

Mario Milani

List of Publications by Year in descending order

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94
papers

3,516
citations

117453

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docs citations

99
times ranked

3822
citing authors

#	ARTICLE	IF	CITATIONS
1	Virucidal Activity of the Pyridobenzothiazolone Derivative HeE1-17Y against Enveloped RNA Viruses. <i>Viruses</i> , 2022, 14, 1157.	1.5	4
2	Combined in silico and in vitro approaches identified the antipsychotic drug lurasidone and the antiviral drug elbasvir as SARS-CoV2 and HCoV-OC43 inhibitors. <i>Antiviral Research</i> , 2021, 189, 105055.	1.9	26
3	Synthesis and Characterization of Novel Mono- and Bis-Guanyl Hydrazones as Potent and Selective ASIC1 Inhibitors Able to Reduce Brain Ischemic Insult. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 8333-8353.	2.9	3
4	Structure-based identification of a new IAP-targeting compound that induces cancer cell death inducing NF- κ B pathway. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6366-6374.	1.9	7
5	A novel hotspot of gelsolin instability triggers an alternative mechanism of amyloid aggregation. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6355-6365.	1.9	2
6	The structure of N184K amyloidogenic variant of gelsolin highlights the role of the H-bond network for protein stability and aggregation properties. <i>European Biophysics Journal</i> , 2020, 49, 11-19.	1.2	4
7	Retromer stabilization results in neuroprotection in a model of Amyotrophic Lateral Sclerosis. <i>Nature Communications</i> , 2020, 11, 3848.	5.8	44
8	Computational and Experimental Characterization of NF023, A Candidate Anticancer Compound Inhibiting cIAP2/TRAF2 Assembly. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5036-5044.	2.5	3
9	Modulation of Guanylate Cyclase Activating Protein 1 (GCAP1) Dimeric Assembly by Ca ²⁺ or Mg ²⁺ : Hints to Understand Protein Activity. <i>Biomolecules</i> , 2020, 10, 1408.	1.8	11
10	Missense mutations affecting Ca ²⁺ -coordination in GCAP1 lead to cone-rod dystrophies by altering protein structural and functional properties. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020, 1867, 118794.	1.9	7
11	An alternative non-proteolytic mechanism may underlie AGel amyloidosis. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2019, 26, 150-151.	1.4	1
12	High-resolution crystal structure of gelsolin domain 2 in complex with the physiological calcium ion. <i>Biochemical and Biophysical Research Communications</i> , 2019, 518, 94-99.	1.0	5
13	Structure-Activity Relationship of NF023 Derivatives Binding to XIAP-BIR1. <i>ChemistryOpen</i> , 2019, 8, 476-482.	0.9	6
14	Broad spectrum anti-flavivirus pyridobenzothiazolones leading to less infective virions. <i>Antiviral Research</i> , 2019, 167, 6-12.	1.9	24
15	Targeting the BIR Domains of Inhibitor of Apoptosis (IAP) Proteins in Cancer Treatment. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 142-150.	1.9	65
16	Structural and functional characterization of TgpA, a critical protein for the viability of <i>Pseudomonas aeruginosa</i> . <i>Journal of Structural Biology</i> , 2019, 205, 18-25.	1.3	1
17	Nanobody interaction unveils structure, dynamics and proteotoxicity of the Finnish-type amyloidogenic gelsolin variant. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 648-660.	1.8	21
18	Gelsolin pathogenic Gly167Arg mutation promotes domain-swap dimerization of the protein. <i>Human Molecular Genetics</i> , 2018, 27, 53-65.	1.4	16

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19	Glycine Amidinotransferase (GATM), Renal Fanconi Syndrome, and Kidney Failure. Journal of the American Society of Nephrology: JASN, 2018, 29, 1849-1858.	3.0	53
20	A stereospecific carboxyl esterase from <i>Bacillus coagulans</i> hosting nonlipase activity within a lipase-like fold. FEBS Journal, 2018, 285, 903-914.	2.2	10
21	Identification of a Small Molecule That Compromises the Structural Integrity of Viroplasm and Rotavirus Double-Layered Particles. Journal of Virology, 2018, 92, .	1.5	20
22	Functionalized 2,1-benzothiazine 2,2-dioxides as new inhibitors of Dengue NS5 RNA-dependent RNA polymerase. European Journal of Medicinal Chemistry, 2018, 143, 1667-1676.	2.6	24
23	Structure-based design and molecular profiling of Smac-mimetics selective for cellular XIAPs. FEBS Journal, 2018, 285, 3286-3298.	2.2	10
24	Role and inhibition of GLI1 protein in cancer. Lung Cancer: Targets and Therapy, 2018, Volume 9, 35-43.	1.3	29
25	Structural bases of the altered catalytic properties of a pathogenic variant of apoptosis inducing factor. Biochemical and Biophysical Research Communications, 2017, 490, 1011-1017.	1.0	9
26	Targeting flavivirus RNA dependent RNA polymerase through a pyridobenzothiazole inhibitor. Antiviral Research, 2016, 134, 226-235.	1.9	49
27	Molecular basis of a novel renal amyloidosis due to N184K gelsolin variant. Scientific Reports, 2016, 6, 33463.	1.6	12
28	Crystal structure of YeaZ from Pseudomonas aeruginosa. Biochemical and Biophysical Research Communications, 2016, 470, 460-465.	1.0	9
29	The Activator of Apoptosis Smac-DIABLO Acts as a Tetramer in Solution. Biophysical Journal, 2015, 108, 714-723.	0.2	12
30	NF023 binding to XIAP-BIR1: Searching drugs for regulation of the NF- κ B pathway. Proteins: Structure, Function and Bioinformatics, 2015, 83, 612-620.	1.5	6
31	Structural Bases of Norovirus RNA Dependent RNA Polymerase Inhibition by Novel Suramin-Related Compounds. PLoS ONE, 2014, 9, e91765.	1.1	53
32	Naphthalene-sulfonate inhibitors of human norovirus RNA-dependent RNA-polymerase. Antiviral Research, 2014, 102, 23-28.	1.9	39
33	Delivery of Suramin as an Antiviral Agent through Liposomal Systems. ChemMedChem, 2014, 9, 933-939.	1.6	28
34	PPNDS inhibits murine Norovirus RNA-dependent RNA-polymerase mimicking two RNA stacking bases. FEBS Letters, 2014, 588, 1720-1725.	1.3	21
35	Evidence for self-association of the alternative sigma factor σ^{54} . FEBS Journal, 2013, 280, 1371-1378.	2.2	0
36	Is Renalase a Novel Player in Catecholaminergic Signaling? The Mystery of the Catalytic Activity of an Intriguing New Flavoenzyme. Current Pharmaceutical Design, 2013, 19, 2540-2551.	0.9	26

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37	Structure-Based Inhibition of Norovirus RNA-Dependent RNA Polymerases. <i>Journal of Molecular Biology</i> , 2012, 419, 198-210.	2.0	86
38	Flaviviral helicase: Insights into the mechanism of action of a motor protein. <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 84-87.	1.0	19
39	Dimeric Smac mimetics/IAP inhibitors as in vivo-active pro-apoptotic agents. Part II: Structural and biological characterization. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 6709-6723.	1.4	29
40	Structure Based Inhibition of the Calicivirus RNA-Dependent RNA-Polymerase. <i>Biophysical Journal</i> , 2012, 102, 462a.	0.2	0
41	Structural Insight into Inhibitor of Apoptosis Proteins Recognition by a Potent Divalent Smac-Mimetic. <i>PLoS ONE</i> , 2012, 7, e49527.	1.1	13
42	Ivermectin is a potent inhibitor of flavivirus replication specifically targeting NS3 helicase activity: new prospects for an old drug. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 1884-1894.	1.3	329
43	FAD-Binding Site and NADP Reactivity in Human Renalase: A New Enzyme Involved in Blood Pressure Regulation. <i>Journal of Molecular Biology</i> , 2011, 411, 463-473.	2.0	67
44	Structure and functionality in flavivirus NS-proteins: Perspectives for drug design. <i>Antiviral Research</i> , 2010, 87, 125-148.	1.9	289
45	Recognition of Smac-mimetic compounds by the BIR domain of cIAP1. <i>Protein Science</i> , 2010, 19, 2418-2429.	3.1	25
46	Crystal Structure of a Novel Conformational State of the Flavivirus NS3 Protein: Implications for Polyprotein Processing and Viral Replication. <i>Journal of Virology</i> , 2009, 83, 12895-12906.	1.5	115
47	Flaviviral methyltransferase/RNA interaction: Structural basis for enzyme inhibition. <i>Antiviral Research</i> , 2009, 83, 28-34.	1.9	64
48	Rational design, synthesis and characterization of potent, non-peptidic Smac mimics/XIAP inhibitors as proapoptotic agents for cancer therapy. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 5834-5856.	1.4	36
49	Plasmodium falciparum Ferredoxin-NADP+ Reductase His286 Plays a Dual Role in NADP(H) Binding and Catalysis. <i>Biochemistry</i> , 2009, 48, 9525-9533.	1.2	11
50	Designing Smac-mimetics as antagonists of XIAP, cIAP1, and cIAP2. <i>Biochemical and Biophysical Research Communications</i> , 2009, 378, 162-167.	1.0	50
51	Crystal structure of a methyltransferase from a no-known-vector Flavivirus. <i>Biochemical and Biophysical Research Communications</i> , 2009, 382, 200-204.	1.0	14
52	Recognition of RNA Cap in the Wesselsbron Virus NS5 Methyltransferase Domain: Implications for RNA-Capping Mechanisms in Flavivirus. <i>Journal of Molecular Biology</i> , 2009, 385, 140-152.	2.0	78
53	Structural Basis for Bivalent Smac-Mimetics Recognition in the IAP Protein Family. <i>Journal of Molecular Biology</i> , 2009, 392, 630-644.	2.0	40
54	Structural determinants of ligand migration in <i>Mycobacterium tuberculosis</i> truncated hemoglobin O. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 372-379.	1.5	47

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55	Hemoprotein time-resolved X-ray crystallography. IUBMB Life, 2008, 60, 154-158.	1.5	7
56	Mapping Heme-Ligand Tunnels in Group I Truncated(2/2) Hemoglobins. Methods in Enzymology, 2008, 436, 303-315.	0.4	17
57	Targeting the X-Linked Inhibitor of Apoptosis Protein through 4-Substituted Azabicyclo[5.3.0]alkane Smac Mimetics. Structure, Activity, and Recognition Principles. Journal of Molecular Biology, 2008, 384, 673-689.	2.0	40
58	Ligand Binding to Truncated Hemoglobin N from Mycobacterium tuberculosis Is Strongly Modulated by the Interplay between the Distal Heme Pocket Residues and Internal Water. Journal of Biological Chemistry, 2008, 283, 27270-27278.	1.6	29
59	A Crystallographer's Perspective on the 2/2Hb Family. , 2008, , 17-30.		0
60	Mycobacterial truncated hemoglobins: From genes to functions. Gene, 2007, 398, 42-51.	1.0	51
61	Protein fold and structure in the truncated (2/2) globin family. Gene, 2007, 398, 2-11.	1.0	66
62	Ferredoxin-NADP+ Reductase from Plasmodium falciparum Undergoes NADP+-dependent Dimerization and Inactivation: Functional and Crystallographic Analysis. Journal of Molecular Biology, 2007, 367, 501-513.	2.0	40
63	Crystal Structure and Activity of Kunjin Virus NS3 Helicase; Protease and Helicase Domain Assembly in the Full Length NS3 Protein. Journal of Molecular Biology, 2007, 372, 444-455.	2.0	78
64	The Roles of Tyr(CD1) and Trp(G8) in Mycobacterium tuberculosis Truncated Hemoglobin O in Ligand Binding and on the Heme Distal Site Architecture,. Biochemistry, 2007, 46, 11440-11450.	1.2	38
65	Structural bases for substrate recognition and activity in Meaban virus nucleoside-2'-O-methyltransferase. Protein Science, 2007, 16, 1133-1145.	3.1	39
66	Protein structure in the truncated (2/2) hemoglobin family. IUBMB Life, 2007, 59, 535-541.	1.5	15
67	Structure and activity of Kunjin virus NS3 helicase domain. Acta Crystallographica Section A: Foundations and Advances, 2007, 63, s290-s290.	0.3	0
68	Ligand Interactions in the Distal Heme Pocket of Mycobacterium tuberculosis Truncated Hemoglobin N: Roles of TyrB10 and GlnE11 Residues. Biochemistry, 2006, 45, 8770-8781.	1.2	45
69	Nitric oxide scavenging by Mycobacterium leprae GbO involves the formation of the ferric heme-bound peroxynitrite intermediate. Biochemical and Biophysical Research Communications, 2006, 339, 450-456.	1.0	33
70	Peroxynitrite scavenging by ferrous truncated hemoglobin GbO from Mycobacterium leprae. Biochemical and Biophysical Research Communications, 2006, 351, 528-533.	1.0	21
71	Preliminary characterization of (nucleoside-2'-O-)methyltransferase crystals from Meaban and Yokose flaviviruses. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 768-770.	0.7	5
72	Preliminary crystallographic characterization of an RNA helicase from Kunjin virus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 876-879.	0.7	5

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73	Ligand-induced dynamical regulation of NO conversion in Mycobacterium tuberculosis truncated hemoglobin-N. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 457-464.	1.5	95
74	Structural bases for heme binding and diatomic ligand recognition in truncated hemoglobins. <i>Journal of Inorganic Biochemistry</i> , 2005, 99, 97-109.	1.5	117
75	An Active-like Structure in the Unphosphorylated StyR Response Regulator Suggests a Phosphorylation-Dependent Allosteric Activation Mechanism. <i>Structure</i> , 2005, 13, 1289-1297.	1.6	46
76	Heme-Ligand Tunneling in Group I Truncated Hemoglobins. <i>Journal of Biological Chemistry</i> , 2004, 279, 21520-21525.	1.6	117
77	Viscosity-dependent Relaxation Significantly Modulates the Kinetics of CO Recombination in the Truncated Hemoglobin TrHbN from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , 2004, 279, 38844-38853.	1.6	18
78	CO Sniffing through Heme-based Sensor Proteins. <i>IUBMB Life</i> , 2004, 56, 309-315.	1.5	18
79	Truncated Hemoglobins and Nitric Oxide Action. <i>IUBMB Life</i> , 2004, 55, 623-627.	1.5	38
80	Cyanide Binding to Truncated Hemoglobins: A Crystallographic and Kinetic Study. <i>Biochemistry</i> , 2004, 43, 5213-5221.	1.2	65
81	Substrate channeling: Molecular bases. <i>Biochemistry and Molecular Biology Education</i> , 2003, 31, 228-233.	0.5	26
82	A TyrCD1/TrpG8 hydrogen bond network and a TyrB10-TyrCD1 covalent link shape the heme distal site of Mycobacterium tuberculosis hemoglobin O. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5766-5771.	3.3	111
83	The truncated hemoglobin from Mycobacterium leprae. <i>Biochemical and Biophysical Research Communications</i> , 2002, 294, 1064-1070.	1.0	40
84	Structural plasticity in the eight-helix fold of a trematode haemoglobin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 719-722.	2.5	3
85	Nitric Oxide and Mycobacterium leprae Pathogenicity. <i>IUBMB Life</i> , 2002, 54, 95-99.	1.5	26
86	Single mutations at the subunit interface modulate copper reactivity in Photobacterium leiognathi Cu,Zn superoxide dismutase. <i>Journal of Molecular Biology</i> , 2001, 308, 555-563.	2.0	19
87	Very high resolution structure of a trematode hemoglobin displaying a TyrB10-TyrE7 heme distal residue pair and high oxygen affinity. <i>Journal of Molecular Biology</i> , 2001, 309, 1153-1164.	2.0	44
88	Single mutations at the subunit interface modulate copper reactivity in photobacterium leiognathi Cu, Zn superoxide dismutase. <i>Journal of Molecular Biology</i> , 2001, 309, 1003.	2.0	0
89	The 1.6 Å resolution crystal structure of a mutant plastocyanin bearing a 21 engineered disulfide bridge. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1735-1738.	2.5	12
90	Mycobacterium tuberculosis hemoglobin N displays a protein tunnel suited for O ₂ diffusion to the heme. <i>EMBO Journal</i> , 2001, 20, 3902-3909.	3.5	198

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91	Truncated hemoglobins: trimming the classical 'three-over-three' globin fold to a minimal size. <i>Biochemistry and Molecular Biology Education</i> , 2001, 29, 123-125.	0.5	0
92	Truncated hemoglobins: trimming the classical 'three-over-three' globin fold to a minimal size. <i>Biochemistry and Molecular Biology Education</i> , 2001, 29, 123-125.	0.5	1
93	Scattering mechanism of electrons interacting with surfaces in specular reflection geometry: Graphite. <i>Physical Review B</i> , 1999, 59, 13359-13364.	1.1	19
94	On the scattering mechanism of the electron impact on surfaces in specular reflection geometry : Nickel (110). <i>European Physical Journal Special Topics</i> , 1999, 09, Pr6-149-Pr6-152.	0.2	0