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	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
2	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
3	Discovery of cyclic guanidine-linked sulfonamides as inhibitors of LMTK3 kinase. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 127108.	2.2	5
4	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
5	Activity of Selected Nucleoside Analogue ProTides against Zika Virus in Human Neural Stem Cells. Viruses, 2019, 11, 365.	3.3	10
6	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
7	CUREs in biochemistryâ€"where we are and where we should go. Biochemistry and Molecular Biology Education, 2017, 45, 7-12.	1.2	52
8	Structure-based analysis of Bacilli and plasmid dihydrofolate reductase evolution. Journal of Molecular Graphics and Modelling, 2017, 71, 135-153.	2.4	3
9	The Preorganization of Atropisomers to Increase Target Selectivity. Synlett, 2016, 27, 977-983.	1.8	11
10	Enhancing the selectivity of kinase inhibitors in oncology: a chemical biology perspective. Future Medicinal Chemistry, 2016, 8, 241-244.	2.3	4
11	Exploiting Atropisomerism to Increase the Target Selectivity of Kinase Inhibitors. Angewandte Chemie - International Edition, 2015, 54, 11754-11759.	13.8	51
12	Modeling the evolution of drug resistance in Plasmodium falciparum DHFR. , 2013, , .		0
13	Semantic Computing and Drug Discovery - A Preliminary Report. , 2013, , .		4
14	Modeling the evolution of drug resistance in malaria. Journal of Computer-Aided Molecular Design, 2012, 26, 1343-1353.	2.9	9
15	BioFactory: Semantic Integration of Biomedical Data and Applications. , 2012, , .		0
16	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
17	Towards predictive structure-based models of evolved drug resistance. , 2012, , .		2
18	Molecular Modeling Studies of AmpR Mediated AmpC ß-Lactamase Repression. , 2011, , .		1

#	Article	IF	Citations
19	Applications of machine learning and computational intelligence to drug discovery and development. Drug Development Research, 2011, 72, 53-65.	2.9	19
20	Structural-based analysis of dihydrofolate reductase evolution. Molecular Phylogenetics and Evolution, 2011, 61, 212-230.	2.7	14
21	Machine learning approaches for customized docking scores: Modeling of inhibition of Mycobacterium tuberculosis enoyl acyl carrier protein reductase. , 2010, , .		4
22	Computational Intelligence Methods for Docking Scores. Current Computer-Aided Drug Design, 2009, 5, 56-68.	1.2	33
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	Describing Dynamic Biological Systems in SPDL and SCDL. , 2009, , .		0
25	SCDL Applications to Drug Discovery. , 2009, , .		1
26	A Novel In Silico Approach to Drug Discovery via Computational Intelligence. Journal of Chemical Information and Modeling, 2009, 49, 1105-1121.	5.4	32
27	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
28	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
29	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
30	QSAR using evolved neural networks for the inhibition of mutant PfDHFR by pyrimethamine derivatives. BioSystems, 2008, 92, 10-15.	2.0	31
31	Quantitative structure-property relationships for drug solubility prediction using evolved neural networks. , 2008, , .		7
32	USING SCDL FOR INTEGRATING TOOLS AND DATA FOR COMPLEX BIOMEDICAL APPLICATIONS. International Journal of Semantic Computing, 2008, 02, 291-308.	0.5	10
33	BioSemantic System: Applications of Structured Natural Language to Biological and Biochemical Research. , 2008, , .		1
34	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
35	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
36	Correlating hydration shell structure with amino acid hydrophobicity. Journal of the American Chemical Society, 1993, 115, 3336-3337.	13.7	77

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37	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