

Thom Vreven

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

3,060
citations

471509

17
h-index

610901

24
g-index

25
all docs

25
docs citations

25
times ranked

4750
citing authors

#	ARTICLE	IF	CITATIONS
1	High-throughput modeling and scoring of TCR-pMHC complexes to predict cross-reactive peptides. <i>Bioinformatics</i> , 2021, 36, 5377-5385.	4.1	13
2	An expanded benchmark for antibody-antigen docking and affinity prediction reveals insights into antibody recognition determinants. <i>Structure</i> , 2021, 29, 606-621.e5.	3.3	65
3	Integrating <i>ab initio</i> and template-based algorithms for protein-protein complex structure prediction. <i>Bioinformatics</i> , 2020, 36, 751-757.	4.1	14
4	Performance of ZDOCK and IRAD in CAPRI rounds 39-45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1050-1054.	2.6	8
5	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
6	Computational investigation into the fluorescence of luciferin analogues. <i>Journal of Computational Chemistry</i> , 2019, 40, 527-531.	3.3	7
7	Integrating Cross-Linking Experiments with <i>Ab Initio</i> Protein-Protein Docking. <i>Journal of Molecular Biology</i> , 2018, 430, 1814-1828.	4.2	22
8	Performance of ZDOCK and IRAD in CAPRI rounds 28-34. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 408-416.	2.6	13
9	IRaPPA: information retrieval based integration of biophysical models for protein assembly selection. <i>Bioinformatics</i> , 2017, 33, 1806-1813.	4.1	36
10	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	2.6	148
11	Updates to the Integrated Protein-Protein Interaction Benchmarks: Docking Benchmark Version 5 and Affinity Benchmark Version 2. <i>Journal of Molecular Biology</i> , 2015, 427, 3031-3041.	4.2	348
12	Evaluating template-based and template-free protein-protein complex structure prediction. <i>Briefings in Bioinformatics</i> , 2014, 15, 169-176.	6.5	35
13	Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 620-632.	2.6	50
14	ZDOCK server: interactive docking prediction of protein-protein complexes and symmetric multimers. <i>Bioinformatics</i> , 2014, 30, 1771-1773.	4.1	1,313
15	The HP1 Homolog Rhino Anchors a Nuclear Complex that Suppresses piRNA Precursor Splicing. <i>Cell</i> , 2014, 157, 1353-1363.	28.9	198
16	Performance of ZDOCK in CAPRI rounds 20-26. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2175-2182.	2.6	22
17	Exploring Angular Distance in Protein-Protein Docking Algorithms. <i>PLoS ONE</i> , 2013, 8, e56645.	2.5	11
18	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1980-1987.	2.6	87

#	ARTICLE	IF	CITATIONS
19	UAP56 Couples piRNA Clusters to the Perinuclear Transposon Silencing Machinery. <i>Cell</i> , 2012, 151, 871-884.	28.9	204
20	Prediction of proteinâ€“protein binding free energies. <i>Protein Science</i> , 2012, 21, 396-404.	7.6	74
21	Oscillator Strengths in ONIOM Excited State Calculations. <i>Journal of Chemical Theory and Computation</i> , 2011, 7, 180-187.	5.3	10
22	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	4.2	131
23	Integrating atomâ€“based and residueâ€“based scoring functions for proteinâ€“protein docking. <i>Protein Science</i> , 2011, 20, 1576-1586.	7.6	80
24	Performance of ZDOCK and ZRANK in CAPRI rounds 13â€“19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3104-3110.	2.6	72