

Alberto Marina

List of Publications by Year in descending order

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67
papers

3,227
citations

186265

28
h-index

161849

54
g-index

72
all docs

72
docs citations

72
times ranked

3673
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Insight into Partner Specificity and Phosphoryl Transfer in Two-Component Signal Transduction. <i>Cell</i> , 2009, 139, 325-336.	28.9	351
2	Structure of the entire cytoplasmic portion of a sensor histidine-kinase protein. <i>EMBO Journal</i> , 2005, 24, 4247-4259.	7.8	266
3	The mechanism of signal transduction by two-component systems. <i>Current Opinion in Structural Biology</i> , 2010, 20, 763-771.	5.7	206
4	Bacterial Histidine Kinases as Novel Antibacterial Drug Targets. <i>ACS Chemical Biology</i> , 2015, 10, 213-224.	3.4	174
5	Mitochondrial DNA depletion and <i>dGK</i> gene mutations. <i>Annals of Neurology</i> , 2002, 52, 311-317.	5.3	152
6	Evolutionary Diversification in Polyamine Biosynthesis. <i>Molecular Biology and Evolution</i> , 2008, 25, 2119-2128.	8.9	150
7	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
8	Visualizing autophosphorylation in histidine kinases. <i>Nature Communications</i> , 2014, 5, 3258.	12.8	115
9	Structural and Mutational Analysis of the PhoQ Histidine Kinase Catalytic Domain. <i>Journal of Biological Chemistry</i> , 2001, 276, 41182-41190.	3.4	111
10	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
11	Structural and Functional Insights into Endoglin Ligand Recognition and Binding. <i>PLoS ONE</i> , 2012, 7, e29948.	2.5	86
12	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
13	Structural Basis of a Rationally Rewired Protein-Protein Interface Critical to Bacterial Signaling. <i>Structure</i> , 2013, 21, 1636-1647.	3.3	69
14	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
15	Structural Basis of Rap Phosphatase Inhibition by Phr Peptides. <i>PLoS Biology</i> , 2013, 11, e1001511.	5.6	53
16	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
17	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
18	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 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 299, 463-476.	4.2	49

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19	Virus Satellites Drive Viral Evolution and Ecology. PLoS Genetics, 2015, 11, e1005609.	3.5	49
20	Carbamate kinase: New structural machinery for making carbamoyl phosphate, the common precursor of pyrimidines and arginine. Protein Science, 1999, 8, 934-940.	7.6	46
21	Environmental control of phosphorylation pathways in a branched two-component system. Molecular Microbiology, 2010, 78, 475-489.	2.5	46
22	Hijacking the Hijackers: Escherichia coli Pathogenicity Islands Redirect Helper Phage Packaging for Their Own Benefit. Molecular Cell, 2019, 75, 1020-1030.e4.	9.7	45
23	Phosphorylation-independent activation of the atypical response regulator NblR. Microbiology (United Kingdom), 2008, 154, 3002-3015.	1.8	44
24	Deciphering the Molecular Mechanism Underpinning Phage Arbitrium Communication Systems. Molecular Cell, 2019, 74, 59-72.e3.	9.7	42
25	Unraveling the role of the secretor antigen in human rotavirus attachment to histo-blood group antigens. PLoS Pathogens, 2019, 15, e1007865.	4.7	41
26	Putative histidine kinase inhibitors with antibacterial effect against multi-drug resistant clinical isolates identified by in vitro and in silico screens. Scientific Reports, 2016, 6, 26085.	3.3	36
27	The regulatory factor SipA provides a link between NblS and NblR signal transduction pathways in the cyanobacterium Synechococcus sp. PCC 7942. Molecular Microbiology, 2007, 66, 071120025032002-???.	2.5	32
28	dUTPases, the unexplored family of signalling molecules. Current Opinion in Microbiology, 2013, 16, 163-170.	5.1	32
29	Molecular Basis of Lysis—Lysogeny Decisions in Gram-Positive Phages. Annual Review of Microbiology, 2021, 75, 563-581.	7.3	31
30	Carbamate kinase from Enterococcus faecalis and Enterococcus faecium . Cloning of the genes, studies on the enzyme expressed in Escherichia coli, and sequence similarity with N-acetyl- L-glutamate kinase. FEBS Journal, 1998, 253, 280-291.	0.2	29
31	The Carbamoyl-phosphate Synthetase of Pyrococcus furiosus Is Enzymologically and Structurally a Carbamate Kinase. Journal of Biological Chemistry, 1999, 274, 16295-16303.	3.4	29
32	Laforin, a dual-specificity phosphatase involved in Lafora disease, is phosphorylated at Ser25 by AMP-activated protein kinase. Biochemical Journal, 2011, 439, 265-275.	3.7	29
33	Convergent evolution of pathogenicity islands in helper <i>cos</i> phage interference. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150505.	4.0	29
34	Beyond the CRISPR-Cas safeguard: PICI-encoded innate immune systems protect bacteria from bacteriophage predation. Current Opinion in Microbiology, 2020, 56, 52-58.	5.1	28
35	Laforin, a Dual Specificity Phosphatase Involved in Lafora Disease, Is Present Mainly as Monomeric Form with Full Phosphatase Activity. PLoS ONE, 2011, 6, e24040.	2.5	25
36	Pirating conserved phage mechanisms promotes promiscuous staphylococcal pathogenicity island transfer. ELife, 2017, 6, .	6.0	25

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37	The arbitrium system controls prophage induction. <i>Current Biology</i> , 2021, 31, 5037-5045.e3.	3.9	22
38	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
39	A regulatory cascade controls <i>Staphylococcus aureus</i> pathogenicity island activation. <i>Nature Microbiology</i> , 2021, 6, 1300-1308.	13.3	20
40	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
41	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
42	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
43	Revisiting the pH-gated conformational switch on the activities of HisKA-family histidine kinases. <i>Nature Communications</i> , 2020, 11, 769.	12.8	19
44	Structure-function analysis of the $\hat{I}\pm 5$ and the $\hat{I}\pm 13$ helices of human glucokinase: Description of two novel activating mutations. <i>Protein Science</i> , 2005, 14, 2080-2086.	7.6	18
45	Conformational dynamism for DNA interaction in the <i>Salmonella</i> RcsB response regulator. <i>Nucleic Acids Research</i> , 2018, 46, 456-472.	14.5	17
46	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
47	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
48	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
49	Structures of collagen IV globular domains: insight into associated pathologies, folding and network assembly. <i>IUCr</i> , 2018, 5, 765-779.	2.2	12
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 structure of a polygamous repressor reveals how phage-inducible chromosomal islands spread in nature. <i>Nature Communications</i> , 2019, 10, 3676.	12.8	11
52	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
53	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
54	Structure-based analyses of <i>Salmonella</i> RcsB variants unravel new features of the Rcs regulon. <i>Nucleic Acids Research</i> , 2021, 49, 2357-2374.	14.5	10

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55	Convergent evolution involving dimeric and trimeric dUTPases in pathogenicity island mobilization. <i>PLoS Pathogens</i> , 2017, 13, e1006581.	4.7	9
56	[21] Carbamoyl phosphate synthesis: Carbamate kinase from <i>Pyrococcus furiosus</i> . <i>Methods in Enzymology</i> , 2001, 331, 236-247.	1.0	8
57	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
58	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
59	Dissecting the link between the enzymatic activity and the SaPI inducing capacity of the phage 80 \pm dUTPase. <i>Scientific Reports</i> , 2017, 7, 11234.	3.3	6
60	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
61	Insights into the mechanism of action of the arbitrium communication system in SPbeta phages. <i>Nature Communications</i> , 2022, 13, .	12.8	6
62	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
63	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
64	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
65	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
66	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
67	Structural and Functional Characterization of Autophosphorylation in Bacterial Histidine Kinases. <i>Methods in Molecular Biology</i> , 2020, 2077, 121-140.	0.9	1