

# Samuel Schmitz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/150391/publications.pdf>

Version: 2024-02-01

10  
papers

149  
citations

1307594

7  
h-index

1474206

9  
g-index

10  
all docs

10  
docs citations

10  
times ranked

281  
citing authors

#	ARTICLE	IF	CITATIONS
1	Small integral membrane protein 10 like 1 downregulation enhances differentiation of adipose progenitor cells. <i>Biochemical and Biophysical Research Communications</i> , 2022, 604, 57-62.	2.1	1
2	The human antibody sequence space and structural design of the V, J regions, and CDRH3 with Rosetta. <i>MAbs</i> , 2022, 14, 2068212.	5.2	0
3	Identification of a novel leptin receptor (LEPR) variant and proof of functional relevance directing treatment decisions in patients with morbid obesity. <i>Metabolism: Clinical and Experimental</i> , 2021, 116, 154438.	3.4	17
4	Rosetta design with co-evolutionary information retains protein function. <i>PLoS Computational Biology</i> , 2021, 17, e1008568.	3.2	12
5	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. <i>Biochemistry</i> , 2021, 60, 825-846.	2.5	24
6	<scp>RosettaCM</scp> for antibodies with very long <scp>HCDR3s</scp> and low template availability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1458-1472.	2.6	3
7	PyIR: a scalable wrapper for processing billions of immunoglobulin and T cell receptor sequences using IgBLAST. <i>BMC Bioinformatics</i> , 2020, 21, 314.	2.6	21
8	Human-likeness of antibody biologics determined by back-translation and comparison with large antibody variable gene repertoires. <i>MAbs</i> , 2020, 12, 1758291.	5.2	10
9	Rosetta:MSF: a modular framework for multi-state computational protein design. <i>PLoS Computational Biology</i> , 2017, 13, e1005600.	3.2	43
10	<i>Plasmodium falciparum</i> Nucleosomes Exhibit Reduced Stability and Lost Sequence Dependent Nucleosome Positioning. <i>PLoS Pathogens</i> , 2016, 12, e1006080.	4.7	18