

Luisa Di Paola

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

1,320
citations

430874

18
h-index

377865

34
g-index

60
all docs

60
docs citations

60
times ranked

1676
citing authors

#	ARTICLE	IF	CITATIONS
1	Symmetric versus Asymmetric Features of Homologous Homodimeric Amine Oxidases: When Water and Cavities Make the Difference. <i>Symmetry</i> , 2022, 14, 522.	2.2	1
2	One for All, All for One: The Peculiar Dynamics of TNF-Receptor-Associated Factor (TRAF2) Subunits. <i>Symmetry</i> , 2022, 14, 720.	2.2	3
3	Biophysical Insight into the SARS-CoV2 Spike-ACE2 Interaction and Its Modulation by Hepcidin through a Multifaceted Computational Approach. <i>ACS Omega</i> , 2022, 7, 17024-17042.	3.5	9
4	PCN-Miner: an open-source extensible tool for the analysis of Protein Contact Networks. <i>Bioinformatics</i> , 2022, 38, 4235-4237.	4.1	11
5	Non-symmetrical structural behavior of a symmetric protein: the case of homo-trimeric TRAF2 (tumor) Tj ETQq1 1 0.784314 rgBT /Over 39, 319-329.	3.5	10
6	Polymorphism on human aromatase affects protein dynamics and substrate binding: spectroscopic evidence. <i>Biology Direct</i> , 2021, 16, 8.	4.6	2
7	Integrated Biophysical Modeling of the SARS-CoV-2 Spike Protein Binding and Allosteric Interactions with Antibodies. <i>Journal of Physical Chemistry B</i> , 2021, 125, 4596-4619.	2.6	60
8	The Odd Faces of Oligomers: The Case of TRAF2-C, A Trimeric C-Terminal Domain of TNF Receptor-Associated Factor. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5871.	4.1	7
9	Network models of biological adaptation at the molecular scale. <i>Physics of Life Reviews</i> , 2021, 38, 124-126.	2.8	2
10	Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and Signal Transmission via Cascades of Regulatory Switches. <i>Journal of Physical Chemistry B</i> , 2021, 125, 850-873.	2.6	66
11	Disclosing Allostery Through Protein Contact Networks. <i>Methods in Molecular Biology</i> , 2021, 2253, 7-20.	0.9	9
12	Protein Assembly: Defining the Strength of Protein-Protein Interactions Coupling the Theory with Experiments. <i>Methods in Molecular Biology</i> , 2021, 2253, 77-88.	0.9	0
13	Cardiovascular Active Peptides of Marine Origin with ACE Inhibitory Activities: Potential Role as Anti-Hypertensive Drugs and in Prevention of SARS-CoV-2 Infection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8364.	4.1	14
14	Fishery Wastes as a Yet Undiscovered Treasure from the Sea: Biomolecules Sources, Extraction Methods and Valorization. <i>Marine Drugs</i> , 2020, 18, 622.	4.6	86
15	The Discovery of a Putative Allosteric Site in the SARS-CoV-2 Spike Protein Using an Integrated Structural/Dynamic Approach. <i>Journal of Proteome Research</i> , 2020, 19, 4576-4586.	3.7	66
16	Effects of protein-protein interface disruptors at the ligand of the glucocorticoid-induced tumor necrosis factor receptor-related gene (GITR). <i>Biochemical Pharmacology</i> , 2020, 178, 114110.	4.4	9
17	Novel indole derivatives targeting HuR-mRNA complex to counteract high glucose damage in retinal endothelial cells. <i>Biochemical Pharmacology</i> , 2020, 175, 113908.	4.4	27
18	Characterization of innovative sensors for volatile organic compounds trace compounds in biogas. <i>Asia-Pacific Journal of Chemical Engineering</i> , 2019, 14, e2321.	1.5	1

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19	Ethanol From Biomass. , 2019, , 25-59.		18
20	AN ACCURATE EXPLICIT EXPRESSION FOR THE SELF INDUCTANCE OF THIN-WIRE ROUND PANCAKE COILS. Progress in Electromagnetics Research Letters, 2019, 84, 147-153.	0.7	0
21	The basic principles of topology-dynamics relations in networks: An empirical approach. Physica A: Statistical Mechanics and Its Applications, 2018, 508, 584-594.	2.6	7
22	The Two Faces of Protein Flexibility: A Topological Approach. Current Chemical Biology, 2018, 12, 14-22.	0.5	1
23	Design of microfluidic bioreactors: Transport regimes. Asia-Pacific Journal of Chemical Engineering, 2018, 13, e2238.	1.5	2
24	Auxin minimum triggers the developmental switch from cell division to cell differentiation in the <i>Arabidopsis</i> root. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7641-E7649.	7.1	193
25	Comparative Study of Elastic Network Model and Protein Contact Network for Protein Complexes: The Hemoglobin Case. BioMed Research International, 2017, 2017, 1-15.	1.9	20
26	Network Proteomics: From Protein Structure to Protein-Protein Interaction. BioMed Research International, 2017, 2017, 1-1.	1.9	4
27	P2X7 receptor antagonism: Implications in diabetic retinopathy. Biochemical Pharmacology, 2017, 138, 130-139.	4.4	71
28	Two phase partitioning bioreactor applied to produced water treatment. Journal of Water Reuse and Desalination, 2016, 6, 274-279.	2.3	1
29	Are biofuels sustainable? An LCA/multivariate perspective on feedstocks and processes. Asia-Pacific Journal of Chemical Engineering, 2016, 11, 650-663.	1.5	8
30	GH32 family activity: a topological approach through protein contact networks. Plant Molecular Biology, 2016, 92, 401-410.	3.9	15
31	Biodiesel production from microalgae: ionic liquid process simulation. Journal of Cleaner Production, 2016, 111, 62-68.	9.3	51
32	Are Proteins Just Coiled Cords? Local and Global Analysis of Contact Maps Reveals the Backbone-Dependent Nature of Proteins. Current Protein and Peptide Science, 2015, 17, 26-29.	1.4	6
33	Exploring the stability of dimers through protein structure topology. Current Protein and Peptide Science, 2015, 17, 30-36.	1.4	18
34	Characterization of Protein-Protein Interfaces through a Protein Contact Network Approach. Frontiers in Bioengineering and Biotechnology, 2015, 3, 170.	4.1	20
35	Molecular features of interaction between VEGFA and anti-angiogenic drugs used in retinal diseases: a computational approach. Frontiers in Pharmacology, 2015, 6, 248.	3.5	73
36	Editorial (Thematic Issue: Protein as Networks: Will Contact Maps Hold the Promise to Represent the) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	1.4	4

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37	Reverse osmosis membranes for treatment of produced water: a process analysis. <i>Desalination and Water Treatment</i> , 2015, 55, 565-574.	1.0	27
38	Protein contact network topology: a natural language for allostery. <i>Current Opinion in Structural Biology</i> , 2015, 31, 43-48.	5.7	141
39	Comment-Protein Contact Networks: A New Framework for Structural Biology. , 2014, 4, .		1
40	Sequencing batch reactors (SBRs) for BioH ₂ production: Reactor operation criteria. <i>International Journal of Hydrogen Energy</i> , 2014, 39, 4863-4869.	7.1	12
41	Modules Identification in Protein Structures: The Topological and Geometrical Solutions. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 159-168.	5.4	38
42	Chemical reaction engineering methodologies for post-contrastographic biomedical imaging analysis. <i>Asia-Pacific Journal of Chemical Engineering</i> , 2014, 9, 354-363.	1.5	0
43	Biomedical and biotechnological applications of chemical engineering methodologies. <i>Asia-Pacific Journal of Chemical Engineering</i> , 2014, 9, 317-317.	1.5	0
44	GIANT: A Cytoscape Plugin for Modular Networks. <i>PLoS ONE</i> , 2014, 9, e105001.	2.5	39
45	Assessing protein resilience via a complex network approach. , 2013, , .		5
46	Structural and Functional Analysis of Hemoglobin and Serum Albumin Through Protein Long-Range Interaction Networks. <i>Current Proteomics</i> , 2012, 9, 160-166.	0.3	12
47	Sym-Bio GUI: A graphical user interface to analyze protein aminoacid residue contact networks. , 2012, , .		3
48	Extracorporeal membrane blood oxygenators: effect of membrane wetting on gas transfer and device performance. <i>Asia-Pacific Journal of Chemical Engineering</i> , 2012, 7, S348.	1.5	5
49	Proteins as Sponges: A Statistical Journey along Protein Structure Organization Principles. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 474-482.	5.4	29
50	Shedding light on protein-ligand binding by graph theory: The topological nature of allostery. <i>Biophysical Chemistry</i> , 2012, 165-166, 21-29.	2.8	48
51	Characterizing Protein Shape by a Volume Distribution Asymmetry Index. <i>Open Bioinformatics Journal</i> , 2012, 6, 20-27.	1.0	3
52	Observer-based techniques for the identification and analysis of avascular tumor growth. <i>Mathematical Biosciences</i> , 2011, 234, 147-153.	1.9	7
53	Proteins as Networks: A Mesoscopic Approach Using Haemoglobin Molecule as Case Study. <i>Current Proteomics</i> , 2009, 6, 235-245.	0.3	43
54	A novel process of humidification-dehumidification with brine recirculation for desalination in remote areas of the world. , 0, 69, 244-251.		6