

# Yu Xia

## List of Publications by Year in descending order

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88  
papers

7,734  
citations

126907

33  
h-index

60623

81  
g-index

93  
all docs

93  
docs citations

93  
times ranked

11156  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Proteome-Scale Map of the Human Interactome Network. <i>Cell</i> , 2014, 159, 1212-1226.	28.9	1,199
2	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	27.8	724
3	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. <i>Genome Research</i> , 2004, 14, 1107-1118.	5.5	516
4	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
5	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	28.9	479
6	Relating Three-Dimensional Structures to Protein Networks Provides Evolutionary Insights. <i>Science</i> , 2006, 314, 1938-1941.	12.6	447
7	Diverse Cellular Functions of the Hsp90 Molecular Chaperone Uncovered Using Systems Approaches. <i>Cell</i> , 2007, 131, 121-135.	28.9	437
8	Defining the TRiC/CCT interactome links chaperonin function to stabilization of newly made proteins with complex topologies. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1255-1262.	8.2	340
9	The role of disorder in interaction networks: a structural analysis. <i>Molecular Systems Biology</i> , 2008, 4, 179.	7.2	206
10	Genome-wide prioritization of disease genes and identification of disease-disease associations from an integrated human functional linkage network. <i>Genome Biology</i> , 2009, 10, R91.	9.6	196
11	Assessing the limits of genomic data integration for predicting protein networks. <i>Genome Research</i> , 2005, 15, 945-953.	5.5	182
12	Structural Determinants of Protein Evolution Are Context-Sensitive at the Residue Level. <i>Molecular Biology and Evolution</i> , 2009, 26, 2387-2395.	8.9	175
13	Ab initio construction of protein tertiary structures using a hierarchical approach. <i>Journal of Molecular Biology</i> , 2000, 300, 171-185.	4.2	162
14	Analyzing Cellular Biochemistry in Terms of Molecular Networks. <i>Annual Review of Biochemistry</i> , 2004, 73, 1051-1087.	11.1	133
15	Use of Thioredoxin as a Reporter To Identify a Subset of Escherichia coli Signal Sequences That Promote Signal Recognition Particle-Dependent Translocation. <i>Journal of Bacteriology</i> , 2005, 187, 2983-2991.	2.2	128
16	Structural principles within the human-virus protein-protein interaction network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10538-10543.	7.1	120
17	A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. <i>Cell</i> , 2016, 164, 310-323.	28.9	106
18	Simulating protein evolution in sequence and structure space. <i>Current Opinion in Structural Biology</i> , 2004, 14, 202-207.	5.7	89

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19	Production of a reference transcriptome and transcriptomic database (PocilloporaBase) for the cauliflower coral, <i>Pocillopora damicornis</i> . <i>BMC Genomics</i> , 2011, 12, 585.	2.8	75
20	Ab initio protein structure prediction using a combined hierarchical approach. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 194-198.	2.6	66
21	A High-Resolution Genome-Wide CRISPR/Cas9 Viability Screen Reveals Structural Features and Contextual Diversity of the Human Cell-Essential Proteome. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	66
22	Discovering causal signaling pathways through gene-expression patterns. <i>Nucleic Acids Research</i> , 2010, 38, W109-W117.	14.5	65
23	Roles of mutation and recombination in the evolution of protein thermodynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 10382-10387.	7.1	63
24	Computational analysis of membrane proteins: genomic occurrence, structure prediction and helix interactions. <i>Quarterly Reviews of Biophysics</i> , 2004, 37, 121-146.	5.7	62
25	Finding local communities in protein networks. <i>BMC Bioinformatics</i> , 2009, 10, 297.	2.6	59
26	Integrated Assessment of Genomic Correlates of Protein Evolutionary Rate. <i>PLoS Computational Biology</i> , 2009, 5, e1000413.	3.2	55
27	Selection and Characterization of Small Random Transmembrane Proteins that Bind and Activate the Platelet-derived Growth Factor $\beta$ Receptor. <i>Journal of Molecular Biology</i> , 2004, 338, 907-920.	4.2	54
28	Predicting eukaryotic transcriptional cooperativity by Bayesian network integration of genome-wide data. <i>Nucleic Acids Research</i> , 2009, 37, 5943-5958.	14.5	48
29	Signatures of Pleiotropy, Economy and Convergent Evolution in a Domain-Resolved Map of Human "Virus Protein" Protein Interaction Networks. <i>PLoS Pathogens</i> , 2013, 9, e1003778.	4.7	47
30	An inter-species protein-protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016, 12, 865.	7.2	42
31	Therapeutics of Ebola Hemorrhagic Fever: Whole-Genome Transcriptional Analysis of Successful Disease Mitigation. <i>Journal of Infectious Diseases</i> , 2011, 204, S1043-S1052.	4.0	38
32	Sequence variation in G-protein-coupled receptors: analysis of single nucleotide polymorphisms. <i>Nucleic Acids Research</i> , 2005, 33, 1710-1721.	14.5	37
33	Spectral affinity in protein networks. <i>BMC Systems Biology</i> , 2009, 3, 112.	3.0	37
34	A COMBINED APPROACH FOR AB INITIO CONSTRUCTION OF LOW RESOLUTION PROTEIN TERTIARY STRUCTURES FROM SEQUENCE. , 1998, , 505-16.		34
35	Funnel-like organization in sequence space determines the distributions of protein stability and folding rate preferred by evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 107-114.	2.6	33
36	High-precision high-coverage functional inference from integrated data sources. <i>BMC Bioinformatics</i> , 2008, 9, 119.	2.6	33

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37	Domain-based prediction of the human isoform interactome provides insights into the functional impact of alternative splicing. <i>PLoS Computational Biology</i> , 2017, 13, e1005717.	3.2	30
38	Worldwide malaria incidence and cancer mortality are inversely associated. <i>Infectious Agents and Cancer</i> , 2017, 12, 14.	2.6	29
39	Ab initio protein structure prediction using a combined hierarchical approach. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 194-198.	2.6	27
40	Extracting knowledge-based energy functions from protein structures by error rate minimization: Comparison of methods using lattice model. <i>Journal of Chemical Physics</i> , 2000, 113, 9318-9330.	3.0	26
41	Heterozygous Yeast Deletion Collection Screens Reveal Essential Targets of Hsp90. <i>PLoS ONE</i> , 2011, 6, e28211.	2.5	26
42	Toward a three-dimensional view of protein networks between species. <i>Frontiers in Microbiology</i> , 2012, 3, 428.	3.5	26
43	Integrated Prediction of the Helical Membrane Protein Interactome in Yeast. <i>Journal of Molecular Biology</i> , 2006, 357, 339-349.	4.2	25
44	Consequences of domain insertion on sequence-structure divergence in a superfold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3381-7.	7.1	25
45	A Computational Framework for Heparan Sulfate Sequencing Using High-resolution Tandem Mass Spectra. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2490-2502.	3.8	25
46	Molecular Modeling and Design of Invariant Chain Peptides with Altered Dissociation Kinetics from Class II MHC. <i>Biochemistry</i> , 1996, 35, 14734-14742.	2.5	24
47	Design of an optimal Chebyshev-expanded discrimination function for globular proteins. <i>Protein Science</i> , 2002, 11, 2010-2021.	7.6	24
48	Interactome evolution: insights from genome-wide analyses of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2018, 50, 42-48.	5.7	24
49	Protein evolution in yeast transcription factor subnetworks. <i>Nucleic Acids Research</i> , 2010, 38, 5959-5969.	14.5	23
50	Transcriptional Correlates of Disease Outcome in Anticoagulant-Treated Non-Human Primates Infected with Ebolavirus. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3061.	3.0	22
51	Independent Effects of Protein Core Size and Expression on Residue-Level Structure-Evolution Relationships. <i>PLoS ONE</i> , 2012, 7, e46602.	2.5	22
52	The Impact of Native State Switching on Protein Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 1378-1390.	8.9	20
53	Design principles of molecular networks revealed by global comparisons and composite motifs. <i>Genome Biology</i> , 2006, 7, R55.	9.6	19
54	Photodissociation of methylazide: Observation of triplet methylnitrene radical. <i>Journal of Chemical Physics</i> , 1996, 105, 5798-5805.	3.0	17

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55	A pooled genome-wide screening strategy to identify and rank influenza host restriction factors in cell-based vaccine production platforms. <i>Scientific Reports</i> , 2020, 10, 12166.	3.3	17
56	Precipitation patterns with polygonal boundaries between electrolytes. <i>Physical Chemistry Chemical Physics</i> , 2009, 11, 11033.	2.8	15
57	Nature of Long-Range Evolutionary Constraint in Enzymes: Insights from Comparison to Pseudoenzymes with Similar Structures. <i>Molecular Biology and Evolution</i> , 2018, 35, 2597-2606.	8.9	15
58	Computational Reconstruction of Protein-Protein Interaction Networks: Algorithms and Issues. <i>Methods in Molecular Biology</i> , 2009, 541, 89-100.	0.9	15
59	Haplotype-resolved de novo assembly of the Vero cell line genome. <i>Npj Vaccines</i> , 2021, 6, 106.	6.0	14
60	Bioinformatics Analysis of Macrophages Exposed to <i>Porphyromonas gingivalis</i> : Implications in Acute vs. Chronic Infections. <i>PLoS ONE</i> , 2010, 5, e15613.	2.5	14
61	Network Centrality Analysis in Fungi Reveals Complex Regulation of Lost and Gained Genes. <i>PLoS ONE</i> , 2017, 12, e0169459.	2.5	12
62	Quantitative Residue-Level Structure-Evolution Relationships in the Yeast Membrane Proteome. <i>Genome Biology and Evolution</i> , 2013, 5, 734-744.	2.5	11
63	Structural Perspectives on Protein Evolution. <i>Annual Reports in Computational Chemistry</i> , 2008, 4, 3-21.	1.7	10
64	Multi-Edge Gene Set Networks Reveal Novel Insights into Global Relationships between Biological Themes. <i>PLoS ONE</i> , 2012, 7, e45211.	2.5	10
65	Are transient protein-protein interactions more dispensable?. <i>PLoS Computational Biology</i> , 2022, 18, e1010013.	3.2	10
66	Construction of Functional Linkage Gene Networks by Data Integration. <i>Methods in Molecular Biology</i> , 2013, 939, 215-232.	0.9	9
67	Upon Accounting for the Impact of Isoenzyme Loss, Gene Deletion Costs Anticorrelate with Their Evolutionary Rates. <i>PLoS ONE</i> , 2017, 12, e0170164.	2.5	9
68	Estimating dispensable content in the human interactome. <i>Nature Communications</i> , 2019, 10, 3205.	12.8	9
69	Non-catalytic Binding Sites Induce Weaker Long-Range Evolutionary Rate Gradients than Catalytic Sites in Enzymes. <i>Journal of Molecular Biology</i> , 2019, 431, 3860-3870.	4.2	9
70	Quantifying evolutionary importance of protein sites: A Tale of two measures. <i>PLoS Genetics</i> , 2021, 17, e1009476.	3.5	8
71	Convergent perturbation of the human domain-resolved interactome by viruses and mutations inducing similar disease phenotypes. <i>PLoS Computational Biology</i> , 2019, 15, e1006762.	3.2	7
72	Regulatory Network Structure as a Dominant Determinant of Transcription Factor Evolutionary Rate. <i>PLoS Computational Biology</i> , 2012, 8, e1002734.	3.2	6

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73	Using Pseudoenzymes to Probe Evolutionary Design Principles of Enzymes. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431985593.	1.2	6
74	Structural models for host-pathogen protein-protein interactions: assessing coverage and bias. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 287-98.	0.7	6
75	Overview of recent advances in Vero cells genomic characterization and engineering for high-throughput vaccine manufacturing. <i>Clinical and Translational Discovery</i> , 2022, 2, .	0.5	5
76	Research Resource: EPSLiM: Ensemble Predictor for Short Linear Motifs in Nuclear Hormone Receptors. <i>Molecular Endocrinology</i> , 2014, 28, 768-777.	3.7	4
77	Structural Profiling of Bacterial Effectors Reveals Enrichment of Host-Interacting Domains and Motifs. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 626600.	3.5	4
78	Principal component analysis of alpha-helix deformations in transmembrane proteins. <i>PLoS ONE</i> , 2021, 16, e0257318.	2.5	4
79	A High-Throughput Method to Examine Protein-Nucleotide Interactions Identifies Targets of the Bacterial Transcriptional Regulatory Protein Fur. <i>PLoS ONE</i> , 2014, 9, e96832.	2.5	4
80	Protein Interaction Prediction by Integrating Genomic Features and Protein Interaction Network Analysis. , 2005, , 61-81.		3
81	Structure-guided approach for detecting large domain inserts in protein sequences as illustrated using the haloacid dehalogenase superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1896-1906.	2.6	3
82	Mutation Edgotype Drives Fitness Effect in Human. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	2.1	2
83	STRUCTURAL MODELS FOR HOST-PATHOGEN PROTEIN-PROTEIN INTERACTIONS: ASSESSING COVERAGE AND BIAS. , 2011, , .		2
84	Probing structure-function relationships of the DNA polymerase alpha-associated zinc-finger protein using computational approaches. , 1999, , 179-90.		1
85	The Wnt signaling network in cancer. , 0, , 222-255.		0
86	Using Functional Linkage Gene Networks to Study Human Diseases. , 2011, , 275-293.		0
87	The nature of sequence and structure divergence in the Haloalkanoate Dehalogenase SuperFamily (HADSF). <i>FASEB Journal</i> , 2013, 27, 797.2.	0.5	0
88	Structural Determinants of Yeast Protein-Protein Interaction Interface Evolution at the Residue Level. <i>Journal of Molecular Biology</i> , 2022, 434, 167750.	4.2	0