

# Matteo Lambrughi

## List of Publications by Year in descending order

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35  
papers

1,642  
citations

430874

18  
h-index

395702

33  
g-index

41  
all docs

41  
docs citations

41  
times ranked

3220  
citing authors

#	ARTICLE	IF	CITATIONS
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	14.5	117
2	Cancer-related Mutations with Local or Long-range Effects on an Allosteric Loop of p53. <i>Journal of Molecular Biology</i> , 2022, 434, 167663.	4.2	17
3	Unraveling membrane properties at the organelle-level with LipidDyn. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3604-3614.	4.1	8
4	The conformational and mutational landscape of the ubiquitin-like marker for autophagosome formation in cancer. <i>Autophagy</i> , 2021, 17, 2818-2841.	9.1	19
5	Characterization of a natural variant of human NDP52 and its functional consequences on mitophagy. <i>Cell Death and Differentiation</i> , 2021, 28, 2499-2516.	11.2	12
6	TFG binds LC3C to regulate ULK1 localization and autophagosome formation. <i>EMBO Journal</i> , 2021, 40, e103563.	7.8	15
7	Ubiquitin Interacting Motifs: Duality Between Structured and Disordered Motifs. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 676235.	3.5	6
8	The PyInteraph Workflow for the Study of Interaction Networks From Protein Structural Ensembles. <i>Methods in Molecular Biology</i> , 2021, 2253, 153-174.	0.9	0
9	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	14.5	141
10	Structure and Dynamics in the ATG8 Family From Experimental to Computational Techniques. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 420.	3.7	24
11	S-nitrosylation affects TRAP1 structure and ATPase activity and modulates cell response to apoptotic stimuli. <i>Biochemical Pharmacology</i> , 2020, 176, 113869.	4.4	19
12	Conformational gating in ammonia lyases. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129605.	2.4	1
13	Structure-function investigation of 3-methylaspartate ammonia lyase reveals substrate molecular determinants for the deamination reaction. <i>PLoS ONE</i> , 2020, 15, e0233467.	2.5	1
14	Analyzing Biomolecular Ensembles. <i>Methods in Molecular Biology</i> , 2019, 2022, 415-451.	0.9	1
15	Selective autophagy maintains centrosome integrity and accurate mitosis by turnover of centriolar satellites. <i>Nature Communications</i> , 2019, 10, 4176.	12.8	61
16	Myoglobinopathy is an adult-onset autosomal dominant myopathy with characteristic sarcoplasmic inclusions. <i>Nature Communications</i> , 2019, 10, 1396.	12.8	11
17	Alterations of the interactome of Bcl-2 proteins in breast cancer at the transcriptional, mutational and structural level. <i>PLoS Computational Biology</i> , 2019, 15, e1007485.	3.2	42
18	Release of transcriptional repression via ErbB2-induced, SUMO-directed phosphorylation of myeloid zinc finger-1 serine 27 activates lysosome redistribution and invasion. <i>Oncogene</i> , 2019, 38, 3170-3184.	5.9	17

#	ARTICLE	IF	CITATIONS
19	Catalytic Mechanism of Fungal Lytic Polysaccharide Monoxygenases Investigated by First-Principles Calculations. <i>Inorganic Chemistry</i> , 2018, 57, 86-97.	4.0	72
20	Bi-allelic mutations in MYL1 cause a severe congenital myopathy. <i>Human Molecular Genetics</i> , 2018, 27, 4263-4272.	2.9	31
21	HUWE1 E3 ligase promotes PINK1/PARKIN-independent mitophagy by regulating AMBRA1 activation via IKK $\hat{\pm}$ . <i>Nature Communications</i> , 2018, 9, 3755.	12.8	198
22	Absence of Neurofibromin Induces an Oncogenic Metabolic Switch via Mitochondrial ERK-Mediated Phosphorylation of the Chaperone TRAP1. <i>Cell Reports</i> , 2017, 18, 659-672.	6.4	81
23	A phosphorylation-motif for tuneable helix stabilisation in intrinsically disordered proteins â€“ Lessons from the sodium proton exchanger 1 (NHE1). <i>Cellular Signalling</i> , 2017, 37, 40-51.	3.6	34
24	Hybrid Voronoi diagrams, their computation and reduction for applications in computational biochemistry. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 74, 225-233.	2.4	6
25	An optimal distance cutoff for contact-based Protein Structure Networks using side-chain centers of mass. <i>Scientific Reports</i> , 2017, 7, 2838.	3.3	70
26	The Mutational Landscape of the Oncogenic MZF1 SCAN Domain in Cancer. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 78.	3.5	34
27	The dynamics of the Î²-propeller domain in Kelch protein KLHL40 changes upon nemaline myopathy-associated mutation. <i>RSC Advances</i> , 2016, 6, 34043-34054.	3.6	6
28	DNA-binding protects p53 from interactions with cofactors involved in transcription-independent functions. <i>Nucleic Acids Research</i> , 2016, 44, gkw770.	14.5	40
29	The Role of Protein Loops and Linkers in Conformational Dynamics and Allostery. <i>Chemical Reviews</i> , 2016, 116, 6391-6423.	47.7	302
30	E2 superfamily of ubiquitin-conjugating enzymes: constitutively active or activated through phosphorylation in the catalytic cleft. <i>Scientific Reports</i> , 2015, 5, 14849.	3.3	43
31	Communication Routes in ARID Domains between Distal Residues in Helix 5 and the DNA-Binding Loops. <i>PLoS Computational Biology</i> , 2014, 10, e1003744.	3.2	40
32	PyInterph: A Framework for the Analysis of Interaction Networks in Structural Ensembles of Proteins. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 1537-1551.	5.4	107
33	The conformational ensemble of the disordered and aggregation-protective 182â€“291 region of ataxin-3. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 5236-5247.	2.4	14
34	A comparative study of Whi5 and retinoblastoma proteins: from sequence and structure analysis to intracellular networks. <i>Frontiers in Physiology</i> , 2013, 4, 315.	2.8	17
35	Intramolecular interactions stabilizing compact conformations of the intrinsically disordered kinase-inhibitor domain of Sic1: a molecular dynamics investigation. <i>Frontiers in Physiology</i> , 2012, 3, 435.	2.8	25