

# Maria Jesus Martin

## List of Publications by Year in descending order

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Version: 2024-02-01

78  
papers

24,513  
citations

71061

41  
h-index

62565

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. <i>Nucleic Acids Research</i> , 2021, 49, D480-D489.	6.5	4,709
2	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , 2003, 31, 365-370.	6.5	3,096
3	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , 2004, 32, 115D-119.	6.5	2,994
4	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	6.5	2,416
5	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2004, 33, D154-D159.	6.5	1,681
6	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2012, 40, D71-D75.	6.5	1,196
7	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006, 34, D187-D191.	6.5	961
8	Update on activities at the Universal Protein Resource (UniProt) in 2013. <i>Nucleic Acids Research</i> , 2012, 41, D43-D47.	6.5	620
9	Uniclust databases of clustered and deeply annotated protein sequences and alignments. <i>Nucleic Acids Research</i> , 2017, 45, D170-D176.	6.5	520
10	The GOA database: Gene Ontology annotation updates for 2015. <i>Nucleic Acids Research</i> , 2015, 43, D1057-D1063.	6.5	493
11	Gene Ontology Annotations and Resources. <i>Nucleic Acids Research</i> , 2012, 41, D530-D535.	6.5	456
12	Infrastructure for the life sciences: design and implementation of the UniProt website. <i>BMC Bioinformatics</i> , 2009, 10, 136.	1.2	405
13	The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , 2012, 40, D565-D570.	6.5	349
14	Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases. <i>Briefings in Bioinformatics</i> , 2019, 20, 1878-1912.	3.2	310
15	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
16	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. <i>Briefings in Bioinformatics</i> , 2002, 3, 275-284.	3.2	273
17	UniProt Protein Knowledgebase. <i>Methods in Molecular Biology</i> , 2017, 1558, 41-55.	0.4	263
18	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261

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19	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. Nucleic Acids Research, 2012, 41, D483-D489.	6.5	238
20	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
21	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	6.5	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.	6.5	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.	3.7	131
25	GlyGen: Computational and Informatics Resources for Glycoscience. Glycobiology, 2020, 30, 72-73.	1.3	123
26	BioJS: an open source JavaScript framework for biological data visualization. Bioinformatics, 2013, 29, 1103-1104.	1.8	110
27	Big data and other challenges in the quest for orthologs. Bioinformatics, 2014, 30, 2993-2998.	1.8	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.	1.2	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.	2.6	97
30	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	6.5	89
31	DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks. Scientific Reports, 2019, 9, 7344.	1.6	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.	3.3	70
34	The Proteins API: accessing key integrated protein and genome information. Nucleic Acids Research, 2017, 45, W539-W544.	6.5	69
35	MDeePred: novel multi-channel protein featurization for deep learning-based binding affinity prediction in drug discovery. Bioinformatics, 2021, 37, 693-704.	1.8	61
36	ProtVista: visualization of protein sequence annotations. Bioinformatics, 2017, 33, 2040-2041.	1.8	58

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37	HAMAP in 2013, new developments in the protein family classification and annotation system. <i>Nucleic Acids Research</i> , 2013, 41, D584-D589.	6.5	57
38	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2003, 31, 43-50.	6.5	56
39	UniProtJAPI: a remote API for accessing UniProt data. <i>Bioinformatics</i> , 2008, 24, 1321-1322.	1.8	56
40	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	2.6	54
41	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. <i>Bioinformatics</i> , 2020, 36, 4643-4648.	1.8	42
42	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020, 48, W538-W545.	6.5	41
43	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
44	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. <i>Bioinformatics</i> , 2016, 32, 2264-2271.	1.8	37
45	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
46	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325.	1.8	35
47	UniProt genomic mapping for deciphering functional effects of missense variants. <i>Human Mutation</i> , 2019, 40, 694-705.	1.1	29
48	The Quest for Orthologs orthology benchmark service in 2022. <i>Nucleic Acids Research</i> , 2022, 50, W623-W632.	6.5	29
49	Expanding the horizons of microRNA bioinformatics. <i>Rna</i> , 2018, 24, 1005-1017.	1.6	27
50	Comparing Bacterial Genomes Through Conservation Profiles. <i>Genome Research</i> , 2003, 13, 991-998.	2.4	26
51	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> , 2014, 10, e1003733.	1.5	25
52	Minimizing proteome redundancy in the UniProt Knowledgebase. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw139.	1.4	24
53	The role SWISS-PROT and TrEMBL play in the genome research environment. <i>Journal of Biotechnology</i> , 2000, 78, 221-234.	1.9	23
54	The Impact of Focused Gene Ontology Curation of Specific Mammalian Systems. <i>PLoS ONE</i> , 2011, 6, e27541.	1.1	23

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55	GlyGen data model and processing workflow. <i>Bioinformatics</i> , 2020, 36, 3941-3943.	1.8	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.	1.6	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.	1.4	20
58	The EBI enzyme portal. <i>Nucleic Acids Research</i> , 2013, 41, D773-D780.	6.5	19
59	CROssBAR: comprehensive resource of biomedical relations with knowledge graph representations. <i>Nucleic Acids Research</i> , 2021, 49, e96-e96.	6.5	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.	1.2	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.	1.4	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.	1.0	15
63	A GO catalogue of human DNA-binding transcription factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194765.	0.9	15
64	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. <i>Journal of Proteome Research</i> , 2022, 21, 1510-1524.	1.8	15
65	Dasty3, a WEB framework for DAS. <i>Bioinformatics</i> , 2011, 27, 2616-2617.	1.8	14
66	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1603-1615.	1.8	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.	1.5	13
68	Prediction of Metabolic Pathway Involvement in Prokaryotic UniProtKB Data by Association Rule Mining. <i>PLoS ONE</i> , 2016, 11, e0158896.	1.1	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.	1.5	13
70	FAIR adoption, assessment and challenges at UniProt. <i>Scientific Data</i> , 2019, 6, 175.	2.4	11
71	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. <i>F1000Research</i> , 2014, 3, 47.	0.8	11
72	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. <i>F1000Research</i> , 2014, 3, 47.	0.8	8

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73	Managing core resources for genomics and proteomics. <i>Pharmacogenomics</i> , 2003, 4, 343-350.	0.6	4
74	SLPred: a multi-view subcellular localization prediction tool for multi-location human proteins. <i>Bioinformatics</i> , 2022, 38, 4226-4229.	1.8	3
75	Enhancing the interoperability of glycan data flow between ChEBI, PubChem, and GlyGen. <i>Glycobiology</i> , 2021, , .	1.3	2
76	The Enzyme Portal: an integrative tool for enzyme information and analysis. <i>FEBS Journal</i> , 2021, , .	2.2	2
77	MyDas, an Extensible Java DAS Server. <i>PLoS ONE</i> , 2012, 7, e44180.	1.1	2
78	Protein Sequence Database Methods. , 2004, , 13-17.		0