Michal Vieth

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5607075/publications.pdf

Version: 2024-02-01

41	4,058	218677	265206
papers	citations	26 h-index	42 g-index

42	42	42	5175
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of Î²-Lactams Active against Mycobacterium tuberculosis by a Consortium of Pharmaceutical Companies and Academic Institutions. ACS Infectious Diseases, 2022, 8, 557-573.	3.8	13
2	Structural determinants of dual incretin receptor agonism by tirzepatide. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2116506119.	7.1	31
3	Structural insights into probe-dependent positive allosterism of the GLP-1 receptor. Nature Chemical Biology, 2020, 16, 1105-1110.	8.0	58
4	Identification of tyrosine kinase inhibitors that halt Plasmodium falciparum parasitemia. PLoS ONE, 2020, 15, e0242372.	2.5	13
5	Crystal structure of human RIOK2 bound to a specific inhibitor. Open Biology, 2019, 9, 190037.	3.6	15
6	Predicting the Conformational Variability of Abl Tyrosine Kinase using Molecular Dynamics Simulations and Markov State Models. Journal of Chemical Theory and Computation, 2018, 14, 2721-2732.	5.3	47
7	Molecular Basis for Necitumumab Inhibition of EGFR Variants Associated with Acquired Cetuximab Resistance. Molecular Cancer Therapeutics, 2018, 17, 521-531.	4.1	45
8	Are induced fit protein conformational changes caused by ligandâ€binding predictable? A molecular dynamics investigation. Journal of Computational Chemistry, 2017, 38, 1229-1237.	3.3	10
9	Reconstruction of 3D structures of MET antibodies from electron microscopy 2D class averages. PLoS ONE, 2017, 12, e0175758.	2.5	10
10	Oxadiazoles Have Butyrate-Specific Conditional Activity against Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2016, 60, 3608-3616.	3.2	26
11	Knowledge-Based Strategy to Improve Ligand Pose Prediction Accuracy for Lead Optimization. Journal of Chemical Information and Modeling, 2015, 55, 1460-1468.	5.4	12
12	Perspective on computational and structural aspects of kinase discovery from IPK2014. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1595-1604.	2.3	4
13	Selectivity Data: Assessment, Predictions, Concordance, and Implications. Journal of Medicinal Chemistry, 2013, 56, 6991-7002.	6.4	11
14	What general conclusions can we draw from kinase profiling data sets?. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1425-1433.	2.3	28
15	A High-Throughput Screen against Pantothenate Synthetase (PanC) Identifies 3-Biphenyl-4-Cyanopyrrole-2-Carboxylic Acids as a New Class of Inhibitor with Activity against Mycobacterium tuberculosis. PLoS ONE, 2013, 8, e72786.	2.5	35
16	Structure-guided expansion of kinase fragment libraries driven by support vector machine models. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 642-652.	2.3	23
17	Kinase Inhibitor Data Modeling and de Novo Inhibitor Design with Fragment Approaches. Journal of Medicinal Chemistry, 2009, 52, 6456-6466.	6.4	41
18	Chemical Fragments as Foundations for Understanding Target Space and Activity Prediction. Journal of Medicinal Chemistry, 2008, 51, 2689-2700.	6.4	70

#	Article	IF	Citations
19	Lessons in Molecular Recognition. 2. Assessing and Improving Cross-Docking Accuracy. Journal of Chemical Information and Modeling, 2007, 47, 2293-2302.	5.4	112
20	Drugs in other drugs: a new look at drugs as fragments. Drug Discovery Today, 2007, 12, 71-79.	6.4	73
21	Geometric Accuracy of Three-Dimensional Molecular Overlays. Journal of Chemical Information and Modeling, 2006, 46, 1996-2002.	5.4	17
22	Dependence of Molecular Properties on Proteomic Family for Marketed Oral Drugs. Journal of Medicinal Chemistry, 2006, 49, 3451-3453.	6.4	95
23	Novel route to the synthesis of 4-quinolyl isothiocyanates. Tetrahedron Letters, 2006, 47, 2161-2164.	1.4	17
24	Kinomics: characterizing the therapeutically validated kinase space. Drug Discovery Today, 2005, 10, 839-846.	6.4	164
25	Design of Potent and Selective 2-Aminobenzimidazole-Based p38Î± MAP Kinase Inhibitors with Excellent in Vivo Efficacy. Journal of Medicinal Chemistry, 2005, 48, 2270-2273.	6.4	49
26	Aminoimidazo[1,2-a]pyridines as a new structural class of cyclin-dependent kinase inhibitors. Part 1: Design, synthesis, and biological evaluation. Bioorganic and Medicinal Chemistry Letters, 2004, 14, 6095-6099.	2.2	34
27	Kinomicsâ€"structural biology and chemogenomics of kinase inhibitors and targets. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1697, 243-257.	2.3	168
28	SDOCKER:Â A Method Utilizing Existing X-ray Structures To Improve Docking Accuracy. Journal of Medicinal Chemistry, 2004, 47, 3142-3148.	6.4	47
29	Characteristic Physical Properties and Structural Fragments of Marketed Oral Drugs. Journal of Medicinal Chemistry, 2004, 47, 224-232.	6.4	350
30	Lessons in Molecular Recognition:â€‰ The Effects of Ligand and Protein Flexibility on Molecular Docking Accuracy. Journal of Medicinal Chemistry, 2004, 47, 45-55.	6.4	358
31	The discovery of a new structural class of cyclin-dependent kinase inhibitors, aminoimidazo[1,2-a]pyridines. Molecular Cancer Therapeutics, 2004, 3, 1-9.	4.1	8
32	Molecular properties that influence oral drug-like behavior. Current Opinion in Drug Discovery & Development, 2004, 7, 470-7.	1.9	29
33	Detailed analysis of grid-based molecular docking: A case study of CDOCKER?A CHARMm-based MD docking algorithm. Journal of Computational Chemistry, 2003, 24, 1549-1562.	3.3	1,299
34	Synthesis and Activity of New Aryl- and Heteroaryl-Substituted Pyrazole Inhibitors of the Transforming Growth Factor-Î² Type I Receptor Kinase Domain. Journal of Medicinal Chemistry, 2003, 46, 3953-3956.	6.4	225
35	DoMCoSAR:Â A Novel Approach for Establishing the Docking Mode That Is Consistent with the Structureâ"Activity Relationship. Application to HIV-1 Protease Inhibitors and VEGF Receptor Tyrosine Kinase Inhibitors. Journal of Medicinal Chemistry, 2000, 43, 3020-3032.	6.4	77
36	Do active site conformations of small ligands correspond to low free-energy solution structures?. Journal of Computer-Aided Molecular Design, 1998, 12, 563-572.	2.9	94

#	Article	IF	Citations
37	Assessing energy functions for flexible docking. Journal of Computational Chemistry, 1998, 19, 1612-1622.	3.3	144
38	Assessing search strategies for flexible docking. Journal of Computational Chemistry, 1998, 19, 1623-1631.	3.3	112
39	Predicting leucine zipper structures from sequence. Protein Engineering, Design and Selection, 1996, 9, 657-662.	2.1	35
40	A simple technique to estimate partition functions and equilibrium constants from Monte Carlo simulations. Journal of Chemical Physics, 1995, 102, 6189-6193.	3.0	12
41	Prediction of Quaternary Structure of Coiled Coils. Application to Mutants of the GCN4 Leucine Zipper. Journal of Molecular Biology, 1995, 251, 448-467.	4.2	45