

# Wendy D Cornell

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10790413/publications.pdf>

Version: 2024-02-01

12  
papers

15,168  
citations

932766

10  
h-index

1281420

11  
g-index

14  
all docs

14  
docs citations

14  
times ranked

13999  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | A Second Generation Force Field for the Simulation of Proteins, Nucleic Acids, and Organic Molecules. <i>Journal of the American Chemical Society</i> , 1995, 117, 5179-5197.   | 6.6 | 12,116    |
| 2  | Application of RESP charges to calculate conformational energies, hydrogen bond energies, and free energies of solvation. <i>Journal of the American Chemical Society</i> , 1993, 115, 9620-9631.   | 6.6 | 1,229     |
| 3  | Application of the multimolecule and multiconformational RESP methodology to biopolymers: Charge derivation for DNA, RNA, and proteins. <i>Journal of Computational Chemistry</i> , 1995, 16, 1357-1377.  | 1.5 | 944       |
| 4  | Comparison of Topological, Shape, and Docking Methods in Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 1504-1519.  | 2.5 | 384       |
| 5  | 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> , 1994, 116, 9250-9256.   | 6.6 | 155       |
| 6  | 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> , 2010, 50, 2029-2040.  | 2.5 | 100       |
| 7  | 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> , 1995, 16, 1483-1506. | 1.5 | 99        |
| 8  | 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> , 2020, 60, 4170-4179.  | 2.5 | 64        |
| 9  | Multiple protein structures and multiple ligands: effects on the apparent goodness of virtual screening results. <i>Journal of Computer-Aided Molecular Design</i> , 2008, 22, 257-265.   | 1.3 | 52        |
| 10 | 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> , 1997, 392, 101-109.  | 1.5 | 19        |
| 11 | Application of a simple diagonal force field to the simulation of cyclopentane conformational dynamics. <i>Journal of Computational Chemistry</i> , 1996, 17, 1541-1548.  | 1.5 | 5         |
| 12 | Application of a simple diagonal force field to the simulation of cyclopentane conformational dynamics. , 1996, 17, 1541.   |     | 1         |