

# Cristina Marino-Buslje

## List of Publications by Year in descending order

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Version: 2024-02-01

55  
papers

1,647  
citations

304602

22  
h-index

345118

36  
g-index

61  
all docs

61  
docs citations

61  
times ranked

2268  
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.	6.5	117
2	DisPhaseDB: An integrative database of diseases related variations in liquidâ€“liquid phase separation proteins. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2551-2557.	1.9	4
3	Insight into membraneless organelles and their associated proteins: Drivers, Clients and Regulators. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3964-3977.	1.9	24
4	Panels and models for accurate prediction of tumor mutation burden in tumor samples. <i>Npj Precision Oncology</i> , 2021, 5, 31.	2.3	7
5	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	6.5	95
6	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
7	The role of P-type IIA and P-type IIB Ca <sup>2+</sup> -ATPases in plant development and growth. <i>Journal of Experimental Botany</i> , 2020, 71, 1239-1248.	2.4	39
8	Chasing coevolutionary signals in intrinsically disordered proteins complexes. <i>Scientific Reports</i> , 2020, 10, 17962.	1.6	7
9	Characterization of intellectual disability and autism comorbidity through gene panel sequencing. <i>Human Mutation</i> , 2019, 40, 1346-1363.	1.1	54
10	Comutation and exclusion analysis in human tumors: A tool for cancer biology studies and for rational selection of multitargeted therapeutic approaches. <i>Human Mutation</i> , 2019, 40, 413-425.	1.1	0
11	On the dynamical incompleteness of the Protein Data Bank. <i>Briefings in Bioinformatics</i> , 2019, 20, 356-359.	3.2	13
12	Cooperative RNA Recognition by a Viral Transcription Antiterminator. <i>Journal of Molecular Biology</i> , 2018, 430, 777-792.	2.0	10
13	How Does pH Fit in with Oscillating Polar Growth?. <i>Trends in Plant Science</i> , 2018, 23, 479-489.	4.3	33
14	How is structural divergence related to evolutionary information?. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 859-866.	1.2	13
15	MISTIC2: comprehensive server to study coevolution in protein families. <i>Nucleic Acids Research</i> , 2018, 46, W323-W328.	6.5	30
16	MIToS.jl: mutual information tools for protein sequence analysis in the Julia language. <i>Bioinformatics</i> , 2017, 33, 564-565.	1.8	17
17	Organization of Circadian Behavior Relies on Glycinergic Transmission. <i>Cell Reports</i> , 2017, 19, 72-85.	2.9	70
18	Proteinâ€“protein interactions leave evolutionary footprints: High molecular coevolution at the core of interfaces. <i>Protein Science</i> , 2017, 26, 2438-2444.	3.1	23

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19	Homology modeling in a dynamical world. <i>Protein Science</i> , 2017, 26, 2195-2206.	3.1	17
20	The conundrum of UDP-Glc entrance into the yeast ER lumen. <i>Glycobiology</i> , 2017, 27, 64-79.	1.3	4
21	Using coevolution to improve protein subfamily classification. <i>BMC Bioinformatics</i> , 2015, 16, .	1.2	1
22	I-COMS: Interprotein-CORrelated Mutations Server. <i>Nucleic Acids Research</i> , 2015, 43, W320-W325.	6.5	26
23	Conformational diversity and the emergence of sequence signatures during evolution. <i>Current Opinion in Structural Biology</i> , 2015, 32, 58-65.	2.6	35
24	The Arabidopsis DNA Polymerase $\delta$ Has a Role in the Deposition of Transcriptionally Active Epigenetic Marks, Development and Flowering. <i>PLoS Genetics</i> , 2015, 11, e1004975.	1.5	36
25	Differential Contributions of Tacaribe Arenavirus Nucleoprotein N-Terminal and C-Terminal Residues to Nucleocapsid Functional Activity. <i>Journal of Virology</i> , 2014, 88, 6492-6505.	1.5	10
26	Kin-Driver: a database of driver mutations in protein kinases. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau104-bau104.	1.4	23
27	Activating Mutations Cluster in the $\alpha$ -Molecular Brake Regions of Protein Kinases and Do Not Associate with Conserved or Catalytic Residues. <i>Human Mutation</i> , 2014, 35, 318-328.	1.1	20
28	Protein Conformational Diversity Correlates with Evolutionary Rate. <i>Molecular Biology and Evolution</i> , 2013, 30, 1500-1503.	3.5	36
29	Oligomerization of the reversibly glycosylated polypeptide: its role during rice plant development and in the regulation of self-glycosylation. <i>Protoplasma</i> , 2013, 250, 111-119.	1.0	3
30	The role of the N-terminal tail for the oligomerization, folding and stability of human frataxin. <i>FEBS Open Bio</i> , 2013, 3, 310-320.	1.0	11
31	MISTIC: mutual information server to infer coevolution. <i>Nucleic Acids Research</i> , 2013, 41, W8-W14.	6.5	157
32	Transcriptional Regulation of Insulin-degrading Enzyme Modulates Mitochondrial Amyloid $A\beta$ Peptide Catabolism and Functionality. <i>Journal of Biological Chemistry</i> , 2013, 288, 12920-12931.	1.6	31
33	Disentangling evolutionary signals: conservation, specificity determining positions and coevolution. Implication for catalytic residue prediction. <i>BMC Bioinformatics</i> , 2012, 13, 235.	1.2	35
34	A Naturally Occurring Hypoallergenic Variant of Vespid Antigen 5 from <i>Polybia scutellaris</i> Venom as a Candidate for Allergen-Specific Immunotherapy. <i>PLoS ONE</i> , 2012, 7, e41351.	1.1	8
35	Mapping the Mutual Information Network of Enzymatic Families in the Protein Structure to Unveil Functional Features. <i>PLoS ONE</i> , 2012, 7, e41430.	1.1	33
36	Sequence Evolution of the Intrinsically Disordered and Globular Domains of a Model Viral Oncoprotein. <i>PLoS ONE</i> , 2012, 7, e47661.	1.1	25

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37	The residue 179 is involved in product specificity of the <i>Bacillus circulans</i> DF 9R cyclodextrin glycosyltransferase. <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 123-130.	1.7	18
38	Molecular Determinants of Arenavirus Z Protein Homo-Oligomerization and L Polymerase Binding. <i>Journal of Virology</i> , 2011, 85, 12304-12314.	1.5	33
39	Biochemical characterization of serine acetyltransferase and cysteine desulfhydrase from <i>Leishmania major</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 173, 170-174.	0.5	11
40	Networks of High Mutual Information Define the Structural Proximity of Catalytic Sites: Implications for Catalytic Residue Identification. <i>PLoS Computational Biology</i> , 2010, 6, e1000978.	1.5	74
41	A New Conformation in Sarcoplasmic Reticulum Calcium Pump and Plasma Membrane Ca <sup>2+</sup> Pumps Revealed by a Photoactivatable Phospholipidic Probe. <i>Journal of Biological Chemistry</i> , 2009, 284, 4823-4828.	1.6	18
42	Correction for phylogeny, small number of observations and data redundancy improves the identification of coevolving amino acid pairs using mutual information. <i>Bioinformatics</i> , 2009, 25, 1125-1131.	1.8	88
43	Structural Selection of a Native Fold by Peptide Recognition. Insights into the Thioredoxin Folding Mechanism. <i>Biochemistry</i> , 2009, 48, 595-607.	1.2	10
44	Interactions between $\hat{\pm}$ -conotoxin MI and the <i>Torpedo marmorata</i> receptor $\hat{\pm}$ interface. <i>Biochemical and Biophysical Research Communications</i> , 2007, 355, 275-279.	1.0	8
45	Consolidation of the Thioredoxin Fold by Peptide Recognition: Interaction between <i>E. coli</i> Thioredoxin Fragments 1 <sup>âˆ’</sup> 93 and 94 <sup>âˆ’</sup> 108. <i>Biochemistry</i> , 2007, 46, 5148-5159.	1.2	13
46	Structural aspects of the <i>Mucor bacilliformis</i> proteinase, a new member of the aspartyl-proteinase family. <i>Journal of Biotechnology</i> , 2006, 123, 443-452.	1.9	12
47	Structural determinants of binding and specificity in transforming growth factor-receptor interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 408-420.	1.5	11
48	Contribution of C-tail residues of potato carboxypeptidase inhibitor to the binding to carboxypeptidase $\hat{\pm}$ A. <i>FEBS Journal</i> , 2000, 267, 1502-1509.	0.2	18
49	Replacement of methionine-161 with threonine eliminates a major by-product of human glutamate decarboxylase 65-kDa variant expression in <i>Escherichia coli</i> . <i>Biotechnology and Applied Biochemistry</i> , 2000, 31, 205.	1.4	4
50	Structural domains of the insulin receptor and IGF receptor required for dimerisation and ligand binding. <i>FEBS Letters</i> , 2000, 467, 226-230.	1.3	23
51	The Insulin Receptor: from Protein Sequence to Structure. <i>Biochemical Society Transactions</i> , 1999, 27, 715-726.	1.6	36
52	Cloning, sequencing and functional expression of a cDNA encoding porcine pancreatic procarboxypeptidase A1. <i>FEBS Journal</i> , 1999, 259, 719-726.	0.2	8
53	A third fibronectin type III domain in the extracellular region of the insulin receptor family. <i>FEBS Letters</i> , 1998, 441, 331-336.	1.3	28
54	On the Entropic and Hydrophobic Properties Involved in the Inhibitory Mechanism of Carboxypeptidase A by its Natural Inhibitor from Potato. <i>Journal of Molecular Modeling</i> , 1995, 1, 54-67.	0.8	3

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55	Overproduction of a recombinant carboxypeptidase inhibitor by optimization of fermentation conditions. <i>Applied Microbiology and Biotechnology</i> , 1994, 41, 632-637.	1.7	13