

Krzysztof Fidelis

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6253119/publications.pdf>

Version: 2024-02-01

55
papers

5,055
citations

136950

32
h-index

161849

54
g-index

58
all docs

58
docs citations

58
times ranked

3815
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling SARS-CoV-2 proteins in the CASP-commons experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1987-1996.	2.6	24
2	Target highlights in <sc>CASP14</sc>: Analysis of models by structure providers. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1647-1672.	2.6	27
3	Assessment of prediction methods for protein structures determined by <sc>NMR</sc> in <sc>CASP14</sc>: Impact of <sc>AlphaFold2</sc>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1959-1976.	2.6	30
4	Critical assessment of methods of protein structure prediction (CASP)â€”Round <sc>XIV</sc>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1607-1617.	2.6	281
5	Small angle X-ray scatteringâ€”assisted protein structure prediction in CASP13 and emergence of solution structure differences. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1298-1314.	2.6	24
6	Protein structure prediction assisted with sparse NMR data in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1315-1332.	2.6	21
7	Assessment of chemicalâ€”crosslinkâ€”assisted protein structure modeling in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1283-1297.	2.6	27
8	Critical assessment of methods of protein structure prediction (CASP)â€”Round XIII. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1011-1020.	2.6	380
9	Target highlights in CASP13: Experimental target structures through the eyes of their authors. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1037-1057.	2.6	12
10	Cover Image, Volume 87, Issue 12. Proteins: Structure, Function and Bioinformatics, 2019, 87, C4.	2.6	0
11	Small angle X-ray scattering and crossâ€”linking for data assisted protein structure prediction in CASP 12 with prospects for improved accuracy. Proteins: Structure, Function and Bioinformatics, 2018, 86, 202-214.	2.6	23
12	Target highlights from the first postâ€”PSI CASP experiment (CASP12, Mayâ€”August 2016). Proteins: Structure, Function and Bioinformatics, 2018, 86, 27-50.	2.6	11
13	Assessment of model accuracy estimations in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 345-360.	2.6	61
14	A tribute to Anna Tramontano (1957â€”2017). Proteins: Structure, Function and Bioinformatics, 2018, 86, 5-6.	2.6	1
15	Critical assessment of methods of protein structure prediction (CASP)â€”Round XII. Proteins: Structure, Function and Bioinformatics, 2018, 86, 7-15.	2.6	296
16	Evaluation of the templateâ€”based modeling in <sc>CASP12</sc>. Proteins: Structure, Function and Bioinformatics, 2018, 86, 321-334.	2.6	61
17	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in <sc>CASP</sc> 11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 349-369.	2.6	63
18	Critical assessment of methods of protein structure prediction: Progress and new directions in round XI. Proteins: Structure, Function and Bioinformatics, 2016, 84, 4-14.	2.6	198

#	ARTICLE	IF	CITATIONS
19	Cover Image, Volume 84, Issue S1. Proteins: Structure, Function and Bioinformatics, 2016, 84, C4.	2.6	13
20	New encouraging developments in contact prediction: Assessment of the <scp>CASP</scp> 11 results. Proteins: Structure, Function and Bioinformatics, 2016, 84, 131-144.	2.6	81
21	<scp>CASP</scp> 11 statistics and the prediction center evaluation system. Proteins: Structure, Function and Bioinformatics, 2016, 84, 15-19.	2.6	42
22	Critical assessment of methods of protein structure prediction (CASP) â€” round x. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1-6.	2.6	366
23	Assessment of the assessment: Evaluation of the model quality estimates in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 112-126.	2.6	114
24	Evaluation of residueâ€”residue contact prediction in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 138-153.	2.6	72
25	CASP prediction center infrastructure and evaluation measures in CASP10 and CASP ROLL. Proteins: Structure, Function and Bioinformatics, 2014, 82, 7-13.	2.6	91
26	CASP10 results compared to those of previous CASP experiments. Proteins: Structure, Function and Bioinformatics, 2014, 82, 164-174.	2.6	91
27	Evaluation of residueâ€”residue contact predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 119-125.	2.6	75
28	Evaluation of model quality predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 91-106.	2.6	83
29	CASP9 results compared to those of previous casp experiments. Proteins: Structure, Function and Bioinformatics, 2011, 79, 196-207.	2.6	91
30	Critical assessment of methods of protein structure prediction (CASP)â€”round IX. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1-5.	2.6	187
31	Protein structure prediction center in CASP8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 5-9.	2.6	28
32	Evaluation of templateâ€”based models in CASP8 with standard measures. Proteins: Structure, Function and Bioinformatics, 2009, 77, 18-28.	2.6	114
33	New tools and expanded data analysis capabilities at the protein structure prediction center. Proteins: Structure, Function and Bioinformatics, 2007, 69, 19-26.	2.6	31
34	CASP6 data processing and automatic evaluation at the protein structure prediction center. Proteins: Structure, Function and Bioinformatics, 2005, 61, 19-23.	2.6	23
35	Progress over the first decade of CASP experiments. Proteins: Structure, Function and Bioinformatics, 2005, 61, 225-236.	2.6	172
36	The Significance of Performance Ranking in CASPâ€”Response to Marti-Renom et al.. Structure, 2002, 10, 291-292.	3.3	5

#	ARTICLE	IF	CITATIONS
37	Processing and evaluation of predictions in CASP4. Proteins: Structure, Function and Bioinformatics, 2001, 45, 13-21.	2.6	131
38	Comparison of performance in successive CASP experiments. Proteins: Structure, Function and Bioinformatics, 2001, 45, 163-170.	2.6	62
39	Critical assessment of methods of protein structure prediction (CASP): Round IV. Proteins: Structure, Function and Bioinformatics, 2001, 45, 2-7.	2.6	146
40	Structure-based sequence alignment for the $\hat{1}2$ -trefoil subdomain of the clostridial neurotoxin family provides residue level information about the putative ganglioside binding site. FEBS Letters, 2000, 482, 119-124.	2.8	39
41	Critical assessment of methods of protein structure prediction (CASP): Round III. Proteins: Structure, Function and Bioinformatics, 1999, 37, 2-6.	2.6	137
42	Processing and analysis of CASP3 protein structure predictions. Proteins: Structure, Function and Bioinformatics, 1999, 37, 22-29.	2.6	206
43	Some measures of comparative performance in the three CASPs. Proteins: Structure, Function and Bioinformatics, 1999, 37, 231-237.	2.6	39
44	Addressing the issue of sequence-to-structure alignments in comparative modeling of CASP3 target proteins. Proteins: Structure, Function and Bioinformatics, 1999, 37, 73-80.	2.6	21
45	A modified definition of Sov, a segment-based measure for protein secondary structure prediction assessment. , 1999, 34, 220-223.		323
46	Processing and analysis of CASP3 protein structure predictions. Proteins: Structure, Function and Bioinformatics, 1999, 37, 22-29.	2.6	142
47	Critical assessment of methods of protein structure prediction (CASP): Round III. Proteins: Structure, Function and Bioinformatics, 1999, 37, 2-6.	2.6	103
48	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, 29, 140-150.	2.6	21
49	Critical assessment of methods of protein structure prediction (CASP): Round II. , 1997, 29, 2-6.		114
50	Criteria for evaluating protein structures derived from comparative modeling. Proteins: Structure, Function and Bioinformatics, 1997, 29, 7-13.	2.6	28
51	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, 29, 140-150.	2.6	2
52	Critical assessment of methods of protein structure prediction (CASP): Round II. Proteins: Structure, Function and Bioinformatics, 1997, 29, 2-6.	2.6	22
53	Critical assessment of methods of protein structure prediction (CASP): Round II. Proteins: Structure, Function and Bioinformatics, 1997, 29, 2-6.	2.6	82
54	Confronting the problem of interconnected structural changes in the comparative modeling of proteins. Proteins: Structure, Function and Bioinformatics, 1995, 23, 327-336.	2.6	25

#	ARTICLE	IF	CITATIONS
55	Comparison of systematic search and database methods for constructing segments of protein structure. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 953-960.	2.1	113