

Hung-Ju Chang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8168708/publications.pdf>

Version: 2024-02-01

14
papers

502
citations

858243

12
h-index

1181555

14
g-index

16
all docs

16
docs citations

16
times ranked

804
citing authors

#	ARTICLE	IF	CITATIONS
1	Programmable receptors enable bacterial biosensors to detect pathological biomarkers in clinical samples. <i>Nature Communications</i> , 2021, 12, 5216.	5.8	28
2	Synthetic receptors to understand and control cellular functions. <i>Methods in Enzymology</i> , 2020, 633, 143-167.	0.4	11
3	Structural basis for chemically-induced homodimerization of a single domain antibody. <i>Scientific Reports</i> , 2019, 9, 1840.	1.6	20
4	A Modular Receptor Platform To Expand the Sensing Repertoire of Bacteria. <i>ACS Synthetic Biology</i> , 2018, 7, 166-175.	1.9	50
5	Microbially derived biosensors for diagnosis, monitoring and epidemiology. <i>Microbial Biotechnology</i> , 2017, 10, 1031-1035.	2.0	59
6	A part toolbox to tune genetic expression in <i>Bacillus subtilis</i> . <i>Nucleic Acids Research</i> , 2016, 44, gkw624.	6.5	157
7	Loop-Sequence Features and Stability Determinants in Antibody Variable Domains by High-Throughput Experiments. <i>Structure</i> , 2014, 22, 9-21.	1.6	26
8	Design of Phage-Displayed Cystine-Stabilized Mini-Protein Libraries for Proteinaceous Binder Engineering. <i>Methods in Molecular Biology</i> , 2014, 1088, 1-17.	0.4	3
9	Antibody Variable Domain Interface and Framework Sequence Requirements for Stability and Function by High-Throughput Experiments. <i>Structure</i> , 2014, 22, 22-34.	1.6	22
10	Rationalization and Design of the Complementarity Determining Region Sequences in an Antibody-Antigen Recognition Interface. <i>PLoS ONE</i> , 2012, 7, e33340.	1.1	42
11	Engineering Anti-vascular Endothelial Growth Factor Single Chain Disulfide-stabilized Antibody Variable Fragments (sc-dsFv) with Phage-displayed sc-dsFv Libraries. <i>Journal of Biological Chemistry</i> , 2010, 285, 7880-7891.	1.6	15
12	Molecular Evolution of Cystine-Stabilized Miniproteins as Stable Proteinaceous Binders. <i>Structure</i> , 2009, 17, 620-631.	1.6	17
13	Factor Xa Active Site Substrate Specificity with Substrate Phage Display and Computational Molecular Modeling. <i>Journal of Biological Chemistry</i> , 2008, 283, 12343-12353.	1.6	25
14	Assessing Computational Amino Acid β -Turn Propensities with a Phage-Displayed Combinatorial Library and Directed Evolution. <i>Structure</i> , 2006, 14, 1499-1510.	1.6	24