

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	On the calculation of pK _a s in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 252-265.	2.6	514
2	On the pH Dependence of Protein Stability. <i>Journal of Molecular Biology</i> , 1993, 231, 459-474.	4.2	409
3	Structural Repertoire of HIV-1-Neutralizing Antibodies Targeting the CD4 Supersite in 14 Donors. <i>Cell</i> , 2015, 161, 1280-1292.	28.9	305
4	Free Energy Determinants of Secondary Structure Formation: I. α -Helices. <i>Journal of Molecular Biology</i> , 1995, 252, 351-365.	4.2	227
5	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
6	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 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 665-678.	4.2	194
7	Structural Origins of pH and Ionic Strength Effects on Protein Stability. <i>Journal of Molecular Biology</i> , 1994, 237, 602-614.	4.2	184
8	Free Energy Determinants of Secondary Structure Formation: II. Antiparallel β -Sheets. <i>Journal of Molecular Biology</i> , 1995, 252, 366-376.	4.2	170
9	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
10	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
11	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
12	The Na ⁺ Channel Inactivation Gate Is a Molecular Complex. <i>Journal of General Physiology</i> , 2004, 123, 155-165.	1.9	133
13	Secondary Structure of the Human Cardiac Na ⁺ Channel C Terminus. <i>Journal of Biological Chemistry</i> , 2002, 277, 9233-9241.	3.4	121
14	Analysis of the heat capacity dependence of protein folding. <i>Journal of Molecular Biology</i> , 1992, 227, 889-900.	4.2	108
15	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
16	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
17	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 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 691-711.	4.2	94
18	Electrostatic effects on protein stability. <i>Current Opinion in Structural Biology</i> , 1992, 2, 40-45.	5.7	83

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19	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
20	E339â€ 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
21	Protein backbone angle prediction with machine learning approaches. <i>Bioinformatics</i> , 2004, 20, 1612-1621.	4.1	72
22	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
23	Population-based study of SR-BI genetic variation and lipid profile. <i>Atherosclerosis</i> , 2004, 175, 159-168.	0.8	69
24	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
25	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
26	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
27	Sequence to structure alignment in comparative modeling using PrISM. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 66-72.	2.6	48
28	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
29	Local structure prediction with local structure-based sequence profiles. <i>Bioinformatics</i> , 2003, 19, 1267-1274.	4.1	39
30	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
31	Characterization of a Novel Isoform of Caspase-9 That Inhibits Apoptosis. <i>Journal of Biological Chemistry</i> , 2001, 276, 12190-12200.	3.4	38
32	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
33	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
34	Modeling protein loops with knowledge-based prediction of sequence-structure alignment. <i>Bioinformatics</i> , 2007, 23, 2836-2842.	4.1	34
35	Structure-Based Design and Synthesis of Highly Potent SARS-CoV 3CL Protease Inhibitors. <i>ChemBioChem</i> , 2007, 8, 1654-1657.	2.6	33
36	Antibodyomics: bioinformatics technologies for understanding B-cell immunity to HIV-1. <i>Immunological Reviews</i> , 2017, 275, 108-128.	6.0	32

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37	Structure-dependent sequence alignment for remotely related proteins. <i>Bioinformatics</i> , 2002, 18, 1658-1665.	4.1	28
38	Loop-Sequence Features and Stability Determinants in Antibody Variable Domains by High-Throughput Experiments. <i>Structure</i> , 2014, 22, 9-21.	3.3	26
39	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
40	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
41	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
42	Assessing Computational Amino Acid $\hat{\tau}$ -Turn Propensities with a Phage-Displayed Combinatorial Library and Directed Evolution. <i>Structure</i> , 2006, 14, 1499-1510.	3.3	24
43	SIGLEC-3 (CD33) serves as an immune checkpoint receptor for HBV infection. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	23
44	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
45	Local structure-based sequence profile database for local and global protein structure predictions. <i>Bioinformatics</i> , 2002, 18, 1650-1657.	4.1	21
46	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
47	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
48	Protease substrate site predictors derived from machine learning on multilevel substrate phage display data. <i>Bioinformatics</i> , 2008, 24, 2691-2697.	4.1	18
49	Molecular Evolution of Cystine-Stabilized Mini-proteins as Stable Proteinaceous Binders. <i>Structure</i> , 2009, 17, 620-631.	3.3	17
50	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
51	Predominant structural configuration of natural antibody repertoires enables potent antibody responses against protein antigens. <i>Scientific Reports</i> , 2015, 5, 12411.	3.3	17
52	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
53	Sequence to structure alignment in comparative modeling using PrISM. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 66-72.	2.6	17
54	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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55	High throughput discovery of influenza virus neutralizing antibodies from phage-displayed synthetic antibody libraries. <i>Scientific Reports</i> , 2017, 7, 14455.	3.3	15
56	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
57	A non-neutralizing antibody broadly protects against influenza virus infection by engaging effector cells. <i>PLoS Pathogens</i> , 2021, 17, e1009724.	4.7	13
58	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
59	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
60	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
61	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
62	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
63	Preparation and characterization of antibody-drug conjugates acting on HER2-positive cancer cells. <i>PLoS ONE</i> , 2020, 15, e0239813.	2.5	9
64	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
65	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
66	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
67	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
68	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
69	Electrostatic effects on protein stability. <i>Current Biology</i> , 1992, 2, 82.	3.9	1
70	Attitude towards hereditary cancer risk management among women with cancer in Taiwan. <i>Supportive Care in Cancer</i> , 2022, 30, 3625.	2.2	1
71	EPR detection of kinetic responses to photochemically generated protein cofactors. <i>Journal of Magnetic Resonance</i> , 1990, 90, 580-583.	0.5	0
72	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

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73	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