

# Fabrizio Pucci

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Physical and molecular bases of protein thermal stability and cold adaptation. <i>Current Opinion in Structural Biology</i> , 2017, 42, 117-128.	5.7	124
2	Quantification of biases in predictions of protein stability changes upon mutations. <i>Bioinformatics</i> , 2018, 34, 3659-3665.	4.1	110
3	Predicting protein thermal stability changes upon point mutations using statistical potentials: Introducing HoTMuSiC. <i>Scientific Reports</i> , 2016, 6, 23257.	3.3	96
4	SCoop: an accurate and fast predictor of protein stability curves as a function of temperature. <i>Bioinformatics</i> , 2017, 33, 3415-3422.	4.1	82
5	Prediction and interpretation of deleterious coding variants in terms of protein structural stability. <i>Scientific Reports</i> , 2018, 8, 4480.	3.3	64
6	Protein Thermostability Prediction within Homologous Families Using Temperature-Dependent Statistical Potentials. <i>PLoS ONE</i> , 2014, 9, e91659.	2.5	50
7	Computational analysis of the amino acid interactions that promote or decrease protein solubility. <i>Scientific Reports</i> , 2018, 8, 14661.	3.3	48
8	Artificial intelligence challenges for predicting the impact of mutations on protein stability. <i>Current Opinion in Structural Biology</i> , 2022, 72, 161-168.	5.7	45
9	SOLart: a structure-based method to predict protein solubility and aggregation. <i>Bioinformatics</i> , 2020, 36, 1445-1452.	4.1	44
10	Correlators of supersymmetric Wilson-loops, protected operators and matrix models in $d = 4$ SYM. <i>Journal of High Energy Physics</i> , 2009, 2009, 061-061.	4.7	41
11	A comprehensive computational study of amino acid interactions in membrane proteins. <i>Scientific Reports</i> , 2019, 9, 12043.	3.3	40
12	Supersymmetric Wilson loops at two loops. <i>Journal of High Energy Physics</i> , 2008, 2008, 083-083.	4.7	39
13	High-quality Thermodynamic Data on the Stability Changes of Proteins Upon Single-site Mutations. <i>Journal of Physical and Chemical Reference Data</i> , 2016, 45, .	4.2	38
14	Stability Curve Prediction of Homologous Proteins Using Temperature-Dependent Statistical Potentials. <i>PLoS Computational Biology</i> , 2014, 10, e1003689.	3.2	32
15	Correlators of supersymmetric Wilson loops at weak and strong coupling. <i>Journal of High Energy Physics</i> , 2010, 2010, 1.	4.7	29
16	Symmetry Principles in Optimization Problems: an application to Protein Stability Prediction. <i>IFAC-PapersOnLine</i> , 2015, 48, 458-463.	0.9	29
17	pydca v1.0: a comprehensive software for direct coupling analysis of RNA and protein sequences. <i>Bioinformatics</i> , 2020, 36, 2264-2265.	4.1	25
18	Prediction and Evolution of the Molecular Fitness of SARS-CoV-2 Variants: Introducing SpikePro. <i>Viruses</i> , 2021, 13, 935.	3.3	22

#	ARTICLE	IF	CITATIONS
19	Quantifying Renin-Angiotensin-System Alterations in COVID-19. <i>Cells</i> , 2021, 10, 2755.	4.1	21
20	Towards an accurate prediction of the thermal stability of homologous proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1132-1142.	3.5	19
21	Improved insights into protein thermal stability: from the molecular to the structurome scale. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20160141.	3.4	18
22	Shedding light on the dark matter of the biomolecular structural universe: Progress in RNA 3D structure prediction. <i>Methods</i> , 2019, 162-163, 68-73.	3.8	18
23	Modeling the Molecular Impact of SARS-CoV-2 Infection on the Renin-Angiotensin System. <i>Viruses</i> , 2020, 12, 1367.	3.3	15
24	Protein Thermal Stability Engineering Using HoTMuSiC. <i>Methods in Molecular Biology</i> , 2020, 2112, 59-73.	0.9	15
25	Evaluating DCA-based method performances for RNA contact prediction by a well-curated data set. <i>Rna</i> , 2020, 26, 794-802.	3.5	13
26	SWOTein: a structure-based approach to predict stability Strengths and Weaknesses of prOTEINs. <i>Bioinformatics</i> , 2021, 37, 1963-1971.	4.1	13
27	<i>NPTX1</i> mutations trigger endoplasmic reticulum stress and cause autosomal dominant cerebellar ataxia. <i>Brain</i> , 2022, 145, 1519-1534.	7.6	10
28	Relation between DNA ionization potentials, single base substitutions and pathogenic variants. <i>BMC Genomics</i> , 2019, 20, 551.	2.8	7
29	Large-scale in silico mutagenesis experiments reveal optimization of genetic code and codon usage for protein mutational robustness. <i>BMC Biology</i> , 2020, 18, 146.	3.8	7
30	Taste symmetry breaking at finite temperature. <i>European Physical Journal C</i> , 2012, 72, 1.	3.9	5
31	Perturbing dimer interactions and allosteric communication modulates the immunosuppressive activity of human galectin-7. <i>Journal of Biological Chemistry</i> , 2021, 297, 101308.	3.4	5
32	Analysis of the Neutralizing Activity of Antibodies Targeting Open or Closed SARS-CoV-2 Spike Protein Conformations. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2078.	4.1	5
33	In Silico Analysis of the Molecular-Level Impact of SMPD1 Variants on Niemann-Pick Disease Severity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4516.	4.1	4
34	CoCoNetâ€”boosting RNA contact prediction by convolutional neural networks. <i>Nucleic Acids Research</i> , 2021, 49, 12661-12672.	14.5	3
35	BRANEart: Identify Stability Strength and Weakness Regions in Membrane Proteins. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	2.1	3
36	Using metagenomic data to boost protein structure prediction and discovery. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 434-442.	4.1	3

#	ARTICLE	IF	CITATIONS
37	More on $\hat{t}$ Hooft loops in $\mathcal{N}=4$ SYM. Journal of High Energy Physics, 2012, 2012, 1.	4.7	2
38	Intrinsic noise modulation in closed oligomerization-type systems $\hat{Z}$ $\hat{Z}$ FP 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
39	Insights into noise modulation in oligomerization systems of increasing complexity. Physical Review E, 2018, 98, 012137.	2.1	2
40	MutaFrame"an interpretative visualization framework for deleteriousness prediction of missense variants in the human exome. Bioinformatics, 2021, 38, 265-266.	4.1	2
41	Exploring the Aoki regime. Journal of High Energy Physics, 2013, 2013, 1.	4.7	1
42	Deciphering noise amplification and reduction in open chemical reaction networks. Journal of the Royal Society Interface, 2018, 15, 20180805.	3.4	1
43	BPS Wilson loops on Hyperbolic space. Journal of Physics A: Mathematical and Theoretical, 2014, 47, 385401.	2.1	0
44	Finite volume corrections to LECs in Wilson and staggered ChPT. , 2012, , .		0
45	Taste symmetry violation at finite temperature. , 2012, , .		0