# Thom Vreven

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8815130/publications.pdf

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|---|---|---|---|
| 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 | ZDOCK server: interactive docking prediction of proteinâ€“protein complexes and symmetric multimers. Bioinformatics, 2014, 30, 1771-1773. | 4.1 | 1,313 |
| 2 | Updates to the Integrated Proteinâ€“Protein Interaction Benchmarks: Docking Benchmark Version 5 and Affinity Benchmark Version 2. Journal of Molecular Biology, 2015, 427, 3031-3041. | 4.2 | 348 |
| 3 | UAP56 Couples piRNA Clusters to the Perinuclear Transposon Silencing Machinery. Cell, 2012, 151, 871-884. | 28.9 | 204 |
| 4 | The HP1 Homolog Rhino Anchors a Nuclear Complex that Suppresses piRNA Precursor Splicing. Cell, 2014, 157, 1353-1363. | 28.9 | 198 |
| 5 | 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. | 2.6 | 148 |
| 6 | Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302. | 4.2 | 131 |
| 7 | Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221. | 2.6 | 99 |
| 8 | Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987. | 2.6 | 87 |
| 9 | Integrating atomâ€based and residueâ€based scoring functions for proteinâ€“protein docking. Protein Science, 2011, 20, 1576-1586. | 7.6 | 80 |
| 10 | Prediction of proteinâ€“protein binding free energies. Protein Science, 2012, 21, 396-404. | 7.6 | 74 |
| 11 | Performance of ZDOCK and ZRANK in CAPRI rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3104-3110. | 2.6 | 72 |
| 12 | An expanded benchmark for antibody-antigen docking and affinity prediction reveals insights into antibody recognition determinants. Structure, 2021, 29, 606-621.e5. | 3.3 | 65 |
| 13 | Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632. | 2.6 | 50 |
| 14 | IRaPPA: information retrieval based integration of biophysical models for protein assembly selection. Bioinformatics, 2017, 33, 1806-1813. | 4.1 | 36 |
| 15 | Evaluating template-based and template-free protein-protein complex structure prediction. Briefings in Bioinformatics, 2014, 15, 169-176. | 6.5 | 35 |
| 16 | Performance of ZDOCK in CAPRI rounds 20â€“26. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2175-2182. | 2.6 | 22 |
| 17 | Integrating Cross-Linking Experiments with Ab Initio Proteinâ€“Protein Docking. Journal of Molecular Biology, 2018, 430, 1814-1828. | 4.2 | 22 |
| 18 | Integrating ab initio and template-based algorithms for proteinâ€“protein complex structure prediction. Bioinformatics, 2020, 36, 751-757. | 4.1 | 14 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Performance of ZDOCK and IRAD in CAPRI rounds 28â€“34. Proteins: Structure, Function and Bioinformatics, 2017, 85, 408-416. | 2.6 | 13 |
| 20 | High-throughput modeling and scoring of TCR-pMHC complexes to predict cross-reactive peptides. Bioinformatics, 2021, 36, 5377-5385. | 4.1 | 13 |
| 21 | Exploring Angular Distance in Protein-Protein Docking Algorithms. PLoS ONE, 2013, 8, e56645. | 2.5 | 11 |
| 22 | Oscillator Strengths in ONIOM Excited State Calculations. Journal of Chemical Theory and Computation, 2011, 7, 180-187. | 5.3 | 10 |
| 23 | Performance of ZDOCK and IRAD in CAPRI rounds 39â€45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1050-1054. | 2.6 | 8 |
| 24 | Computational investigation into the fluorescence of luciferin analogues. Journal of Computational Chemistry, 2019, 40, 527-531. | 3.3 | 7 |