Michel F Sanner

List of Publications by Citations

39 papers	17,247 citations	21 h-index	40 g-index
40 ext. papers	20,764 ext. citations	5.6 avg, IF	6.6 L-index

#	Paper	IF	Citations
39	AutoDock4 and AutoDockTools4: Automated docking with selective receptor flexibility. *Journal of Computational Chemistry*, **2009**, 30, 2785-91	3.5	11655
38	Reduced surface: An efficient way to compute molecular surfaces. *Biopolymers*, **1996**, 38, 305-320	2.2	1616
37	Python: a programming language for software integration and development. *Journal of Molecular Graphics and Modelling*, **1999**, 17, 57-61	2.8	1383
36	Computational protein-ligand docking and virtual drug screening with the AutoDock suite. *Nature Protocols*, **2016**, 11, 905-19	18.8	719
35	Reduced surface: an efficient way to compute molecular surfaces. *Biopolymers*, **1996**, 38, 305-20	2.2	557
34	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	4.2	341
33	AutoDockFR: Advances in Protein-Ligand Docking with Explicitly Specified Binding Site Flexibility. *PLoS Computational Biology*, **2015**, 11, e1004586	5	129
32	Tangible interfaces for structural molecular biology. *Structure*, **2005**, 13, 483-91	5.2	95
31	cellPACK: a virtual mesoscope to model and visualize structural systems biology. *Nature Methods*, **2015**, 12, 85-91	21.6	89
30	FLIPDock: docking flexible ligands into flexible receptors. *Proteins: Structure, Function and Bioinformatics*, **2007**, 68, 726-37	4.2	86
29	ePMV embeds molecular modeling into professional animation software environments. *Structure*, **2011**, 19, 293-303	5.2	60
28	Fast and robust computation of molecular surfaces **1995**,		56
27	A component-based software environment for visualizing large macromolecular assemblies. *Structure*, **2005**, 13, 447-62	5.2	53
26	3D molecular models of whole HIV-1 virions generated with cellPACK. *Faraday Discussions*, **2014**, 169, 23-44	3.6	37
25	AutoDock CrankPep: combining folding and docking to predict protein-peptide complexes. *Bioinformatics*, **2019**, 35, 5121-5127	7.2	34
24	Accelerating AutoDock4 with GPUs and Gradient-Based Local Search. *Journal of Chemical Theory and Computation*, **2021**, 17, 1060-1073	6.4	34
23	AutoSite: an automated approach for pseudo-ligands prediction-from ligand-binding sites identification to predicting key ligand atoms. *Bioinformatics*, **2016**, 32, 3142-3149	7.2	31

22	Reduced surface: An efficient way to compute molecular surfaces **1996**, 38, 305		29
21	Protein-protein docking with F(2)Dock 2.0 and GB-rerank. *PLoS ONE*, **2013**, 8, e51307	3.7	27
20	Protein-ligand docking with multiple flexible side chains. *Journal of Computer-Aided Molecular Design*, **2008**, 22, 673-9	4.2	26
19	Hierarchical and multi-resolution representation of protein flexibility. *Bioinformatics*, **2006**, 22, 2768-74	7.2	24
18	Shape complementarity of protein-protein complexes at multiple resolutions. *Proteins: Structure, Function and Bioinformatics*, **2009**, 75, 453-67	4.2	21
17	The AutoDock suite at 30. *Protein Science*, **2021**, 30, 31-43	6.3	21
16	Evolutionary analysis of HIV-1 protease inhibitors: Methods for design of inhibitors that evade resistance. *Proteins: Structure, Function and Bioinformatics*, **2002**, 48, 63-74	4.2	17
15	Model of the alphaLbeta2 integrin I-domain/ICAM-1 DI interface suggests that subtle changes in loop orientation determine ligand specificity. *Proteins: Structure, Function and Bioinformatics*, **2002**, 48, 151-60	4.2	15
14	Design and Synthesis of Transition State Analogs for Induction of Hydride Transfer Catalytic Antibodies. *Journal of Organic Chemistry*, **1997**, 62, 3220-3229	4.2	13
13	Visualizing nature at work from the nano to the macro scale. *Nanobiotechnology*, **2005**, 1, 007-022		13
12	Docking Flexible Cyclic Peptides with. *Journal of Chemical Theory and Computation*, **2019**, 15, 5161-5168	6.4	12
11	AutoGridFR: Improvements on AutoDock Affinity Maps and Associated Software Tools. *Journal of Computational Chemistry*, **2019**, 40, 2882-2886	3.5	11
10	uPy: a ubiquitous CG Python API with biological-modeling applications. *IEEE Computer Graphics and Applications*, **2012**, 32, 50-61	1.7	10
9	Conformational studies of cyclic peptide structures in solution from 1H-Nmr data by distance geometry calculation and restrained energy minimization. *Biopolymers*, **1990**, 29, 1387-400	2.2	9
8	Adjusting potential energy functions for lattice models of chain molecules. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 379-88	4.2	6
7	Computer-linked autofabricated 3D models for teaching structural biology **2004**,		4
6	Activated protein C light chain provides an extended binding surface for its anticoagulant cofactor, protein S. *Blood Advances*, **2017**, 1, 1423-1426	7.8	3
5	Lattice modeling: Accuracy of energy calculations. *Journal of Computational Chemistry*, **1996**, 17, 1025-1032	3.3	3

4	Improving Docking Power for Short Peptides Using Random Forest. *Journal of Chemical Information and Modeling*, **2021**, 61, 3074-3090	6.1	3
3	Using the Python programming language for bioinformatics **2005**,		2
2	Cyclic Peptides as Protein Kinase Inhibitors: Structure-Activity Relationship and Molecular Modeling. *Journal of Chemical Information and Modeling*, **2021**, 61, 3015-3026	6.1	2
1	C-terminal residues of activated protein C light chain contribute to its anticoagulant and cytoprotective activities. *Journal of Thrombosis and Haemostasis*, **2020**, 18, 1027-1038	15.4	1