

# Jarek Juraszek

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1163389/publications.pdf>

Version: 2024-02-01

22  
papers

1,703  
citations

471509

17  
h-index

677142

22  
g-index

26  
all docs

26  
docs citations

26  
times ranked

2793  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sampling the multiple folding mechanisms of Trp-cage in explicit solvent. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15859-15864.	7.1	228
2	A common solution to group 2 influenza virus neutralization. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 445-450.	7.1	187
3	Stabilizing the closed SARS-CoV-2 spike trimer. Nature Communications, 2021, 12, 244.	12.8	139
4	Mechanisms of Hemagglutinin Targeted Influenza Virus Neutralization. PLoS ONE, 2013, 8, e80034.	2.5	138
5	Potent peptidic fusion inhibitors of influenza virus. Science, 2017, 358, 496-502.	12.6	135
6	Rate Constant and Reaction Coordinate of Trp-Cage Folding in Explicit Water. Biophysical Journal, 2008, 95, 4246-4257.	0.5	130
7	Molecular Mechanism of SSR128129E, an Extracellularly Acting, Small-Molecule, Allosteric Inhibitor of FGF Receptor Signaling. Cancer Cell, 2013, 23, 489-501.	16.8	125
8	A small-molecule fusion inhibitor of influenza virus is orally active in mice. Science, 2019, 363, .	12.6	98
9	Predicting the reaction coordinates of millisecond light-induced conformational changes in photoactive yellow protein. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2397-2402.	7.1	83
10	Relating influenza virus membrane fusion kinetics to stoichiometry of neutralizing antibodies at the single-particle level. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5143-8.	7.1	57
11	Nonlinear reaction coordinate analysis in the reweighted path ensemble. Journal of Chemical Physics, 2010, 133, 174110.	3.0	55
12	The reweighted path ensemble. Journal of Chemical Physics, 2010, 133, 174109.	3.0	49
13	Free-Energy-Based Methods for Binding Profile Determination in a Congeneric Series of CDK2 Inhibitors. Journal of Physical Chemistry B, 2010, 114, 9516-9524.	2.6	48
14	Structure-Based Design of Prefusion-Stabilized Filovirus Glycoprotein Trimers. Cell Reports, 2020, 30, 4540-4550.e3.	6.4	46
15	Epitope mapping of diverse influenza Hemagglutinin drug candidates using HDX-MS. Scientific Reports, 2019, 9, 4735.	3.3	33
16	Transition path sampling of protein conformational changes. Chemical Physics, 2012, 396, 30-44.	1.9	30
17	Effects of a Mutation on the Folding Mechanism of a $\hat{\text{I}}^2$ -Hairpin. Journal of Physical Chemistry B, 2009, 113, 16184-16196.	2.6	28
18	(Un)Folding Mechanisms of the FBP28 WW Domain in Explicit Solvent Revealed by Multiple Rare Event Simulation Methods. Biophysical Journal, 2010, 98, 646-656.	0.5	15

#	ARTICLE	IF	CITATIONS
19	A common antigenic motif recognized by naturally occurring human VH5â€“51/VL4â€“1 anti-tau antibodies with distinct functionalities. <i>Acta Neuropathologica Communications</i> , 2018, 6, 43.	5.2	15
20	Enhancement of therapeutic potential of a naturally occurring human antibody targeting a phosphorylated Ser422 containing epitope on pathological tau. <i>Acta Neuropathologica Communications</i> , 2018, 6, 59.	5.2	13
21	Universal stabilization of the influenza hemagglutinin by structure-based redesign of the pH switch regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	7
22	Universal influenza vaccine design: directing the antibody repertoire. <i>Future Virology</i> , 2016, 11, 451-467.	1.8	2