Andriy Kryshtafovych

List of Publications by Year
in descending order

78 papers	5,354 citations	101384 36 h-index	95083 68 g-index
84 all docs	84 docs citations	84 times ranked	4193 citing authors

#	ARTICLE	IF	CITATIONS
1	Critical assessment of methods of protein structure prediction (CASP)â€"Round XIII. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1011-1020.	1.5	380
2	Critical assessment of methods of protein structure prediction (CASP) â€" round x. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1-6.	1.5	366
3	Critical assessment of methods of protein structure prediction (CASP)â€"Round XII. Proteins: Structure, Function and Bioinformatics, 2018, 86, 7-15.	1.5	296
4	Critical assessment of methods of protein structure prediction (CASP)â€"Round <scp>XIV</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1607-1617.	1.5	281
5	Critical assessment of methods of protein structure predictionâ€"Round VII. Proteins: Structure, Function and Bioinformatics, 2007, 69, 3-9.	1.5	199
6	Critical assessment of methods of protein structure prediction: Progress and new directions in round XI. Proteins: Structure, Function and Bioinformatics, 2016, 84, 4-14.	1.5	198
7	Critical assessment of methods of protein structure prediction (CASP)â€"round IX. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1-5.	1.5	187
8	Assessment of contact predictions in CASP12: Coâ€evolution and deep learning coming of age. Proteins: Structure, Function and Bioinformatics, 2018, 86, 51-66.	1.5	174
9	Progress over the first decade of CASP experiments. Proteins: Structure, Function and Bioinformatics, 2005, 61, 225-236.	1.5	172
10	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	1.5	148
11	Assessment of predictions in the model quality assessment category. Proteins: Structure, Function and Bioinformatics, 2007, 69, 175-183.	1.5	122
12	Evaluation of templateâ€based models in CASP8 with standard measures. Proteins: Structure, Function and Bioinformatics, 2009, 77, 18-28.	1.5	114
13	Assessment of the assessment: Evaluation of the model quality estimates in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 112-126.	1.5	114
14	CASP9 results compared to those of previous casp experiments. Proteins: Structure, Function and Bioinformatics, 2011, 79, 196-207.	1.5	91
15	CASP prediction center infrastructure and evaluation measures in CASP10 and CASP ROLL. Proteins: Structure, Function and Bioinformatics, 2014, 82, 7-13.	1.5	91
16	CASP10 results compared to those of previous CASP experiments. Proteins: Structure, Function and Bioinformatics, 2014, 82, 164-174.	1.5	91
17	Protein structure prediction and model quality assessment. Drug Discovery Today, 2009, 14, 386-393.	3.2	84
18	Evaluation of model quality predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 91-106.	1.5	83

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19	New encouraging developments in contact prediction: Assessment of the <scp>CASP</scp>11 results. Proteins: Structure, Function and Bioinformatics, 2016, 84, 131-144.	1.5	81
20	Assessment of hard target modeling in CASP12 reveals an emerging role of alignment–based contact prediction methods. Proteins: Structure, Function and Bioinformatics, 2018, 86, 97-112.	1.5	79
21	Evaluation of CASP8 model quality predictions. Proteins: Structure, Function and Bioinformatics, 2009, 77, 157-166.	1.5	76
22	Evaluation of residue–residue contact predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 119-125.	1.5	75
23	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	9.0	73
24	Evaluation of residue–residue contact prediction in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 138-153.	1.5	72
25	Evaluation of free modeling targets in CASP11 and ROLL. Proteins: Structure, Function and Bioinformatics, 2016, 84, 51-66.	1.5	70
26	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in <scp>CASP</scp>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 349-369.	1.5	63
27	Assessment of model accuracy estimations in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 345-360.	1.5	61
28	Evaluation of the template–based modeling in <scp>CASP12</scp>. Proteins: Structure, Function and Bioinformatics, 2018, 86, 321-334.	1.5	61
29	Progress from CASP6 to CASP7. Proteins: Structure, Function and Bioinformatics, 2007, 69, 194-207.	1.5	60
30	Evaluation of template–based modeling in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1113-1127.	1.5	56
31	Assessment of protein assembly prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 247-256.	1.5	54
32	Assessment of protein model structure accuracy estimation in CASP13: Challenges in the era of deep learning. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1351-1360.	1.5	54
33	Challenging the state of the art in protein structure prediction: Highlights of experimental target structures for the 10th Critical Assessment of Techniques for Protein Structure Prediction Experiment CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 26-42.	1.5	53
34	Assessment of protein model structure accuracy estimation in <scp>CASP14</scp>: Old and new challenges. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1940-1948.	1.5	48
35	<scp>CASP</scp>11 statistics and the prediction center evaluation system. Proteins: Structure, Function and Bioinformatics, 2016, 84, 15-19.	1.5	42
36	Assessment of protein assembly prediction in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1190-1199.	1.5	40

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37	Using multi-data hidden Markov models trained on local neighborhoods of protein structure to predict residue–residue contacts. Bioinformatics, 2009, 25, 1264-1270.	1.8	39
38	Generalized modeling of enzyme-ligand interactions using proteochemometrics and local protein substructures. Proteins: Structure, Function and Bioinformatics, 2006, 65, 568-579.	1.5	38
39	A Comprehensive Analysis of the Structure-Function Relationship in Proteins Based on Local Structure Similarity. PLoS ONE, 2009, 4, e6266.	1.1	37
40	Computational models in the service of X–ray and <scp>cryo–</scp>electron microscopy structure determination. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1633-1646.	1.5	37
41	Topology evaluation of models for difficult targets in the 14th round of the critical assessment of protein structure prediction (CASP14). Proteins: Structure, Function and Bioinformatics, 2021, 89, 1673-1686.	1.5	35
42	Assessment of the <scp>CASP14</scp> assembly predictions. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1787-1799.	1.5	35
43	CASP13 target classification into tertiary structure prediction categories. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1021-1036.	1.5	34
44	Comparative analysis of methods for evaluation of protein models against native structures. Bioinformatics, 2019, 35, 937-944.	1.8	34
45	Interaction Model Based on Local Protein Substructures Generalizes to the Entire Structural Enzyme-Ligand Space. Journal of Chemical Information and Modeling, 2008, 48, 2278-2288.	2.5	33
46	Assessment of the model refinement category in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 152-167.	1.5	33
47	Target classification in the 14th <scp>round</scp> of the <scp>critical assessment of protein structure prediction</scp> (<scp>CASP14</scp>). Proteins: Structure, Function and Bioinformatics, 2021, 89, 1618-1632.	1.5	32
48	New tools and expanded data analysis capabilities at the protein structure prediction center. Proteins: Structure, Function and Bioinformatics, 2007, 69, 19-26.	1.5	31
49	CASP 11 target classification. Proteins: Structure, Function and Bioinformatics, 2016, 84, 20-33.	1.5	31
50	Assessment of prediction methods for protein structures determined by <scp>NMR</scp> in <scp>CASP14</scp>: Impact of <scp>AlphaFold2</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1959-1976.	1.5	30
51	Protein structure prediction center in CASP8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 5-9.	1.5	28
52	Evaluation of model refinement in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1249-1262.	1.5	28
53	Assessment of chemical–crosslink–assisted protein structure modeling in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1283-1297.	1.5	27
54	Target highlights in <scp>CASP14</scp>: Analysis of models by structure providers. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1647-1672.	1.5	27

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55	A novel approach to fold recognition using sequence-derived properties from sets of structurally similar local fragments of proteins. Bioinformatics, 2003, 19, ii81-ii91.	1.8	25
56	Assessment of CASP11 contact‑assisted predictions. Proteins: Structure, Function and Bioinformatics, 2016, 84, 164-180.	1.5	24
57	Small angle X‑ray scattering‑assisted protein structure prediction in CASP13 and emergence of solution structure differences. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1298-1314.	1.5	24
58	Modeling SARS‑CoV‑2 proteins in the CASP‑commons experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1987-1996.	1.5	24
59	CASP6 data processing and automatic evaluation at the protein structure prediction center. Proteins: Structure, Function and Bioinformatics, 2005, 61, 19-23.	1.5	23
60	Small angle X‑ray scattering and cross‑linking for data assisted protein structure prediction in CASP 12 with prospects for improved accuracy. Proteins: Structure, Function and Bioinformatics, 2018, 86, 202-214.	1.5	23
61	Protein structure prediction assisted with sparse NMR data in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1315-1332.	1.5	21
62	Cryo‑electron microscopy targets in CASP13: Overview and evaluation of results. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1128-1140.	1.5	21
63	Evaluation of model refinement in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1852-1869.	1.5	21
64	Definition and classification of evaluation units for CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 14-25.	1.5	20
65	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 6-20.	1.5	19
66	Some of the most interesting <scp>CASP</scp>11 targets through the eyes of their authors. Proteins: Structure, Function and Bioinformatics, 2016, 84, 34-50.	1.5	16
67	Local descriptors of protein structure: A systematic analysis of the sequence‑structure relationship in proteins using short‑and long‑range interactions. Proteins: Structure, Function and Bioinformatics, 2009, 75, 870-884.	1.5	15
68	Assessing the accuracy of contact and distance predictions in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1888-1900.	1.5	15
69	Cover Image, Volume 84, Issue S1. Proteins: Structure, Function and Bioinformatics, 2016, 84, C4.	1.5	13
70	Definition and classification of evaluation units for tertiary structure prediction in CASP12 facilitated through semi‑automated metrics. Proteins: Structure, Function and Bioinformatics, 2018, 86, 16-26.	1.5	12
71	Target highlights in CASP13: Experimental target structures through the eyes of their authors. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1037-1057.	1.5	12
72	Target highlights from the first post‑PSI CASP experiment (CASP12, May‑August 2016). Proteins: Structure, Function and Bioinformatics, 2018, 86, 27-50.	1.5	11

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73	Evaluation system and web infrastructure for the second cryo-EM model challenge. Journal of Structural Biology, 2018, 204, 96-108.	1.3	11
74	<scp>Cryoâ€EM</scp> targets in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1949-1958.	1.5	11
75	Assessment of domain interactions in the fourteenth round of the Critical Assessment of Structure Prediction (CASP14). Proteins: Structure, Function and Bioinformatics, 2021, 89, 1700-1710.	1.5	8
76	Distribution of evaluation scores for the models submitted to the second cryo-EM model challenge. Data in Brief, 2018, 20, 1629-1638.	0.5	5
77	A tribute to Anna Tramontano (1957â€"2017). Proteins: Structure, Function and Bioinformatics, 2018, 86, 5-6.	1.5	1
78	Cover Image, Volume 87, Issue 12. Proteins: Structure, Function and Bioinformatics, 2019, 87, C4.	1.5	0