Domenico Cozzetto

List of Publications by Year
in descending order

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	TGF-Î²1 potentiates Vγ9Vδ2 T cell adoptive immunotherapy of cancer. Cell Reports Medicine, 2021, 2, 100473.	3.3	16
2	Interleukin-22 orchestrates a pathological endoplasmic reticulum stress response transcriptional programme in colonic epithelial cells. Gut, 2020, 69, 578-590.	6.1	84
3	Cancer-associated hypersialylated MUC1 drives the differentiation of human monocytes into macrophages with a pathogenic phenotype. Communications Biology, 2020, 3, 644.	2.0	36
4	Using deep maxout neural networks to improve the accuracy of function prediction from protein interaction networks. PLoS ONE, 2019, 14, e0209958.	1.1	11
5	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
6	Predicting human protein function with multi-task deep neural networks. PLoS ONE, 2018, 13, e0198216.	1.1	58
7	Computational Methods for Annotation Transfers from Sequence. Methods in Molecular Biology, 2017, 1446, 55-67.	0.4	40
8	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
9	FFPred 3: feature-based function prediction for all Gene Ontology domains. Scientific Reports, 2016, 6, 31865.	1.6	93
10	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	6.5	42
11	DISOPRED3: precise disordered region predictions with annotated protein-binding activity. Bioinformatics, 2015, 31, 857-863.	1.8	744
12	Evaluation of predictions in the CASP10 model refinement category. Proteins: Structure, Function and Bioinformatics, 2014, 82, 98-111.	1.5	101
13	Protein function prediction by massive integration of evolutionary analyses and multiple data sources. BMC Bioinformatics, 2013, 14, S1.	1.2	72
14	The contribution of intrinsic disorder prediction to the elucidation of protein function. Current Opinion in Structural Biology, 2013, 23, 467-472.	2.6	45
15	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
16	FFPred 2.0: Improved Homology-Independent Prediction of Gene Ontology Terms for Eukaryotic Protein Sequences. PLoS ONE, 2013, 8, e63754.	1.1	40
17	PSICOV: precise structural contact prediction using sparse inverse covariance estimation on large multiple sequence alignments. Bioinformatics, 2012, 28, 184-190.	1.8	686
18	Evaluation of Protein Structure Prediction Methods: Issues and Strategies. , 2011, , 315-339.		2

#	Article	IF	Citations
19	Evaluation of CASP8 model quality predictions. Proteins: Structure, Function and Bioinformatics, 2009, 77, 157-166.	1.5	76
20	Evaluation of template‐based models in CASP8 with standard measures. Proteins: Structure, Function and Bioinformatics, 2009, 77, 18-28.	1.5	114
21	The Evaluation of Protein Structure Prediction Results. Molecular Biotechnology, 2008, 39, 1-8.	1.3	13
22	The Assessment of Methods for Protein Structure Prediction. , 2008, 413, 43-57.		11
23	Advances and Pitfalls in Protein Structure Prediction. Current Protein and Peptide Science, 2008, 9, 567-577.	0.7	11
24	Computer-Assisted Protein Domain Boundary Prediction Using the Dom-Pred Server. Current Protein and Peptide Science, 2007, 8, 181-188.	0.7	52
25	Assessment of predictions in the model quality assessment category. Proteins: Structure, Function and Bioinformatics, 2007, 69, 175-183.	1.5	122
26	The PMDB Protein Model Database. Nucleic Acids Research, 2006, 34, D306-D309.	6.5	266
27	An analysis of the Sargasso Sea resource and the consequences for database composition. BMC Bioinformatics, 2006, 7, 213.	1.2	18
28	QUALITY AND EFFECTIVENESS OF PROTEIN STRUCTURE COMPARATIVE MODELS. , 2006, , .		0
29	The Relationship Between Protein Sequence, Structure and Function. , 2005, , 15-29.		4
30	Relationship between multiple sequence alignments and quality of protein comparative models. Proteins: Structure, Function and Bioinformatics, 2004, 58, 151-157.	1.5	46
31	The Assessment of Methods for Protein Structure Prediction. , 0, , 43-58.		0