

Alberto Marina

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

3,227
citations

186265

28
h-index

161849

54
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72
all docs

72
docs citations

72
times ranked

3673
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the mechanism of action of the arbitrium communication system in SPbeta phages. <i>Nature Communications</i> , 2022, 13, .	12.8	6
2	The structural role of SARS-CoV-2 genetic background in the emergence and success of spike mutations: The case of the spike A222V mutation. <i>PLoS Pathogens</i> , 2022, 18, e1010631.	4.7	11
3	Structure-based analyses of Salmonella RcsB variants unravel new features of the Rcs regulon. <i>Nucleic Acids Research</i> , 2021, 49, 2357-2374.	14.5	10
4	Molecular Basis of Lysis—Lysogeny Decisions in Gram-Positive Phages. <i>Annual Review of Microbiology</i> , 2021, 75, 563-581.	7.3	31
5	The arbitrium system controls prophage induction. <i>Current Biology</i> , 2021, 31, 5037-5045.e3.	3.9	22
6	A regulatory cascade controls <i>Staphylococcus aureus</i> pathogenicity island activation. <i>Nature Microbiology</i> , 2021, 6, 1300-1308.	13.3	20
7	Evolutionary and Phenotypic Characterization of Two Spike Mutations in European Lineage 20E of SARS-CoV-2. <i>MBio</i> , 2021, 12, e0231521.	4.1	6
8	SARS-CoV-2 antibodies, serum inflammatory biomarkers and clinical severity of hospitalized COVID-19 patients. <i>Journal of Clinical Virology</i> , 2020, 131, 104611.	3.1	61
9	Beyond the CRISPR-Cas safeguard: PICI-encoded innate immune systems protect bacteria from bacteriophage predation. <i>Current Opinion in Microbiology</i> , 2020, 56, 52-58.	5.1	28
10	Revisiting the pH-gated conformational switch on the activities of HisKA-family histidine kinases. <i>Nature Communications</i> , 2020, 11, 769.	12.8	19
11	The SrrAB two-component system regulates <i>Staphylococcus aureus</i> pathogenicity through redox sensitive cysteines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10989-10999.	7.1	50
12	Structural and Functional Characterization of Autophosphorylation in Bacterial Histidine Kinases. <i>Methods in Molecular Biology</i> , 2020, 2077, 121-140.	0.9	1
13	The structure of a polygamous repressor reveals how phage-inducible chromosomal islands spread in nature. <i>Nature Communications</i> , 2019, 10, 3676.	12.8	11
14	Hijacking the Hijackers: <i>Escherichia coli</i> Pathogenicity Islands Redirect Helper Phage Packaging for Their Own Benefit. <i>Molecular Cell</i> , 2019, 75, 1020-1030.e4.	9.7	45
15	Unraveling the role of the secretor antigen in human rotavirus attachment to histo-blood group antigens. <i>PLoS Pathogens</i> , 2019, 15, e1007865.	4.7	41
16	Deciphering the Molecular Mechanism Underpinning Phage Arbitrium Communication Systems. <i>Molecular Cell</i> , 2019, 74, 59-72.e3.	9.7	42
17	Conformational dynamism for DNA interaction in the Salmonella RcsB response regulator. <i>Nucleic Acids Research</i> , 2018, 46, 456-472.	14.5	17
18	Structures of collagen IV globular domains: insight into associated pathologies, folding and network assembly. <i>IUCr</i> , 2018, 5, 765-779.	2.2	12

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19	Dissecting the link between the enzymatic activity and the SaPI inducing capacity of the phage 80± dUTPase. <i>Scientific Reports</i> , 2017, 7, 11234.	3.3	6
20	Broadening the antibacterial spectrum of histidine kinase autophosphorylation inhibitors via the use of µ-poly-L-lysine capped mesoporous silica-based nanoparticles. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2017, 13, 569-581.	3.3	19
21	Convergent evolution involving dimeric and trimeric dUTPases in pathogenicity island mobilization. <i>PLoS Pathogens</i> , 2017, 13, e1006581.	4.7	9
22	Sak and Sak4 recombinases are required for bacteriophage replication in <i>Staphylococcus aureus</i> . <i>Nucleic Acids Research</i> , 2017, 45, 6507-6519.	14.5	20
23	Pirating conserved phage mechanisms promotes promiscuous staphylococcal pathogenicity island transfer. <i>ELife</i> , 2017, 6, .	6.0	25
24	Convergent evolution of pathogenicity islands in helper <i>cos</i> phage interference. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150505.	4.0	29
25	Putative histidine kinase inhibitors with antibacterial effect against multi-drug resistant clinical isolates identified by in vitro and in silico screens. <i>Scientific Reports</i> , 2016, 6, 26085.	3.3	36
26	Another look at the mechanism involving trimeric dUTPases in <i>Staphylococcus aureus</i> pathogenicity island induction involves novel players in the party. <i>Nucleic Acids Research</i> , 2016, 44, 5457-5469.	14.5	20
27	The closed conformation of the LDL receptor is destabilized by the low Ca ⁺⁺ concentration but favored by the high Mg ⁺⁺ concentration in the endosome. <i>FEBS Letters</i> , 2015, 589, 3534-3540.	2.8	5
28	Bacterial Histidine Kinases as Novel Antibacterial Drug Targets. <i>ACS Chemical Biology</i> , 2015, 10, 213-224.	3.4	174
29	Virus Satellites Drive Viral Evolution and Ecology. <i>PLoS Genetics</i> , 2015, 11, e1005609.	3.5	49
30	Visualizing autophosphorylation in histidine kinases. <i>Nature Communications</i> , 2014, 5, 3258.	12.8	115
31	Staphylococcal pathogenicity island DNA packaging system involving <i>cos</i> -site packaging and phage-encoded HNH endonucleases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6016-6021.	7.1	73
32	Structural Basis of a Rationally Rewired Protein-Protein Interface Critical to Bacterial Signaling. <i>Structure</i> , 2013, 21, 1636-1647.	3.3	69
33	Phage dUTPases Control Transfer of Virulence Genes by a Proto-Oncogenic G Protein-like Mechanism. <i>Molecular Cell</i> , 2013, 49, 947-958.	9.7	51
34	dUTPases, the unexplored family of signalling molecules. <i>Current Opinion in Microbiology</i> , 2013, 16, 163-170.	5.1	32
35	Walk, the Path towards New Antibacterials with Low Potential for Resistance Development. <i>ACS Medicinal Chemistry Letters</i> , 2013, 4, 891-894.	2.8	15
36	Structural Basis of Rap Phosphatase Inhibition by Phr Peptides. <i>PLoS Biology</i> , 2013, 11, e1001511.	5.6	53

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37	Insights into the mechanism of activation of the phosphorylation-independent response regulator NblR. Role of residues Cys69 and Cys96. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 382-390.	1.9	4
38	Structural and Functional Insights into Endoglin Ligand Recognition and Binding. <i>PLoS ONE</i> , 2012, 7, e29948.	2.5	86
39	Laforin, a Dual Specificity Phosphatase Involved in Lafora Disease, Is Present Mainly as Monomeric Form with Full Phosphatase Activity. <i>PLoS ONE</i> , 2011, 6, e24040.	2.5	25
40	Laforin, a dual-specificity phosphatase involved in Lafora disease, is phosphorylated at Ser25 by AMP-activated protein kinase. <i>Biochemical Journal</i> , 2011, 439, 265-275.	3.7	29
41	Does the severity of the LGMD2A phenotype in compound heterozygotes depend on the combination of mutations?. <i>Muscle and Nerve</i> , 2011, 44, 710-714.	2.2	13
42	The mechanism of signal transduction by two-component systems. <i>Current Opinion in Structural Biology</i> , 2010, 20, 763-771.	5.7	206
43	The regulatory factor SipA is a highly stable β class protein with a SH3 fold. <i>FEBS Letters</i> , 2010, 584, 989-994.	2.8	8
44	Environmental control of phosphorylation pathways in a branched two-component system. <i>Molecular Microbiology</i> , 2010, 78, 475-489.	2.5	46
45	Substrate Binding and Catalysis in Carbamate Kinase Ascertained by Crystallographic and Site-Directed Mutagenesis Studies: Movements and Significance of a Unique Globular Subdomain of This Key Enzyme for Fermentative ATP Production in Bacteria. <i>Journal of Molecular Biology</i> , 2010, 397, 1261-1275.	4.2	19
46	Structural Insight into Partner Specificity and Phosphoryl Transfer in Two-Component Signal Transduction. <i>Cell</i> , 2009, 139, 325-336.	28.9	351
47	Biochemical characterization of novel glucokinase mutations isolated from Spanish maturity-onset diabetes of the young (MODY2) patients. <i>Journal of Human Genetics</i> , 2008, 53, 460-466.	2.3	12
48	Phosphorylation-independent activation of the atypical response regulator NblR. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3002-3015.	1.8	44
49	Evolutionary Diversification in Polyamine Biosynthesis. <i>Molecular Biology and Evolution</i> , 2008, 25, 2119-2128.	8.9	150
50	Identification of a novel two component system in <i>Thermotoga maritima</i> . Complex stoichiometry and crystallization. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 603-609.	2.3	11
51	The regulatory factor SipA provides a link between NblS and NblR signal transduction pathways in the cyanobacterium <i>Synechococcus</i> sp. PCC 7942. <i>Molecular Microbiology</i> , 2007, 66, 071120025032002-???	2.5	32
52	Structure-function analysis of the α 5 and the α 13 helices of human glucokinase: Description of two novel activating mutations. <i>Protein Science</i> , 2005, 14, 2080-2086.	7.6	18
53	Structure of the entire cytoplasmic portion of a sensor histidine-kinase protein. <i>EMBO Journal</i> , 2005, 24, 4247-4259.	7.8	266
54	Gene Structure, Organization, Expression, and Potential Regulatory Mechanisms of Arginine Catabolism in <i>Enterococcus faecalis</i> . <i>Journal of Bacteriology</i> , 2002, 184, 6289-6300.	2.2	92

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55	Structure of Acetylglutamate Kinase, a Key Enzyme for Arginine Biosynthesis and a Prototype for the Amino Acid Kinase Enzyme Family, during Catalysis. <i>Structure</i> , 2002, 10, 329-342.	3.3	126
56	Mitochondrial DNA depletion and <i>dGK</i> gene mutations. <i>Annals of Neurology</i> , 2002, 52, 311-317.	5.3	152
57	A crystallographic glimpse of a nucleotide triphosphate (AMPPNP) bound to a protein surface: external and internal AMPPNP molecules in crystalline N-acetyl-L-glutamate kinase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1892-1895.	2.5	3
58	[21] Carbamoyl phosphate synthesis: Carbamate kinase from <i>Pyrococcus furiosus</i> . <i>Methods in Enzymology</i> , 2001, 331, 236-247.	1.0	8
59	Structural and Mutational Analysis of the PhoQ Histidine Kinase Catalytic Domain. <i>Journal of Biological Chemistry</i> , 2001, 276, 41182-41190.	3.4	111
60	The 1.5 Å... resolution crystal structure of the carbamate kinase-like carbamoyl phosphate synthetase from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> , bound to ADP, confirms that this thermostable enzyme is a carbamate kinase, and provides insight into substrate binding and stability in carbamate kinases. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 299, 463-476.	4.2	49
61	The Carbamoyl-phosphate Synthetase of <i>Pyrococcus furiosus</i> Is Enzymologically and Structurally a Carbamate Kinase. <i>Journal of Biological Chemistry</i> , 1999, 274, 16295-16303.	3.4	29
62	Crystallization and preliminary structural results of catalase from human erythrocytes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1066-1068.	2.5	2
63	N-Acetyl-L-glutamate kinase from <i>Escherichia coli</i> : cloning of the gene, purification and crystallization of the recombinant enzyme and preliminary X-ray analysis of the free and ligand-bound forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1350-1352.	2.5	10
64	Carbamate kinase: New structural machinery for making carbamoyl phosphate, the common precursor of pyrimidines and arginine. <i>Protein Science</i> , 1999, 8, 934-940.	7.6	46
65	Carbamate kinase from <i>Enterococcus faecalis</i> and <i>Enterococcus faecium</i> . Cloning of the genes, studies on the enzyme expressed in <i>Escherichia coli</i> , and sequence similarity with N-acetyl-L-glutamate kinase. <i>FEBS Journal</i> , 1998, 253, 280-291.	0.2	29
66	Crystallization, characterization, and preliminary crystallographic studies of mitochondrial carbamoyl phosphate synthetase I of <i>Rana catesbeiana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 193-196.	2.6	3
67	Crystallization, Characterization and Preliminary Crystallographic Studies of Carbamate Kinase of <i>Streptococcus faecium</i> . <i>Journal of Molecular Biology</i> , 1994, 235, 1345-1347.	4.2	7