

An-Suei Yang

List of Publications by Year in descending order

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73
papers

4,842
citations

126907

33
h-index

95266

68
g-index

73
all docs

73
docs citations

73
times ranked

5392
citing authors

#	ARTICLE	IF	CITATIONS
1	Attitude towards hereditary cancer risk management among women with cancer in Taiwan. <i>Supportive Care in Cancer</i> , 2022, 30, 3625.	2.2	1
2	Structure-based Development of Human Interleukin-1 β -Specific Antibody That Simultaneously Inhibits Binding to Both IL-1RI and IL-1RAcP. <i>Journal of Molecular Biology</i> , 2021, 433, 166766.	4.2	10
3	SIGLEC-3 (CD33) serves as an immune checkpoint receptor for HBV infection. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	23
4	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.	3.3	5
5	A non-neutralizing antibody broadly protects against influenza virus infection by engaging effector cells. <i>PLoS Pathogens</i> , 2021, 17, e1009724.	4.7	13
6	Functionalized Terpolymer-Brush-Based Biointerface with Improved Antifouling Properties for Ultra-Sensitive Direct Detection of Virus in Crude Clinical Samples. <i>ACS Applied Materials & Interfaces</i> , 2021, 13, 60612-60624.	8.0	19
7	Preparation and characterization of antibody-drug conjugates acting on HER2-positive cancer cells. <i>PLoS ONE</i> , 2020, 15, e0239813.	2.5	9
8	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.	3.3	5
9	Development of theranostic active-targeting boron-containing gold nanoparticles for boron neutron capture therapy (BNCT). <i>Colloids and Surfaces B: Biointerfaces</i> , 2019, 183, 110387.	5.0	38
10	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.	5.2	10
11	Effective binding to protein antigens by antibodies from antibody libraries designed with enhanced protein recognition propensities. <i>MAbs</i> , 2019, 11, 373-387.	5.2	12
12	Noninvasive assessment of characteristics of novel anti-HER2 antibodies by molecular imaging in a human gastric cancer xenograft-bearing mouse model. <i>Scientific Reports</i> , 2018, 8, 13735.	3.3	15
13	Antibodyomics: bioinformatics technologies for understanding B-cell immunity to HIV-1. <i>Immunological Reviews</i> , 2017, 275, 108-128.	6.0	32
14	High throughput discovery of influenza virus neutralizing antibodies from phage-displayed synthetic antibody libraries. <i>Scientific Reports</i> , 2017, 7, 14455.	3.3	15
15	Predicting Ligand Binding Sites on Protein Surfaces by 3-Dimensional Probability Density Distributions of Interacting Atoms. <i>PLoS ONE</i> , 2016, 11, e0160315.	2.5	17
16	High throughput cytotoxicity screening of anti-HER2 immunotoxins conjugated with antibody fragments from phage-displayed synthetic antibody libraries. <i>Scientific Reports</i> , 2016, 6, 31878.	3.3	19
17	Discovering neutralizing antibodies targeting the stem epitope of H1N1 influenza hemagglutinin with synthetic phage-displayed antibody libraries. <i>Scientific Reports</i> , 2015, 5, 15053.	3.3	17
18	Structural Repertoire of HIV-1-Neutralizing Antibodies Targeting the CD4 Supersite in 14 Donors. <i>Cell</i> , 2015, 161, 1280-1292.	28.9	305

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19	Predominant structural configuration of natural antibody repertoires enables potent antibody responses against protein antigens. <i>Scientific Reports</i> , 2015, 5, 12411.	3.3	17
20	Loop-Sequence Features and Stability Determinants in Antibody Variable Domains by High-Throughput Experiments. <i>Structure</i> , 2014, 22, 9-21.	3.3	26
21	Design of Phage-Displayed Cystine-Stabilized Mini-Protein Libraries for Proteinaceous Binder Engineering. <i>Methods in Molecular Biology</i> , 2014, 1088, 1-17.	0.9	3
22	Antibody Variable Domain Interface and Framework Sequence Requirements for Stability and Function by High-Throughput Experiments. <i>Structure</i> , 2014, 22, 22-34.	3.3	22
23	Substrate Phage Display for Protease Substrate Sequence Characterization: Bovine Factor Xa as a Model System. <i>Methods in Molecular Biology</i> , 2014, 1088, 107-124.	0.9	0
24	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.	1.7	10
25	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.	7.1	163
26	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.	2.8	10
27	Protein-Protein Interaction Site Predictions with Three-Dimensional Probability Distributions of Interacting Atoms on Protein Surfaces. <i>PLoS ONE</i> , 2012, 7, e37706.	2.5	25
28	Prediction of Carbohydrate Binding Sites on Protein Surfaces with 3-Dimensional Probability Density Distributions of Interacting Atoms. <i>PLoS ONE</i> , 2012, 7, e40846.	2.5	25
29	Rationalization and Design of the Complementarity Determining Region Sequences in an Antibody-Antigen Recognition Interface. <i>PLoS ONE</i> , 2012, 7, e33340.	2.5	42
30	Amino Acid Substitutions of MagA in <i>Klebsiella pneumoniae</i> Affect the Biosynthesis of the Capsular Polysaccharide. <i>PLoS ONE</i> , 2012, 7, e46783.	2.5	36
31	A Practical Synthesis of Zanamivir Phosphonate Congeners with Potent Anti-influenza Activity. <i>Journal of the American Chemical Society</i> , 2011, 133, 17959-17965.	13.7	83
32	Effects of signal sequence on phage-displayed disulfide-stabilized single chain antibody variable fragment (sc-dsFv) libraries. <i>Biochemical and Biophysical Research Communications</i> , 2011, 411, 348-353.	2.1	0
33	Structure and Immunological Characterization of the Capsular Polysaccharide of a Pyrogenic Liver Abscess Caused by <i>Klebsiella pneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 21041-21051.	3.4	62
34	E339R/R416 salt bridge of nucleoprotein as a feasible target for influenza virus inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16515-16520.	7.1	73
35	Analogues of zanamivir with modified C4-substituents as the inhibitors against the group-1 neuraminidases of influenza viruses. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 4074-4084.	3.0	57
36	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.	3.4	15

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37	Development of GlcNAc-Inspired Iminocyclitols as Potent and Selective N-Acetyl- β -Hexosaminidase Inhibitors. <i>ACS Chemical Biology</i> , 2010, 5, 489-497.	3.4	39
38	Signal sequence as a determinant in expressing disulfide-stabilized single chain antibody variable fragments (sc-dsFv) against human VEGF. <i>Molecular BioSystems</i> , 2010, 6, 1307.	2.9	2
39	Molecular Evolution of Cystine-Stabilized Mini-proteins as Stable Proteinaceous Binders. <i>Structure</i> , 2009, 17, 620-631.	3.3	17
40	Design, synthesis, and evaluation of trifluoromethyl ketones as inhibitors of SARS-CoV 3CL protease. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 4652-4660.	3.0	68
41	Factor Xa Active Site Substrate Specificity with Substrate Phage Display and Computational Molecular Modeling. <i>Journal of Biological Chemistry</i> , 2008, 283, 12343-12353.	3.4	25
42	Protease substrate site predictors derived from machine learning on multilevel substrate phage display data. <i>Bioinformatics</i> , 2008, 24, 2691-2697.	4.1	18
43	Modeling protein loops with knowledge-based prediction of sequence-structure alignment. <i>Bioinformatics</i> , 2007, 23, 2836-2842.	4.1	34
44	Synthesis of Tamiflu and its Phosphonate Congeners Possessing Potent Anti-Influenza Activity. <i>Journal of the American Chemical Society</i> , 2007, 129, 11892-11893.	13.7	200
45	Structure-Based Design and Synthesis of Highly Potent SARS-CoV 3CL Protease Inhibitors. <i>ChemBioChem</i> , 2007, 8, 1654-1657.	2.6	33
46	Assessing Computational Amino Acid β -Turn Propensities with a Phage-Displayed Combinatorial Library and Directed Evolution. <i>Structure</i> , 2006, 14, 1499-1510.	3.3	24
47	The Na ⁺ Channel Inactivation Gate Is a Molecular Complex. <i>Journal of General Physiology</i> , 2004, 123, 155-165.	1.9	133
48	Protein backbone angle prediction with machine learning approaches. <i>Bioinformatics</i> , 2004, 20, 1612-1621.	4.1	72
49	Population-based study of SR-BI genetic variation and lipid profile. <i>Atherosclerosis</i> , 2004, 175, 159-168.	0.8	69
50	Local structure prediction with local structure-based sequence profiles. <i>Bioinformatics</i> , 2003, 19, 1267-1274.	4.1	39
51	Secondary Structure of the Human Cardiac Na ⁺ Channel C Terminus. <i>Journal of Biological Chemistry</i> , 2002, 277, 9233-9241.	3.4	121
52	Local structure-based sequence profile database for local and global protein structure predictions. <i>Bioinformatics</i> , 2002, 18, 1650-1657.	4.1	21
53	Structure-dependent sequence alignment for remotely related proteins. <i>Bioinformatics</i> , 2002, 18, 1658-1665.	4.1	28
54	Characterization of a Novel Isoform of Caspase-9 That Inhibits Apoptosis. <i>Journal of Biological Chemistry</i> , 2001, 276, 12190-12200.	3.4	38

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55	An integrated approach to the analysis and modeling of protein sequences and structures. I. Protein structural alignment and a quantitative measure for protein structural distance 1 1Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 665-678.	4.2	194
56	An integrated approach to the analysis and modeling of protein sequences and structures. II. On the relationship between sequence and structural similarity for proteins that are not obviously related in sequence 1 1Edited by F. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 679-689.	4.2	69
57	An integrated approach to the analysis and modeling of protein sequences and structures. III. A comparative study of sequence conservation in protein structural families using multiple structural alignments 1 1Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 691-711.	4.2	94
58	Characterization of the Interaction between the Wilson and Menkes Disease Proteins and the Cytoplasmic Copper Chaperone, HAH1p. <i>Journal of Biological Chemistry</i> , 1999, 274, 28497-28504.	3.4	151
59	Sequence to structure alignment in comparative modeling using PrISM. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 66-72.	2.6	48
60	Sequence to structure alignment in comparative modeling using PrISM. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 66-72.	2.6	17
61	Electrostatic Contributions to the Binding Free Energy of the λ CI Repressor to DNA. <i>Biophysical Journal</i> , 1998, 75, 2262-2273.	0.5	105
62	Free Energy of Amide Hydrogen Bond Formation in Vacuum, in Water, and in Liquid Alkane Solution. <i>Journal of Physical Chemistry B</i> , 1997, 101, 450-457.	2.6	143
63	Free Energy Determinants of Secondary Structure Formation: III. β -Turns and their Role in Protein Folding. <i>Journal of Molecular Biology</i> , 1996, 259, 873-882.	4.2	108
64	Thermal access to amplified chemical potential and the determination of equilibrium constants in protein solutions at subfreezing temperatures. <i>Biophysical Chemistry</i> , 1996, 58, 341-354.	2.8	2
65	Free Energy Determinants of Secondary Structure Formation: I. α -Helices. <i>Journal of Molecular Biology</i> , 1995, 252, 351-365.	4.2	227
66	Free Energy Determinants of Secondary Structure Formation: II. Antiparallel β -Sheets. <i>Journal of Molecular Biology</i> , 1995, 252, 366-376.	4.2	170
67	Structural Origins of pH and Ionic Strength Effects on Protein Stability. <i>Journal of Molecular Biology</i> , 1994, 237, 602-614.	4.2	184
68	On the calculation of pKas in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 252-265.	2.6	514
69	On the pH Dependence of Protein Stability. <i>Journal of Molecular Biology</i> , 1993, 231, 459-474.	4.2	409
70	Electrostatic effects on protein stability. <i>Current Opinion in Structural Biology</i> , 1992, 2, 40-45.	5.7	83
71	Analysis of the heat capacity dependence of protein folding. <i>Journal of Molecular Biology</i> , 1992, 227, 889-900.	4.2	108
72	Electrostatic effects on protein stability. <i>Current Biology</i> , 1992, 2, 82.	3.9	1

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73	EPR detection of kinetic responses to photochemically generated protein cofactors. Journal of Magnetic Resonance, 1990, 90, 580-583.	0.5	0