

Lance M Westerhoff

List of Publications by Year in descending order

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15
papers

524
citations

933447

10
h-index

1199594

12
g-index

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all docs

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docs citations

15
times ranked

674
citing authors

#	ARTICLE	IF	CITATIONS
1	The critical role of QM/MM X-ray refinement and accurate tautomer/protomer determination in structure-based drug design. <i>Journal of Computer-Aided Molecular Design</i> , 2021, 35, 433-451.	2.9	15
2	MovableType Software for Fast Free Energy-Based Virtual Screening: Protocol Development, Deployment, Validation, and Assessment. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5437-5456.	5.4	7
3	High-throughput quantum-mechanics/molecular-mechanics (ONIOM) macromolecular crystallographic refinement with <i>PHENIX</i> / <i>DivCon</i> : the impact of mixed Hamiltonian methods on ligand and protein structure. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1063-1077.	2.3	18
4	The Impact of Experimental, Protein Structure on our Ability to Model Protein Function. <i>Biophysical Journal</i> , 2016, 110, 544a.	0.5	0
5	<i>XModeScore</i> : a novel method for accurate protonation/tautomer-state determination using quantum-mechanically driven macromolecular X-ray crystallographic refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 586-598.	2.3	15
6	Accurate Determination of Tautomeric/Protonation States in Quantum-Mechanic Driven Macromolecular Crystallographic Refinement. <i>Biophysical Journal</i> , 2015, 108, 620a.	0.5	0
7	Accurate macromolecular crystallographic refinement: incorporation of the linear scaling, semiempirical quantum-mechanics program <i>DivCon</i> into the <i>PHENIX</i> refinement package. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1233-1247.	2.5	46
8	Computational alanine scanning with linear scaling semiempirical quantum mechanical methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2329-2337.	2.6	17
9	Quantum Mechanical Pairwise Decomposition Analysis of Protein Kinase B Inhibitors: Validating a New Tool for Guiding Drug Design. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 651-661.	5.4	17
10	A Critical Assessment of the Performance of Protein-Ligand Scoring Functions Based on NMR Chemical Shift Perturbations. <i>Journal of Medicinal Chemistry</i> , 2007, 50, 5128-5134.	6.4	35
11	The role of quantum mechanics in structure-based drug design. <i>Drug Discovery Today</i> , 2007, 12, 725-731.	6.4	226
12	Quantum mechanical description of the interactions between DNA and water. <i>Journal of Molecular Graphics and Modelling</i> , 2006, 24, 440-455.	2.4	10
13	Pairwise Decomposition of Residue Interaction Energies Using Semiempirical Quantum Mechanical Methods in Studies of Protein-Ligand Interaction. <i>Journal of the American Chemical Society</i> , 2005, 127, 6583-6594.	13.7	40
14	Quantum mechanical/quantum mechanical methods. I. A divide and conquer strategy for solving the Schrödinger equation for large molecular systems using a composite density functional semiempirical Hamiltonian. <i>Journal of Chemical Physics</i> , 2000, 113, 5604-5613.	3.0	77
15	Fast, Routine Free Energy of Binding Estimation Using MovableType. <i>ACS Symposium Series</i> , 0, , 247-265.	0.5	1