

Domenico Cozzetto

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

4,186
citations

331259

21
h-index

525886

27
g-index

35
all docs

35
docs citations

35
times ranked

5470
citing authors

#	ARTICLE	IF	CITATIONS
1	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
2	DISOPRED3: precise disordered region predictions with annotated protein-binding activity. <i>Bioinformatics</i> , 2015, 31, 857-863.	1.8	744
3	PSICOV: precise structural contact prediction using sparse inverse covariance estimation on large multiple sequence alignments. <i>Bioinformatics</i> , 2012, 28, 184-190.	1.8	686
4	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
5	The PMDB Protein Model Database. <i>Nucleic Acids Research</i> , 2006, 34, D306-D309.	6.5	266
6	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
7	Assessment of predictions in the model quality assessment category. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 175-183.	1.5	122
8	Evaluation of template-based models in CASP8 with standard measures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 18-28.	1.5	114
9	Evaluation of predictions in the CASP10 model refinement category. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 98-111.	1.5	101
10	FFPred 3: feature-based function prediction for all Gene Ontology domains. <i>Scientific Reports</i> , 2016, 6, 31865.	1.6	93
11	Interleukin-22 orchestrates a pathological endoplasmic reticulum stress response transcriptional programme in colonic epithelial cells. <i>Gut</i> , 2020, 69, 578-590.	6.1	84
12	Evaluation of CASP8 model quality predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 157-166.	1.5	76
13	Protein function prediction by massive integration of evolutionary analyses and multiple data sources. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	72
14	Predicting human protein function with multi-task deep neural networks. <i>PLoS ONE</i> , 2018, 13, e0198216.	1.1	58
15	Computer-Assisted Protein Domain Boundary Prediction Using the Dom-Pred Server. <i>Current Protein and Peptide Science</i> , 2007, 8, 181-188.	0.7	52
16	Relationship between multiple sequence alignments and quality of protein comparative models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 151-157.	1.5	46
17	The contribution of intrinsic disorder prediction to the elucidation of protein function. <i>Current Opinion in Structural Biology</i> , 2013, 23, 467-472.	2.6	45
18	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015, 43, D382-D386.	6.5	42

#	ARTICLE	IF	CITATIONS
19	FFPred 2.0: Improved Homology-Independent Prediction of Gene Ontology Terms for Eukaryotic Protein Sequences. PLoS ONE, 2013, 8, e63754.	1.1	40
20	Computational Methods for Annotation Transfers from Sequence. Methods in Molecular Biology, 2017, 1446, 55-67.	0.4	40
21	Cancer-associated hypersialylated MUC1 drives the differentiation of human monocytes into macrophages with a pathogenic phenotype. Communications Biology, 2020, 3, 644.	2.0	36
22	An analysis of the Sargasso Sea resource and the consequences for database composition. BMC Bioinformatics, 2006, 7, 213.	1.2	18
23	TGF- β 1 potentiates V β 9V β 2 T β cell adoptive immunotherapy of cancer. Cell Reports Medicine, 2021, 2, 100473.	3.3	16
24	The Evaluation of Protein Structure Prediction Results. Molecular Biotechnology, 2008, 39, 1-8.	1.3	13
25	The Assessment of Methods for Protein Structure Prediction. , 2008, 413, 43-57.		11
26	Advances and Pitfalls in Protein Structure Prediction. Current Protein and Peptide Science, 2008, 9, 567-577.	0.7	11
27	Using deep maxout neural networks to improve the accuracy of function prediction from protein interaction networks. PLoS ONE, 2019, 14, e0209958.	1.1	11
28	The Relationship Between Protein Sequence, Structure and Function. , 2005, , 15-29.		4
29	Evaluation of Protein Structure Prediction Methods: Issues and Strategies. , 2011, , 315-339.		2
30	QUALITY AND EFFECTIVENESS OF PROTEIN STRUCTURE COMPARATIVE MODELS. , 2006, , .		0
31	The Assessment of Methods for Protein Structure Prediction. , 0, , 43-58.		0