

David Tudor Jones

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

17,462
citations

116194

36
h-index

156644

58
g-index

66
all docs

66
docs citations

66
times ranked

24348
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein secondary structure prediction based on position-specific scoring matrices 1 Edited by G. Von Heijne. Journal of Molecular Biology, 1999, 292, 195-202.	2.0	5,026
2	Improved protein structure prediction using potentials from deep learning. Nature, 2020, 577, 706-710.	13.7	2,112
3	Classification of Intrinsically Disordered Regions and Proteins. Chemical Reviews, 2014, 114, 6589-6631.	23.0	1,618
4	The PSIPRED Protein Analysis Workbench: 20 years on. Nucleic Acids Research, 2019, 47, W402-W407.	6.5	881
5	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
6	Protein superfamilies and domain superfolds. Nature, 1994, 372, 631-634.	13.7	783
7	DISOPRED3: precise disordered region predictions with annotated protein-binding activity. Bioinformatics, 2015, 31, 857-863.	1.8	744
8	PSICOV: precise structural contact prediction using sparse inverse covariance estimation on large multiple sequence alignments. Bioinformatics, 2012, 28, 184-190.	1.8	686
9	A guide to machine learning for biologists. Nature Reviews Molecular Cell Biology, 2022, 23, 40-55.	16.1	626
10	Improving the accuracy of transmembrane protein topology prediction using evolutionary information. Bioinformatics, 2007, 23, 538-544.	1.8	389
11	Transmembrane protein topology prediction using support vector machines. BMC Bioinformatics, 2009, 10, 159.	1.2	377
12	MetaPSICOV: combining coevolution methods for accurate prediction of contacts and long range hydrogen bonding in proteins. Bioinformatics, 2015, 31, 999-1006.	1.8	311
13	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
14	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
15	Prediction of disordered regions in proteins from position specific score matrices. Proteins: Structure, Function and Bioinformatics, 2003, 53, 573-578.	1.5	207
16	High precision in protein contact prediction using fully convolutional neural networks and minimal sequence features. Bioinformatics, 2018, 34, 3308-3315.	1.8	157
17	Getting the most from PSI-BLAST. Trends in Biochemical Sciences, 2002, 27, 161-164.	3.7	145
18	Deep learning extends de novo protein modelling coverage of genomes using iteratively predicted structural constraints. Nature Communications, 2019, 10, 3977.	5.8	144

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19	A structural model for the nucleotide binding domains of the flavocytochrome <i>b₂₄₅</i> chain. <i>Protein Science</i> , 1993, 2, 1675-1685.	3.1	126
20	The impact of AlphaFold2 one year on. <i>Nature Methods</i> , 2022, 19, 15-20.	9.0	107
21	Prediction of interresidue contacts with DeepMetaPSICOV in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1092-1099.	1.5	102
22	Evaluation of predictions in the CASP10 model refinement category. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 98-111.	1.5	101
23	De Novo Structure Prediction of Globular Proteins Aided by Sequence Variation-Derived Contacts. <i>PLoS ONE</i> , 2014, 9, e92197.	1.1	98
24	FFPred 3: feature-based function prediction for all Gene Ontology domains. <i>Scientific Reports</i> , 2016, 6, 31865.	1.6	93
25	Isolation and Comparative Transcriptome Analysis of Human Fetal and iPSC-Derived Cone Photoreceptor Cells. <i>Stem Cell Reports</i> , 2017, 9, 1898-1915.	2.3	90
26	Setting the standards for machine learning in biology. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 659-660.	16.1	83
27	Design of metalloproteins and novel protein folds using variational autoencoders. <i>Scientific Reports</i> , 2018, 8, 16189.	1.6	82
28	Prediction of progress at last. <i>Nature</i> , 1991, 354, 105-106.	13.7	77
29	Assembling novel protein folds from super-secondary structural fragments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 480-485.	1.5	73
30	Protein function prediction by massive integration of evolutionary analyses and multiple data sources. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	72
31	Predicting human protein function with multi-task deep neural networks. <i>PLoS ONE</i> , 2018, 13, e0198216.	1.1	58
32	Recent developments in deep learning applied to protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1179-1189.	1.5	56
33	EigenTHREADER: analogous protein fold recognition by efficient contact map threading. <i>Bioinformatics</i> , 2017, 33, 2684-2690.	1.8	54
34	Improved protein contact predictions with the MetaPSICOV2 server in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 78-83.	1.5	52
35	Accurate contact predictions using covariation techniques and machine learning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 145-151.	1.5	48
36	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015, 43, D382-D386.	6.5	42

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37	FFPred 2.0: Improved Homology-Independent Prediction of Gene Ontology Terms for Eukaryotic Protein Sequences. PLoS ONE, 2013, 8, e63754.	1.1	40
38	Computational Methods for Annotation Transfers from Sequence. Methods in Molecular Biology, 2017, 1446, 55-67.	0.4	40
39	Protein function prediction is improved by creating synthetic feature samples with generative adversarial networks. Nature Machine Intelligence, 2020, 2, 540-550.	8.3	40
40	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	1.1	39
41	Framework engineering to produce dominant T cell receptors with enhanced antigen-specific function. Nature Communications, 2019, 10, 4451.	5.8	38
42	Recurrence of a binding motif?. Nature, 1993, 362, 299-299.	13.7	26
43	Ultrafast end-to-end protein structure prediction enables high-throughput exploration of uncharacterized proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	26
44	Increasing the accuracy of single sequence prediction methods using a deep semi-supervised learning framework. Bioinformatics, 2021, 37, 3744-3751.	1.8	24
45	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. Human Mutation, 2017, 38, 1123-1131.	1.1	17
46	Learning a functional grammar of protein domains using natural language word embedding techniques. Proteins: Structure, Function and Bioinformatics, 2020, 88, 616-624.	1.5	17
47	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. Nucleic Acids Research, 2020, 48, D314-D319.	6.5	13
48	Differentiable molecular simulation can learn all the parameters in a coarse-grained force field for proteins. PLoS ONE, 2021, 16, e0256990.	1.1	13
49	Opportunities and limitations in applying coevolution-derived contacts to protein structure prediction. Bio-Algorithms and Med-Systems, 2014, 10, 243-254.	1.0	12
50	Crohn disease risk predictionâ€”Best practices and pitfalls with exome data. Human Mutation, 2017, 38, 1193-1200.	1.1	12
51	Analysis of temporal transcription expression profiles reveal links between protein function and developmental stages of Drosophila melanogaster. PLoS Computational Biology, 2017, 13, e1005791.	1.5	12
52	Predictions of Backbone Dynamics in Intrinsically Disordered Proteins Using De Novo Fragment-Based Protein Structure Predictions. Scientific Reports, 2017, 7, 6999.	1.6	11
53	Using deep maxout neural networks to improve the accuracy of function prediction from protein interaction networks. PLoS ONE, 2019, 14, e0209958.	1.1	11
54	Assessment of predicted enzymatic activity of Î±-acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	1.1	10

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55	Lessons from the CAGI Hopkins clinical panel challenge. <i>Human Mutation</i> , 2017, 38, 1155-1168.	1.1	6
56	Inferring function using patterns of native disorder in proteins. <i>PLoS Computational Biology</i> , 2005, preprint, e162.	1.5	3
57	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. <i>Methods in Molecular Biology</i> , 2020, 2165, 27-67.	0.4	3
58	Shared structural motif in proteins. <i>Nature</i> , 1993, 365, 21-21.	13.7	1