Ramy Farid

List of Publications by Year
in descending order

12 papers	5,364 citations	758635 12 h-index	1199166 12 g-index
13 all docs	13 docs citations	13 times ranked	7927 citing authors

#	Article	IF	Citations
1	Novel Procedure for Modeling Ligand/Receptor Induced Fit Effects. Journal of Medicinal Chemistry, 2006, 49, 534-553.	2.9	1,671
2	Integrated Modeling Program, Applied Chemical Theory (IMPACT). Journal of Computational Chemistry, 2005, 26, 1752-1780.	1.5	1,194
3	Accurate and Reliable Prediction of Relative Ligand Binding Potency in Prospective Drug Discovery by Way of a Modern Free-Energy Calculation Protocol and Force Field. Journal of the American Chemical Society, 2015, 137, 2695-2703.	6.6	931
4	Role of the Active-Site Solvent in the Thermodynamics of Factor Xa Ligand Binding. Journal of the American Chemical Society, 2008, 130, 2817-2831.	6.6	594
5	New insights about HERG blockade obtained from protein modeling, potential energy mapping, and docking studies. Bioorganic and Medicinal Chemistry, 2006, 14, 3160-3173.	1.4	443
6	Contribution of Explicit Solvent Effects to the Binding Affinity of Smallâ€Molecule Inhibitors in Blood Coagulation Factor Serine Proteases. ChemMedChem, 2011, 6, 1049-1066.	1.6	116
7	Understanding Kinase Selectivity Through Energetic Analysis of Binding Site Waters. ChemMedChem, 2010, 5, 618-627.	1.6	112
8	Highâ€energy water sites determine peptide binding affinity and specificity of PDZ domains. Protein Science, 2009, 18, 1609-1619.	3.1	100
9	WScore: A Flexible and Accurate Treatment of Explicit Water Molecules in Ligandâ€“Receptor Docking. Journal of Medicinal Chemistry, 2016, 59, 4364-4384.	2.9	75
10	Improving database enrichment through ensemble docking. Journal of Computer-Aided Molecular Design, 2008, 22, 621-627.	1.3	63
11	The translocation kinetics of antibiotics through porin OmpC: Insights from structureâ€based solvation mapping using WaterMap. Proteins: Structure, Function and Bioinformatics, 2013, 81, 291-299.	1.5	44
12	Significant reduction in errors associated with nonbonded contacts in protein crystal structures: automated all-atom refinement withPrimeX. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 935-952.	2.5	21