

# Inna Goreshnik

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

14  
papers

787  
citations

8  
h-index

15  
g-index

15  
ext. papers

1,275  
ext. citations

22.6  
avg, IF

3.74  
L-index

#	Paper	IF	Citations
14	Design of protein binding proteins from target structure alone.. <i>Nature</i> , <b>2022</b> ,	50.4	13
13	Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice.. <i>Science Translational Medicine</i> , <b>2022</b> , 14, eabn1252	17.5	3
12	Ultrapotent miniproteins targeting the receptor-binding domain protect against SARS-CoV-2 infection and disease in mice <b>2021</b> ,		1
11	Transferrin receptor targeting by de novo sheet extension. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	6
10	Computational design of a synthetic PD-1 agonist. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	9
9	Multivalent designed proteins protect against SARS-CoV-2 variants of concern <b>2021</b> ,		4
8	Ultrapotent miniproteins targeting the SARS-CoV-2 receptor-binding domain protect against infection and disease. <i>Cell Host and Microbe</i> , <b>2021</b> , 29, 1151-1161.e5	23.4	11
7	Parallelized identification of on- and off-target protein interactions.. <i>Molecular Systems Design and Engineering</i> , <b>2020</b> , 5, 349-357	4.6	0
6	De novo design of picomolar SARS-CoV-2 miniprotein inhibitors. <i>Science</i> , <b>2020</b> , 370, 426-431	33.3	219
5	An enumerative algorithm for de novo design of proteins with diverse pocket structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 22135-22145	11.5	28
4	Massively parallel de novo protein design for targeted therapeutics. <i>Nature</i> , <b>2017</b> , 550, 74-79	50.4	235
3	Global analysis of protein folding using massively parallel design, synthesis, and testing. <i>Science</i> , <b>2017</b> , 357, 168-175	33.3	241
2	A computationally engineered RAS rheostat reveals RAS-ERK signaling dynamics. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 119-126	11.7	15
1	Robust de novo design of protein binding proteins from target structural information alone		1