

# David Tudor Jones

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64  
papers

12,277  
citations

34  
h-index

66  
g-index

66  
ext. papers

15,309  
ext. citations

13.5  
avg, IF

7.22  
L-index

#	Paper	IF	Citations
64	Ultrafast end-to-end protein structure prediction enables high-throughput exploration of uncharacterized proteins.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119,	11.5	3
63	The impact of AlphaFold2 one year on.. <i>Nature Methods</i> , <b>2022</b> , 19, 15-20	21.6	5
62	Increasing the Accuracy of Single Sequence Prediction Methods Using a Deep Semi-Supervised Learning Framework. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	3
61	Differentiable molecular simulation can learn all the parameters in a coarse-grained force field for proteins. <i>PLoS ONE</i> , <b>2021</b> , 16, e0256990	3.7	2
60	A guide to machine learning for biologists. <i>Nature Reviews Molecular Cell Biology</i> , <b>2021</b> ,	48.7	55
59	Improved protein structure prediction using potentials from deep learning. <i>Nature</i> , <b>2020</b> , 577, 706-710	50.4	1007
58	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2165, 27-67	1.4	1
57	Learning a functional grammar of protein domains using natural language word embedding techniques. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2020</b> , 88, 616-624	4.2	8
56	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D314-D319	20.1	7
55	Protein function prediction is improved by creating synthetic feature samples with generative adversarial networks. <i>Nature Machine Intelligence</i> , <b>2020</b> , 2, 540-550	22.5	11
54	Deep learning extends de novo protein modelling coverage of genomes using iteratively predicted structural constraints. <i>Nature Communications</i> , <b>2019</b> , 10, 3977	17.4	95
53	Framework engineering to produce dominant T cell receptors with enhanced antigen-specific function. <i>Nature Communications</i> , <b>2019</b> , 10, 4451	17.4	25
52	Setting the standards for machine learning in biology. <i>Nature Reviews Molecular Cell Biology</i> , <b>2019</b> , 20, 659-660	48.7	34
51	The PSIPRED Protein Analysis Workbench: 20 years on. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, W402-W407	20.1	496
50	Prediction of interresidue contacts with DeepMetaPSICOV in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2019</b> , 87, 1092-1099	4.2	67
49	Using deep maxout neural networks to improve the accuracy of function prediction from protein interaction networks. <i>PLoS ONE</i> , <b>2019</b> , 14, e0209958	3.7	5
48	Assessment of predicted enzymatic activity of N-acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , <b>2019</b> , 40, 1519-1529	4.7	4

47	Recent developments in deep learning applied to protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2019</b> , 87, 1179-1189	4.2	38
46	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , <b>2019</b> , 20, 244	18.3	111
45	High precision in protein contact prediction using fully convolutional neural networks and minimal sequence features. <i>Bioinformatics</i> , <b>2018</b> , 34, 3308-3315	7.2	116
44	Predicting human protein function with multi-task deep neural networks. <i>PLoS ONE</i> , <b>2018</b> , 13, e0198216	3.7	42
43	Improved protein contact predictions with the MetaPSICOV2 server in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2018</b> , 86 Suppl 1, 78-83	4.2	45
42	Design of metalloproteins and novel protein folds using variational autoencoders. <i>Scientific Reports</i> , <b>2018</b> , 8, 16189	4.9	50
41	Computational Methods for Annotation Transfers from Sequence. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1446, 55-67	1.4	28
40	Crohn disease risk prediction-Best practices and pitfalls with exome data. <i>Human Mutation</i> , <b>2017</b> , 38, 1193-1200	4.7	6
39	EigenTHREADER: analogous protein fold recognition by efficient contact map threading. <i>Bioinformatics</i> , <b>2017</b> , 33, 2684-2690	7.2	39
38	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. <i>Human Mutation</i> , <b>2017</b> , 38, 1123-1131	4.1	12
37	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , <b>2017</b> , 38, 1182-1192	4.7	28
36	Analysis of temporal transcription expression profiles reveal links between protein function and developmental stages of <i>Drosophila melanogaster</i> . <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005791	5	6
35	Predictions of Backbone Dynamics in Intrinsically Disordered Proteins Using De Novo Fragment-Based Protein Structure Predictions. <i>Scientific Reports</i> , <b>2017</b> , 7, 6999	4.9	9
34	Lessons from the CAGI-4 Hopkins clinical panel challenge. <i>Human Mutation</i> , <b>2017</b> , 38, 1155-1168	4.7	4
33	Isolation and Comparative Transcriptome Analysis of Human Fetal and iPSC-Derived Cone Photoreceptor Cells. <i>Stem Cell Reports</i> , <b>2017</b> , 9, 1898-1915	8	61
32	FFPred 3: feature-based function prediction for all Gene Ontology domains. <i>Scientific Reports</i> , <b>2016</b> , 6, 31865	4.9	62
31	Accurate contact predictions using covariation techniques and machine learning. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84 Suppl 1, 145-51	4.2	38
30	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , <b>2016</b> , 17, 184	18.3	218

29	MetaPSICOV: combining coevolution methods for accurate prediction of contacts and long range hydrogen bonding in proteins. <i>Bioinformatics</i> , <b>2015</b> , 31, 999-1006	7.2	236
28	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D382-6	20.1	33
27	DISOPRED3: precise disordered region predictions with annotated protein-binding activity. <i>Bioinformatics</i> , <b>2015</b> , 31, 857-63	7.2	483
26	Classification of intrinsically disordered regions and proteins. <i>Chemical Reviews</i> , <b>2014</b> , 114, 6589-631	68.1	1141
25	De novo structure prediction of globular proteins aided by sequence variation-derived contacts. <i>PLoS ONE</i> , <b>2014</b> , 9, e92197	3.7	81
24	Opportunities and limitations in applying coevolution-derived contacts to protein structure prediction. <i>Bio-Algorithms and Med-Systems</i> , <b>2014</b> , 10,	1.2	5
23	Evaluation of predictions in the CASP10 model refinement category. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82 Suppl 2, 98-111	4.2	84
22	Protein function prediction by massive integration of evolutionary analyses and multiple data sources. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 3, S1	3.6	63
21	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , <b>2013</b> , 10, 221-7	21.6	587
20	FFPred 2.0: improved homology-independent prediction of gene ontology terms for eukaryotic protein sequences. <i>PLoS ONE</i> , <b>2013</b> , 8, e63754	3.7	37
19	PSICOV: precise structural contact prediction using sparse inverse covariance estimation on large multiple sequence alignments. <i>Bioinformatics</i> , <b>2012</b> , 28, 184-90	7.2	545
18	Transmembrane protein topology prediction using support vector machines. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 159	3.6	300
17	Improving the accuracy of transmembrane protein topology prediction using evolutionary information. <i>Bioinformatics</i> , <b>2007</b> , 23, 538-44	7.2	355
16	Inferring function using patterns of native disorder in proteins. <i>PLoS Computational Biology</i> , <b>2005</b> , preprint, e162	5	1
15	Prediction of disordered regions in proteins from position specific score matrices. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53 Suppl 6, 573-8	4.2	175
14	Assembling novel protein folds from super-secondary structural fragments. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53 Suppl 6, 480-5	4.2	68
13	Getting the most from PSI-BLAST. <i>Trends in Biochemical Sciences</i> , <b>2002</b> , 27, 161-4	10.3	128
12	Protein secondary structure prediction based on position-specific scoring matrices. <i>Journal of Molecular Biology</i> , <b>1999</b> , 292, 195-202	6.5	4276

11	Protein superfamilies and domain superfolds. <i>Nature</i> , <b>1994</b> , 372, 631-4	50.4	706
10	A structural model for the nucleotide binding domains of the flavocytochrome b-245 beta-chain. <i>Protein Science</i> , <b>1993</b> , 2, 1675-85	6.3	114
9	Shared structural motif in proteins. <i>Nature</i> , <b>1993</b> , 365, 21-21	50.4	1
8	Recurrence of a binding motif?. <i>Nature</i> , <b>1993</b> , 362, 299	50.4	23
7	A Deep Semi-Supervised Framework for Accurate Modelling of Orphan Sequences		1
6	Ultrafast end-to-end protein structure prediction enables high-throughput exploration of uncharacterised proteins		6
5	Prediction of inter-residue contacts with DeepMetaPSICOV in CASP13		6
4	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
3	Improving protein function prediction with synthetic feature samples created by generative adversarial networks		1
2	Differentiable molecular simulation can learn all the parameters in a coarse-grained force field for proteins		1
1	Using AlphaFold for Rapid and Accurate Fixed Backbone Protein Design		4