

# Maria Jesus Martin

## List of Publications by Citations

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**Version:** 2024-04-26

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

76  
papers

14,234  
citations

38  
h-index

89  
g-index

89  
ext. papers

19,956  
ext. citations

10.8  
avg, IF

6.71  
L-index

#	Paper	IF	Citations
76	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 365-70	20.1	2375
75	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D115-9	20.1	2195
74	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D154-9	20.1	1231
73	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D71-5	20.1	1096
72	UniProt: the universal protein knowledgebase in 2021. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D480-D489	20.1	1073
71	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D187-91	20.1	839
70	Update on activities at the Universal Protein Resource (UniProt) in 2013. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D43-7	20.1	589
69	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D325-D334	20.1	494
68	Gene Ontology annotations and resources. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D530-5	20.1	397
67	Infrastructure for the life sciences: design and implementation of the UniProt website. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 136	3.6	366
66	The GOA database: gene Ontology annotation updates for 2015. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D1057-63	20.1	361
65	The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D565-70	20.1	265
64	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , <b>2016</b> , 17, 184	18.3	218
63	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 275-84	13.4	206
62	Uniclust databases of clustered and deeply annotated protein sequences and alignments. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D170-D176	20.1	199
61	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D483-9	20.1	181
60	The Gene Ontology: enhancements for 2011. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D559-64	20.1	166

59	UniProt Protein Knowledgebase. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1558, 41-55	1.4	157
58	Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1878-1912	13.4	155
57	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , <b>2016</b> , 13, 425-30	21.6	133
56	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , <b>2019</b> , 20, 244	18.3	111
55	BioJS: an open source JavaScript framework for biological data visualization. <i>Bioinformatics</i> , <b>2013</b> , 29, 1103-4	7.2	88
54	UniProt Tools. <i>Current Protocols in Bioinformatics</i> , <b>2016</b> , 53, 1.29.1-1.29.15	24.2	77
53	SIFTS: updated Structure Integration with Function, Taxonomy and Sequences resource allows 40-fold increase in coverage of structure-based annotations for proteins. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D482-D489	20.1	69
52	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. <i>PLoS Biology</i> , <b>2017</b> , 15, e2001414	9.7	63
51	Searching and Navigating UniProt Databases. <i>Current Protocols in Bioinformatics</i> , <b>2015</b> , 50, 1.27.1-1.27.10	4.2	61
50	DEEPScreen: high performance drug-target interaction prediction with convolutional neural networks using 2-D structural compound representations. <i>Chemical Science</i> , <b>2020</b> , 11, 2531-2557	9.4	61
49	Understanding how and why the Gene Ontology and its annotations evolve: the GO within UniProt. <i>GigaScience</i> , <b>2014</b> , 3, 4	7.6	58
48	GlyGen: Computational and Informatics Resources for Glycoscience. <i>Glycobiology</i> , <b>2020</b> , 30, 72-73	5.8	53
47	HAMAP in 2013, new developments in the protein family classification and annotation system. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D584-9	20.1	52
46	The COMBREX project: design, methodology, and initial results. <i>PLoS Biology</i> , <b>2013</b> , 11, e1001638	9.7	47
45	ProtVista: visualization of protein sequence annotations. <i>Bioinformatics</i> , <b>2017</b> , 33, 2040-2041	7.2	44
44	ECPred: a tool for the prediction of the enzymatic functions of protein sequences based on the EC nomenclature. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 334	3.6	44
43	The Proteins API: accessing key integrated protein and genome information. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W539-W544	20.1	43
42	DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks. <i>Scientific Reports</i> , <b>2019</b> , 9, 7344	4.9	40

41	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 43-50	20.1	38
40	UniProtJAPI: a remote API for accessing UniProt data. <i>Bioinformatics</i> , <b>2008</b> , 24, 1321-2	7.2	32
39	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 1321-1325	5.6	27
38	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , <b>2018</b> , 34, 323-329	7.2	25
37	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. <i>Bioinformatics</i> , <b>2016</b> , 32, 2264-71	7.2	22
36	The impact of focused Gene Ontology curation of specific mammalian systems. <i>PLoS ONE</i> , <b>2011</b> , 6, e27541	4.17	22
35	Comparing bacterial genomes through conservation profiles. <i>Genome Research</i> , <b>2003</b> , 13, 991-8	9.7	20
34	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. <i>Bioinformatics</i> , <b>2020</b> , 36, 4643-4648	7.2	19
33	Expanding the horizons of microRNA bioinformatics. <i>Rna</i> , <b>2018</b> , 24, 1005-1017	5.8	19
32	AntiFam: a tool to help identify spurious ORFs in protein annotation. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2012</b> , 2012, bas003	5	18
31	The role SWISS-PROT and TrEMBL play in the genome research environment. <i>Journal of Biotechnology</i> , <b>2000</b> , 78, 221-34	3.7	18
30	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W538-W545	20.1	17
29	Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bas062	5	16
28	Minimizing proteome redundancy in the UniProt Knowledgebase. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	16
27	Analysis of the protein domain and domain architecture content in fungi and its application in the search of new antifungal targets. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003733	5	15
26	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	15
25	MDeePred: novel multi-channel protein featurization for deep learning-based binding affinity prediction in drug discovery. <i>Bioinformatics</i> , <b>2021</b> , 37, 693-704	7.2	14
24	UniProt genomic mapping for deciphering functional effects of missense variants. <i>Human Mutation</i> , <b>2019</b> , 40, 694-705	4.7	13

23	The EBI enzyme portal. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D773-80	20.1	13
22	From data repositories to submission portals: rethinking the role of domain-specific databases in CollecTF. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	12
21	Prediction of Metabolic Pathway Involvement in Prokaryotic UniProtKB Data by Association Rule Mining. <i>PLoS ONE</i> , <b>2016</b> , 11, e0158896	3.7	11
20	GlyGen data model and processing workflow. <i>Bioinformatics</i> , <b>2020</b> , 36, 3941-3943	7.2	10
19	Dasty3, a WEB framework for DAS. <i>Bioinformatics</i> , <b>2011</b> , 27, 2616-7	7.2	9
18	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. <i>F1000Research</i> , <b>2014</b> , 3, 47	3.6	7
17	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
16	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. <i>F1000Research</i> , <b>2014</b> , 3, 47	3.6	7
15	FAIR adoption, assessment and challenges at UniProt. <i>Scientific Data</i> , <b>2019</b> , 6, 175	8.2	6
14	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimer's Disease Gene Expression Data. <i>Journal of Alzheimers Disease</i> , <b>2020</b> , 75, 1417-1435	4.3	6
13	Effect of sequence padding on the performance of deep learning models in archaeal protein functional prediction. <i>Scientific Reports</i> , <b>2020</b> , 10, 14634	4.9	6
12	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimer's Disease Data. <i>Genes</i> , <b>2018</b> , 9,	4.2	6
11	Managing core resources for genomics and proteomics. <i>Pharmacogenomics</i> , <b>2003</b> , 4, 343-50	2.6	4
10	A GO catalogue of human DNA-binding transcription factors		4
9	A community-driven roadmap to advance research on translated open reading frames detected by Ribo-seq		4
8	Large-scale automated function prediction of protein sequences and an experimental case study validation on PTEN transcript variants. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2018</b> , 86, 135-151 <sup>4.2</sup>	4.2	4
7	CROssBAR: comprehensive resource of biomedical relations with knowledge graph representations. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e96	20.1	3
6	MyDas, an extensible Java DAS server. <i>PLoS ONE</i> , <b>2012</b> , 7, e44180	3.7	2

5	Protein domain-based prediction of drug/compound-target interactions and experimental validation on LIM kinases. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009171	5	1
4	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data		1
3	Enhancing the interoperability of glycan data flow between ChEBI, PubChem, and GlyGen. <i>Glycobiology</i> , <b>2021</b> ,	5.8	1
2	A GO catalogue of human DNA-binding transcription factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2021</b> , 1864, 194765	6	0
1	Protein Sequence Database Methods <b>2004</b> , 13-17		