risk of schizophrenia. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2013, 1832, 400-410.	3.8	26
44	One hundred years of X-ray diffraction, 50 years of structural biology. <i>Rendiconti Lincei</i> , 2013, 24, 93-99.	2.2	1
45	Molecular mechanism and functional role of brefeldin A-mediated ADP-ribosylation of CtBP1/BARS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9794-9799.	7.1	37
46	The <i>Escherichia coli</i> Lpt Transenvelope Protein Complex for Lipopolysaccharide Export Is Assembled via Conserved Structurally Homologous Domains. <i>Journal of Bacteriology</i> , 2013, 195, 1100-1108.	2.2	90
47	CO Rebinding Kinetics and Molecular Dynamics Simulations Highlight Dynamic Regulation of Internal Cavities in Human Cytochrome c. <i>PLoS ONE</i> , 2013, 8, e49770.	2.5	28
48	Identification of the Molecular Site of Ivabradine Binding to HCN4 Channels. <i>PLoS ONE</i> , 2013, 8, e53132.	2.5	51
49	Structure and Haem-Distal Site Plasticity in <i>Methanosarcina acetivorans</i> Protoglobin. <i>PLoS ONE</i> , 2013, 8, e66144.	2.5	19
50	High Resolution Crystal Structures of the <i>Cerebratulus lacteus</i> Mini-Hb in the Unligated and Carbomonoxy States. <i>International Journal of Molecular Sciences</i> , 2012, 13, 8025-8037.	4.1	4
51	Determination of Ligand Pathways in Globins. <i>Journal of Biological Chemistry</i> , 2012, 287, 33163-33178.	3.4	34
52	Ligation Tunes Protein Reactivity in an Ancient Haemoglobin: Kinetic Evidence for an Allosteric Mechanism in <i>Methanosarcina acetivorans</i> Protoglobin. <i>PLoS ONE</i> , 2012, 7, e33614.	2.5	13
53	Ligand Migration in <i>Methanosarcina acetivorans</i> Protoglobin: Effects of Ligand Binding and Dimeric Assembly. <i>Journal of Physical Chemistry B</i> , 2011, 115, 13771-13780.	2.6	31
54	Structural heterogeneity and ligand gating in ferric <i>Methanosarcina acetivorans</i> protoglobin mutants. <i>IUBMB Life</i> , 2011, 63, 287-294.	3.4	15

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55	Structural characterization of a group II 2/2 hemoglobin from the plant pathogen <i>Agrobacterium tumefaciens</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 810-816.	2.3	13
56	Ligand Migration in the Apolar Tunnel of <i>Cerebratulus lacteus</i> Mini-Hemoglobin. <i>Journal of Biological Chemistry</i> , 2011, 286, 5347-5358.	3.4	23
57	Tetramerization Dynamics of C-terminal Domain Underlies Isoform-specific cAMP Gating in Hyperpolarization-activated Cyclic Nucleotide-gated Channels. <i>Journal of Biological Chemistry</i> , 2011, 286, 44811-44820.	3.4	101
58	Globin-like proteins in <i>Caenorhabditis elegans</i> : in vivo localization, ligand binding and structural properties. <i>BMC Biochemistry</i> , 2010, 11, 17.	4.4	21
59	Probing the active site of the sugar isomerase domain from <i>E. coli</i> arabinose-5-phosphate isomerase via X-ray crystallography. <i>Protein Science</i> , 2010, 19, 2430-2439.	7.6	19
60	Role of Heme Distortion on Oxygen Affinity in Heme Proteins: The Protoglobin Case. <i>Journal of Physical Chemistry B</i> , 2010, 114, 8536-8543.	2.6	49
61	HisE11 and HisF8 Provide Bis-histidyl Heme Hexa-coordination in the Globin Domain of <i>Geobacter sulfurreducens</i> Globin-coupled Sensor. <i>Journal of Molecular Biology</i> , 2009, 386, 246-260.	4.2	47
62	CtBP1/BARS Gly172 → Glu mutant structure: Impairing NAD(H)-binding and dimerization. <i>Biochemical and Biophysical Research Communications</i> , 2009, 381, 70-74.	2.1	21
63	Hemoprotein time-resolved X-ray crystallography. <i>IUBMB Life</i> , 2008, 60, 154-158.	3.4	7
64	Ferrous <i>Campylobacter jejuni</i> truncated hemoglobin _{FP} displays an extremely high reactivity for cyanide → a comparative study. <i>FEBS Journal</i> , 2008, 275, 633-645.	4.7	24
65	Archaeal protoglobin structure indicates new ligand diffusion paths and modulation of haem reactivity. <i>EMBO Reports</i> , 2008, 9, 157-163.	4.5	43
66	Mapping Heme-Ligand Tunnels in Group I Truncated(2/2) Hemoglobins. <i>Methods in Enzymology</i> , 2008, 436, 303-315.	1.0	17
67	The hemoglobins of the trematodes <i>Fasciola hepatica</i> and <i>Paramphistomum epiclitum</i> : A molecular biological, physicochemical, kinetic, and vaccination study. <i>Protein Science</i> , 2008, 17, 1653-1662.	7.6	11
68	Dissecting the Structural Determinants of the Interaction between the Human Cytomegalovirus UL18 Protein and the CD85j Immune Receptor. <i>Journal of Immunology</i> , 2008, 180, 957-968.	0.8	10
69	The Apolar Channel in <i>Cerebratulus lacteus</i> Hemoglobin Is the Route for O ₂ Entry and Exit. <i>Journal of Biological Chemistry</i> , 2008, 283, 35689-35702.	3.4	31
70	A Crystallographer's Perspective on the 2/2Hb Family. , 2008, , 17-30.		0
71	Protein fold and structure in the truncated (2/2) globin family. <i>Gene</i> , 2007, 398, 2-11.	2.2	66
72	Structural Basis of Phospholipase Activity of <i>Staphylococcus hyicus</i> lipase. <i>Journal of Molecular Biology</i> , 2007, 371, 447-456.	4.2	60

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73	Protein structure in the truncated (2/2) hemoglobin family. <i>IUBMB Life</i> , 2007, 59, 535-541.	3.4	15
74	The C-terminal domain of the transcriptional corepressor CtBP is intrinsically unstructured. <i>Protein Science</i> , 2006, 15, 1042-1050.	7.6	44
75	Structural Determinants in the Group III Truncated Hemoglobin from <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 37803-37812.	3.4	54
76	Role of the C-Terminal Binding Protein PXDLS Motif Binding Cleft in Protein Interactions and Transcriptional Repression. <i>Molecular and Cellular Biology</i> , 2006, 26, 8202-8213.	2.3	53
77	Specific Recognition of ZNF217 and Other Zinc Finger Proteins at a Surface Groove of C-Terminal Binding Proteins. <i>Molecular and Cellular Biology</i> , 2006, 26, 8159-8172.	2.3	74
78	Structural bases for heme binding and diatomic ligand recognition in truncated hemoglobins. <i>Journal of Inorganic Biochemistry</i> , 2005, 99, 97-109.	3.5	117
79	Modulation of oxygen binding to insect hemoglobins: The structure of hemoglobin from the botfly <i>Gasterophilus intestinalis</i> . <i>Protein Science</i> , 2005, 14, 3057-3063.	7.6	15
80	Two distinct heme distal site states define <i>Cerebratulus lacteus</i> mini-hemoglobin oxygen affinity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 641-648.	2.6	21
81	Bishistidyl Heme Hexacoordination, a Key Structural Property in <i>Drosophila melanogaster</i> Hemoglobin. <i>Journal of Biological Chemistry</i> , 2005, 280, 27222-27229.	3.4	48
82	Thr-E11 Regulates O ₂ Affinity in <i>Cerebratulus lacteus</i> Mini-hemoglobin. <i>Journal of Biological Chemistry</i> , 2004, 279, 33662-33672.	3.4	38
83	Structure-Function Relationships in the Growing Hexacoordinate Hemoglobin Subfamily. <i>IUBMB Life</i> , 2004, 56, 643-651.	3.4	41
84	Reversible hexa- to penta- coordination of the heme Fe atom modulates ligand binding properties of neuroglobin and cytoglobin. <i>IUBMB Life</i> , 2004, 56, 657-664.	3.4	47
85	The human brain hexacoordinated neuroglobin three-dimensional structure. <i>Micron</i> , 2004, 35, 63-65.	2.2	30
86	Crystal structure of the glutaredoxin-like protein SH3BGRL3 at 1.6Å... resolution. <i>Biochemical and Biophysical Research Communications</i> , 2004, 318, 470-476.	2.1	14
87	Remarkably similar antigen receptors among a subset of patients with chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , 2004, 113, 1008-1016.	8.2	190
88	Remarkably similar antigen receptors among a subset of patients with chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , 2004, 113, 1008-1016.	8.2	28
89	CtBP/BARS: a dual-function protein involved in transcription co-repression and Golgi membrane fission. <i>EMBO Journal</i> , 2003, 22, 3122-3130.	7.8	144
90	Human Brain Neuroglobin Structure Reveals a Distinct Mode of Controlling Oxygen Affinity. <i>Structure</i> , 2003, 11, 1087-1095.	3.3	286

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91	The 109 Residue Nerve Tissue Minihemoglobin from <i>Cerebratulus lacteus</i> Highlights Striking Structural Plasticity of the $\hat{I}\pm$ -Helical Globin Fold. <i>Structure</i> , 2002, 10, 725-735.	3.3	66
92	Nitrophorins: Lipocalin-based heme proteins transporting nitric oxide. <i>Biochemistry and Molecular Biology Education</i> , 2002, 30, 68-71.	1.2	12
93	Crystallization and preliminary X-ray diffraction analysis of brefeldin A-ADP ribosylated substrate (BARS). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1068-1070.	2.5	10
94	Human neuroglobin: crystals and preliminary X-ray diffraction analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1848-1850.	2.5	13
95	Crystallization and preliminary X-ray analysis of neural haemoglobin from the nemertean worm <i>Cerebratulus lacteus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1897-1899.	2.5	8
96	Structure and mechanism of the epoxide hydrolase from <i>Agrobacterium radiobacter</i> AD1. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2001, 11, 1035-1042.	1.8	23
97	Directed evolution of an enantioselective lipase. <i>Chemistry and Biology</i> , 2000, 7, 709-718.	6.0	231
98	Functional and crystallographic characterization of <i>Salmonella typhimurium</i> Cu,Zn superoxide dismutase coded by the <i>sodCI</i> virulence gene 1. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 302, 465-478.	4.2	47
99	Crystal Structure of <i>Pseudomonas aeruginosa</i> Lipase in the Open Conformation. <i>Journal of Biological Chemistry</i> , 2000, 275, 31219-31225.	3.4	248
100	The X-ray Structure of Epoxide Hydrolase from <i>Agrobacterium radiobacter</i> AD1. <i>Journal of Biological Chemistry</i> , 1999, 274, 14579-14586.	3.4	160
101	$\hat{I}\pm/\hat{I}\pm^2$ Hydrolase fold enzymes: the family keeps growing. <i>Current Opinion in Structural Biology</i> , 1999, 9, 732-737.	5.7	752
102	Mutation of Tyrosine Residues Involved in the Alkylation Half Reaction of Epoxide Hydrolase from <i>Agrobacterium radiobacter</i> AD1 Results in Improved Enantioselectivity. <i>Journal of the American Chemical Society</i> , 1999, 121, 7417-7418.	13.7	65
103	BEAMS (BEAds Modelling System): a set of computer programs for the generation, the visualization and the computation of the hydrodynamic and conformational properties of bead models of proteins. <i>European Biophysics Journal</i> , 1997, 25, 373-384.	2.2	46
104	Human $\hat{I}\pm$ -Thrombin Inhibition by the Active Site Titrant $\hat{N}\hat{I}\pm$ -(N,N-dimethylcarbamoyl)- $\hat{I}\pm$ -azalysine p-nitrophenyl ester: A Comparative Kinetic and X-ray Crystallographic Study. <i>Journal of Molecular Biology</i> , 1996, 258, 851-859.	4.2	17
105	Reptile Heme Protein Structure: X-ray Crystallographic Study of the Aquo-met and Cyano-met Derivatives of the Loggerhead Sea Turtle (<i>Caretta caretta</i>) Myoglobin at 2.0 Å... Resolution. <i>Journal of Molecular Biology</i> , 1995, 247, 459-465.	4.2	26