Mark A Olson

List of Publications by Year
in descending order

43 papers	903 citations	471509 17 h-index	477307 29 g-index
45 all docs	45 docs citations	45 times ranked	1093 citing authors

#	Article	IF	Citations
1	Small-Molecule Probes Targeting the Viral PPxY-Host Nedd4 Interface Block Egress of a Broad Range of RNA Viruses. Journal of Virology, 2014, 88, 7294-7306.	3.4	86
2	In Silico Derived Small Molecules Bind the Filovirus VP35 Protein and Inhibit Its Polymerase Cofactor Activity. Journal of Molecular Biology, 2014, 426, 2045-2058.	4.2	75
3	Staphylococcal enterotoxins A and B share a common structural motif for binding class II major histocompatibility complex molecules. Nature Structural Biology, 1995, 2, 554-560.	9.7	68
4	Finding a new vaccine in the ricin protein fold. Protein Engineering, Design and Selection, 2004, 17, 391-397.	2.1	68
5	Evaluation of Disulfide Bond Position to Enhance the Thermal Stability of a Highly Stable Single Domain Antibody. PLoS ONE, 2014, 9, e115405.	2.5	43
6	Prediction of protein loop conformations using multiscale modeling methods with physical energy scoring functions. Journal of Computational Chemistry, 2008, 29, 820-831.	3.3	40
7	Secondary structural predictions for the clostridial neurotoxins. Proteins: Structure, Function and Bioinformatics, 1994, 20, 293-300.	2.6	39
8	Protein Folding Simulations Combining Self-Guided Langevin Dynamics and Temperature-Based Replica Exchange. Journal of Chemical Theory and Computation, 2010, 6, 2477-2487.	5.3	38
9	Ricin A-chain structural determinant for binding substrate analogues: A molecular dynamics simulation analysis. Proteins: Structure, Function and Bioinformatics, 1997, 27, 80-95.	2.6	36
10	Calculation of Protein Heat Capacity from Replica-Exchange Molecular Dynamics Simulations with Different Implicit Solvent Models. Journal of Physical Chemistry B, 2008, 112, 15064-15073.	2.6	35
11	Comparison of two adaptive temperature-based replica exchange methods applied to a sharp phase transition of protein unfolding-folding. Journal of Chemical Physics, 2011, 134, 244111.	3.0	27
12	Modeling implicit reorganization in continuum descriptions of protein-protein interactions. , 2000, 38, 115-119.		26
13	Assessment of Detection and Refinement Strategies for de novo Protein Structures Using Force Field and Statistical Potentials. Journal of Chemical Theory and Computation, 2007, 3, 312-324.	5.3	26
14	Kinetic, Mutational, and Structural Studies of the Venezuelan Equine Encephalitis Virus Nonstructural Protein 2 Cysteine Protease. Biochemistry, 2016, 55, 3007-3019.	2.5	25
15	Efficient Conformational Sampling in Explicit Solvent Using a Hybrid Replica Exchange Molecular Dynamics Method. Journal of Chemical Theory and Computation, 2012, 8, 677-687.	5.3	24
16	Comparison between selfâ€guided Langevin dynamics and molecular dynamics simulations for structure refinement of protein loop conformations. Journal of Computational Chemistry, 2011, 32, 3014-3022.	3.3	23
17	Small Molecule Analogues of the parasitic worm product ES-62 interact with the TIR domain of MyD88 to inhibit pro-inflammatory signalling. Scientific Reports, 2018, 8, 2123.	3.3	21
18	Comparison of volume and surface area nonpolar solvation free energy terms for implicit solvent simulations. Journal of Chemical Physics, 2013, 139, 044119.	3.0	20

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19	Modeling loop reorganization free energies of acetylcholinesterase: A comparison of explicit and implicit solvent models. Proteins: Structure, Function and Bioinformatics, 2004, 57, 645-650.	2.6	17
20	Free-Energy Profiles of Membrane Insertion of the M2 Transmembrane Peptide from Influenza A Virus. Biophysical Journal, 2008, 95, 5021-5029.	0.5	17
21	Stability of isolated antibody-antigen complexes as a predictive tool for selecting toxin neutralizing antibodies. MAbs, 2017, 9, 43-57.	5.2	16
22	Structure refinement of protein model decoys requires accurate sideâ€chain placement. Proteins: Structure, Function and Bioinformatics, 2013, 81, 469-478.	2.6	15
23	Structural and mutational analysis of a monomeric and dimeric form of a single domain antibody with implications for protein misfolding. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3101-3116.	2.6	14
24	Evaluation of Unrestrained Replica-Exchange Simulations Using Dynamic Walkers in Temperature Space for Protein Structure Refinement. PLoS ONE, 2014, 9, e96638.	2.5	12
25	Molecular docking of superantigens with class II major histocompatibility complex proteins. Journal of Molecular Recognition, 1997, 10, 277-289.	2.1	11
26	ExÂvivo inhibition of Clostridium botulinum neurotoxin types B, C, E, and F by small molecular weight inhibitors. Toxicon, 2015, 98, 12-19.	1.6	10
27	Experimental evaluation of singleâ€domain antibodies predicted by molecular dynamics simulations to have elevated thermal stability. Protein Science, 2019, 28, 1909-1912.	7.6	9
28	Predicting differential antigen-antibody contact regions based on solvent accessibility. The Protein Journal, 1997, 16, 607-618.	1.1	8
29	Electrostatic effects on the free-energy balance in folding a ribosome-inactivating protein. Biophysical Chemistry, 2001, 91, 219-229.	2.8	8
30	Application of replica exchange umbrella sampling to protein structure refinement of nontemplate models. Journal of Computational Chemistry, 2013, 34, 1785-1793.	3.3	7
31	Can template-based protein models guide the design of sequence fitness for enhanced thermal stability of single domain antibodies?. Protein Engineering, Design and Selection, 2015, 28, 395-402.	2.1	7
32	Accuracy of secondary structure and solvent accessibility predictions for a clostridial neurotoxin C-fragment. The Protein Journal, 1998, 17, 311-318.	1.1	5
33	Free-energy contributions to complex formation between botulinum neurotoxin type B and synaptobrevin fragment. Protein Engineering, Design and Selection, 2002, 15, 739-743.	2.1	5
34	On the Helix Propensity in Generalized Born Solvent Descriptions of Modeling the Dark Proteome. Frontiers in Molecular Biosciences, 2017, 4, 3.	3.5	5
35	Sequence Tolerance of a Single-Domain Antibody with a High Thermal Stability: Comparison of Computational and Experimental Fitness Profiles. ACS Omega, 2019, 4, 10444-10454.	3.5	4
36	Comparison of Replica Exchange Simulations of a Kinetically Trapped Protein Conformational State and its Native Form. Journal of Physical Chemistry B, 2016, 120, 2234-2240.	2.6	3

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37	Membrane insertion of fusion peptides from Ebola and Marburg viruses studied by replicaâ€exchange molecular dynamics simulations. Journal of Computational Chemistry, 2017, 38, 1342-1352.	3.3	3
38	Parallel Tempering of Dark Matter from the Ebola Virus Proteome: Comparison of CHARMM36m and CHARMM22 Force Fields with Implicit Solvent. Journal of Chemical Information and Modeling, 2018, 58, 111-118.	5.4	2
39	Conformational Selection of a Polyproline Peptide by Ebola Virus VP30. Proteomics, 2018, 18, e1800081.	2.2	2
40	Coarseâ€grained lattice model simulations of sequenceâ€structure fitness of a ribosomeâ€inactivating protein. Biopolymers, 2008, 89, 153-159.	2.4	1
41	Disorderâ€“Order Transitions in Conformational Selection of a Peptide by Ebola Virus Nucleoprotein. ACS Omega, 2020, 5, 5691-5697.	3.5	1
42	Ricin A-chain structural determinant for binding substrate analogues: A molecular dynamics simulation analysis. , 1997, 27, 80.		1
43	Continuum Models of Macromolecular Association in Aqueous Solution. Computational Chemistry - Reviews of Current Trends, 1999, , 153-190.	0.4	0