

# Mario Milani

## List of Publications by Year in descending order

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94  
papers

3,516  
citations

117625

34  
h-index

149698

56  
g-index

99  
all docs

99  
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.	3.3	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.	4.1	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.	6.4	3
4	Structure-based identification of a new IAP-targeting compound that induces cancer cell death inducing NF- $\kappa$ B pathway. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6366-6374.	4.1	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.	4.1	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.	2.2	4
7	Retromer stabilization results in neuroprotection in a model of Amyotrophic Lateral Sclerosis. <i>Nature Communications</i> , 2020, 11, 3848.	12.8	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.	5.4	3
9	Modulation of Guanylate Cyclase Activating Protein 1 (GCAP1) Dimeric Assembly by Ca <sup>2+</sup> or Mg <sup>2+</sup> : Hints to Understand Protein Activity. <i>Biomolecules</i> , 2020, 10, 1408.	4.0	11
10	Missense mutations affecting Ca <sup>2+</sup> -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.	4.1	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.	3.0	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.	2.1	5
13	Structure-Activity Relationship of NF023 Derivatives Binding to XIAP-BIR1. <i>ChemistryOpen</i> , 2019, 8, 476-482.	1.9	6
14	Broad spectrum anti-flavivirus pyridobenzothiazolones leading to less infective virions. <i>Antiviral Research</i> , 2019, 167, 6-12.	4.1	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.	4.1	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.	2.8	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.	3.8	21
18	Gelsolin pathogenic Gly167Arg mutation promotes domain-swap dimerization of the protein. <i>Human Molecular Genetics</i> , 2018, 27, 53-65.	2.9	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.	6.1	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.	4.7	10
21	Identification of a Small Molecule That Compromises the Structural Integrity of Viroplasm and Rotavirus Double-Layered Particles. Journal of Virology, 2018, 92, .	3.4	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.	5.5	24
23	Structure-based design and molecular profiling of Smac-mimetics selective for cellular XIAPs. FEBS Journal, 2018, 285, 3286-3298.	4.7	10
24	Role and inhibition of GLI1 protein in cancer. Lung Cancer: Targets and Therapy, 2018, Volume 9, 35-43.	2.7	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.	2.1	9
26	Targeting flavivirus RNA dependent RNA polymerase through a pyridobenzothiazole inhibitor. Antiviral Research, 2016, 134, 226-235.	4.1	49
27	Molecular basis of a novel renal amyloidosis due to N184K gelsolin variant. Scientific Reports, 2016, 6, 33463.	3.3	12
28	Crystal structure of YeaZ from <i>Pseudomonas aeruginosa</i> . Biochemical and Biophysical Research Communications, 2016, 470, 460-465.	2.1	9
29	The Activator of Apoptosis Smac-DIABLO Acts as a Tetramer in Solution. Biophysical Journal, 2015, 108, 714-723.	0.5	12
30	NF023 binding to XIAP-BIR1: Searching drugs for regulation of the NF- $\kappa$ B pathway. Proteins: Structure, Function and Bioinformatics, 2015, 83, 612-620.	2.6	6
31	Structural Bases of Norovirus RNA Dependent RNA Polymerase Inhibition by Novel Suramin-Related Compounds. PLoS ONE, 2014, 9, e91765.	2.5	53
32	Naphthalene-sulfonate inhibitors of human norovirus RNA-dependent RNA-polymerase. Antiviral Research, 2014, 102, 23-28.	4.1	39
33	Delivery of Suramin as an Antiviral Agent through Liposomal Systems. ChemMedChem, 2014, 9, 933-939.	3.2	28
34	PPNDS inhibits murine Norovirus RNA-dependent RNA-polymerase mimicking two RNA stacking bases. FEBS Letters, 2014, 588, 1720-1725.	2.8	21
35	Evidence for self-association of the alternative sigma factor $\sigma^{54}$ . FEBS Journal, 2013, 280, 1371-1378.	4.7	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.	1.9	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.	4.2	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.	2.1	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.	3.0	29
40	Structure Based Inhibition of the Calicivirus RNA-Dependent RNA-Polymerase. <i>Biophysical Journal</i> , 2012, 102, 462a.	0.5	0
41	Structural Insight into Inhibitor of Apoptosis Proteins Recognition by a Potent Divalent Smac-Mimetic. <i>PLoS ONE</i> , 2012, 7, e49527.	2.5	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.	3.0	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.	4.2	67
44	Structure and functionality in flavivirus NS-proteins: Perspectives for drug design. <i>Antiviral Research</i> , 2010, 87, 125-148.	4.1	289
45	Recognition of Smac-mimetic compounds by the BIR domain of cIAP1. <i>Protein Science</i> , 2010, 19, 2418-2429.	7.6	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.	3.4	115
47	Flaviviral methyltransferase/RNA interaction: Structural basis for enzyme inhibition. <i>Antiviral Research</i> , 2009, 83, 28-34.	4.1	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.	3.0	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.	2.5	11
50	Designing Smac-mimetics as antagonists of XIAP, cIAP1, and cIAP2. <i>Biochemical and Biophysical Research Communications</i> , 2009, 378, 162-167.	2.1	50
51	Crystal structure of a methyltransferase from a no-known-vector Flavivirus. <i>Biochemical and Biophysical Research Communications</i> , 2009, 382, 200-204.	2.1	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.	4.2	78
53	Structural Basis for Bivalent Smac-Mimetics Recognition in the IAP Protein Family. <i>Journal of Molecular Biology</i> , 2009, 392, 630-644.	4.2	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.	2.6	47

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55	Hemoprotein time-resolved X-ray crystallography. IUBMB Life, 2008, 60, 154-158.	3.4	7
56	Mapping Heme-Ligand Tunnels in Group I Truncated(2/2) Hemoglobins. Methods in Enzymology, 2008, 436, 303-315.	1.0	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.	4.2	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.	3.4	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.	2.2	51
61	Protein fold and structure in the truncated (2/2) globin family. Gene, 2007, 398, 2-11.	2.2	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.	4.2	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.	4.2	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.	2.5	38
65	Structural bases for substrate recognition and activity in Meaban virus nucleoside-2'-O-methyltransferase. Protein Science, 2007, 16, 1133-1145.	7.6	39
66	Protein structure in the truncated (2/2) hemoglobin family. IUBMB Life, 2007, 59, 535-541.	3.4	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.	2.5	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.	2.1	33
70	Peroxynitrite scavenging by ferrous truncated hemoglobin GbO from Mycobacterium leprae. Biochemical and Biophysical Research Communications, 2006, 351, 528-533.	2.1	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.	2.6	95
74	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
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.	3.3	46
76	Heme-Ligand Tunneling in Group I Truncated Hemoglobins. <i>Journal of Biological Chemistry</i> , 2004, 279, 21520-21525.	3.4	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.	3.4	18
78	CO Sniffing through Heme-based Sensor Proteins. <i>IUBMB Life</i> , 2004, 56, 309-315.	3.4	18
79	Truncated Hemoglobins and Nitric Oxide Action. <i>IUBMB Life</i> , 2004, 55, 623-627.	3.4	38
80	Cyanide Binding to Truncated Hemoglobins: A Crystallographic and Kinetic Study. <i>Biochemistry</i> , 2004, 43, 5213-5221.	2.5	65
81	Substrate channeling: Molecular bases. <i>Biochemistry and Molecular Biology Education</i> , 2003, 31, 228-233.	1.2	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.	7.1	111
83	The truncated hemoglobin from Mycobacterium leprae. <i>Biochemical and Biophysical Research Communications</i> , 2002, 294, 1064-1070.	2.1	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.	3.4	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.	4.2	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.	4.2	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.	4.2	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 O2 diffusion to the heme. <i>EMBO Journal</i> , 2001, 20, 3902-3909.	7.8	198

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91	Truncated hemoglobins: trimming the classical 'three-over-three' globin fold to a minimal size. Biochemistry and Molecular Biology Education, 2001, 29, 123-125.	1.2	0
92	Truncated hemoglobins: trimming the classical 'three-over-three' globin fold to a minimal size. Biochemistry and Molecular Biology Education, 2001, 29, 123-125.	1.2	1
93	Scattering mechanism of electrons interacting with surfaces in specular reflection geometry: Graphite. Physical Review B, 1999, 59, 13359-13364.	3.2	19
94	On the scattering mechanism of the electron impact on surfaces in specular reflection geometry : Nickel (110). European Physical Journal Special Topics, 1999, 09, Pr6-149-Pr6-152.	0.2	0