Fabrizio Pucci

List of Publications by Year
in descending order

45 papers	1,168 citations	471509 17 h-index	434195 31 g-index
56 all docs	56 docs citations	56 times ranked	1261 citing authors

#	Article	IF	Citations
1	*NPTX1* mutations trigger endoplasmic reticulum stress and cause autosomal dominant cerebellar ataxia. Brain, 2022, 145, 1519-1534.	7.6	10
2	Artificial intelligence challenges for predicting the impact of mutations on protein stability. Current Opinion in Structural Biology, 2022, 72, 161-168.	5.7	45
3	Using metagenomic data to boost protein structure prediction and discovery. Computational and Structural Biotechnology Journal, 2022, 20, 434-442.	4.1	3
4	Analysis of the Neutralizing Activity of Antibodies Targeting Open or Closed SARS-CoV-2 Spike Protein Conformations. International Journal of Molecular Sciences, 2022, 23, 2078.	4.1	5
5	SWOTein: a structure-based approach to predict stability Strengths and Weaknesses of prOTEINs. Bioinformatics, 2021, 37, 1963-1971.	4.1	13
6	In Silico Analysis of the Molecular-Level Impact of SMPD1 Variants on Niemann-Pick Disease Severity. International Journal of Molecular Sciences, 2021, 22, 4516.	4.1	4
7	Prediction and Evolution of the Molecular Fitness of SARS-CoV-2 Variants: Introducing SpikePro. Viruses, 2021, 13, 935.	3.3	22
8	MutaFrameâ€"an interpretative visualization framework for deleteriousness prediction of missense variants in the human exome. Bioinformatics, 2021, 38, 265-266.	4.1	2
9	Perturbing dimer interactions and allosteric communication modulates the immunosuppressive activity of human galectin-7. Journal of Biological Chemistry, 2021, 297, 101308.	3.4	5
10	Quantifying Renin-Angiotensin-System Alterations in COVID-19. Cells, 2021, 10, 2755.	4.1	21
11	CoCoNetâ€"boosting RNA contact prediction by convolutional neural networks. Nucleic Acids Research, 2021, 49, 12661-12672.	14.5	3
12	BRANEart: Identify Stability Strength and Weakness Regions in Membrane Proteins. Frontiers in Bioinformatics, 2021, 1, .	2.1	3
13	SOLart: a structure-based method to predict protein solubility and aggregation. Bioinformatics, 2020, 36, 1445-1452.	4.1	44
14	pydca v1.0: a comprehensive software for direct coupling analysis of RNA and protein sequences. Bioinformatics, 2020, 36, 2264-2265.	4.1	25
15	Modeling the Molecular Impact of SARS-CoV-2 Infection on the Renin-Angiotensin System. Viruses, 2020, 12, 1367.	3.3	15
16	Large-scale in silico mutagenesis experiments reveal optimization of genetic code and codon usage for protein mutational robustness. BMC Biology, 2020, 18, 146.	3.8	7
17	Evaluating DCA-based method performances for RNA contact prediction by a well-curated data set. Rna, 2020, 26, 794-802.	3.5	13
18	Protein Thermal Stability Engineering Using HoTMuSiC. Methods in Molecular Biology, 2020, 2112, 59-73.	0.9	15

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19	Relation between DNA ionization potentials, single base substitutions and pathogenic variants. BMC Genomics, 2019, 20, 551.	2.8	7
20	A comprehensive computational study of amino acid interactions in membrane proteins. Scientific Reports, 2019, 9, 12043.	3.3	40
21	Shedding light on the dark matter of the biomolecular structural universe: Progress in RNA 3D structure prediction. Methods, 2019, 162-163, 68-73.	3.8	18
22	Quantification of biases in predictions of protein stability changes upon mutations. Bioinformatics, 2018, 34, 3659-3665.	4.1	110
23	Prediction and interpretation of deleterious coding variants in terms of protein structural stability. Scientific Reports, 2018, 8, 4480.	3.3	64
24	Deciphering noise amplification and reduction in open chemical reaction networks. Journal of the Royal Society Interface, 2018, 15, 20180805.	3.4	1
25	Intrinsic noise modulation in closed oligomerization-type systems âŽ âŽFP and MR are research assistant and research director, respectively, at the Belgian Fund for scientific research (FNRS).. IFAC-PapersOnLine, 2018, 51, 649-654.	0.9	2
26	Computational analysis of the amino acid interactions that promote or decrease protein solubility. Scientific Reports, 2018, 8, 14661.	3.3	48
27	Insights into noise modulation in oligomerization systems of increasing complexity. Physical Review E, 2018, 98, 012137.	2.1	2
28	Physical and molecular bases of protein thermal stability and cold adaptation. Current Opinion in Structural Biology, 2017, 42, 117-128.	5.7	124
29	SCooP: an accurate and fast predictor of protein stability curves as a function of temperature. Bioinformatics, 2017, 33, 3415-3422.	4.1	82
30	High-quality Thermodynamic Data on the Stability Changes of Proteins Upon Single-site Mutations. Journal of Physical and Chemical Reference Data, 2016, 45, .	4.2	38
31	Improved insights into protein thermal stability: from the molecular to the structurome scale. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2016, 374, 20160141.	3.4	18
32	Predicting protein thermal stability changes upon point mutations using statistical potentials: Introducing HoTMuSiC. Scientific Reports, 2016, 6, 23257.	3.3	96
33	Towards an accurate prediction of the thermal stability of homologous proteins. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1132-1142.	3.5	19
34	Symmetry Principles in Optimization Problems: an application to Protein Stability Prediction. IFAC-PapersOnLine, 2015, 48, 458-463.	0.9	29
35	Stability Curve Prediction of Homologous Proteins Using Temperature-Dependent Statistical Potentials. PLoS Computational Biology, 2014, 10, e1003689.	3.2	32
36	BPS Wilson loops on Hyperbolic space. Journal of Physics A: Mathematical and Theoretical, 2014, 47, 385401.	2.1	0

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37	Protein Thermostability Prediction within Homologous Families Using Temperature-Dependent Statistical Potentials. PLoS ONE, 2014, 9, e91659.	2.5	50
38	Exploring the Aoki regime. Journal of High Energy Physics, 2013, 2013, 1.	4.7	1
39	More on â€™t Hooft loops in $ \mathcal{N}=4 $ SYM. Journal of High Energy Physics, 2012, 2012, 1.	4.7	2
40	Taste symmetry breaking at finite temperature. European Physical Journal C, 2012, 72, 1.	3.9	5
41	Finite volume corrections to LECs in Wilson and staggered ChPT. , 2012, , .		0
42	Taste symmetry violation at finite temperature. , 2012, , .		0
43	Correlators of supersymmetric Wilson loops at weak and strong coupling. Journal of High Energy Physics, 2010, 2010, 1.	4.7	29
44	Correlators of supersymmetric Wilson-loops, protected operators and matrix models in ? = 4 SYM. Journal of High Energy Physics, 2009, 2009, 061-061.	4.7	41
45	Supersymmetric Wilson loops at two loops. Journal of High Energy Physics, 2008, 2008, 083-083.	4.7	39