

# Shion A Lim

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10683412/publications.pdf>

Version: 2024-02-01

11  
papers

725  
citations

1040056

9  
h-index

1281871

11  
g-index

15  
all docs

15  
docs citations

15  
times ranked

1665  
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting a proteolytic neoepitope on CUB domain containing protein 1 (CDCP1) for RAS-driven cancers. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	13
2	Bi-paratopic and multivalent VH domains block ACE2 binding and neutralize SARS-CoV-2. <i>Nature Chemical Biology</i> , 2021, 17, 113-121.	8.0	78
3	Exploring the Evolutionary History of Kinetic Stability in the Î±-Lytic Protease Family. <i>Biochemistry</i> , 2021, 60, 170-181.	2.5	2
4	Bispecific VH/Fab antibodies targeting neutralizing and non-neutralizing Spike epitopes demonstrate enhanced potency against SARS-CoV-2. <i>MAbs</i> , 2021, 13, 1893426.	5.2	22
5	Engineering luminescent biosensors for point-of-care SARS-CoV-2 antibody detection. <i>Nature Biotechnology</i> , 2021, 39, 928-935.	17.5	106
6	Engineered ACE2 receptor traps potentially neutralize SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28046-28055.	7.1	219
7	Competitive SARS-CoV-2 Serology Reveals Most Antibodies Targeting the Spike Receptor-Binding Domain Compete for ACE2 Binding. <i>MSphere</i> , 2020, 5, .	2.9	62
8	Theranostic Targeting of CUB Domain Containing Protein 1 (CDCP1) in Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 3608-3615.	7.0	24
9	The burstâ€phase folding intermediate of ribonuclease H changes conformation over evolutionary history. <i>Biopolymers</i> , 2018, 109, e23086.	2.4	8
10	Evolutionary trend toward kinetic stability in the folding trajectory of RNases H. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13045-13050.	7.1	37
11	The thermostability and specificity of ancient proteins. <i>Current Opinion in Structural Biology</i> , 2016, 38, 37-43.	5.7	106