Haiyuan Yu

List of Publications by Year
in descending order

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66 papers	6,926 citations	147726 31 h-index	110317 64 g-index
85 all docs	85 docs citations	85 times ranked	10438 citing authors

#	Article	IF	Citations
1	Implications of disease-related mutations at proteinâ€“protein interfaces. Current Opinion in Structural Biology, 2022, 72, 219-225.	2.6	17
2	Agingâ€related cell typeâ€specific pathophysiologic immune responses that exacerbate disease severity in aged COVIDâ€19 patients. Aging Cell, 2022, 21, e13544.	3.0	11
3	Deep learning methods for 3D structural proteome and interactome modeling. Current Opinion in Structural Biology, 2022, 73, 102329.	2.6	19
4	A comparison of experimental assays and analytical methods for genome-wide identification of active enhancers. Nature Biotechnology, 2022, 40, 1056-1065.	9.4	28
5	Advancing discovery of risk-altering variants for complex diseases by functionally informed fine-mapping. Neuron, 2022, 110, 905-907.	3.8	1
6	A full-proteome, interaction-specific characterization of mutational hotspots across human cancers. Genome Research, 2022, 32, 135-149.	2.4	2
7	SAAMBE-SEQ: a sequence-based method for predicting mutation effect on proteinâ€“protein binding affinity. Bioinformatics, 2021, 37, 992-999.	1.8	17
8	Structural basis of TRAPPIIIâ€mediated Rab1 activation. EMBO Journal, 2021, 40, e107607.	3.5	24
9	Network medicine links SARS-CoV-2/COVID-19 infection to brain microvascular injury and neuroinflammation in dementia-like cognitive impairment. Alzheimer's Research and Therapy, 2021, 13, 110.	3.0	108
10	A multifaceted role of progranulin in regulating amyloid-beta dynamics and responses. Life Science Alliance, 2021, 4, e202000874.	1.3	10
11	Human MLH1/3 variants causing aneuploidy, pregnancy loss, and premature reproductive aging. Nature Communications, 2021, 12, 5005.	5.8	13
12	Handcuffing intrinsically disordered regions in Mlh1â€“Pms1 disrupts mismatch repair. Nucleic Acids Research, 2021, 49, 9327-9341.	6.5	5
13	Inâ€depth and 3â€dimensional exploration of the budding yeast phosphoproteome. EMBO Reports, 2021, 22, e51121.	2.0	99
14	Progress in methodologies and qualityâ€control strategies in protein crossâ€linking mass spectrometry. Proteomics, 2021, 21, e2100145.	1.3	5
15	A 3D structural SARS-CoV-2â€“human interactome to explore genetic and drug perturbations. Nature Methods, 2021, 18, 1477-1488.	9.0	17
16	Combining views for newly sequenced organisms. Nature Machine Intelligence, 2021, 3, 1011-1012.	8.3	0
17	Variants in RABL2A causing male infertility and ciliopathy. Human Molecular Genetics, 2020, 29, 3402-3411.	1.4	11
18	De novo missense variants disrupting proteinâ€“protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. Molecular Autism, 2020, 11, 76.	2.6	19

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19	Glucosylation by the Legionella Effector SetA Promotes the Nuclear Localization of the Transcription Factor TFEB. IScience, 2020, 23, 101300.	1.9	18
20	Structure-based validation can drastically underestimate error rate in proteome-wide cross-linking mass spectrometry studies. Nature Methods, 2020, 17, 985-988.	9.0	23
21	Genetics of extreme human longevity to guide drug discovery for healthy ageing. Nature Metabolism, 2020, 2, 663-672.	5.1	32
22	Maximized quantitative phosphoproteomics allows high confidence dissection of the DNA damage signaling network. Scientific Reports, 2020, 10, 18056.	1.6	9
23	Transcription imparts architecture, function and logic to enhancer units. Nature Genetics, 2020, 52, 1067-1075.	9.4	60
24	BraInMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. Cell Systems, 2020, 10, 333-350.e14.	2.9	48
25	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11836-11842.	3.3	16
26	Revealing new therapeutic opportunities through drug target prediction: a class imbalance-tolerant machine learning approach. Bioinformatics, 2020, 36, 4490-4497.	1.8	9
27	MaXLinker: Proteome-wide Cross-link Identifications with High Specificity and Sensitivity. Molecular and Cellular Proteomics, 2020, 19, 554-568.	2.5	38
28	SAAMBE-3D: Predicting Effect of Mutations on Proteinâ€“Protein Interactions. International Journal of Molecular Sciences, 2020, 21, 2563.	1.8	66
29	Loss of <scp>TMEM</scp> 106B and <scp>PGRN</scp> leads to severe lysosomal abnormalities and neurodegeneration in mice. EMBO Reports, 2020, 21, e50219.	2.0	52
30	Inferring Protein-Protein Interaction Networks From Mass Spectrometry-Based Proteomic Approaches: A Mini-Review. Computational and Structural Biotechnology Journal, 2019, 17, 805-811.	1.9	39
31	GRAM: A GeneRAlized Model to predict the molecular effect of a non-coding variant in a cell-type specific manner. PLoS Genetics, 2019, 15, e1007860.	1.5	1
32	Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. Nature Communications, 2019, 10, 4141.	5.8	48
33	Leveraging genetic interactions for adverse drug-drug interaction prediction. PLoS Computational Biology, 2019, 15, e1007068.	1.5	18
34	Interactome INSIDER: a structural interactome browser for genomic studies. Nature Methods, 2018, 15, 107-114.	9.0	133
35	Germline Lysine-Specific Demethylase 1 (LSD1/KDM1A) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759.	0.4	56
36	Extracting complementary insights from molecular phenotypes for prioritization of disease-associated mutations. Current Opinion in Systems Biology, 2018, 11, 107-116.	1.3	4

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37	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Nature Genetics, 2018, 50, 1032-1040.	9.4	64
38	iRegNet3D: three-dimensional integrated regulatory network for the genomic analysis of coding and non-coding disease mutations. Genome Biology, 2017, 18, 10.	3.8	9
39	GeMSTONE: orchestrated prioritization of human germline mutations in the cloud. Nucleic Acids Research, 2017, 45, W207-W214.	6.5	2
40	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF-Î¹B Signaling. Cell Systems, 2017, 5, 564-577.e12.	2.9	44
41	mutation3D: Cancer Gene Prediction Through Atomic Clustering of Coding Variants in the Structural Proteome. Human Mutation, 2016, 37, 447-456.	1.1	94
42	Systems level analysis of the Chlamydomonas reinhardtii metabolic network reveals variability in evolutionary co-conservation. Molecular BioSystems, 2016, 12, 2394-2407.	2.9	12
43	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. Cell, 2016, 167, 1734-1749.e22.	13.5	195
44	Pooledâ€matrix protein interaction screens using Barcode Fusion Genetics. Molecular Systems Biology, 2016, 12, 863.	3.2	102
45	Integrated network analysis reveals distinct regulatory roles of transcription factors and microRNAs. Rna, 2016, 22, 1663-1672.	1.6	36
46	A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. Cell, 2016, 164, 310-323.	13.5	106
47	BISQUE: locus- and variant-specific conversion of genomic, transcriptomic and proteomic database identifiers. Bioinformatics, 2016, 32, 1598-1600.	1.8	4
48	Studying Autism in Context. Cell Systems, 2015, 1, 312-313.	2.9	0
49	Phosphoproteomics Reveals Distinct Modes of Mec1/ATR Signaling during DNA Replication. Molecular Cell, 2015, 57, 1124-1132.	4.5	106
50	ENCAPP: elastic-net-based prognosis prediction and biomarker discovery for human cancers. BMC Genomics, 2015, 16, 263.	1.2	30
51	Trimethylation of Lys36 on H3 restricts gene expression change during aging and impacts life span. Genes and Development, 2015, 29, 718-731.	2.7	121
52	Regulatory network features in Listeria monocytogenesâ€"changing the way we talk. Frontiers in Cellular and Infection Microbiology, 2014, 4, 14.	1.8	23
53	A Massively Parallel Pipeline to Clone DNA Variants and Examine Molecular Phenotypes of Human Disease Mutations. PLoS Genetics, 2014, 10, e1004819.	1.5	47
54	Predicting Cancer Prognosis Using Functional Genomics Data Sets. Cancer Informatics, 2014, 13s5, CIN.S14064.	0.9	9

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55	Exploring mechanisms of human disease through structurally resolved protein interactome networks. Molecular BioSystems, 2014, 10, 9-17.	2.9	27
56	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
57	INstruct: a database of high-quality 3D structurally resolved protein interactome networks. Bioinformatics, 2013, 29, 1577-1579.	1.8	129
58	Cross-Species Protein Interactome Mapping Reveals Species-Specific Wiring of Stress Response Pathways. Science Signaling, 2013, 6, ra38.	1.6	47
59	Three-dimensional reconstruction of protein networks provides insight into human genetic disease. Nature Biotechnology, 2012, 30, 159-164.	9.4	378
60	HINT: High-quality protein interactomes and their applications in understanding human disease. BMC Systems Biology, 2012, 6, 92.	3.0	366
61	Next-generation sequencing to generate interactome datasets. Nature Methods, 2011, 8, 478-480.	9.0	258
62	Edgetic perturbation models of human inherited disorders. Molecular Systems Biology, 2009, 5, 321.	3.2	326
63	An empirical framework for binary interactome mapping. Nature Methods, 2009, 6, 83-90.	9.0	800
64	An experimentally derived confidence score for binary protein-protein interactions. Nature Methods, 2009, 6, 91-97.	9.0	397
65	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. Science, 2008, 322, 104-110.	6.0	1,297
66	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. Genes and Development, 2005, 19, 2816-2826.	2.7	443