

# Fan Zheng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4503710/publications.pdf>

Version: 2024-02-01

15  
papers

517  
citations

758635

12  
h-index

1058022

14  
g-index

17  
all docs

17  
docs citations

17  
times ranked

1001  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Functional landscape of SARS-CoV-2 cellular restriction. <i>Molecular Cell</i> , 2021, 81, 2656-2668.e8.  | 4.5  | 137       |
| 2  | A protein interaction landscape of breast cancer. <i>Science</i> , 2021, 374, eabf3066.   | 6.0  | 66        |
| 3  | A multi-scale map of cell structure fusing protein images and interactions. <i>Nature</i> , 2021, 600, 536-542.   | 13.7 | 43        |
| 4  | A protein network map of head and neck cancer reveals PIK3CA mutant drug sensitivity. <i>Science</i> , 2021, 374, eabf2911.   | 6.0  | 37        |
| 5  | Multiscale community detection in Cytoscape. <i>PLoS Computational Biology</i> , 2020, 16, e1008239.  | 1.5  | 34        |
| 6  | Design and designability of protein-based assemblies. <i>Current Opinion in Structural Biology</i> , 2014, 27, 79-86.   | 2.6  | 31        |
| 7  | Interpretation of cancer mutations using a multiscale map of protein systems. <i>Science</i> , 2021, 374, eabf3067.   | 6.0  | 29        |
| 8  | HiDeF: identifying persistent structures in multiscale omics data. <i>Genome Biology</i> , 2021, 22, 21.  | 3.8  | 29        |
| 9  | Tertiary Structural Propensities Reveal Fundamental Sequence/Structure Relationships. <i>Structure</i> , 2015, 23, 961-971.   | 1.6  | 27        |
| 10 | Sequence statistics of tertiary structural motifs reflect protein stability. <i>PLoS ONE</i> , 2017, 12, e0178272.  | 1.1  | 26        |
| 11 | Computational Design of Selective Peptides to Discriminate between Similar PDZ Domains in an Oncogenic Pathway. <i>Journal of Molecular Biology</i> , 2015, 427, 491-510.             | 2.0  | 23        |
| 12 | DDOT: A Swiss Army Knife for Investigating Data-Driven Biological Ontologies. <i>Cell Systems</i> , 2019, 8, 267-273.e3.  | 2.9  | 22        |
| 13 | Annotating gene sets by mining large literature collections with protein networks. , 2018, , .  |      | 6         |
| 14 | Simplifying the Design of Protein-Peptide Interaction Specificity with Sequence-Based Representations of Atomistic Models. <i>Methods in Molecular Biology</i> , 2017, 1561, 189-200. | 0.4  | 2         |
| 15 | Design of Specific Peptide-Protein Recognition. <i>Methods in Molecular Biology</i> , 2016, 1414, 249-263.  | 0.4  | 1         |