

# Dilyana Dimova

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

427  
citations

758635

12  
h-index

752256

20  
g-index

28  
all docs

28  
docs citations

28  
times ranked

459  
citing authors

#	ARTICLE	IF	CITATIONS
1	Redundancy in two major compound databases. <i>Drug Discovery Today</i> , 2018, 23, 1183-1186.	3.2	8
2	Mapping Biological Activities to Different Types of Molecular Scaffolds: Exemplary Application to Protein Kinase Inhibitors. <i>Methods in Molecular Biology</i> , 2018, 1825, 327-337.	0.4	1
3	Collection of analog series-based scaffolds from public compound sources. <i>Future Science OA</i> , 2018, 4, FSO287.	0.9	8
4	Computational design of new molecular scaffolds for medicinal chemistry, part II: generalization of analog series-based scaffolds. <i>Future Science OA</i> , 2018, 4, FSO267.	0.9	8
5	Identification and analysis of promiscuity cliffs formed by bioactive compounds and experimental implications. <i>RSC Advances</i> , 2017, 7, 58-66.	1.7	15
6	Systematic analysis of structural and activity relationships between conventional hierarchical and analog series-based scaffolds. <i>RSC Advances</i> , 2017, 7, 18718-18723.	1.7	3
7	Application of a New Scaffold Concept for Computational Target Deconvolution of Chemical Cancer Cell Line Screens. <i>ACS Omega</i> , 2017, 2, 1463-1468.	1.6	14
8	Is scaffold hopping a reliable indicator for the ability of computational methods to identify structurally diverse active compounds?. <i>Journal of Computer-Aided Molecular Design</i> , 2017, 31, 603-608.	1.3	2
9	Exploring Structural Relationships between Bioactive and Commercial Chemical Space and Developing Target Hypotheses for Compound Acquisition. <i>ACS Omega</i> , 2017, 2, 7760-7766.	1.6	2
10	Assessing Scaffold Diversity of Kinase Inhibitors Using Alternative Scaffold Concepts and Estimating the Scaffold Hopping Potential for Different Kinases. <i>Molecules</i> , 2017, 22, 730.	1.7	12
11	Computational Method for the Systematic Identification of Analog Series and Key Compounds Representing Series and Their Biological Activity Profiles. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 7667-7676.	2.9	50
12	Analog series-based scaffolds: computational design and exploration of a new type of molecular scaffolds for medicinal chemistry. <i>Future Science OA</i> , 2016, 2, FSO149.	0.9	28
13	Highly Promiscuous Small Molecules from Biological Screening Assays Include Many Pan-Assay Interference Compounds but Also Candidates for Polypharmacology. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 10285-10290.	2.9	38
14	Classification of matching molecular series on the basis of SAR phenotypes and structural relationships. <i>MedChemComm</i> , 2016, 7, 237-246.	3.5	8
15	Monitoring the Progression of Structure-Activity Relationship Information during Lead Optimization. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 4235-4244.	2.9	27
16	Identification of Orthologous Target Pairs with Shared Active Compounds and Comparison of Organism-specific Activity Patterns. <i>Chemical Biology and Drug Design</i> , 2015, 86, 1105-1114.	1.5	2
17	Systematic assessment of scaffold hopping versus activity cliff formation across bioactive compound classes following a molecular hierarchy. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 3183-3191.	1.4	4
18	Activity cliff clusters as a source of structure-activity relationship information. <i>Expert Opinion on Drug Discovery</i> , 2015, 10, 441-447.	2.5	12

#	ARTICLE	IF	CITATIONS
19	Systematic assessment of coordinated activity cliffs formed by kinase inhibitors and detailed characterization of activity cliff clusters and associated SAR information. <i>European Journal of Medicinal Chemistry</i> , 2015, 90, 414-427.	2.6	9
20	Extraction of SAR information from activity cliff clusters via matching molecular series. <i>European Journal of Medicinal Chemistry</i> , 2014, 87, 454-460.	2.6	12
21	Method for the Evaluation of Structure-Activity Relationship Information Associated with Coordinated Activity Cliffs. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 6553-6563.	2.9	17
22	Advancing the activity cliff concept, part II. <i>F1000Research</i> , 2014, 3, 75.	0.8	23
23	Quantifying the Fingerprint Descriptor Dependence of Structure-Activity Relationship Information on a Large Scale. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 2275-2281.	2.5	12
24	Do Medicinal Chemists Learn from Activity Cliffs? A Systematic Evaluation of Cliff Progression in Evolving Compound Data Sets. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 3339-3345.	2.9	23
25	Assessing the Target Differentiation Potential of Imidazole-Based Protein Kinase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 11067-11071.	2.9	24
26	Advances in Computational Medicinal Chemistry: Matched Molecular Pair Analysis. <i>Drug Development Research</i> , 2012, 73, 518-527.	1.4	21
27	Matched Molecular Pair Analysis of Small Molecule Microarray Data Identifies Promiscuity Cliffs and Reveals Molecular Origins of Extreme Compound Promiscuity. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 10220-10228.	2.9	41
28	Computational Chemical Biology: Identification of Small Molecular Probes that Discriminate between Members of Target Protein Families. <i>Chemical Biology and Drug Design</i> , 2012, 79, 369-375.	1.5	3