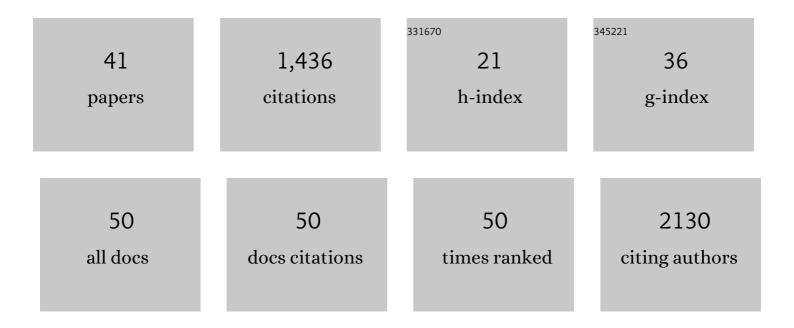
Oscar Méndez-Lucio

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	De novo generation of hit-like molecules from gene expression signatures using artificial intelligence. Nature Communications, 2020, 11, 10.	12.8	253
2	Polypharmacology modelling using proteochemometrics (PCM): recent methodological developments, applications to target families, and future prospects. MedChemComm, 2015, 6, 24-50.	3.4	109
3	The many roles of molecular complexity in drug discovery. Drug Discovery Today, 2017, 22, 120-126.	6.4	107
4	Lysine harvesting is an antioxidant strategy and triggers underground polyamine metabolism. Nature, 2019, 572, 249-253.	27.8	99
5	Toward Drug Repurposing in Epigenetics: Olsalazine as a Hypomethylating Compound Active in a Cellular Context. ChemMedChem, 2014, 9, 560-565.	3.2	67
6	A geometric deep learning approach to predict binding conformations of bioactive molecules. Nature Machine Intelligence, 2021, 3, 1033-1039.	16.0	64
7	Molecular basis for benzimidazole resistance from a novel β-tubulin binding site model. Journal of Molecular Graphics and Modelling, 2013, 45, 26-37.	2.4	61
8	Towards the identification of the binding site of benzimidazoles to Î ² -tubulin of Trichinella spiralis: Insights from computational and experimental data. Journal of Molecular Graphics and Modelling, 2013, 41, 12-19.	2.4	54
9	Discovery and development of DNA methyltransferase inhibitors using in silico approaches. Drug Discovery Today, 2015, 20, 569-577.	6.4	53
10	Synthesis and antiprotozoal activity of novel 2-{[2-(1H-imidazol-1-yl)ethyl]sulfanyl}-1H-benzimidazole derivatives. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 4221-4224.	2.2	48
11	Chemoinformatic expedition of the chemical space of fungal products. Future Medicinal Chemistry, 2016, 8, 1399-1412.	2.3	42
12	Identifying Activity Cliff Generators of PPAR Ligands Using SAS Maps. Molecular Informatics, 2012, 31, 837-846.	2.5	32
13	Design, synthesis and evaluation of semi-synthetic triazole-containing caffeic acid analogues as 5-lipoxygenase inhibitors. European Journal of Medicinal Chemistry, 2015, 101, 573-583.	5.5	30
14	A chemical space odyssey of inhibitors of histone deacetylases and bromodomains. RSC Advances, 2016, 6, 56225-56239.	3.6	28
15	Modelling ligand selectivity of serine proteases using integrative proteochemometric approaches improves model performance and allows the multi-target dependent interpretation of features. Integrative Biology (United Kingdom), 2014, 6, 1023-1033.	1.3	26
16	Activity and property landscape modeling is at the interface of chemoinformatics and medicinal chemistry. Future Medicinal Chemistry, 2015, 7, 1197-1211.	2.3	26
17	Rationalization of Activity Cliffs of a Sulfonamide Inhibitor of DNA Methyltransferases with Induced-Fit Docking. International Journal of Molecular Sciences, 2014, 15, 3253-3261.	4.1	25
18	The Interplay Between Molecular Modeling and Chemoinformatics to Characterize Protein–Ligand and Protein–Protein Interactions Landscapes for Drug Discovery. Advances in Protein Chemistry and Structural Biology, 2014, 96, 1-37.	2.3	23

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19	Analyzing Multitarget Activity Landscapes Using Protein–Ligand Interaction Fingerprints: Interaction Cliffs. Journal of Chemical Information and Modeling, 2015, 55, 251-262.	5.4	23
20	Activity cliffs and activity cliff generators based on chemotype-related activity landscapes. Molecular Diversity, 2015, 19, 1021-1035.	3.9	22
21	Activity Landscape Plotter: A Web-Based Application for the Analysis of Structure–Activity Relationships. Journal of Chemical Information and Modeling, 2017, 57, 397-402.	5.4	22
22	Homology modeling, docking and molecular dynamics of the Leishmania mexicana arginase: A description of the catalytic site useful for drug design. Journal of Molecular Graphics and Modelling, 2012, 38, 50-59.	2.4	19
23	Activity landscape modeling of PPAR ligands with dual-activity difference maps. Bioorganic and Medicinal Chemistry, 2012, 20, 3523-3532.	3.0	17
24	Data-driven approaches used for compound library design, hit triage and bioactivity modeling in high-throughput screening. Briefings in Bioinformatics, 2018, 19, bbw105.	6.5	17
25	ARWAR: A network approach for predicting Adverse Drug Reactions. Computers in Biology and Medicine, 2016, 68, 101-108.	7.0	17
26	Advances in the development of pyridinone derivatives as non-nucleoside reverse transcriptase inhibitors. RSC Advances, 2016, 6, 2119-2130.	3.6	15
27	Computational study on the inhibition mechanism of cruzain by nitrile-containing molecules. Journal of Molecular Graphics and Modelling, 2012, 35, 28-35.	2.4	12
28	Exploring the Use of Compound-Induced Transcriptomic Data Generated From Cell Lines to Predict Compound Activity Toward Molecular Targets. Frontiers in Chemistry, 2020, 8, 296.	3.6	12
29	CASE Plots for the Chemotypeâ€Based Activity and Selectivity Analysis: A CASE Study of Cyclooxygenase Inhibitors. Chemical Biology and Drug Design, 2012, 80, 752-762.	3.2	11
30	Diversity selection, screening and quantitative structure–activity relationships of osmolyte-like additive effects on the thermal stability of a monoclonal antibody. European Journal of Pharmaceutical Sciences, 2017, 97, 151-157.	4.0	11
31	3D-QSAR studies on purine-carbonitriles as cruzain inhibitors: comparative molecular field analysis (CoMFA) and comparative molecular similarity indices analysis (CoMSIA). MedChemComm, 2011, 2, 1058.	3.4	10
32	Two-step radical reactions that switch low multiplicity channels leading to the carbene and carbyne species detected for Ru(5F) + CH4â^'nFn (n = 2–4) interactions under matrix isolation conditions. RSC Advances, 2013, 3, 11607.	3.6	10
33	One Drug for Multiple Targets: A Computational Perspective. Journal of the Mexican Chemical Society, 2017, 60, .	0.6	10
34	Synthesis, Screening and in silico Simulations of Anti-Parasitic Propamidine/Benzimidazole Derivatives. Medicinal Chemistry, 2017, 13, 137-148.	1.5	9
35	Activity landscape analysis, CoMFA and CoMSIA studies of pyrazole CB1 antagonists. Medicinal Chemistry Research, 2013, 22, 4133-4145.	2.4	8
36	Molecular Modeling and Chemoinformatics to Advance the Development of Modulators of Epigenetic Targets. Advances in Protein Chemistry and Structural Biology, 2016, 105, 1-26.	2.3	6

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37	Statistical correlation of nonconservative substitutions of HIV gp41 variable amino acid residues with the R5X4 HIV-1 phenotype. Virology Journal, 2016, 13, 28.	3.4	4
38	Cyclic Systems Distribution Along Similarity Measures: Insights for an Application to Activity Landscape Modeling. Molecular Informatics, 2013, 32, 179-190.	2.5	3
39	Theoretical Study of the Reactions M ⁺ +CH ₃ F (M=Ge, As, Se, Sb). ChemPhysChem, 2010, 11, 1909-1917.	2.1	2
40	Towards understanding polyol additive effects on the pH shift-induced aggregation of a monoclonal antibody using high throughput screening and quantitative structure-activity modeling. International Journal of Pharmaceutics, 2017, 530, 165-172.	5.2	2
41	Computational Structure–Activity Relationship Studies of Epigenetic Target Inhibitors. , 2016, , 359-384.		1