Michel F Sanner

List of Publications by Year
in descending order

39 papers	24,301 citations	279701 23 h-index	360920 35 g-index
40 all docs	40 docs citations	40 times ranked	31787 citing authors

#	Article	IF	Citations
1	AutoDock4 and AutoDockTools4: Automated docking with selective receptor flexibility. Journal of Computational Chemistry, 2009, 30, 2785-2791.	1.5	16,850
2	Reduced surface: An efficient way to compute molecular surfaces. Biopolymers, 1996, 38, 305-320.	1.2	1,818
3	Python: a programming language for software integration and development. Journal of Molecular Graphics and Modelling, 1999, 17, 57-61.	1.3	1,586
4	Computational proteinâ€“ligand docking and virtual drug screening with the AutoDock suite. Nature Protocols, 2016, 11, 905-919.	5.5	1,370
5	Reduced surface: an efficient way to compute molecular surfaces. Biopolymers, 1996, 38, 305-20.	1.2	657
6	Automated docking to multiple target structures: Incorporation of protein mobility and structural water heterogeneity in AutoDock. Proteins: Structure, Function and Bioinformatics, 2002, 46, 34-40.	1.5	394
7	AutoDockFR: Advances in Protein-Ligand Docking with Explicitly Specified Binding Site Flexibility. PLoS Computational Biology, 2015, 11, e1004586.	1.5	287
8	cellPACK: a virtual mesoscope to model and visualize structural systems biology. Nature Methods, 2015, 12, 85-91.	9.0	130
9	Accelerating A<scp>uto</scp>D<scp>ock</scp>4 with GPUs and Gradient-Based Local Search. Journal of Chemical Theory and Computation, 2021, 17, 1060-1073.	2.3	128
10	Tangible Interfaces for Structural Molecular Biology. Structure, 2005, 13, 483-491.	1.6	111
11	FLIPDock: Docking flexible ligands into flexible receptors. Proteins: Structure, Function and Bioinformatics, 2007, 68, 726-737.	1.5	97
12	AutoDock CrankPep: combining folding and docking to predict proteinâ€“peptide complexes. Bioinformatics, 2019, 35, 5121-5127.	1.8	96
13	The <scp>AutoDock</scp> suite at 30. Protein Science, 2021, 30, 31-43.	3.1	85
14	ePMV Embeds Molecular Modeling into Professional Animation Software Environments. Structure, 2011, 19, 293-303.	1.6	82
15	Fast and robust computation of molecular surfaces. , 1995, , .		75
16	A Component-Based Software Environment for Visualizing Large Macromolecular Assemblies. Structure, 2005, 13, 447-462.	1.6	67
17	AutoSite: an automated approach for pseudo-ligands predictionâ€”from ligand-binding sites identification to predicting key ligand atoms. Bioinformatics, 2016, 32, 3142-3149.	1.8	59
18	3D molecular models of whole HIV-1 virions generated with cellPACK. Faraday Discussions, 2014, 169, 23-44.	1.6	52

#	Article	IF	Citations
19	Reduced surface: An efficient way to compute molecular surfaces. Biopolymers, 1996, 38, 305-320.	1.2	48
20	Protein-Protein Docking with F2Dock 2.0 and GB-Rerank. PLoS ONE, 2013, 8, e51307.	1.1	33
21	Docking Flexible Cyclic Peptides with AutoDock CrankPep. Journal of Chemical Theory and Computation, 2019, 15, 5161-5168.	2.3	33
22	Proteinâ€“ligand docking with multiple flexible side chains. Journal of Computer-Aided Molecular Design, 2008, 22, 673-679.	1.3	30
23	Hierarchical and multi-resolution representation of protein flexibility. Bioinformatics, 2006, 22, 2768-2774.	1.8	29
24	Shape complementarity of proteinâ€“protein complexes at multiple resolutions. Proteins: Structure, Function and Bioinformatics, 2009, 75, 453-467.	1.5	29
25	AutoGridFR: Improvements on AutoDock Affinity Maps and Associated Software Tools. Journal of Computational Chemistry, 2019, 40, 2882-2886.	1.5	23
26	Evolutionary analysis of HIV-1 protease inhibitors: Methods for design of inhibitors that evade resistance. Proteins: Structure, Function and Bioinformatics, 2002, 48, 63-74.	1.5	17
27	Design and Synthesis of Transition State Analogs for Induction of Hydride Transfer Catalytic Antibodies. Journal of Organic Chemistry, 1997, 62, 3220-3229.	1.7	16
28	Model of the ?L?2 integrin I-domain/ICAM-1 DI interface suggests that subtle changes in loop orientation determine ligand specificity. Proteins: Structure, Function and Bioinformatics, 2002, 48, 151-160.	1.5	15
29	Visualizing Nature at Work from the Nano to the Macro Scale. Nanobiotechnology, 2005, 1, 007-022.	1.2	13
30	Conformational studies of cyclic peptide structures in solution from1H-Nmr data by distance geometry calculation and restrained energy minimization. Biopolymers, 1990, 29, 1387-1400.	1.2	12
31	uPy: A Ubiquitous CG Python API with Biological-Modeling Applications. IEEE Computer Graphics and Applications, 2012, 32, 50-61.	1.0	11
32	Improving Docking Power for Short Peptides Using Random Forest. Journal of Chemical Information and Modeling, 2021, 61, 3074-3090.	2.5	11
33	Adjusting potential energy functions for lattice models of chain molecules. , 1996, 25, 379-388.		8
34	Cyclic Peptides as Protein Kinase Inhibitors: Structureâ€“Activity Relationship and Molecular Modeling. Journal of Chemical Information and Modeling, 2021, 61, 3015-3026.	2.5	7
35	Computer-linked autofabricated 3D models for teaching structural biology. , 2004, , .		6
36	Lattice modeling: Accuracy of energy calculations. Journal of Computational Chemistry, 1996, 17, 1025-1032.	1.5	5

#	Article	IF	Citations
37	Using the Python programming language for bioinformatics. , 2005, , .		4
38	Câ€terminal residues of activated protein C light chain contribute to its anticoagulant and cytoprotective activities. Journal of Thrombosis and Haemostasis, 2020, 18, 1027-1038.	1.9	4
39	Activated protein C light chain provides an extended binding surface for its anticoagulant cofactor, protein S. Blood Advances, 2017, 1, 1423-1426.	2.5	3