David A Hecht

List of Publications by Year
in descending order

37	729	623734	580821
papers	citations	14 h-index	25 g-index

38	38	38	1010
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Oral IDN-6556, an antiapoptotic caspase inhibitor, may lower aminotransferase activity in patients with chronic hepatitis C. Hepatology, 2007, 46, 324-329.	7.3	177
2	Correlating hydration shell structure with amino acid hydrophobicity. Journal of the American Chemical Society, 1993, 115, 3336-3337.	13.7	77
3	CUREs in biochemistryâ€"where we are and where we should go. Biochemistry and Molecular Biology Education, 2017, 45, 7-12.	1.2	52
4	Exploiting Atropisomerism to Increase the Target Selectivity of Kinase Inhibitors. Angewandte Chemie - International Edition, 2015, 54, 11754-11759.	13.8	51
5	Computational Intelligence Methods for Docking Scores. Current Computer-Aided Drug Design, 2009, 5, 56-68.	1.2	33
6	A Novel In Silico Approach to Drug Discovery via Computational Intelligence. Journal of Chemical Information and Modeling, 2009, 49, 1105-1121.	5.4	32
7	QSAR using evolved neural networks for the inhibition of mutant PfDHFR by pyrimethamine derivatives. BioSystems, 2008, 92, 10-15.	2.0	31
8	Modeling the structural origins of drug resistance to isoniazid via key mutations in Mycobacterium tuberculosis catalase-peroxidase, KatG. Tuberculosis, 2018, 108, 155-162.	1.9	26
9	Defining hydrophobicity: probing the structure of solute-induced hydration shells by Fourier transform infrared spectroscopy. Journal of the American Chemical Society, 1992, 114, 4336-4339.	13.7	25
10	High-Throughput Ligand Screening via Preclustering and Evolved Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 476-484.	3.0	20
11	Modeling the inhibition of quadruple mutant Plasmodium falciparum dihydrofolate reductase by pyrimethamine derivatives. Journal of Computer-Aided Molecular Design, 2008, 22, 29-38.	2.9	20
12	In silico screening against wild-type and mutant Plasmodium falciparum dihydrofolate reductase. Journal of Molecular Graphics and Modelling, 2008, 26, 1145-1152.	2.4	20
13	Applications of machine learning and computational intelligence to drug discovery and development. Drug Development Research, 2011, 72, 53-65.	2.9	19
14	Structural-based analysis of dihydrofolate reductase evolution. Molecular Phylogenetics and Evolution, 2011, 61, 212-230.	2.7	14
15	The Preorganization of Atropisomers to Increase Target Selectivity. Synlett, 2016, 27, 977-983.	1.8	11
16	USING SCDL FOR INTEGRATING TOOLS AND DATA FOR COMPLEX BIOMEDICAL APPLICATIONS. International Journal of Semantic Computing, 2008, 02, 291-308.	0.5	10
17	Activity of Selected Nucleoside Analogue ProTides against Zika Virus in Human Neural Stem Cells. Viruses, 2019, 11, 365.	3.3	10
18	On the relationship between GC content and the number of predicted microRNA binding sites by MicroInspector. Computational Biology and Chemistry, 2008, 32, 222-226.	2.3	9

#	Article	IF	Citations
19	Modeling the evolution of drug resistance in malaria. Journal of Computer-Aided Molecular Design, 2012, 26, 1343-1353.	2.9	9
20	Quantitative structure-property relationships for drug solubility prediction using evolved neural networks. , 2008, , .		7
21	Cefoxitin is both an inhibitor of class A beta-lactamase of Xanthomonas campestris pv. campestris str. 17 and an inducer of its gene. Research in Microbiology, 2012, 163, 550-556.	2.1	6
22	The novel protein homeostatic modulator BTX306 is active in myeloma and overcomes bortezomib and lenalidomide resistance. Journal of Molecular Medicine, 2020, 98, 1161-1173.	3.9	6
23	Docking scores and QSAR using evolved neural networks for the Pan-inhibition of wild-type and mutant PfDHFR by cycloguanil derivatives. , 2009, , .		5
24	Discovery of cyclic guanidine-linked sulfonamides as inhibitors of LMTK3 kinase. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 127108.	2.2	5
25	Machine learning approaches for customized docking scores: Modeling of inhibition of Mycobacterium tuberculosis enoyl acyl carrier protein reductase. , 2010, , .		4
26	Semantic Computing and Drug Discovery - A Preliminary Report. , 2013, , .		4
27	Enhancing the selectivity of kinase inhibitors in oncology: a chemical biology perspective. Future Medicinal Chemistry, 2016, 8, 241-244.	2.3	4
28	Structure-based analysis of Bacilli and plasmid dihydrofolate reductase evolution. Journal of Molecular Graphics and Modelling, 2017, 71, 135-153.	2.4	3
29	Towards predictive structure-based models of evolved drug resistance. , 2012, , .		2
30	BioSemantic System: Applications of Structured Natural Language to Biological and Biochemical Research. , 2008, , .		1
31	SCDL Applications to Drug Discovery. , 2009, , .		1
32	Molecular Modeling Studies of AmpR Mediated AmpC ß-Lactamase Repression. , 2011, , .		1
33	Describing Dynamic Biological Systems in SPDL and SCDL. , 2009, , .		0
34	BioFactory: Semantic Integration of Biomedical Data and Applications. , 2012, , .		0
35	Modeling the evolution of drug resistance in Plasmodium falciparum DHFR. , 2013, , .		0
36	Structure-based design of guanosine analogue inhibitors targeting GTP cyclohydrolase IB towards a new class of antibiotics. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 126818.	2.2	0

#	Article	IF	Citations
37	Syntheses and Binding Testing of N1-Alkylamino-Substituted 2-Aminobenzimidazole Analogues Targeting the Hepatitis C Virus Internal Ribosome Entry Site. Australian Journal of Chemistry, 2020, 73, 212.	0.9	0