Martino Bertoni

List of Publications by Year in Descending Order

20 papers	8,361 citations	8 h-index	23 g-index
23 ext. papers	11,621 ext. citations	9.3 avg, IF	5.98 L-index

#	Paper	IF	Citations
20	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data.. *Cell Reports Medicine*, **2022**, 3, 100492	18	5
19	Bioactivity descriptors for uncharacterized chemical compounds. *Nature Communications*, **2021**, 12, 3932	17.4	8
18	Extending the small-molecule similarity principle to all levels of biology with the Chemical Checker. *Nature Biotechnology*, **2020**, 38, 1087-1096	44.5	29
17	Bioactivity Profile Similarities to Expand the Repertoire of COVID-19 Drugs. *Journal of Chemical Information and Modeling*, **2020**, 60, 5730-5734	6.1	1
16	Introducing "best single template" models as reference baseline for the Continuous Automated Model Evaluation (CAMEO). *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1378-1387	4.2	17
15	Cover Image, Volume 9, Issue 6. *Wiley Interdisciplinary Reviews: Computational Molecular Science*, **2019**, 9, e1451	7.9	
14	Formatting biological big data for modern machine learning in drug discovery. *Wiley Interdisciplinary Reviews: Computational Molecular Science*, **2019**, 9, e1408	7.9	6
13	Modeling of Protein Tertiary and Quaternary Structures Based on Evolutionary Information. *Methods in Molecular Biology*, **2019**, 1851, 301-316	1.4	6
12	Assessment of protein assembly prediction in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 247-256	4.2	37
11	Continuous Automated Model EvaluatiOn (CAMEO) complementing the critical assessment of structure prediction in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 387-398	4.2	75
10	DynBench3D, a Web-Resource to Dynamically Generate Benchmark Sets of Large Heteromeric Protein Complexes. *Journal of Molecular Biology*, **2018**, 430, 4431-4438	6.5	3
9	SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic Acids Research*, **2018**, 46, W296-W303	20.1	4367
8	Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. *Scientific Reports*, **2017**, 7, 10480	4.9	357
7	A non-deterministic approach to forecasting the trophic evolution of lakes. *Journal of Limnology*, **2016**, 75,	1.5	2
6	SWISS-MODEL: modelling protein tertiary and quaternary structure using evolutionary information. *Nucleic Acids Research*, **2014**, 42, W252-8	20.1	3437
5	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	
4	GeNet: A Graph-Based Genetic Programming Framework for the Reverse Engineering of Gene Regulatory Networks. *Lecture Notes in Computer Science*, **2012**, 97-109	0.9	2

List of Publications

3	Extending the small molecule similarity principle to all levels of biology	1
2	Bioactivity descriptors for uncharacterized compounds	3
1	A Community Challenge for Pancancer Drug Mechanism of Action Inference from Perturbational Profile Data	3