Claire Marks

List of Publications by Year
in descending order

17 papers	1,030 citations	840776 11 h-index	1125743 13 g-index
23 all docs	23 docs citations	23 times ranked	1543 citing authors

#	Article	IF	Citations
1	CoV-AbDab: the coronavirus antibody database. Bioinformatics, 2021, 37, 734-735.	4.1	273
2	Five computational developability guidelines for therapeutic antibody profiling. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4025-4030.	7.1	221
3	SAbPred: a structure-based antibody prediction server. Nucleic Acids Research, 2016, 44, W474-W478.	14.5	155
4	Thera-SAbDab: the Therapeutic Structural Antibody Database. Nucleic Acids Research, 2020, 48, D383-D388.	14.5	88
5	Sphinx: merging knowledge-based and *ab initio* approaches to improve protein loop prediction. Bioinformatics, 2017, 33, 1346-1353.	4.1	49
6	Humanization of antibodies using a machine learning approach on large-scale repertoire data. Bioinformatics, 2021, 37, 4041-4047.	4.1	49
7	How repertoire data are changing antibody science. Journal of Biological Chemistry, 2020, 295, 9823-9837.	3.4	43
8	Epitope profiling using computational structural modelling demonstrated on coronavirus-binding antibodies. PLoS Computational Biology, 2021, 17, e1009675.	3.2	33
9	Structural diversity of B-cell receptor repertoires along the B-cell differentiation axis in humans and mice. PLoS Computational Biology, 2020, 16, e1007636.	3.2	27
10	Public Baseline and shared response structures support the theory of antibody repertoire functional commonality. PLoS Computational Biology, 2021, 17, e1008781.	3.2	26
11	Predicting loop conformational ensembles. Bioinformatics, 2018, 34, 949-956.	4.1	20
12	TCRBuilder: multi-state T-cell receptor structure prediction. Bioinformatics, 2020, 36, 3580-3581.	4.1	10
13	Increasing the accuracy of protein loop structure prediction with evolutionary constraints. Bioinformatics, 2019, 35, 2585-2592.	4.1	8
14	Title is missing!. , 2020, 16, e1007636.		0
15	Title is missing!. , 2020, 16, e1007636.		0
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