Stefano Pascarella

List of Publications by Year
in descending order

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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	SARSâ€CoVâ€2 AY.4.2 variant circulating in Italy: Genomic preliminary insight. Journal of Medical Virology, 2022, 94, 1689-1692.	5.0	15
2	The electrostatic potential of the Omicron variant spike is higher than in Delta and Deltaâ€plus variants: A hint to higher transmissibility?. Journal of Medical Virology, 2022, 94, 1277-1280.	5.0	60
3	The SARSâ€CoVâ€2 Mu variant should not be left aside: It warrants attention for its immunoâ€escaping ability. Journal of Medical Virology, 2022, 94, 2479-2486.	5.0	6
4	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. Journal of Infection, 2022, 84, e62-e63.	3.3	17
5	SARS-CoV-2 Pandemic Tracing in Italy Highlights Lineages with Mutational Burden in Growing Subsets. International Journal of Molecular Sciences, 2022, 23, 4155.	4.1	3
6	A Novel Human Neutralizing mAb Recognizes Delta, Gamma and Omicron Variants of SARS-CoV-2 and Can Be Used in Combination with Sotrovimab. International Journal of Molecular Sciences, 2022, 23, 5556.	4.1	3
7	SARS-Cov-2 ORF3a: Mutability and function. International Journal of Biological Macromolecules, 2021, 170, 820-826.	7.5	77
8	The importance of genomic analysis in cracking the coronavirus pandemic. Expert Review of Molecular Diagnostics, 2021, 21, 547-562.	3.1	14
9	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. Communications Biology, 2021, 4, 489.	4.4	23
10	SARSâ€CoVâ€2 B.1.617 Indian variants: Are electrostatic potential changes responsible for a higher transmission rate?. Journal of Medical Virology, 2021, 93, 6551-6556.	5.0	79
11	Long-chain polyphosphates impair SARS-CoV-2 infection and replication. Science Signaling, 2021, 14, .	3.6	27
12	Shortening Epitopes to Survive: The Case of SARS-CoV-2 Lambda Variant. Biomolecules, 2021, 11, 1494.	4.0	5
13	Structural Analysis of Merkel Cell Polyomavirus (MCPyV) Viral Capsid Protein 1 (VP1) in HIV-1 Infected Individuals. International Journal of Molecular Sciences, 2020, 21, 7998.	4.1	11
14	Evidence for mutations in SARSâ€CoVâ€2 Italian isolates potentially affecting virus transmission. Journal of Medical Virology, 2020, 92, 2232-2237.	5.0	28
15	Molecular dynamics of an asymmetric form of GabR, a bacterial transcriptional regulator. Biophysical Chemistry, 2020, 262, 106380.	2.8	4
16	Sars-CoV-2 Envelope and Membrane Proteins: Structural Differences Linked to Virus Characteristics?. BioMed Research International, 2020, 2020, 1-6.	1.9	150
17	Interaction of Bacillus subtilis GabR with the gabTD promoter: role of repeated sequences and effect of GABA in transcriptional activation. FEBS Journal, 2020, 287, 4952-4970.	4.7	7
18	COVIDâ€2019: The role of the nsp2 and nsp3 in its pathogenesis. Journal of Medical Virology, 2020, 92, 584-588.	5.0	308

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19	Response to Ribeiro da Silva et al,â€œRole of nonstructural proteins in the pathogenesis of SARSâ€CoVâ€2â€: Journal of Medical Virology, 2020, 92, 1430-1430.	5.0	2
20	Evolutionary analysis of SARS-CoV-2: how mutation of Non-Structural Protein 6 (NSP6) could affect viral autophagy. Journal of Infection, 2020, 81, e24-e27.	3.3	211
21	Conformational transitions induced by Î³-amino butyrate binding in GabR, a bacterial transcriptional regulator. Scientific Reports, 2019, 9, 19319.	3.3	5
22	Computational classification of MocR transcriptional regulators into subgroups as a support for experimental and functional characterization. Bioinformation, 2019, 15, 151-159.	0.5	3
23	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. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 111-125.	3.6	3
24	The MocRâ€like transcription factors: pyridoxal 5â€²â€phosphateâ€dependent regulators of bacterial metabolism. FEBS Journal, 2018, 285, 3925-3944.	4.7	28
25	Multi-drug resistant Pseudomonas aeruginosa nosocomial strains: Molecular epidemiology and evolution. Microbial Pathogenesis, 2018, 123, 233-241.	2.9	19
26	Salmonella typhimurium PtsJ is a novel MocRâ€like transcriptional repressor involved in regulating the vitamin B₆ salvage pathway. FEBS Journal, 2017, 284, 466-484.	4.7	14
27	Study of DNA binding and bending by Bacillus subtilis GabR, a PLP-dependent transcription factor. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3474-3489.	2.4	18
28	Molecular dynamics simulation unveils the conformational flexibility of the interdomain linker in the bacterial transcriptional regulator GabR from Bacillus subtilis bound to pyridoxal 5â€™-phosphate. PLoS ONE, 2017, 12, e0189270.	2.5	10
29	A Bioinformatics Analysis Reveals a Group of MocR Bacterial Transcriptional Regulators Linked to a Family of Genes Coding for Membrane Proteins. Biochemistry Research International, 2016, 2016, 1-13.	3.3	9
30	Data from computational analysis of the peptide linkers in the MocR bacterial transcriptional regulators. Data in Brief, 2016, 9, 292-313.	1.0	7
31	Structural properties of the linkers connecting the N- and C- terminal domains in the MocR bacterial transcriptional regulators. Biochimie Open, 2016, 3, 8-18.	3.2	10
32	Molecular mechanism of PdxRÂâ€“Âa transcriptional activator involved in the regulation of vitamin B₆ biosynthesis in the probiotic bacterium BacillusÂclausii. FEBS Journal, 2015, 282, 2966-2984.	4.7	33
33	The aspartate aminotransferase-like domain of Firmicutes MocR transcriptional regulators. Computational Biology and Chemistry, 2015, 58, 55-61.	2.3	16
34	Conserved water molecules in bacterial serine hydroxymethyltransferases. Protein Engineering, Design and Selection, 2015, 28, 415-426.	2.1	4
35	Conformational transitions driven by pyridoxal-5â€²-phosphate uptake in the psychrophilic serine hydroxymethyltransferase fromPsychromonas ingrahamii. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2831-2841.	2.6	17
36	Structural stability of cold-adapted serine hydroxymethyltransferase, a tool for Î²-hydroxy-Î±-amino acid biosynthesis. Journal of Molecular Catalysis B: Enzymatic, 2014, 110, 171-177.	1.8	2

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37	Structural mimicry between SLA/LP and Rickettsia surface antigens as a driver of autoimmune hepatitis: insights from an in silico study. Theoretical Biology and Medical Modelling, 2013, 10, 25.	2.1	12
38	Chemogenomics of pyridoxal 5â€²-phosphate dependent enzymes. Journal of Enzyme Inhibition and Medicinal Chemistry, 2013, 28, 183-194.	5.2	12
39	Type I pyridoxal 5â€²-phosphate dependent enzymatic domains embedded within multimodular nonribosomal peptide synthetase and polyketide synthase assembly lines. BMC Structural Biology, 2013, 13, 26.	2.3	22
40	Serine Hydroxymethyltransferase from the Cold Adapted Microorganism Psychromonas ingrahamii: A Low Temperature Active Enzyme with Broad Substrate Specificity. International Journal of Molecular Sciences, 2012, 13, 1314-1326.	4.1	24
41	PyMod: sequence similarity searches, multiple sequence-structure alignments, and homology modeling within PyMOL. BMC Bioinformatics, 2012, 13, S2.	2.6	141
42	Structural adaptation of extreme halophilic proteins through decrease of conserved hydrophobic contact surface. BMC Structural Biology, 2011, 11, 50.	2.3	139
43	â€œCold spotsâ€•in protein cold adaptation: Insights from normalized atomic displacement parameters (Bâ€²-factors). Biophysical Chemistry, 2010, 153, 104-114.	2.8	30
44	Structural adaptation of serine hydroxymethyltransferase to low temperatures. International Journal of Biological Macromolecules, 2010, 46, 37-46.	7.5	15
45	Structural adaptation of the subunit interface of oligomeric thermophilic and hyperthermophilic enzymes. Computational Biology and Chemistry, 2009, 33, 137-148.	2.3	21
46	Subunit interfaces of oligomeric hyperthermophilic enzymes display enhanced compactness. International Journal of Biological Macromolecules, 2009, 44, 353-360.	7.5	6
47	"Hot cores" in proteins: Comparative analysis of the apolar contact area in structures from hyper/thermophilic and mesophilic organisms. BMC Structural Biology, 2008, 8, 14.	2.3	18
48	Evolutionarily conserved regions and hydrophobic contacts at the superfamily level: The case of the fold-type I, pyridoxal-5â€²-phosphate-dependent enzymes. Protein Science, 2008, 13, 2992-3005.	7.6	35
49	Structural adaptation to low temperaturesâ€ƒâ€”â€ƒanalysis of the subunit interface of oligomeric psychrophilic enzymes. FEBS Journal, 2007, 274, 4595-4608.	4.7	44
50	A consensus procedure improving solvent accessibility prediction. Journal of Computational Chemistry, 2006, 27, 621-626.	3.3	10
51	CAMPO, SCR_FIND and CHC_FIND: a suite of web tools for computational structural biology. Nucleic Acids Research, 2005, 33, W50-W55.	14.5	22
52	Improvement in prediction of solvent accessibility by probability profiles. Protein Engineering, Design and Selection, 2003, 16, 987-992.	2.1	40
53	Comparative structural analysis of psychrophilic and meso- and thermophilic enzymes. Proteins: Structure, Function and Bioinformatics, 2002, 47, 236-249.	2.6	144
54	Structural plasticity of thermophilic serine hydroxymethyltransferases. Proteins: Structure, Function and Bioinformatics, 2002, 50, 122-134.	2.6	32

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55	Structural adaptation of enzymes to low temperatures. Protein Engineering, Design and Selection, 2001, 14, 141-148.	2.1	104
56	l-Threonine aldolase, serine hydroxymethyltransferase and fungal alanine racemase. FEBS Journal, 2001, 268, 6508-6525.	0.2	85
57	Structureâ^'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. Biochemistry, 2000, 39, 658-666.	2.5	39
58	Easy method to predict solvent accessibility from multiple protein sequence alignments. Proteins: Structure, Function and Bioinformatics, 1998, 32, 190-199.	2.6	34
59	A data bank merging related protein structures and sequences. Protein Engineering, Design and Selection, 1992, 5, 121-137.	2.1	130