

# Claire Marks

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/445664/publications.pdf>

Version: 2024-02-01

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