

# Wendy D Cornell

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/10790413/wendy-d-cornell-publications-by-year.pdf>

**Version:** 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

12  
papers

13,603  
citations

10  
h-index

14  
g-index

14  
ext. papers

14,423  
ext. citations

8  
avg, IF

5.21  
L-index

#	Paper	IF	Citations
12	Combining Docking Pose Rank and Structure with Deep Learning Improves Protein-Ligand Binding Mode Prediction over a Baseline Docking Approach. <i>Journal of Chemical Information and Modeling</i> , <b>2020</b> , 60, 4170-4179	6.1	30
11	Drug-like density: a method of quantifying the "bindability" of a protein target based on a very large set of pockets and drug-like ligands from the Protein Data Bank. <i>Journal of Chemical Information and Modeling</i> , <b>2010</b> , 50, 2029-40	6.1	78
10	Multiple protein structures and multiple ligands: effects on the apparent goodness of virtual screening results. <i>Journal of Computer-Aided Molecular Design</i> , <b>2008</b> , 22, 257-65	4.2	46
9	Comparison of topological, shape, and docking methods in virtual screening. <i>Journal of Chemical Information and Modeling</i> , <b>2007</b> , 47, 1504-19	6.1	349
8	The effects of basis set and blocking groups on the conformational energies of glycyI and alanyl dipeptides A Hartree-Fock and MP2 study. <i>Computational and Theoretical Chemistry</i> , <b>1997</b> , 392, 101-109		18
7	Application of a simple diagonal force field to the simulation of cyclopentane conformational dynamics. <i>Journal of Computational Chemistry</i> , <b>1996</b> , 17, 1541-1548	3.5	4
6	Application of a simple diagonal force field to the simulation of cyclopentane conformational dynamics <b>1996</b> , 17, 1541		1
5	A Second Generation Force Field for the Simulation of Proteins, Nucleic Acids, and Organic Molecules. <i>Journal of the American Chemical Society</i> , <b>1995</b> , 117, 5179-5197	16.4	10990
4	Application of the multimolecule and multiconformational RESP methodology to biopolymers: Charge derivation for DNA, RNA, and proteins. <i>Journal of Computational Chemistry</i> , <b>1995</b> , 16, 1357-1377	3.5	820
3	Calculation of molecular geometries, relative conformational energies, dipole moments, and molecular electrostatic potential fitted charges of small organic molecules of biochemical interest by density functional theory. <i>Journal of Computational Chemistry</i> , <b>1995</b> , 16, 1483-1506	3.5	90
2	A quantum Mechanical Investigation of the Conformational Energetics of the Alanine and Glycine Dipeptides in the Gas Phase and in Aqueous Solution. <i>Journal of the American Chemical Society</i> , <b>1994</b> , 116, 9250-9256	16.4	146
1	Application of RESP charges to calculate conformational energies, hydrogen bond energies, and free energies of solvation. <i>Journal of the American Chemical Society</i> , <b>1993</b> , 115, 9620-9631	16.4	1031