

# Luca Parca

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2837937/publications.pdf>

Version: 2024-02-01

27  
papers

1,313  
citations

687363

13  
h-index

552781

26  
g-index

29  
all docs

29  
docs citations

29  
times ranked

2750  
citing authors

#	ARTICLE	IF	CITATIONS
1	In situ structural analysis of the human nuclear pore complex. <i>Nature</i> , 2015, 526, 140-143.	27.8	361
2	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012, 8, 599.	7.2	216
3	PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. <i>Nucleic Acids Research</i> , 2012, 41, D306-D311.	14.5	116
4	Spatiotemporal variation of mammalian protein complex stoichiometries. <i>Genome Biology</i> , 2016, 17, 47.	8.8	115
5	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. <i>Nucleic Acids Research</i> , 2015, 43, D494-D502.	14.5	90
6	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	14.5	87
7	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 810-825.	3.8	65
8	Systematic identification of phosphorylation-mediated protein interaction switches. <i>PLoS Computational Biology</i> , 2017, 13, e1005462.	3.2	44
9	Modeling cancer drug response through drug-specific informative genes. <i>Scientific Reports</i> , 2019, 9, 15222.	3.3	42
10	Histone Deacetylase Inhibitors (HDACi) Cause the Selective Depletion of Bromodomain Containing Proteins (BCPs). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1350-1360.	3.8	23
11	MitImpact 3: modeling the residue interaction network of the Respiratory Chain subunits. <i>Nucleic Acids Research</i> , 2021, 49, D1282-D1288.	14.5	21
12	Discovering sequence and structure landscapes in RNA interaction motifs. <i>Nucleic Acids Research</i> , 2019, 47, 4958-4969.	14.5	17
13	Phosphate binding sites identification in protein structures. <i>Nucleic Acids Research</i> , 2011, 39, 1231-1242.	14.5	15
14	Quantifying compartment-associated variations of protein abundance in proteomics data. <i>Molecular Systems Biology</i> , 2018, 14, e8131.	7.2	14
15	Phosfinder: a web server for the identification of phosphate-binding sites on protein structures. <i>Nucleic Acids Research</i> , 2011, 39, W278-W282.	14.5	13
16	Pyntacle: a parallel computing-enabled framework for large-scale network biology analysis. <i>GigaScience</i> , 2020, 9, .	6.4	11
17	Mapping protein carboxymethylation sites provides insights into their role in proteostasis and cell proliferation. <i>Nature Communications</i> , 2021, 12, 6743.	12.8	11
18	Phosphorylation within Intrinsic Disordered Region Discriminates Histone Variant macroH2A1 Splicing Isoforms macroH2A1.1 and macroH2A1.2. <i>Biology</i> , 2021, 10, 659.	2.8	10

#	ARTICLE	IF	CITATIONS
19	Kinome-wide identification of phosphorylation networks in eukaryotic proteomes. <i>Bioinformatics</i> , 2019, 35, 372-379.	4.1	9
20	Mechanisms of pathogenesis of missense mutations on the KDM6A-H3 interaction in type 2 Kabuki Syndrome. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2033-2042.	4.1	9
21	Nucleos: a web server for the identification of nucleotide-binding sites in protein structures. <i>Nucleic Acids Research</i> , 2013, 41, W281-W285.	14.5	7
22	Identification of Nucleotide-Binding Sites in Protein Structures: A Novel Approach Based on Nucleotide Modularity. <i>PLoS ONE</i> , 2012, 7, e50240.	2.5	6
23	Variants in MHY7 Gene Cause Arrhythmogenic Cardiomyopathy. <i>Genes</i> , 2021, 12, 793.	2.4	4
24	Transcriptome and Gene Fusion Analysis of Synchronous Lesions Reveals IncMRPS31P5 as a Novel Transcript Involved in Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7120.	4.1	3
25	Variation in the co-expression profile highlights a loss of miRNA-mRNA regulation in multiple cancer types. <i>Non-coding RNA Research</i> , 2022, 7, 98-105.	4.6	2
26	Dissecting the Genome for Drug Response Prediction. <i>Methods in Molecular Biology</i> , 2022, 2449, 187-196.	0.9	1
27	Conserved exchange of paralog proteins during neuronal differentiation. <i>Life Science Alliance</i> , 2022, 5, e202201397.	2.8	0