

Stefano Pascarella

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

2,423
citations

304743

22
h-index

214800

47
g-index

65
all docs

65
docs citations

65
times ranked

3949
citing authors

#	ARTICLE	IF	CITATIONS
1	COVID-2019: The role of the nsp2 and nsp3 in its pathogenesis. <i>Journal of Medical Virology</i> , 2020, 92, 584-588.	5.0	308
2	Evolutionary analysis of SARS-CoV-2: how mutation of Non-Structural Protein 6 (NSP6) could affect viral autophagy. <i>Journal of Infection</i> , 2020, 81, e24-e27.	3.3	211
3	Sars-CoV-2 Envelope and Membrane Proteins: Structural Differences Linked to Virus Characteristics?. <i>BioMed Research International</i> , 2020, 2020, 1-6.	1.9	150
4	Comparative structural analysis of psychrophilic and meso- and thermophilic enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 236-249.	2.6	144
5	PyMod: sequence similarity searches, multiple sequence-structure alignments, and homology modeling within PyMOL. <i>BMC Bioinformatics</i> , 2012, 13, S2.	2.6	141
6	Structural adaptation of extreme halophilic proteins through decrease of conserved hydrophobic contact surface. <i>BMC Structural Biology</i> , 2011, 11, 50.	2.3	139
7	A data bank merging related protein structures and sequences. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 121-137.	2.1	130
8	Structural adaptation of enzymes to low temperatures. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 141-148.	2.1	104
9	l-Threonine aldolase, serine hydroxymethyltransferase and fungal alanine racemase. <i>FEBS Journal</i> , 2001, 268, 6508-6525.	0.2	85
10	SARS-CoV-2 B.1.617 Indian variants: Are electrostatic potential changes responsible for a higher transmission rate?. <i>Journal of Medical Virology</i> , 2021, 93, 6551-6556.	5.0	79
11	SARS-Cov-2 ORF3a: Mutability and function. <i>International Journal of Biological Macromolecules</i> , 2021, 170, 820-826.	7.5	77
12	The electrostatic potential of the Omicron variant spike is higher than in Delta and Delta plus variants: A hint to higher transmissibility?. <i>Journal of Medical Virology</i> , 2022, 94, 1277-1280.	5.0	60
13	Structural adaptation to low temperatures—analysis of the subunit interface of oligomeric psychrophilic enzymes. <i>FEBS Journal</i> , 2007, 274, 4595-4608.	4.7	44
14	Improvement in prediction of solvent accessibility by probability profiles. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 987-992.	2.1	40
15	Structure-Function Relationships in Sorcin, a Member of the Penta EF-Hand Family. Interaction of Sorcin Fragments with the Ryanodine Receptor and an Escherichia coli Model System. <i>Biochemistry</i> , 2000, 39, 658-666.	2.5	39
16	Evolutionarily conserved regions and hydrophobic contacts at the superfamily level: The case of the fold-type I, pyridoxal-5-phosphate-dependent enzymes. <i>Protein Science</i> , 2008, 13, 2992-3005.	7.6	35
17	Easy method to predict solvent accessibility from multiple protein sequence alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 32, 190-199.	2.6	34
18	Molecular mechanism of PdxR—transcriptional activator involved in the regulation of vitamin B ₆ biosynthesis in the probiotic bacterium <i>Bacillus clausii</i> . <i>FEBS Journal</i> , 2015, 282, 2966-2984.	4.7	33

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19	Structural plasticity of thermophilic serine hydroxymethyltransferases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 50, 122-134.	2.6	32
20	“Cold spots” in protein cold adaptation: Insights from normalized atomic displacement parameters (B ² -factors). <i>Biophysical Chemistry</i> , 2010, 153, 104-114.	2.8	30
21	The MocR-like transcription factors: pyridoxal 5-phosphate-dependent regulators of bacterial metabolism. <i>FEBS Journal</i> , 2018, 285, 3925-3944.	4.7	28
22	Evidence for mutations in SARS-CoV-2 Italian isolates potentially affecting virus transmission. <i>Journal of Medical Virology</i> , 2020, 92, 2232-2237.	5.0	28
23	Long-chain polyphosphates impair SARS-CoV-2 infection and replication. <i>Science Signaling</i> , 2021, 14, .	3.6	27
24	Serine Hydroxymethyltransferase from the Cold Adapted Microorganism <i>Psychromonas ingrahamii</i> : A Low Temperature Active Enzyme with Broad Substrate Specificity. <i>International Journal of Molecular Sciences</i> , 2012, 13, 1314-1326.	4.1	24
25	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021, 4, 489.	4.4	23
26	CAMPO, SCR_FIND and CHC_FIND: a suite of web tools for computational structural biology. <i>Nucleic Acids Research</i> , 2005, 33, W50-W55.	14.5	22
27	Type I pyridoxal 5-phosphate dependent enzymatic domains embedded within multimodular nonribosomal peptide synthetase and polyketide synthase assembly lines. <i>BMC Structural Biology</i> , 2013, 13, 26.	2.3	22
28	Structural adaptation of the subunit interface of oligomeric thermophilic and hyperthermophilic enzymes. <i>Computational Biology and Chemistry</i> , 2009, 33, 137-148.	2.3	21
29	Multi-drug resistant <i>Pseudomonas aeruginosa</i> nosocomial strains: Molecular epidemiology and evolution. <i>Microbial Pathogenesis</i> , 2018, 123, 233-241.	2.9	19
30	"Hot cores" in proteins: Comparative analysis of the apolar contact area in structures from hyper/thermophilic and mesophilic organisms. <i>BMC Structural Biology</i> , 2008, 8, 14.	2.3	18
31	Study of DNA binding and bending by <i>Bacillus subtilis</i> GabR, a PLP-dependent transcription factor. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3474-3489.	2.4	18
32	Conformational transitions driven by pyridoxal-5-phosphate uptake in the psychrophilic serine hydroxymethyltransferase from <i>Psychromonas ingrahamii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2831-2841.	2.6	17
33	The value of electrostatic potentials of the spike receptor binding and N-terminal domains in addressing transmissibility and infectivity of SARS-CoV-2 variants of concern. <i>Journal of Infection</i> , 2022, 84, e62-e63.	3.3	17
34	The aspartate aminotransferase-like domain of Firmicutes MocR transcriptional regulators. <i>Computational Biology and Chemistry</i> , 2015, 58, 55-61.	2.3	16
35	Structural adaptation of serine hydroxymethyltransferase to low temperatures. <i>International Journal of Biological Macromolecules</i> , 2010, 46, 37-46.	7.5	15
36	SARS-CoV-2 AY.4.2 variant circulating in Italy: Genomic preliminary insight. <i>Journal of Medical Virology</i> , 2022, 94, 1689-1692.	5.0	15

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37	<i>Salmonella typhimurium</i> PtsJ is a novel MocR-like transcriptional repressor involved in regulating the vitamin B ₆ salvage pathway. <i>FEBS Journal</i> , 2017, 284, 466-484.	4.7	14
38	The importance of genomic analysis in cracking the coronavirus pandemic. <i>Expert Review of Molecular Diagnostics</i> , 2021, 21, 547-562.	3.1	14
39	Structural mimicry between SLA/LP and Rickettsia surface antigens as a driver of autoimmune hepatitis: insights from an in silico study. <i>Theoretical Biology and Medical Modelling</i> , 2013, 10, 25.	2.1	12
40	Chemogenomics of pyridoxal 5-phosphate dependent enzymes. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2013, 28, 183-194.	5.2	12
41	Structural Analysis of Merkel Cell Polyomavirus (MCPyV) Viral Capsid Protein 1 (VP1) in HIV-1 Infected Individuals. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7998.	4.1	11
42	A consensus procedure improving solvent accessibility prediction. <i>Journal of Computational Chemistry</i> , 2006, 27, 621-626.	3.3	10
43	Structural properties of the linkers connecting the N- and C- terminal domains in the MocR bacterial transcriptional regulators. <i>Biochimie Open</i> , 2016, 3, 8-18.	3.2	10
44	Molecular dynamics simulation unveils the conformational flexibility of the interdomain linker in the bacterial transcriptional regulator GabR from <i>Bacillus subtilis</i> bound to pyridoxal 5-phosphate. <i>PLoS ONE</i> , 2017, 12, e0189270.	2.5	10
45	A Bioinformatics Analysis Reveals a Group of MocR Bacterial Transcriptional Regulators Linked to a Family of Genes Coding for Membrane Proteins. <i>Biochemistry Research International</i> , 2016, 2016, 1-13.	3.3	9
46	Data from computational analysis of the peptide linkers in the MocR bacterial transcriptional regulators. <i>Data in Brief</i> , 2016, 9, 292-313.	1.0	7
47	Interaction of <i>Bacillus subtilis</i> GabR with the gabTD promoter: role of repeated sequences and effect of GABA in transcriptional activation. <i>FEBS Journal</i> , 2020, 287, 4952-4970.	4.7	7
48	Subunit interfaces of oligomeric hyperthermophilic enzymes display enhanced compactness. <i>International Journal of Biological Macromolecules</i> , 2009, 44, 353-360.	7.5	6
49	The SARS-CoV-2 Mu variant should not be left aside: It warrants attention for its immuno-escaping ability. <i>Journal of Medical Virology</i> , 2022, 94, 2479-2486.	5.0	6
50	Conformational transitions induced by $\hat{\text{I}}^3$ -amino butyrate binding in GabR, a bacterial transcriptional regulator. <i>Scientific Reports</i> , 2019, 9, 19319.	3.3	5
51	Shortening Epitopes to Survive: The Case of SARS-CoV-2 Lambda Variant. <i>Biomolecules</i> , 2021, 11, 1494.	4.0	5
52	Conserved water molecules in bacterial serine hydroxymethyltransferases. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 415-426.	2.1	4
53	Molecular dynamics of an asymmetric form of GabR, a bacterial transcriptional regulator. <i>Biophysical Chemistry</i> , 2020, 262, 106380.	2.8	4
54	A Comprehensive Computational Analysis of Mycobacterium Genomes Pinpoints the Genes Co-occurring with YczE, a Membrane Protein Coding Gene Under the Putative Control of a MocR, and Predicts its Function. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 111-125.	3.6	3

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55	Computational classification of MoxR transcriptional regulators into subgroups as a support for experimental and functional characterization. <i>Bioinformatics</i> , 2019, 15, 151-159.	0.5	3
56	SARS-CoV-2 Pandemic Tracing in Italy Highlights Lineages with Mutational Burden in Growing Subsets. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4155.	4.1	3
57	A Novel Human Neutralizing mAb Recognizes Delta, Gamma and Omicron Variants of SARS-CoV-2 and Can Be Used in Combination with Sotrovimab. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5556.	4.1	3
58	Structural stability of cold-adapted serine hydroxymethyltransferase, a tool for β -hydroxy- α -amino acid biosynthesis. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2014, 110, 171-177.	1.8	2
59	Response to Ribeiro da Silva et al., "Role of nonstructural proteins in the pathogenesis of SARS-CoV-2". <i>Journal of Medical Virology</i> , 2020, 92, 1430-1430.	5.0	2