

# Marco Punta

## List of Publications by Year in descending order

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Version: 2024-02-01

58  
papers

21,040  
citations

147566

31  
h-index

143772

57  
g-index

64  
all docs

64  
docs citations

64  
times ranked

36402  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014, 42, D222-D230.	6.5	5,425
2	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016, 44, D279-D285.	6.5	5,391
3	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012, 40, D290-D301.	6.5	3,306
4	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. <i>Nucleic Acids Research</i> , 2013, 41, e121-e121.	6.5	1,214
5	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	1,205
6	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
7	PredictProteinâ€”an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014, 42, W337-W343.	6.5	589
8	New mini- zincin structures provide a minimal scaffold for members of this metallopeptidase superfamily. <i>BMC Bioinformatics</i> , 2014, 15, 1.	1.2	541
9	Genomic and Transcriptomic Determinants of Therapy Resistance and Immune Landscape Evolution during Anti-EGFR Treatment in Colorectal Cancer. <i>Cancer Cell</i> , 2019, 36, 35-50.e9.	7.7	179
10	Improved Disorder Prediction by Combination of Orthogonal Approaches. <i>PLoS ONE</i> , 2009, 4, e4433.	1.1	170
11	PROFcon: novel prediction of long-range contacts. <i>Bioinformatics</i> , 2005, 21, 2960-2968.	1.8	138
12	Protein disorderâ€”a breakthrough invention of evolution?. <i>Current Opinion in Structural Biology</i> , 2011, 21, 412-418.	2.6	134
13	Crystal structure of a potassium ion transporter, TrkH. <i>Nature</i> , 2011, 471, 336-340.	13.7	120
14	Natively unstructured regions in proteins identified from contact predictions. <i>Bioinformatics</i> , 2007, 23, 2376-2384.	1.8	118
15	Homologue structure of the SLAC1 anion channel for closing stomata in leaves. <i>Nature</i> , 2010, 467, 1074-1080.	13.7	118
16	Clinical <i>BRCA1/2</i> Reversion Analysis Identifies Hotspot Mutations and Predicted Neoantigens Associated with Therapy Resistance. <i>Cancer Discovery</i> , 2020, 10, 1475-1488.	7.7	109
17	Membrane protein prediction methods. <i>Methods</i> , 2007, 41, 460-474.	1.9	104
18	CASP6 assessment of contact prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 214-224.	1.5	86

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19	Identifying cysteines and histidines in transition-metal-binding sites using support vector machines and neural networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 305-316.	1.5	86
20	Beyond annotation transfer by homology: novel protein-function prediction methods to assist drug discovery. <i>Drug Discovery Today</i> , 2005, 10, 1475-1482.	3.2	84
21	Protein Folding Rates Estimated from Contact Predictions. <i>Journal of Molecular Biology</i> , 2005, 348, 507-512.	2.0	84
22	The Rough Guide to In Silico Function Prediction, or How To Use Sequence and Structure Information To Predict Protein Function. <i>PLoS Computational Biology</i> , 2008, 4, e1000160.	1.5	83
23	Crystal structure of a phosphorylation-coupled saccharide transporter. <i>Nature</i> , 2011, 473, 50-54.	13.7	77
24	Large-Scale Analysis of Thermostable, Mammalian Proteins Provides Insights into the Intrinsically Disordered Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 211-226.	1.8	76
25	The New York Consortium on Membrane Protein Structure (NYCOMPS): a high-throughput platform for structural genomics of integral membrane proteins. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 191-199.	1.2	57
26	MetalDetector: a web server for predicting metal-binding sites and disulfide bridges in proteins from sequence. <i>Bioinformatics</i> , 2008, 24, 2094-2095.	1.8	47
27	Structural genomics target selection for the New York consortium on membrane protein structure. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 255-268.	1.2	46
28	Extreme intratumour heterogeneity and driver evolution in mismatch repair deficient gastro-oesophageal cancer. <i>Nature Communications</i> , 2020, 11, 139.	5.8	44
29	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015, 43, D382-D386.	6.5	42
30	Characterization of metalloproteins by high-throughput X-ray absorption spectroscopy. <i>Genome Research</i> , 2011, 21, 898-907.	2.4	41
31	AntiFam: a tool to help identify spurious ORFs in protein annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas003-bas003.	1.4	38
32	Structural genomics plucks high-hanging membrane proteins. <i>Current Opinion in Structural Biology</i> , 2012, 22, 326-332.	2.6	38
33	Microenvironmental niche divergence shapes BRCA1-dysregulated ovarian cancer morphological plasticity. <i>Nature Communications</i> , 2018, 9, 3917.	5.8	33
34	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, 4725-4725.	6.5	31
35	Structural genomics reveals EVE as a new ASCH/PUA-related domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 760-773.	1.5	29
36	A knowledge-based scale for amino acid membrane propensity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 50, 114-121.	1.5	27

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37	Carbon dating cancer: defining the chronology of metastatic progression in colorectal cancer. <i>Annals of Oncology</i> , 2017, 28, 1243-1249.	0.6	25
38	Movement of the C-Helix during the Gating of Cyclic Nucleotide-Gated Channels. <i>Biophysical Journal</i> , 2002, 83, 3283-3295.	0.2	22
39	The challenge of increasing Pfam coverage of the human proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat023.	1.4	22
40	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. <i>Journal of Proteomics</i> , 2013, 87, 134-138.	1.2	19
41	An estimated 5% of new protein structures solved today represent a new Pfam family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2186-2193.	2.5	12
42	Identification of single nucleotide variants using position-specific error estimation in deep sequencing data. <i>BMC Medical Genomics</i> , 2019, 12, 115.	0.7	10
43	Structure-based analysis of CysZ-mediated cellular uptake of sulfate. <i>ELife</i> , 2018, 7, .	2.8	10
44	Prediction and Analysis of Intrinsically Disordered Proteins. <i>Methods in Molecular Biology</i> , 2015, 1261, 35-59.	0.4	9
45	Molecular modeling studies on CNG channel from bovine retinal rod: A structural model of the cyclic nucleotide-binding domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 332-338.	1.5	8
46	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013, 14, 341.	1.2	8
47	Structure and sequence analyses of <i>Bacteroides</i> proteins BVU_4064 and BF1687 reveal presence of two novel predominantly-beta domains, predicted to be involved in lipid and cell surface interactions. <i>BMC Bioinformatics</i> , 2015, 16, 7.	1.2	8
48	Neural Networks Predict Protein Structure and Function. <i>Methods in Molecular Biology</i> , 2008, 458, 198-225.	0.4	8
49	The Immunogenic Potential of Recurrent Cancer Drug Resistance Mutations: An In Silico Study. <i>Frontiers in Immunology</i> , 2020, 11, 524968.	2.2	7
50	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. <i>Briefings in Bioinformatics</i> , 2015, 16, 865-872.	3.2	6
51	NMR Structure of Lipoprotein YxeF from <i>Bacillus subtilis</i> Reveals a Calycin Fold and Distant Homology with the Lipocalin Blc from <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2012, 7, e37404.	1.1	6
52	The SHOCT Domain: A Widespread Domain Under-Represented in Model Organisms. <i>PLoS ONE</i> , 2013, 8, e57848.	1.1	6
53	The challenge of increasing Pfam coverage of the human proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, .	1.4	5
54	Crystal structures of three representatives of a new <sc>P</sc>fam family PF14869 (DUF4488) suggest they function in sugar binding/uptake. <i>Protein Science</i> , 2014, 23, 1380-1391.	3.1	3

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55	Density Peak clustering of protein sequences associated to a Pfam clan reveals clear similarities and interesting differences with respect to manual family annotation. BMC Bioinformatics, 2021, 22, 121.	1.2	1
56	Metal Binding in Proteins: Machine Learning Complements X-Ray Absorption Spectroscopy. Lecture Notes in Computer Science, 2012, , 854-857.	1.0	1
57	Solution NMR structures of proteins VPA0419 from <i>Vibrio parahaemolyticus</i> and yiiS from <i>Shigella flexneri</i> provide structural coverage for protein domain family PFAM 04175. Proteins: Structure, Function and Bioinformatics, 2010, 78, 779-784.	1.5	0
58	Homology-Based Annotation of Large Protein Datasets. Methods in Molecular Biology, 2016, 1415, 153-176.	0.4	0