Martino Bertoni

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7525493/publications.pdf

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18 papers	13,776 citations	840776 11 h-index	888059 17 g-index
23 all docs	23 docs citations	23 times ranked	27346 citing authors

#	Article	IF	Citations
1	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. Cell Reports Medicine, 2022, 3, 100492.	6.5	33
2	Bioactivity descriptors for uncharacterized chemical compounds. Nature Communications, 2021, 12, 3932.	12.8	44
3	Bioactivity Profile Similarities to Expand the Repertoire of COVID-19 Drugs. Journal of Chemical Information and Modeling, 2020, 60, 5730-5734.	5.4	3
4	Extending the small-molecule similarity principle to all levels of biology with the Chemical Checker. Nature Biotechnology, 2020, 38, 1087-1096.	17.5	78
5	Introducing â€œbest single templateâ€•models as reference baseline for the Continuous Automated Model Evaluation (CAMEO). Proteins: Structure, Function and Bioinformatics, 2019, 87, 1378-1387.	2.6	31
6	Cover Image, Volume 9, Issue 6. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2019, 9, e1451.	14.6	0
7	Formatting biological big data for modern machine learning in drug discovery. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2019, 9, e1408.	14.6	17
8	Modeling of Protein Tertiary and Quaternary Structures Based on Evolutionary Information. Methods in Molecular Biology, 2019, 1851, 301-316.	0.9	13
9	Assessment of protein assembly prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 247-256.	2.6	54
10	Continuous Automated Model EvaluatiOn (CAMEO) complementing the critical assessment of structure prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 387-398.	2.6	127
11	DynBench3D, a Web-Resource to Dynamically Generate Benchmark Sets of Large Heteromeric Protein Complexes. Journal of Molecular Biology, 2018, 430, 4431-4438.	4.2	3
12	SWISS-MODEL: homology modelling of protein structures and complexes. Nucleic Acids Research, 2018, 46, W296-W303.	14.5	8,474
13	Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. Scientific Reports, 2017, 7, 10480.	3.3	608
14	A non-deterministic approach to forecasting the trophic evolution of lakes. Journal of Limnology, 2016, 75, .	1.1	8
15	SWISS-MODEL: modelling protein tertiary and quaternary structure using evolutionary information. Nucleic Acids Research, 2014, 42, W252-W258.	14.5	4,247
16	Gene regulatory networks reconstruction from time series datasets using genetic programming: a comparison between tree-based and graph-based approaches. Genetic Programming and Evolvable Machines, 2013, 14, 431-455.	2.2	1
17	GeNet: A Graph-Based Genetic Programming Framework for the Reverse Engineering of Gene Regulatory Networks. Lecture Notes in Computer Science, 2012, , 97-109.	1.3	2
18	Extending the Small Molecule Similarity Principle to All Levels of Biology. SSRN Electronic Journal, 0, , .	0.4	0