

Michel F Sanner

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Cyclic Peptides as Protein Kinase Inhibitors: Structure-Activity Relationship and Molecular Modeling. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 3015-3026	6.1	2
38	Improving Docking Power for Short Peptides Using Random Forest. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 3074-3090	6.1	3
37	The AutoDock suite at 30. <i>Protein Science</i> , 2021 , 30, 31-43	6.3	21
36	Accelerating AutoDock4 with GPUs and Gradient-Based Local Search. <i>Journal of Chemical Theory and Computation</i> , 2021 , 17, 1060-1073	6.4	34
35	C-terminal residues of activated protein C light chain contribute to its anticoagulant and cytoprotective activities. <i>Journal of Thrombosis and Haemostasis</i> , 2020 , 18, 1027-1038	15.4	1
34	AutoGridFR: Improvements on AutoDock Affinity Maps and Associated Software Tools. <i>Journal of Computational Chemistry</i> , 2019 , 40, 2882-2886	3.5	11
33	Docking Flexible Cyclic Peptides with. <i>Journal of Chemical Theory and Computation</i> , 2019 , 15, 5161-5168	6.4	12
32	AutoDock CrankPep: combining folding and docking to predict protein-peptide complexes. <i>Bioinformatics</i> , 2019 , 35, 5121-5127	7.2	34
31	Activated protein C light chain provides an extended binding surface for its anticoagulant cofactor, protein S. <i>Blood Advances</i> , 2017 , 1, 1423-1426	7.8	3
30	AutoSite: an automated approach for pseudo-ligands prediction-from ligand-binding sites identification to predicting key ligand atoms. <i>Bioinformatics</i> , 2016 , 32, 3142-3149	7.2	31
29	Computational protein-ligand docking and virtual drug screening with the AutoDock suite. <i>Nature Protocols</i> , 2016 , 11, 905-19	18.8	719
28	cellPACK: a virtual mesoscope to model and visualize structural systems biology. <i>Nature Methods</i> , 2015 , 12, 85-91	21.6	89
27	AutoDockFR: Advances in Protein-Ligand Docking with Explicitly Specified Binding Site Flexibility. <i>PLoS Computational Biology</i> , 2015 , 11, e1004586	5	129
26	3D molecular models of whole HIV-1 virions generated with cellPACK. <i>Faraday Discussions</i> , 2014 , 169, 23-44	3.6	37
25	Protein-protein docking with F(2)Dock 2.0 and GB-rerank. <i>PLoS ONE</i> , 2013 , 8, e51307	3.7	27
24	uPy: a ubiquitous CG Python API with biological-modeling applications. <i>IEEE Computer Graphics and Applications</i> , 2012 , 32, 50-61	1.7	10
23	ePMV embeds molecular modeling into professional animation software environments. <i>Structure</i> , 2011 , 19, 293-303	5.2	60

22	AutoDock4 and AutoDockTools4: Automated docking with selective receptor flexibility. <i>Journal of Computational Chemistry</i> , 2009 , 30, 2785-91	3.5	11655
21	Shape complementarity of protein-protein complexes at multiple resolutions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 453-67	4.2	21
20	Protein-ligand docking with multiple flexible side chains. <i>Journal of Computer-Aided Molecular Design</i> , 2008 , 22, 673-9	4.2	26
19	FLIPDock: docking flexible ligands into flexible receptors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 726-37	4.2	86
18	Hierarchical and multi-resolution representation of protein flexibility. <i>Bioinformatics</i> , 2006 , 22, 2768-74	7.2	24
17	Using the Python programming language for bioinformatics 2005 ,		2
16	Visualizing nature at work from the nano to the macro scale. <i>Nanobiotechnology</i> , 2005 , 1, 007-022		13
15	Tangible interfaces for structural molecular biology. <i>Structure</i> , 2005 , 13, 483-91	5.2	95
14	A component-based software environment for visualizing large macromolecular assemblies. <i>Structure</i> , 2005 , 13, 447-62	5.2	53
13	Computer-linked autofabricated 3D models for teaching structural biology 2004 ,		4
12	Automated docking to multiple target structures: incorporation of protein mobility and structural water heterogeneity in AutoDock. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 46, 34-40	4.2	341
11	Evolutionary analysis of HIV-1 protease inhibitors: Methods for design of inhibitors that evade resistance. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 48, 63-74	4.2	17
10	Model of the alphaLbeta2 integrin I-domain/ICAM-1 DI interface suggests that subtle changes in loop orientation determine ligand specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 48, 151-60	4.2	15
9	Python: a programming language for software integration and development. <i>Journal of Molecular Graphics and Modelling</i> , 1999 , 17, 57-61	2.8	1383
8	Design and Synthesis of Transition State Analogs for Induction of Hydride Transfer Catalytic Antibodies. <i>Journal of Organic Chemistry</i> , 1997 , 62, 3220-3229	4.2	13
7	Reduced surface: An efficient way to compute molecular surfaces. <i>Biopolymers</i> , 1996 , 38, 305-320	2.2	1616
6	Lattice modeling: Accuracy of energy calculations. <i>Journal of Computational Chemistry</i> , 1996 , 17, 1025-1032	3.2	3
5	Adjusting potential energy functions for lattice models of chain molecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 379-88	4.2	6

4	Reduced surface: an efficient way to compute molecular surfaces. <i>Biopolymers</i> , 1996 , 38, 305-20	2.2	557
3	Reduced surface: An efficient way to compute molecular surfaces 1996 , 38, 305		29
2	Fast and robust computation of molecular surfaces 1995 ,		56
1	Conformational studies of cyclic peptide structures in solution from ¹ H-Nmr data by distance geometry calculation and restrained energy minimization. <i>Biopolymers</i> , 1990 , 29, 1387-400	2.2	9