

Daniel W A Buchan

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

3,826
citations

933447

10
h-index

1199594

12
g-index

12
all docs

12
docs citations

12
times ranked

7594
citing authors

#	ARTICLE	IF	CITATIONS
1	Learning a functional grammar of protein domains using natural language word embedding techniques. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 616-624.	2.6	17
2	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. <i>Nucleic Acids Research</i> , 2020, 48, D314-D319.	14.5	13
3	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. <i>Methods in Molecular Biology</i> , 2020, 2165, 27-67.	0.9	3
4	The PSIPRED Protein Analysis Workbench: 20 years on. <i>Nucleic Acids Research</i> , 2019, 47, W402-W407.	14.5	881
5	Improved protein contact predictions with the MetaPSICOV2 server in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 78-83.	2.6	52
6	EigenTHREADER: analogous protein fold recognition by efficient contact map threading. <i>Bioinformatics</i> , 2017, 33, 2684-2690.	4.1	54
7	Predictions of Backbone Dynamics in Intrinsically Disordered Proteins Using De Novo Fragment-Based Protein Structure Predictions. <i>Scientific Reports</i> , 2017, 7, 6999.	3.3	11
8	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015, 43, D382-D386.	14.5	42
9	Protein function prediction by massive integration of evolutionary analyses and multiple data sources. <i>BMC Bioinformatics</i> , 2013, 14, S1.	2.6	72
10	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
11	Scalable web services for the PSIPRED Protein Analysis Workbench. <i>Nucleic Acids Research</i> , 2013, 41, W349-W357.	14.5	1,206
12	PSICOV: precise structural contact prediction using sparse inverse covariance estimation on large multiple sequence alignments. <i>Bioinformatics</i> , 2012, 28, 184-190.	4.1	686