

CITATION REPORT

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Predicting kinase inhibitors using bioactivity matrix derived informer sets

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PLoS Computational Biology, 2019, 15, e1006813.

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7	Spectrum of deep learning algorithms in drug discovery. <i>Chemical Biology and Drug Design</i> , 2020 , 96, 886-901	2.9	6
6	Non-linear Deep Neural Network for Rapid and Accurate Prediction of Phenotypic Responses to Kinase Inhibitors. <i>IScience</i> , 2020 , 23, 101129	6.1	4
5	Machine learning and AI-based approaches for bioactive ligand discovery and GPCR-ligand recognition. <i>Methods</i> , 2020 , 180, 89-110	4.6	18
4	Engineering Selectivity for Reduced Toxicity of Bacterial Kinase Inhibitors Using Structure-Guided Medicinal Chemistry.. <i>ACS Medicinal Chemistry Letters</i> , 2021 , 12, 228-235	4.3	1
3	The Use of Informer Sets in Screening: Perspectives on an Efficient Strategy to Identify New Probes. <i>SLAS Discovery</i> , 2021 , 26, 855-861	3.4	1
2	Bayes optimal informer sets for early-stage drug discovery.. <i>Biometrics</i> , 2022 ,	1.8	
1	A Perturbation Bound on the Subspace Estimator from Canonical Projections. 2022 ,		