# Jianyi Yang

## List of Publications by Year in Descending Order



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| 56 papers | 8,172 citations | 27 h-index | 62 g-index |
| 62 ext. papers | 11,273 ext. citations | 8.1 avg, IF | 6.74 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 56 | SARS-CoV-2 nucleocapsid protein binds host mRNAs and attenuates stress granules to impair host stress response.. *IScience*, **2022**, 25, 103562 | 6.1 | 15 |
| 55 | Toward the assessment of predicted inter-residue distance. *Bioinformatics*, **2021**, | 7.2 | 3 |
| 54 | The trRosetta server for fast and accurate protein structure prediction. *Nature Protocols*, **2021**, 16, 5634-5651 | 13.5 | 36 |
| 53 | Improved Protein Structure Prediction Using a New Multi-Scale Network and Homologous Templates. *Advanced Science*, **2021**, e2102592 | 13.6 | 11 |
| 52 | RNA Flexibility Prediction With Sequence Profile and Predicted Solvent Accessibility. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2021**, 18, 2017-2022 | 3 | 3 |
| 51 | RNA inter-nucleotide 3D closeness prediction by deep residual neural networks. *Bioinformatics*, **2021**, 37, 1093-1098 | 7.2 | 4 |
| 50 | Recognition of small molecule-RNA binding sites using RNA sequence and structure. *Bioinformatics*, **2021**, | 7.2 | 5 |
| 49 | Improved protein structure prediction using predicted interresidue orientations. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 1496-1503 | 11.5 | 496 |
| 48 | CATHER: a novel threading algorithm with predicted contacts. *Bioinformatics*, **2020**, 36, 2119-2125 | 7.2 | 6 |
| 47 | Comprehensive Survey and Comparative Assessment of RNA-Binding Residue Predictions with Analysis by RNA Type. *International Journal of Molecular Sciences*, **2020**, 21, | 6.3 | 5 |
| 46 | Protein contact prediction using metagenome sequence data and residual neural networks. *Bioinformatics*, **2020**, 36, 41-48 | 7.2 | 43 |
| 45 | Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. *Computational and Structural Biotechnology Journal*, **2019**, 17, 454-462 | 6.8 | 20 |
| 44 | Enhanced prediction of RNA solvent accessibility with long short-term memory neural networks and improved sequence profiles. *Bioinformatics*, **2019**, 35, 1686-1691 | 7.2 | 9 |
| 43 | Improving the prediction of protein-nucleic acids binding residues via multiple sequence profiles and the consensus of complementary methods. *Bioinformatics*, **2019**, 35, 930-936 | 7.2 | 18 |
| 42 | mTM-align: an algorithm for fast and accurate multiple protein structure alignment. *Bioinformatics*, **2018**, 34, 1719-1725 | 7.2 | 31 |
| 41 | CoABind: a novel algorithm for Coenzyme A (CoA)- and CoA derivatives-binding residues prediction. *Bioinformatics*, **2018**, 34, 2598-2604 | 7.2 | 8 |
| 40 | A large-scale comparative assessment of methods for residue-residue contact prediction. *Briefings in Bioinformatics*, **2018**, 19, 219-230 | 13.4 | 20 |

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| 39 | COACH-D: improved protein-ligand binding sites prediction with refined ligand-binding poses through molecular docking. *Nucleic Acids Research*, **2018**, 46, W438-W442 | 20.1 | 77 |
| 38 | Improving Sequence-Based Prediction of Protein-Peptide Binding Residues by Introducing Intrinsic Disorder and a Consensus Method. *Journal of Chemical Information and Modeling*, **2018**, 58, 1459-1468 | 6.1 | 14 |
| 37 | The structure of the large regulatory subunit of phosphorylase kinase examined by modeling and hydrogen-deuterium exchange. *Protein Science*, **2018**, 27, 472-484 | 6.3 | 1 |
| 36 | PotentialNet for Molecular Property Prediction. *ACS Central Science*, **2018**, 4, 1520-1530 | 16.8 | 155 |
| 35 | mTM-align: a server for fast protein structure database search and multiple protein structure alignment. *Nucleic Acids Research*, **2018**, 46, W380-W386 | 20.1 | 32 |
| 34 | DLTree: efficient and accurate phylogeny reconstruction using the dynamical language method. *Bioinformatics*, **2017**, 33, 2214-2215 | 7.2 | 7 |
| 33 | Structural and Sequence Similarity Makes a Significant Impact on Machine-Learning-Based Scoring Functions for Protein-Ligand Interactions. *Journal of Chemical Information and Modeling*, **2017**, 57, 1007-1012 | 6.1 | 46 |
| 32 | An ensemble approach to protein fold classification by integration of template-based assignment and support vector machine classifier. *Bioinformatics*, **2017**, 33, 863-870 | 7.2 | 15 |
| 31 | ResQ: An Approach to Unified Estimation of B-Factor and Residue-Specific Error in Protein Structure Prediction. *Journal of Molecular Biology*, **2016**, 428, 693-701 | 6.5 | 76 |
| 30 | Template-based protein structure prediction in CASP11 and retrospect of I-TASSER in the last decade. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 233-46 | 4.2 | 42 |
| 29 | Integration of QUARK and I-TASSER for Ab Initio Protein Structure Prediction in CASP11. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 76-86 | 4.2 | 47 |
| 28 | Recognizing metal and acid radical ion-binding sites by integrating ab initio modeling with template-based transferals. *Bioinformatics*, **2016**, 32, 3260-3269 | 7.2 | 56 |
| 27 | GPCR-I-TASSER: A Hybrid Approach to G Protein-Coupled Receptor Structure Modeling and the Application to the Human Genome. *Structure*, **2015**, 23, 1538-1549 | 5.2 | 121 |
| 26 | I-TASSER server: new development for protein structure and function predictions. *Nucleic Acids Research*, **2015**, 43, W174-81 | 20.1 | 1059 |
| 25 | Protein Structure and Function Prediction Using I-TASSER. *Current Protocols in Bioinformatics*, **2015**, 52, 5.8.1-5.8.15 | 24.2 | 214 |
| 24 | GLASS: a comprehensive database for experimentally validated GPCR-ligand associations. *Bioinformatics*, **2015**, 31, 3035-42 | 7.2 | 57 |
| 23 | In various protein complexes, disordered protomers have large per-residue surface areas and area of protein-, DNA- and RNA-binding interfaces. *FEBS Letters*, **2015**, 589, 2561-9 | 3.8 | 30 |
| 22 | The I-TASSER Suite: protein structure and function prediction. *Nature Methods*, **2015**, 12, 7-8 | 21.6 | 3430 |

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| 21 | Histatin 5 binds to Porphyromonas gingivalis hemagglutinin B (HagB) and alters HagB-induced chemokine responses. *Scientific Reports*, **2014**, 4, 3904 | 4.9 | 20 |
| 20 | Advances in GPCR modeling evaluated by the GPCR Dock 2013 assessment: meeting new challenges. *Structure*, **2014**, 22, 1120-1139 | 5.2 | 136 |
| 19 | Antimicrobial Activity of Chemokine CXCL10 for Dermal and Oral Microorganisms. *Antibiotics*, **2014**, 3, 527-39 | 4.9 | 6 |
| 18 | Super Spy variants implicate flexibility in chaperone action. *ELife*, **2014**, 3, e01584 | 8.9 | 38 |
| 17 | A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. *Scientific Reports*, **2013**, 3, 2619 | 4.9 | 128 |
| 16 | Protein-ligand binding site recognition using complementary binding-specific substructure comparison and sequence profile alignment. *Bioinformatics*, **2013**, 29, 2588-95 | 7.2 | 483 |
| 15 | A small shared epitope-mimetic compound potently accelerates osteoclast-mediated bone damage in autoimmune arthritis. *Journal of Immunology*, **2013**, 191, 2096-103 | 5.3 | 18 |
| 14 | BioLiP: a semi-manually curated database for biologically relevant ligand-protein interactions. *Nucleic Acids Research*, **2013**, 41, D1096-103 | 20.1 | 348 |
| 13 | Identification of partially linear structure in additive models with an application to gene expression prediction from sequences. *Biometrics*, **2012**, 68, 437-45 | 1.8 | 10 |
| 12 | COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. *Nucleic Acids Research*, **2012**, 40, W471-7 | 20.1 | 448 |
| 11 | Improving taxonomy-based protein fold recognition by using global and local features. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 2053-64 | 4.2 | 50 |
| 10 | Constructing consensus genetic maps in comparative analysis. *Journal of Computational Biology*, **2010**, 17, 1561-73 | 1.7 | 5 |
| 9 | An improved classification of G-protein-coupled receptors using sequence-derived features. *BMC Bioinformatics*, **2010**, 11, 420 | 3.6 | 27 |
| 8 | Prediction of protein structural classes for low-homology sequences based on predicted secondary structure. *BMC Bioinformatics*, **2010**, 11 Suppl 1, S9 | 3.6 | 62 |
| 7 | Prediction of protein structural classes by recurrence quantification analysis based on chaos game representation. *Journal of Theoretical Biology*, **2009**, 257, 618-26 | 2.3 | 97 |
| 6 | Clustering structures of large proteins using multifractal analyses based on a 6-letter model and hydrophobicity scale of amino acids. *Chaos, Solitons and Fractals*, **2009**, 40, 607-620 | 9.3 | 22 |
| 5 | Human Pol II promoter recognition based on primary sequences and free energy of dinucleotides. *BMC Bioinformatics*, **2008**, 9, 113 | 3.6 | 21 |
| 4 | Correlations between designability and various structural characteristics of protein lattice models. *Journal of Chemical Physics*, **2007**, 126, 195101 | 3.9 | 6 |

# List of Publications

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| 3 | Single-sequence protein structure prediction using supervised transformer protein language models | 1 |
| 2 | SARS-CoV-2 Nucleocapsid protein attenuates stress granule formation and alters gene expression via direct interaction with host mRNAs | 17 |
| 1 | Improved protein structure prediction using predicted inter-residue orientations | 17 |