

# An-Suei Yang

## List of Publications by Year in descending order

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73  
papers

4,842  
citations

145106

33  
h-index

107981

68  
g-index

73  
all docs

73  
docs citations

73  
times ranked

6094  
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.   | 1.0  | 1         |
| 2  | Structure-based Development of Human Interleukin-1 $\beta$ -Specific Antibody That Simultaneously Inhibits Binding to Both IL-1RI and IL-1RAcP. <i>Journal of Molecular Biology</i> , 2021, 433, 166766.   | 2.0  | 10        |
| 3  | SIGLEC-3 (CD33) serves as an immune checkpoint receptor for HBV infection. <i>Journal of Clinical Investigation</i> , 2021, 131, .   | 3.9  | 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.                    | 1.6  | 5         |
| 5  | A non-neutralizing antibody broadly protects against influenza virus infection by engaging effector cells. <i>PLoS Pathogens</i> , 2021, 17, e1009724.   | 2.1  | 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 &amp; Interfaces</i> , 2021, 13, 60612-60624.            | 4.0  | 19        |
| 7  | Preparation and characterization of antibody-drug conjugates acting on HER2-positive cancer cells. <i>PLoS ONE</i> , 2020, 15, e0239813.   | 1.1  | 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. | 1.6  | 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.   | 2.5  | 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.  | 2.6  | 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.  | 2.6  | 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.  | 1.6  | 15        |
| 13 | Antibodyomics: bioinformatics technologies for understanding B-cell immunity to HIV-1. <i>Immunological Reviews</i> , 2017, 275, 108-128.  | 2.8  | 32        |
| 14 | High throughput discovery of influenza virus neutralizing antibodies from phage-displayed synthetic antibody libraries. <i>Scientific Reports</i> , 2017, 7, 14455.  | 1.6  | 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.   | 1.1  | 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.   | 1.6  | 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.  | 1.6  | 17        |
| 18 | Structural Repertoire of HIV-1-Neutralizing Antibodies Targeting the CD4 Supersite in 14 Donors. <i>Cell</i> , 2015, 161, 1280-1292.   | 13.5 | 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.   | 1.6 | 17        |
| 20 | Loop-Sequence Features and Stability Determinants in Antibody Variable Domains by High-Throughput Experiments. <i>Structure</i> , 2014, 22, 9-21.  | 1.6 | 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.  | 0.4 | 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.  | 1.6 | 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.   | 0.4 | 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.  | 0.8 | 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.  | 3.3 | 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.  | 1.5 | 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.   | 1.1 | 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.   | 1.1 | 25        |
| 29 | 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        |
| 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.  | 1.1 | 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.  | 6.6 | 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.                   | 1.0 | 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.                 | 1.6 | 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.                      | 3.3 | 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.                                   | 1.4 | 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. | 1.6 | 15        |

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|----|---|-----|-----------|
| 37 | Development of GlcNAc-Inspired Iminocyclitols as Potent and Selective N-Acetyl- $\beta$ -Hexosaminidase Inhibitors. <i>ACS Chemical Biology</i> , 2010, 5, 489-497.                     | 1.6 | 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.  | 1.6 | 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.                   | 1.4 | 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.         | 1.6 | 25        |
| 42 | Protease substrate site predictors derived from machine learning on multilevel substrate phage display data. <i>Bioinformatics</i> , 2008, 24, 2691-2697.                               | 1.8 | 18        |
| 43 | Modeling protein loops with knowledge-based prediction of sequence-structure alignment. <i>Bioinformatics</i> , 2007, 23, 2836-2842.  | 1.8 | 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.                 | 6.6 | 200       |
| 45 | Structure-Based Design and Synthesis of Highly Potent SARS-CoV 3CL Protease Inhibitors. <i>ChemBioChem</i> , 2007, 8, 1654-1657.  | 1.3 | 33        |
| 46 | Assessing Computational Amino Acid $\beta$ -Turn Propensities with a Phage-Displayed Combinatorial Library and Directed Evolution. <i>Structure</i> , 2006, 14, 1499-1510.              | 1.6 | 24        |
| 47 | The Na <sup>+</sup> Channel Inactivation Gate Is a Molecular Complex. <i>Journal of General Physiology</i> , 2004, 123, 155-165.  | 0.9 | 133       |
| 48 | Protein backbone angle prediction with machine learning approaches. <i>Bioinformatics</i> , 2004, 20, 1612-1621.  | 1.8 | 72        |
| 49 | Population-based study of SR-BI genetic variation and lipid profile. <i>Atherosclerosis</i> , 2004, 175, 159-168.   | 0.4 | 69        |
| 50 | Local structure prediction with local structure-based sequence profiles. <i>Bioinformatics</i> , 2003, 19, 1267-1274.   | 1.8 | 39        |
| 51 | Secondary Structure of the Human Cardiac Na <sup>+</sup> Channel C Terminus. <i>Journal of Biological Chemistry</i> , 2002, 277, 9233-9241.   | 1.6 | 121       |
| 52 | Local structure-based sequence profile database for local and global protein structure predictions. <i>Bioinformatics</i> , 2002, 18, 1650-1657.  | 1.8 | 21        |
| 53 | Structure-dependent sequence alignment for remotely related proteins. <i>Bioinformatics</i> , 2002, 18, 1658-1665.  | 1.8 | 28        |
| 54 | Characterization of a Novel Isoform of Caspase-9 That Inhibits Apoptosis. <i>Journal of Biological Chemistry</i> , 2001, 276, 12190-12200.  | 1.6 | 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 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 665-678.                              | 2.0 | 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 Edited by F. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 679-689. | 2.0 | 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 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 691-711.   | 2.0 | 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.  | 1.6 | 151       |
| 59 | Sequence to structure alignment in comparative modeling using PrISM. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 66-72.   | 1.5 | 48        |
| 60 | Sequence to structure alignment in comparative modeling using PrISM. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, Suppl 3, 66-72.  | 1.5 | 17        |
| 61 | Electrostatic Contributions to the Binding Free Energy of the $\lambda$ CI Repressor to DNA. <i>Biophysical Journal</i> , 1998, 75, 2262-2273.  | 0.2 | 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.   | 1.2 | 143       |
| 63 | Free Energy Determinants of Secondary Structure Formation: III. $\beta$ -Turns and their Role in Protein Folding. <i>Journal of Molecular Biology</i> , 1996, 259, 873-882.   | 2.0 | 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.   | 1.5 | 2         |
| 65 | Free Energy Determinants of Secondary Structure Formation: I. $\alpha$ -Helices. <i>Journal of Molecular Biology</i> , 1995, 252, 351-365.  | 2.0 | 227       |
| 66 | Free Energy Determinants of Secondary Structure Formation: II. Antiparallel $\beta$ -Sheets. <i>Journal of Molecular Biology</i> , 1995, 252, 366-376.  | 2.0 | 170       |
| 67 | Structural Origins of pH and Ionic Strength Effects on Protein Stability. <i>Journal of Molecular Biology</i> , 1994, 237, 602-614.   | 2.0 | 184       |
| 68 | On the calculation of pKas in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 252-265.  | 1.5 | 514       |
| 69 | On the pH Dependence of Protein Stability. <i>Journal of Molecular Biology</i> , 1993, 231, 459-474.  | 2.0 | 409       |
| 70 | Electrostatic effects on protein stability. <i>Current Opinion in Structural Biology</i> , 1992, 2, 40-45.  | 2.6 | 83        |
| 71 | Analysis of the heat capacity dependence of protein folding. <i>Journal of Molecular Biology</i> , 1992, 227, 889-900.  | 2.0 | 108       |
| 72 | Electrostatic effects on protein stability. <i>Current Biology</i> , 1992, 2, 82.   | 1.8 | 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         |