

# Daniel Reker

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9474367/publications.pdf>

Version: 2024-02-01

40  
papers

2,649  
citations

236612

25  
h-index

243296

44  
g-index

47  
all docs

47  
docs citations

47  
times ranked

3559  
citing authors

#	ARTICLE	IF	CITATIONS
1	Oral mRNA delivery using capsule-mediated gastrointestinal tissue injections. <i>Matter</i> , 2022, 5, 975-987.	5.0	48
2	Computationally guided high-throughput design of self-assembling drug nanoparticles. <i>Nature Nanotechnology</i> , 2021, 16, 725-733.	15.6	64
3	Combating small-molecule aggregation with machine learning. <i>Cell Reports Physical Science</i> , 2021, 2, 100573.	2.8	11
4	Adaptive Optimization of Chemical Reactions with Minimal Experimental Information. <i>Cell Reports Physical Science</i> , 2020, 1, 100247.	2.8	42
5	Historical Evolution and Provider Awareness of Inactive Ingredients in Oral Medications. <i>Pharmaceutical Research</i> , 2020, 37, 234.	1.7	0
6	Artificial intelligence in chemistry and drug design. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 709-715.	1.3	79
7	Machine Learning Uncovers Food- and Excipient-Drug Interactions. <i>Cell Reports</i> , 2020, 30, 3710-3716.e4.	2.9	37
8	Robotically handled whole-tissue culture system for the screening of oral drug formulations. <i>Nature Biomedical Engineering</i> , 2020, 4, 544-559.	11.6	35
9	Predicting protein-ligand interactions based on bow-pharmacological space and Bayesian additive regression trees. <i>Scientific Reports</i> , 2019, 9, 7703.	1.6	37
10	Computational advances in combating colloidal aggregation in drug discovery. <i>Nature Chemistry</i> , 2019, 11, 402-418.	6.6	51
11	“Inactive” ingredients in oral medications. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	68
12	Practical considerations for active machine learning in drug discovery. <i>Drug Discovery Today: Technologies</i> , 2019, 32-33, 73-79.	4.0	46
13	Advanced Editorial to announce a JCAMD Special Issue on Artificial Intelligence and Machine Learning. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 941-941.	1.3	0
14	Cheminformatic Analysis of Natural Product Fragments. <i>Progress in the Chemistry of Organic Natural Products</i> , 2019, 110, 143-175.	0.8	1
15	Selection of Informative Examples in Chemogenomic Datasets. <i>Methods in Molecular Biology</i> , 2018, 1825, 369-410.	0.4	9
16	Active learning for computational chemogenomics. <i>Future Medicinal Chemistry</i> , 2017, 9, 381-402.	1.1	75
17	Matrix-based Molecular Descriptors for Prospective Virtual Compound Screening. <i>Molecular Informatics</i> , 2017, 36, 1600091.	1.4	18
18	Small Random Forest Models for Effective Chemogenomic Active Learning. <i>Journal of Computer Aided Chemistry</i> , 2017, 18, 124-142.	0.3	14

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19	New use of an old drug: inhibition of breast cancer stem cells by benztropine mesylate. <i>Oncotarget</i> , 2017, 8, 1007-1022.	0.8	22
20	Counting on natural products for drug design. <i>Nature Chemistry</i> , 2016, 8, 531-541.	6.6	879
21	Deorphaning the Macromolecular Targets of the Natural Anticancer Compound Dolicolide. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 12408-12411.	7.2	31
22	Deorphaning the Macromolecular Targets of the Natural Anticancer Compound Dolicolide. <i>Angewandte Chemie</i> , 2016, 128, 12596-12599.	1.6	3
23	Multi-objective active machine learning rapidly improves structure-activity models and reveals new protein-protein interaction inhibitors. <i>Chemical Science</i> , 2016, 7, 3919-3927.	3.7	55
24	Spotting and designing promiscuous ligands for drug discovery. <i>Chemical Communications</i> , 2016, 52, 1135-1138.	2.2	33
25	De Novo Fragment Design for Drug Discovery and Chemical Biology. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 15079-15083.	7.2	30
26	Fragment-Based De Novo Design Reveals a Small Molecule Inhibitor of <i>Helicobacter Pylori</i> HtrA. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 10244-10248.	7.2	37
27	Revealing the Macromolecular Targets of Fragment-Like Natural Products. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 10516-10520.	7.2	54
28	Multidimensional De Novo Design Reveals 5-HT <sub>2B</sub> Receptor-Selective Ligands. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 1551-1555.	7.2	39
29	Chemography of Natural Product Space. <i>Planta Medica</i> , 2015, 81, 429-435.	0.7	23
30	Active-learning strategies in computer-assisted drug discovery. <i>Drug Discovery Today</i> , 2015, 20, 458-465.	3.2	169
31	Coping with Polypharmacology by Computational Medicinal Chemistry. <i>Chimia</i> , 2014, 68, 648.	0.3	6
32	Identifying the macromolecular targets of de novo-designed chemical entities through self-organizing map consensus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4067-4072.	3.3	196
33	Revealing the macromolecular targets of complex natural products. <i>Nature Chemistry</i> , 2014, 6, 1072-1078.	6.6	114
34	Target prediction by cascaded self-organizing maps for ligand de-orphaning and side-effect investigation. <i>Journal of Cheminformatics</i> , 2014, 6, .	2.8	1
35	Deorphaning Pyrrolopyrazines as Potent Multi-Target Antimalarial Agents. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 7079-7084.	7.2	30
36	Common non-epigenetic drugs as epigenetic modulators. <i>Trends in Molecular Medicine</i> , 2013, 19, 742-753.	3.5	68

#	ARTICLE	IF	CITATIONS
37	De novo design and optimization of Aurora A kinase inhibitors. <i>Chemical Science</i> , 2013, 4, 1229.	3.7	23
38	Chemically Advanced Template Search (CATS) for Scaffold Hopping and Prospective Target Prediction for "Orphan" Molecules. <i>Molecular Informatics</i> , 2013, 32, 133-138.	1.4	132
39	Bioinformatic Challenges in Targeted Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 4393-4402.	1.8	20
40	Computation of mutual information from Hidden Markov Models. <i>Computational Biology and Chemistry</i> , 2010, 34, 328-333.	1.1	4