

# Maria Jesus Martin

## List of Publications by Year in descending order

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Version: 2024-02-01

78  
papers

24,513  
citations

71102

41  
h-index

62596

80  
g-index

89  
all docs

89  
docs citations

89  
times ranked

32291  
citing authors

#	ARTICLE	IF	CITATIONS
1	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	14.5	4,709
2	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. Nucleic Acids Research, 2003, 31, 365-370.	14.5	3,096
3	UniProt: the Universal Protein knowledgebase. Nucleic Acids Research, 2004, 32, 115D-119.	14.5	2,994
4	The Gene Ontology resource: enriching a GOLD mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
5	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2004, 33, D154-D159.	14.5	1,681
6	Reorganizing the protein space at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2012, 40, D71-D75.	14.5	1,196
7	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	14.5	961
8	Update on activities at the Universal Protein Resource (UniProt) in 2013. Nucleic Acids Research, 2012, 41, D43-D47.	14.5	620
9	Uniclust databases of clustered and deeply annotated protein sequences and alignments. Nucleic Acids Research, 2017, 45, D170-D176.	14.5	520
10	The GOA database: Gene Ontology annotation updates for 2015. Nucleic Acids Research, 2015, 43, D1057-D1063.	14.5	493
11	Gene Ontology Annotations and Resources. Nucleic Acids Research, 2012, 41, D530-D535.	14.5	456
12	Infrastructure for the life sciences: design and implementation of the UniProt website. BMC Bioinformatics, 2009, 10, 136.	2.6	405
13	The UniProt-GO Annotation database in 2011. Nucleic Acids Research, 2012, 40, D565-D570.	14.5	349
14	Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases. Briefings in Bioinformatics, 2019, 20, 1878-1912.	6.5	310
15	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
16	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. Briefings in Bioinformatics, 2002, 3, 275-284.	6.5	273
17	UniProt Protein Knowledgebase. Methods in Molecular Biology, 2017, 1558, 41-55.	0.9	263
18	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261

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19	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. Nucleic Acids Research, 2012, 41, D483-D489.	14.5	238
20	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	19.0	198
21	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	14.5	191
22	SIFTS: updated Structure Integration with Function, Taxonomy and Sequences resource allows 40-fold increase in coverage of structure-based annotations for proteins. Nucleic Acids Research, 2019, 47, D482-D489.	14.5	165
23	UniProt Tools. Current Protocols in Bioinformatics, 2016, 53, 1.29.1-1.29.15.	25.8	150
24	DEEPScreen: high performance drug–target interaction prediction with convolutional neural networks using 2-D structural compound representations. Chemical Science, 2020, 11, 2531-2557.	7.4	131
25	GlyGen: Computational and Informatics Resources for Glycoscience. Glycobiology, 2020, 30, 72-73.	2.5	123
26	BioJS: an open source JavaScript framework for biological data visualization. Bioinformatics, 2013, 29, 1103-1104.	4.1	110
27	Big data and other challenges in the quest for orthologs. Bioinformatics, 2014, 30, 2993-2998.	4.1	109
28	ECPred: a tool for the prediction of the enzymatic functions of protein sequences based on the EC nomenclature. BMC Bioinformatics, 2018, 19, 334.	2.6	99
29	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. PLoS Biology, 2017, 15, e2001414.	5.6	97
30	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	14.5	89
31	DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks. Scientific Reports, 2019, 9, 7344.	3.3	80
32	Searching and Navigating UniProt Databases. Current Protocols in Bioinformatics, 2015, 50, 1.27.1-1.27.10.	25.8	72
33	Understanding how and why the Gene Ontology and its annotations evolve: the GO within UniProt. GigaScience, 2014, 3, 4.	6.4	70
34	The Proteins API: accessing key integrated protein and genome information. Nucleic Acids Research, 2017, 45, W539-W544.	14.5	69
35	MDeePred: novel multi-channel protein featurization for deep learning-based binding affinity prediction in drug discovery. Bioinformatics, 2021, 37, 693-704.	4.1	61
36	ProtVista: visualization of protein sequence annotations. Bioinformatics, 2017, 33, 2040-2041.	4.1	58

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37	HAMAP in 2013, new developments in the protein family classification and annotation system. Nucleic Acids Research, 2013, 41, D584-D589.	14.5	57
38	The European Bioinformatics Institute's data resources. Nucleic Acids Research, 2003, 31, 43-50.	14.5	56
39	UniProtJAPI: a remote API for accessing UniProt data. Bioinformatics, 2008, 24, 1321-1322.	4.1	56
40	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	5.6	54
41	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. Bioinformatics, 2020, 36, 4643-4648.	4.1	42
42	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	14.5	41
43	AntiFam: a tool to help identify spurious ORFs in protein annotation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas003-bas003.	3.0	38
44	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. Bioinformatics, 2016, 32, 2264-2271.	4.1	37
45	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	4.1	36
46	ProForma: A Standard Proteoform Notation. Journal of Proteome Research, 2018, 17, 1321-1325.	3.7	35
47	UniProt genomic mapping for deciphering functional effects of missense variants. Human Mutation, 2019, 40, 694-705.	2.5	29
48	The Quest for Orthologs orthology benchmark service in 2022. Nucleic Acids Research, 2022, 50, W623-W632.	14.5	29
49	Expanding the horizons of microRNA bioinformatics. Rna, 2018, 24, 1005-1017.	3.5	27
50	Comparing Bacterial Genomes Through Conservation Profiles. Genome Research, 2003, 13, 991-998.	5.5	26
51	Analysis of the Protein Domain and Domain Architecture Content in Fungi and Its Application in the Search of New Antifungal Targets. PLoS Computational Biology, 2014, 10, e1003733.	3.2	25
52	Minimizing proteome redundancy in the UniProt Knowledgebase. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw139.	3.0	24
53	The role SWISS-PROT and TrEMBL play in the genome research environment. Journal of Biotechnology, 2000, 78, 221-234.	3.8	23
54	The Impact of Focused Gene Ontology Curation of Specific Mammalian Systems. PLoS ONE, 2011, 6, e27541.	2.5	23

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55	GlyGen data model and processing workflow. <i>Bioinformatics</i> , 2020, 36, 3941-3943.	4.1	22
56	Effect of sequence padding on the performance of deep learning models in archaeal protein functional prediction. <i>Scientific Reports</i> , 2020, 10, 14634.	3.3	21
57	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> , 2016, 2016, baw055.	3.0	20
58	The EBI enzyme portal. <i>Nucleic Acids Research</i> , 2013, 41, D773-D780.	14.5	19
59	CROssBAR: comprehensive resource of biomedical relations with knowledge graph representations. <i>Nucleic Acids Research</i> , 2021, 49, e96-e96.	14.5	19
60	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimer's Disease Gene Expression Data. <i>Journal of Alzheimer's Disease</i> , 2020, 75, 1417-1435.	2.6	18
61	Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bas062.	3.0	17
62	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimer's Disease Data. <i>Genes</i> , 2018, 9, 593.	2.4	15
63	A GO catalogue of human DNA-binding transcription factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194765.	1.9	15
64	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. <i>Journal of Proteome Research</i> , 2022, 21, 1510-1524.	3.7	15
65	Dasty3, a WEB framework for DAS. <i>Bioinformatics</i> , 2011, 27, 2616-2617.	4.1	14
66	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1603-1615.	3.7	14
67	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> , 2018, 86, 135-151.	2.6	13
68	Prediction of Metabolic Pathway Involvement in Prokaryotic UniProtKB Data by Association Rule Mining. <i>PLoS ONE</i> , 2016, 11, e0158896.	2.5	13
69	Protein domain-based prediction of drug/compound-target interactions and experimental validation on LIM kinases. <i>PLoS Computational Biology</i> , 2021, 17, e1009171.	3.2	13
70	FAIR adoption, assessment and challenges at UniProt. <i>Scientific Data</i> , 2019, 6, 175.	5.3	11
71	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. <i>F1000Research</i> , 2014, 3, 47.	1.6	11
72	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. <i>F1000Research</i> , 2014, 3, 47.	1.6	8

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73	Managing core resources for genomics and proteomics. Pharmacogenomics, 2003, 4, 343-350.	1.3	4
74	SLPred: a multi-view subcellular localization prediction tool for multi-location human proteins. Bioinformatics, 2022, 38, 4226-4229.	4.1	3
75	Enhancing the interoperability of glycan data flow between ChEBI, PubChem, and GlyGen. Glycobiology, 2021, , .	2.5	2
76	The Enzyme Portal: an integrative tool for enzyme information and analysis. FEBS Journal, 2021, , .	4.7	2
77	MyDas, an Extensible Java DAS Server. PLoS ONE, 2012, 7, e44180.	2.5	2
78	Protein Sequence Database Methods. , 2004, , 13-17.		0