Yen-Ting Lai

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8952661/publications.pdf Version: 2024-02-01

		394421	642732
23	1,921 citations	19	23
papers	citations	h-index	g-index
23	23	23	2889
all docs	docs citations	times ranked	citing authors

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#	Article	IF	CITATIONS
1	Structure of a designed protein cage that self-assembles into a highly porous cube. Nature Chemistry, 2014, 6, 1065-1071.	13.6	267
2	Structure of a 16-nm Cage Designed by Using Protein Oligomers. Science, 2012, 336, 1129-1129.	12.6	260
3	Epitope-based vaccine design yields fusion peptide-directed antibodies that neutralize diverse strains of HIV-1. Nature Medicine, 2018, 24, 857-867.	30.7	256
4	Crystal structure of the membrane-bound bifunctional transglycosylase PBP1b from <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8824-8829.	7.1	180
5	Principles for designing ordered protein assemblies. Trends in Cell Biology, 2012, 22, 653-661.	7.9	120
6	lterative structure-based improvement of a fusion-glycoprotein vaccine against RSV. Nature Structural and Molecular Biology, 2016, 23, 811-820.	8.2	110
7	Crystal structures of trimeric HIV envelope with entry inhibitors BMS-378806 and BMS-626529. Nature Chemical Biology, 2017, 13, 1115-1122.	8.0	110
8	Structure and Flexibility of Nanoscale Protein Cages Designed by Symmetric Self-Assembly. Journal of the American Chemical Society, 2013, 135, 7738-7743.	13.7	82
9	Longitudinal Analysis Reveals Early Development of Three MPER-Directed Neutralizing Antibody Lineages from an HIV-1-Infected Individual. Immunity, 2019, 50, 677-691.e13.	14.3	77
10	Practical approaches to designing novel protein assemblies. Current Opinion in Structural Biology, 2013, 23, 632-638.	5.7	74
11	Structure of Super-Potent Antibody CAP256-VRC26.25 in Complex with HIV-1 Envelope Reveals a Combined Mode of Trimer-Apex Recognition. Cell Reports, 2020, 31, 107488.	6.4	53
12	Lattice engineering enables definition of molecular features allowing for potent small-molecule inhibition of HIV-1 entry. Nature Communications, 2019, 10, 47.	12.8	50
13	Solution structure of family 21 carbohydrate-binding module from Rhizopus oryzae glucoamylase. Biochemical Journal, 2007, 403, 21-30.	3.7	44
14	Protection of calves by a prefusion-stabilized bovine RSV F vaccine. Npj Vaccines, 2017, 2, 7.	6.0	38
15	Designing and defining dynamic protein cage nanoassemblies in solution. Science Advances, 2016, 2, e1501855.	10.3	37
16	Automated Design by Structure-Based Stabilization and Consensus Repair to Achieve Prefusion-Closed Envelope Trimers in a Wide Variety of HIV Strains. Cell Reports, 2020, 33, 108432.	6.4	32
17	Mutagenesis study of rice nonspecific lipid transfer protein 2 reveals residues that contribute to structure and ligand binding. Proteins: Structure, Function and Bioinformatics, 2008, 70, 695-706.	2.6	28
18	Improvement of antibody functionality by structure-guided paratope engraftment. Nature Communications, 2019, 10, 721.	12.8	27

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#	Article	IF	CITATIONS
19	On the predictability of the orientation of protein domains joined by a spanning alpha-helical linker. Protein Engineering, Design and Selection, 2015, 28, 491-500.	2.1	23
20	Development of a 3Mut-Apex-Stabilized Envelope Trimer That Expands HIV-1 Neutralization Breadth When Used To Boost Fusion Peptide-Directed Vaccine-Elicited Responses. Journal of Virology, 2020, 94,	3.4	21
21	Small Molecule HIV-1 Attachment Inhibitors: Discovery, Mode of Action and Structural Basis of Inhibition. Viruses, 2021, 13, 843.	3.3	15
22	Antigenic analysis of the HIV-1 envelope trimer implies small differences between structural states 1 and 2. Journal of Biological Chemistry, 2022, 298, 101819.	3.4	9
23	Effects of ligand binding on the dynamics of rice nonspecific lipid transfer protein 1: A model from molecular simulations. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1189-1198.	2.6	8