

# Yu Xia

## List of Publications by Year in descending order

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88  
papers

7,734  
citations

126907

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60623

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g-index

93  
all docs

93  
docs citations

93  
times ranked

11156  
citing authors

#	ARTICLE	IF	CITATIONS
1	Are transient protein-protein interactions more dispensable?. PLoS Computational Biology, 2022, 18, e1010013.	3.2	10
2	Overview of recent advances in Vero cells genomic characterization and engineering for high-throughput vaccine manufacturing. Clinical and Translational Discovery, 2022, 2, .	0.5	5
3	Structural Determinants of Yeast Protein-Protein Interaction Interface Evolution at the Residue Level. Journal of Molecular Biology, 2022, 434, 167750.	4.2	0
4	Quantifying evolutionary importance of protein sites: A Tale of two measures. PLoS Genetics, 2021, 17, e1009476.	3.5	8
5	Structural Profiling of Bacterial Effectors Reveals Enrichment of Host-Interacting Domains and Motifs. Frontiers in Molecular Biosciences, 2021, 8, 626600.	3.5	4
6	Haplotype-resolved de novo assembly of the Vero cell line genome. Npj Vaccines, 2021, 6, 106.	6.0	14
7	Mutation Edgotype Drives Fitness Effect in Human. Frontiers in Bioinformatics, 2021, 1, .	2.1	2
8	Principal component analysis of alpha-helix deformations in transmembrane proteins. PLoS ONE, 2021, 16, e0257318.	2.5	4
9	A pooled genome-wide screening strategy to identify and rank influenza host restriction factors in cell-based vaccine production platforms. Scientific Reports, 2020, 10, 12166.	3.3	17
10	A reference map of the human binary protein interactome. Nature, 2020, 580, 402-408.	27.8	724
11	Estimating dispensable content in the human interactome. Nature Communications, 2019, 10, 3205.	12.8	9
12	Non-catalytic Binding Sites Induce Weaker Long-Range Evolutionary Rate Gradients than Catalytic Sites in Enzymes. Journal of Molecular Biology, 2019, 431, 3860-3870.	4.2	9
13	Using Pseudoenzymes to Probe Evolutionary Design Principles of Enzymes. Evolutionary Bioinformatics, 2019, 15, 117693431985593.	1.2	6
14	Convergent perturbation of the human domain-resolved interactome by viruses and mutations inducing similar disease phenotypes. PLoS Computational Biology, 2019, 15, e1006762.	3.2	7
15	A High-Resolution Genome-Wide CRISPR/Cas9 Viability Screen Reveals Structural Features and Contextual Diversity of the Human Cell-Essential Proteome. Molecular and Cellular Biology, 2018, 38, .	2.3	66
16	Interactome evolution: insights from genome-wide analyses of protein-protein interactions. Current Opinion in Structural Biology, 2018, 50, 42-48.	5.7	24
17	Nature of Long-Range Evolutionary Constraint in Enzymes: Insights from Comparison to Pseudoenzymes with Similar Structures. Molecular Biology and Evolution, 2018, 35, 2597-2606.	8.9	15
18	The Impact of Native State Switching on Protein Sequence Evolution. Molecular Biology and Evolution, 2017, 34, 1378-1390.	8.9	20

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19	Worldwide malaria incidence and cancer mortality are inversely associated. <i>Infectious Agents and Cancer</i> , 2017, 12, 14.	2.6	29
20	Network Centrality Analysis in Fungi Reveals Complex Regulation of Lost and Gained Genes. <i>PLoS ONE</i> , 2017, 12, e0169459.	2.5	12
21	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
22	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
23	An inter-species protein-protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016, 12, 865.	7.2	42
24	A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. <i>Cell</i> , 2016, 164, 310-323.	28.9	106
25	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	28.9	479
26	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
27	Research Resource: EPSLiM: Ensemble Predictor for Short Linear Motifs in Nuclear Hormone Receptors. <i>Molecular Endocrinology</i> , 2014, 28, 768-777.	3.7	4
28	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
29	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
30	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
31	A Proteome-Scale Map of the Human Interactome Network. <i>Cell</i> , 2014, 159, 1212-1226.	28.9	1,199
32	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
33	Construction of Functional Linkage Gene Networks by Data Integration. <i>Methods in Molecular Biology</i> , 2013, 939, 215-232.	0.9	9
34	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
35	Quantitative Residue-Level Structure-Evolution Relationships in the Yeast Membrane Proteome. <i>Genome Biology and Evolution</i> , 2013, 5, 734-744.	2.5	11
36	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

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37	The nature of sequence and structure divergence in the Haloalkanoate Dehalogenase SuperFamily (HADSF). <i>FASEB Journal</i> , 2013, 27, 797.2.	0.5	0
38	Regulatory Network Structure as a Dominant Determinant of Transcription Factor Evolutionary Rate. <i>PLoS Computational Biology</i> , 2012, 8, e1002734.	3.2	6
39	Multi-Edge Gene Set Networks Reveal Novel Insights into Global Relationships between Biological Themes. <i>PLoS ONE</i> , 2012, 7, e45211.	2.5	10
40	Toward a three-dimensional view of protein networks between species. <i>Frontiers in Microbiology</i> , 2012, 3, 428.	3.5	26
41	Independent Effects of Protein Core Size and Expression on Residue-Level Structure-Evolution Relationships. <i>PLoS ONE</i> , 2012, 7, e46602.	2.5	22
42	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
43	Heterozygous Yeast Deletion Collection Screens Reveal Essential Targets of Hsp90. <i>PLoS ONE</i> , 2011, 6, e28211.	2.5	26
44	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
45	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
46	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
47	STRUCTURAL MODELS FOR HOST-PATHOGEN PROTEIN-PROTEIN INTERACTIONS: ASSESSING COVERAGE AND BIAS. , 2011, , .		2
48	Using Functional Linkage Gene Networks to Study Human Diseases. , 2011, , 275-293.		0
49	Protein evolution in yeast transcription factor subnetworks. <i>Nucleic Acids Research</i> , 2010, 38, 5959-5969.	14.5	23
50	Discovering causal signaling pathways through gene-expression patterns. <i>Nucleic Acids Research</i> , 2010, 38, W109-W117.	14.5	65
51	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
52	Integrated Assessment of Genomic Correlates of Protein Evolutionary Rate. <i>PLoS Computational Biology</i> , 2009, 5, e1000413.	3.2	55
53	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
54	Predicting eukaryotic transcriptional cooperativity by Bayesian network integration of genome-wide data. <i>Nucleic Acids Research</i> , 2009, 37, 5943-5958.	14.5	48

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55	Finding local communities in protein networks. BMC Bioinformatics, 2009, 10, 297.	2.6	59
56	Spectral affinity in protein networks. BMC Systems Biology, 2009, 3, 112.	3.0	37
57	Precipitation patterns with polygonal boundaries between electrolytes. Physical Chemistry Chemical Physics, 2009, 11, 11033.	2.8	15
58	Genome-wide prioritization of disease genes and identification of disease-disease associations from an integrated human functional linkage network. Genome Biology, 2009, 10, R91.	9.6	196
59	Computational Reconstruction of Protein-Protein Interaction Networks: Algorithms and Issues. Methods in Molecular Biology, 2009, 541, 89-100.	0.9	15
60	Defining the TRiC/CCT interactome links chaperonin function to stabilization of newly made proteins with complex topologies. Nature Structural and Molecular Biology, 2008, 15, 1255-1262.	8.2	340
61	High-precision high-coverage functional inference from integrated data sources. BMC Bioinformatics, 2008, 9, 119.	2.6	33
62	The role of disorder in interaction networks: a structural analysis. Molecular Systems Biology, 2008, 4, 179.	7.2	206
63	Structural Perspectives on Protein Evolution. Annual Reports in Computational Chemistry, 2008, 4, 3-21.	1.7	10
64	Diverse Cellular Functions of the Hsp90 Molecular Chaperone Uncovered Using Systems Approaches. Cell, 2007, 131, 121-135.	28.9	437
65	Design principles of molecular networks revealed by global comparisons and composite motifs. Genome Biology, 2006, 7, R55.	9.6	19
66	Relating Three-Dimensional Structures to Protein Networks Provides Evolutionary Insights. Science, 2006, 314, 1938-1941.	12.6	447
67	Integrated Prediction of the Helical Membrane Protein Interactome in Yeast. Journal of Molecular Biology, 2006, 357, 339-349.	4.2	25
68	Protein Interaction Prediction by Integrating Genomic Features and Protein Interaction Network Analysis. , 2005, , 61-81.		3
69	Use of Thioredoxin as a Reporter To Identify a Subset of Escherichia coli Signal Sequences That Promote Signal Recognition Particle-Dependent Translocation. Journal of Bacteriology, 2005, 187, 2983-2991.	2.2	128
70	Assessing the limits of genomic data integration for predicting protein networks. Genome Research, 2005, 15, 945-953.	5.5	182
71	Sequence variation in G-protein-coupled receptors: analysis of single nucleotide polymorphisms. Nucleic Acids Research, 2005, 33, 1710-1721.	14.5	37
72	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. Genome Research, 2004, 14, 1107-1118.	5.5	516

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73	Analyzing Cellular Biochemistry in Terms of Molecular Networks. Annual Review of Biochemistry, 2004, 73, 1051-1087.	11.1	133
74	Simulating protein evolution in sequence and structure space. Current Opinion in Structural Biology, 2004, 14, 202-207.	5.7	89
75	Funnel-like organization in sequence space determines the distributions of protein stability and folding rate preferred by evolution. Proteins: Structure, Function and Bioinformatics, 2004, 55, 107-114.	2.6	33
76	Selection and Characterization of Small Random Transmembrane Proteins that Bind and Activate the Platelet-derived Growth Factor $\beta$ Receptor. Journal of Molecular Biology, 2004, 338, 907-920.	4.2	54
77	Computational analysis of membrane proteins: genomic occurrence, structure prediction and helix interactions. Quarterly Reviews of Biophysics, 2004, 37, 121-146.	5.7	62
78	Roles of mutation and recombination in the evolution of protein thermodynamics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10382-10387.	7.1	63
79	Design of an optimal Chebyshev-expanded discrimination function for globular proteins. Protein Science, 2002, 11, 2010-2021.	7.6	24
80	Extracting knowledge-based energy functions from protein structures by error rate minimization: Comparison of methods using lattice model. Journal of Chemical Physics, 2000, 113, 9318-9330.	3.0	26
81	Ab initio construction of protein tertiary structures using a hierarchical approach. Journal of Molecular Biology, 2000, 300, 171-185.	4.2	162
82	Ab initio protein structure prediction using a combined hierarchical approach. Proteins: Structure, Function and Bioinformatics, 1999, 37, 194-198.	2.6	66
83	Ab initio protein structure prediction using a combined hierarchical approach. Proteins: Structure, Function and Bioinformatics, 1999, 37, 194-198.	2.6	27
84	Probing structure-function relationships of the DNA polymerase alpha-associated zinc-finger protein using computational approaches. , 1999, , 179-90.		1
85	A COMBINED APPROACH FOR AB INITIO CONSTRUCTION OF LOW RESOLUTION PROTEIN TERTIARY STRUCTURES FROM SEQUENCE. , 1998, , 505-16.		34
86	Molecular Modeling and Design of Invariant Chain Peptides with Altered Dissociation Kinetics from Class II MHC. Biochemistry, 1996, 35, 14734-14742.	2.5	24
87	Photodissociation of methylazide: Observation of triplet methylnitrene radical. Journal of Chemical Physics, 1996, 105, 5798-5805.	3.0	17
88	The Wnt signaling network in cancer. , 0, , 222-255.		0