

# Hung-Pin Peng

## List of Publications by Year in descending order

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Version: 2024-02-01

15  
papers

406  
citations

1051969

10  
h-index

1113639

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g-index

15  
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15  
docs citations

15  
times ranked

864  
citing authors

#	ARTICLE	IF	CITATIONS
1	Eradicating mesothelin-positive human gastric and pancreatic tumors in xenograft models with optimized anti-mesothelin antibody-drug conjugates from synthetic antibody libraries. <i>Scientific Reports</i> , 2021, 11, 15430.	1.6	5
2	A panel of anti-influenza virus nucleoprotein antibodies selected from phage-displayed synthetic antibody libraries with rapid diagnostic capability to distinguish diverse influenza virus subtypes. <i>Scientific Reports</i> , 2020, 10, 13318.	1.6	5
3	Antibody-drug conjugates with HER2-targeting antibodies from synthetic antibody libraries are highly potent against HER2-positive human gastric tumor in xenograft models. <i>MAbs</i> , 2019, 11, 153-165.	2.6	10
4	Effective binding to protein antigens by antibodies from antibody libraries designed with enhanced protein recognition propensities. <i>MAbs</i> , 2019, 11, 373-387.	2.6	12
5	Predicting Ligand Binding Sites on Protein Surfaces by 3-Dimensional Probability Density Distributions of Interacting Atoms. <i>PLoS ONE</i> , 2016, 11, e0160315.	1.1	17
6	Discovering neutralizing antibodies targeting the stem epitope of H1N1 influenza hemagglutinin with synthetic phage-displayed antibody libraries. <i>Scientific Reports</i> , 2015, 5, 15053.	1.6	17
7	Predominant structural configuration of natural antibody repertoires enables potent antibody responses against protein antigens. <i>Scientific Reports</i> , 2015, 5, 12411.	1.6	17
8	Loop-Sequence Features and Stability Determinants in Antibody Variable Domains by High-Throughput Experiments. <i>Structure</i> , 2014, 22, 9-21.	1.6	26
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	Prediction of FMN-binding residues with three-dimensional probability distributions of interacting atoms on protein surfaces. <i>Journal of Theoretical Biology</i> , 2014, 343, 154-161.	0.8	10
11	Origins of specificity and affinity in antibody-protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2656-65.	3.3	163
12	Prediction of fatty acid-binding residues on protein surfaces with three-dimensional probability distributions of interacting atoms. <i>Biophysical Chemistry</i> , 2014, 192, 10-19.	1.5	10
13	Protein-Protein Interaction Site Predictions with Three-Dimensional Probability Distributions of Interacting Atoms on Protein Surfaces. <i>PLoS ONE</i> , 2012, 7, e37706.	1.1	25
14	Prediction of Carbohydrate Binding Sites on Protein Surfaces with 3-Dimensional Probability Density Distributions of Interacting Atoms. <i>PLoS ONE</i> , 2012, 7, e40846.	1.1	25
15	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