Marco Bellinzoni

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Mycobacterial Ser/Thr protein kinases and phosphatases: Physiological roles and therapeutic potential. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 193-202.	2.3	153
2	Rv2686c-Rv2687c-Rv2688c, an ABC Fluoroquinolone Efflux Pump in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2004, 48, 3175-3178.	3.2	148
3	Regulation of glutamate metabolism by protein kinases in mycobacteria. Molecular Microbiology, 2008, 70, 1408-1423.	2.5	147
4	The Multidrug Transporters Belonging to Major Facilitator Superfamily (MFS) in Mycobacterium tuberculosis. Molecular Medicine, 2002, 8, 714-724.	4.4	111
5	The structure of PknB in complex with mitoxantrone, an ATP-competitive inhibitor, suggests a mode of protein kinase regulation in mycobacteria. FEBS Letters, 2006, 580, 3018-3022.	2.8	100
6	The TB structural genomics consortium: a resource for Mycobacterium tuberculosis biology. Tuberculosis, 2003, 83, 223-249.	1.9	95
7	Conserved autophosphorylation pattern in activation loops and juxtamembrane regions of Mycobacterium tuberculosis Ser/Thr protein kinases. Biochemical and Biophysical Research Communications, 2005, 333, 858-867.	2.1	83
8	PknG senses amino acid availability to control metabolism and virulence of Mycobacterium tuberculosis. PLoS Pathogens, 2017, 13, e1006399.	4.7	81
9	Functional Plasticity and Allosteric Regulation of α-Ketoglutarate Decarboxylase in Central Mycobacterial Metabolism. Chemistry and Biology, 2011, 18, 1011-1020.	6.0	75
10	Thiophenecarboxamide Derivatives Activated by EthA Kill Mycobacterium tuberculosis by Inhibiting the CTP Synthetase PyrG. Chemistry and Biology, 2015, 22, 917-927.	6.0	72
11	Structural and Binding Studies of the Three-metal Center in Two Mycobacterial PPM Ser/Thr Protein Phosphatases. Journal of Molecular Biology, 2007, 374, 890-898.	4.2	66
12	Biological and structural characterization of the Mycobacterium smegmatis nitroreductase NfnB, and its role in benzothiazinone resistance. Molecular Microbiology, 2010, 77, 1172-1185.	2.5	63
13	<scp>GarA</scp> is an essential regulator of metabolism in <i><scp>M</scp>ycobacterium tuberculosis</i> . Molecular Microbiology, 2013, 90, 356-366.	2.5	59
14	The multidrug transporters belonging to major facilitator superfamily in Mycobacterium tuberculosis. Molecular Medicine, 2002, 8, 714-24.	4.4	56
15	CNTN6 mutations are risk factors for abnormal auditory sensory perception in autism spectrum disorders. Molecular Psychiatry, 2017, 22, 625-633.	7.9	55
16	Insights into the Catalytic Mechanism of PPM Ser/Thr Phosphatases from the Atomic Resolution Structures of a Mycobacterial Enzyme. Structure, 2007, 15, 863-872.	3.3	46
17	Secondary structure reshuffling modulates glycosyltransferase function at the membrane. Nature Chemical Biology, 2015, 11, 16-18.	8.0	44
18	Tolerance of the archaeal Sac7d scaffold protein to alternative library designs: characterization of anti-immunoglobulin G Affitins. Protein Engineering, Design and Selection, 2013, 26, 267-275.	2.1	38

MARCO BELLINZONI

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19	Contactin 4, -5 and -6 differentially regulate neuritogenesis while they display identical PTPRG binding sites. Biology Open, 2013, 2, 324-334.	1.2	38
20	The crystal structure ofMycobacterium tuberculosisadenylate kinase in complex with two molecules of ADP and Mg2+supports an associative mechanism for phosphoryl transfer. Protein Science, 2006, 15, 1489-1493.	7.6	36
21	Structural Plasticity and Distinct Drug-Binding Modes of LfrR, a Mycobacterial Efflux Pump Regulator. Journal of Bacteriology, 2009, 191, 7531-7537.	2.2	34
22	New substrates and interactors of the mycobacterial Serine/Threonine protein kinase PknG identified by a tailored interactomic approach. Journal of Proteomics, 2019, 192, 321-333.	2.4	30
23	A Novel Role of Malonyl-ACP in Lipid Homeostasis,. Biochemistry, 2010, 49, 3161-3167.	2.5	28
24	A dual conformation of the post-decarboxylation intermediate is associated with distinct enzyme states in mycobacterial KGD (α-ketoglutarate decarboxylase). Biochemical Journal, 2014, 457, 425-434.	3.7	27
25	Transmission of SEN virus from mothers to their babies. Journal of Medical Virology, 2002, 66, 421-427.	5.0	26
26	New insight into structure-activity of furan-based salicylate synthase (Mbtl) inhibitors as potential antitubercular agents. Journal of Enzyme Inhibition and Medicinal Chemistry, 2019, 34, 823-828.	5.2	25
27	Structural insights into the functional versatility of an FHA domain protein in mycobacterial signaling. Science Signaling, 2019, 12, .	3.6	22
28	Shedding X-ray Light on the Role of Magnesium in the Activity of <i>Mycobacterium tuberculosis</i> Salicylate Synthase (Mbtl) for Drug Design. Journal of Medicinal Chemistry, 2020, 63, 7066-7080.	6.4	21
29	3-Keto-5-aminohexanoate Cleavage Enzyme. Journal of Biological Chemistry, 2011, 286, 27399-27405.	3.4	20
30	Conformational changes upon ligand binding in the essential class II fumarase Rv1098c from <i>Mycobacterium tuberculosis</i> . FEBS Letters, 2012, 586, 1606-1611.	2.8	20
31	Heterologous expression, purification, and enzymatic activity of Mycobacterium tuberculosis NAD+ synthetase. Protein Expression and Purification, 2002, 25, 547-557.	1.3	18
32	Glutamine amidotransferase activity of NAD+ synthetase from Mycobacterium tuberculosis depends on an amino-terminal nitrilase domain. Research in Microbiology, 2005, 156, 173-177.	2.1	17
33	Novel mechanistic insights into physiological signaling pathways mediated by mycobacterial Ser/Thr protein kinases. Genes and Immunity, 2019, 20, 383-393.	4.1	16
34	High prevalence of a variant of SENV in intravenous drug user HIVâ€infected patients. Journal of Medical Virology, 2002, 68, 18-23.	5.0	15
35	Ser/Thr Phosphorylation Regulates the Fatty Acyl-AMP Ligase Activity of FadD32, an Essential Enzyme in Mycolic Acid Biosynthesis. Journal of Biological Chemistry, 2016, 291, 22793-22805.	3.4	14
36	Techniques and Applications: The heterologous expression of Mycobacterium tuberculosis genes is an uphill road. Trends in Microbiology, 2003, 11, 351-358.	7.7	12

MARCO BELLINZONI

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37	The crystal structure of the catalytic domain of the ser/thr kinase PknA from <i>M. tuberculosis</i> shows an Src-like autoinhibited conformation. Proteins: Structure, Function and Bioinformatics, 2015, 83, 982-988.	2.6	11
38	Conformational transitions in the active site of mycobacterial 2-oxoglutarate dehydrogenase upon binding phosphonate analogues of 2-oxoglutarate: From a Michaelis-like complex to ThDP adducts. Journal of Structural Biology, 2019, 208, 182-190.	2.8	11
39	Actinobacteria challenge the paradigm: A unique protein architecture for a well-known, central metabolic complex. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	10
40	Structural studies suggest a peptidoglycan hydrolase function for the Mycobacterium tuberculosis Tat-secreted protein Rv2525c. Journal of Structural Biology, 2014, 188, 156-164.	2.8	9
41	Structure-Based Drug Design for Tuberculosis: Challenges Still Ahead. Applied Sciences (Switzerland), 2020, 10, 4248.	2.5	9
42	Selective Inhibition of 2-Oxoglutarate and 2-Oxoadipate Dehydrogenases by the Phosphonate Analogs of Their 2-Oxo Acid Substrates. Frontiers in Chemistry, 2020, 8, 596187.	3.6	8
43	Structure ofMycobacterium tuberculosisRv2714, a representative of a duplicated gene family in Actinobacteria. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 972-977.	0.7	6
44	Novel mechanistic insights into physiological signaling pathways mediated by mycobacterial Ser/Thr protein kinases. Microbes and Infection, 2019, 21, 222-229.	1.9	6
45	Proteome remodeling in the Mycobacterium tuberculosis PknG knockout: Molecular evidence for the role of this kinase in cell envelope biogenesis and hypoxia response. Journal of Proteomics, 2021, 244, 104276.	2.4	6
46	The crystal structure of PknI from <i>Mycobacterium tuberculosis</i> shows an inactive, pseudokinaseâ€like conformation. FEBS Journal, 2017, 284, 602-614.	4.7	4
47	Crystal structure of <i>Mycobacterium tuberculosis</i> LppA, a lipoprotein confined to pathogenic mycobacteria. Proteins: Structure, Function and Bioinformatics, 2010, 78, 769-772.	2.6	2
48	A Tetratricopeptide Repeat Scaffold Couples Signal Detection to Odhl Phosphorylation in Metabolic Control by the Protein Kinase PknG. MBio, 2021, 12, e0171721.	4.1	2
49	Bacterial Metabolism under FHA Control. Structure, 2009, 17, 487-488.	3.3	1

50 Energy Metabolism | 2-Oxoglutarate Dehydrogenase Complex., 2021, , 259-271.

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