

Haiyuan Yu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1243503/publications.pdf>

Version: 2024-02-01

66
papers

6,926
citations

147801

31
h-index

110387

64
g-index

85
all docs

85
docs citations

85
times ranked

10438
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. <i>Science</i> , 2008, 322, 104-110.	12.6	1,297
2	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	19.0	800
3	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. <i>Genes and Development</i> , 2005, 19, 2816-2826.	5.9	443
4	An experimentally derived confidence score for binary protein-protein interactions. <i>Nature Methods</i> , 2009, 6, 91-97.	19.0	397
5	Three-dimensional reconstruction of protein networks provides insight into human genetic disease. <i>Nature Biotechnology</i> , 2012, 30, 159-164.	17.5	378
6	HINT: High-quality protein interactomes and their applications in understanding human disease. <i>BMC Systems Biology</i> , 2012, 6, 92.	3.0	366
7	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235587.	12.6	341
8	Edgetic perturbation models of human inherited disorders. <i>Molecular Systems Biology</i> , 2009, 5, 321.	7.2	326
9	Next-generation sequencing to generate interactome datasets. <i>Nature Methods</i> , 2011, 8, 478-480.	19.0	258
10	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. <i>Cell</i> , 2016, 167, 1734-1749.e22.	28.9	195
11	Interactome INSIDER: a structural interactome browser for genomic studies. <i>Nature Methods</i> , 2018, 15, 107-114.	19.0	133
12	INstruct: a database of high-quality 3D structurally resolved protein interactome networks. <i>Bioinformatics</i> , 2013, 29, 1577-1579.	4.1	129
13	Trimethylation of Lys36 on H3 restricts gene expression change during aging and impacts life span. <i>Genes and Development</i> , 2015, 29, 718-731.	5.9	121
14	Network medicine links SARS-CoV-2/COVID-19 infection to brain microvascular injury and neuroinflammation in dementia-like cognitive impairment. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 110.	6.2	108
15	Phosphoproteomics Reveals Distinct Modes of Mec1/ATR Signaling during DNA Replication. <i>Molecular Cell</i> , 2015, 57, 1124-1132.	9.7	106
16	A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. <i>Cell</i> , 2016, 164, 310-323.	28.9	106
17	Pooled matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016, 12, 863.	7.2	102
18	In-depth and 3-dimensional exploration of the budding yeast phosphoproteome. <i>EMBO Reports</i> , 2021, 22, e51121.	4.5	99

#	ARTICLE	IF	CITATIONS
19	mutation3D: Cancer Gene Prediction Through Atomic Clustering of Coding Variants in the Structural Proteome. <i>Human Mutation</i> , 2016, 37, 447-456.	2.5	94
20	SAAMBE-3D: Predicting Effect of Mutations on Protein-Protein Interactions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2563.	4.1	66
21	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. <i>Nature Genetics</i> , 2018, 50, 1032-1040.	21.4	64
22	Transcription imparts architecture, function and logic to enhancer units. <i>Nature Genetics</i> , 2020, 52, 1067-1075.	21.4	60
23	Germline Lysine-Specific Demethylase 1 (<i>LSD1/KDM1A</i>) Mutations Confer Susceptibility to Multiple Myeloma. <i>Cancer Research</i> , 2018, 78, 2747-2759.	0.9	56
24	Loss of <i>TMEM106B</i> and <i>PCRN</i> leads to severe lysosomal abnormalities and neurodegeneration in mice. <i>EMBO Reports</i> , 2020, 21, e50219.	4.5	52
25	Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. <i>Nature Communications</i> , 2019, 10, 4141.	12.8	48
26	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	6.2	48
27	Cross-Species Protein Interactome Mapping Reveals Species-Specific Wiring of Stress Response Pathways. <i>Science Signaling</i> , 2013, 6, ra38.	3.6	47
28	A Massively Parallel Pipeline to Clone DNA Variants and Examine Molecular Phenotypes of Human Disease Mutations. <i>PLoS Genetics</i> , 2014, 10, e1004819.	3.5	47
29	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- κ B Signaling. <i>Cell Systems</i> , 2017, 5, 564-577.e12.	6.2	44
30	Inferring Protein-Protein Interaction Networks From Mass Spectrometry-Based Proteomic Approaches: A Mini-Review. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 805-811.	4.1	39
31	MaXLinker: Proteome-wide Cross-link Identifications with High Specificity and Sensitivity. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 554-568.	3.8	38
32	Integrated network analysis reveals distinct regulatory roles of transcription factors and microRNAs. <i>Rna</i> , 2016, 22, 1663-1672.	3.5	36
33	Genetics of extreme human longevity to guide drug discovery for healthy ageing. <i>Nature Metabolism</i> , 2020, 2, 663-672.	11.9	32
34	ENCAPP: elastic-net-based prognosis prediction and biomarker discovery for human cancers. <i>BMC Genomics</i> , 2015, 16, 263.	2.8	30
35	A comparison of experimental assays and analytical methods for genome-wide identification of active enhancers. <i>Nature Biotechnology</i> , 2022, 40, 1056-1065.	17.5	28
36	Exploring mechanisms of human disease through structurally resolved protein interactome networks. <i>Molecular BioSystems</i> , 2014, 10, 9-17.	2.9	27

#	ARTICLE	IF	CITATIONS
37	Structural basis of TRAPP3-mediated Rab1 activation. <i>EMBO Journal</i> , 2021, 40, e107607.	7.8	24
38	Regulatory network features in <i>Listeria monocytogenes</i> "changing the way we talk". <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 14.	3.9	23
39	Structure-based validation can drastically underestimate error rate in proteome-wide cross-linking mass spectrometry studies. <i>Nature Methods</i> , 2020, 17, 985-988.	19.0	23
40	De novo missense variants disrupting protein-protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. <i>Molecular Autism</i> , 2020, 11, 76.	4.9	19
41	Deep learning methods for 3D structural proteome and interactome modeling. <i>Current Opinion in Structural Biology</i> , 2022, 73, 102329.	5.7	19
42	Leveraging genetic interactions for adverse drug-drug interaction prediction. <i>PLoS Computational Biology</i> , 2019, 15, e1007068.	3.2	18
43	Glucosylation by the <i>Legionella</i> Effector SetA Promotes the Nuclear Localization of the Transcription Factor TFEB. <i>IScience</i> , 2020, 23, 101300.	4.1	18
44	SAAMBE-SEQ: a sequence-based method for predicting mutation effect on protein-protein binding affinity. <i>Bioinformatics</i> , 2021, 37, 992-999.	4.1	17
45	A 3D structural SARS-CoV-2-human interactome to explore genetic and drug perturbations. <i>Nature Methods</i> , 2021, 18, 1477-1488.	19.0	17
46	Implications of disease-related mutations at protein-protein interfaces. <i>Current Opinion in Structural Biology</i> , 2022, 72, 219-225.	5.7	17
47	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11836-11842.	7.1	16
48	Human MLH1/3 variants causing aneuploidy, pregnancy loss, and premature reproductive aging. <i>Nature Communications</i> , 2021, 12, 5005.	12.8	13
49	Systems level analysis of the <i>Chlamydomonas reinhardtii</i> metabolic network reveals variability in evolutionary co-conservation. <i>Molecular BioSystems</i> , 2016, 12, 2394-2407.	2.9	12
50	Variants in <i>RABL2A</i> causing male infertility and ciliopathy. <i>Human Molecular Genetics</i> , 2020, 29, 3402-3411.	2.9	11
51	Aging-related cell type-specific pathophysiologic immune responses that exacerbate disease severity in aged COVID-19 patients. <i>Aging Cell</i> , 2022, 21, e13544.	6.7	11
52	A multifaceted role of progranulin in regulating amyloid-beta dynamics and responses. <i>Life Science Alliance</i> , 2021, 4, e202000874.	2.8	10
53	Predicting Cancer Prognosis Using Functional Genomics Data Sets. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14064.	1.9	9
54	iRegNet3D: three-dimensional integrated regulatory network for the genomic analysis of coding and non-coding disease mutations. <i>Genome Biology</i> , 2017, 18, 10.	8.8	9

#	ARTICLE	IF	CITATIONS
55	Maximized quantitative phosphoproteomics allows high confidence dissection of the DNA damage signaling network. <i>Scientific Reports</i> , 2020, 10, 18056.	3.3	9
56	Revealing new therapeutic opportunities through drug target prediction: a class imbalance-tolerant machine learning approach. <i>Bioinformatics</i> , 2020, 36, 4490-4497.	4.1	9
57	Handcuffing intrinsically disordered regions in Mlh1-Pms1 disrupts mismatch repair. <i>Nucleic Acids Research</i> , 2021, 49, 9327-9341.	14.5	5
58	Progress in methodologies and quality control strategies in protein cross-linking mass spectrometry. <i>Proteomics</i> , 2021, 21, e2100145.	2.2	5
59	BISQUE: locus- and variant-specific conversion of genomic, transcriptomic and proteomic database identifiers. <i>Bioinformatics</i> , 2016, 32, 1598-1600.	4.1	4
60	Extracting complementary insights from molecular phenotypes for prioritization of disease-associated mutations. <i>Current Opinion in Systems Biology</i> , 2018, 11, 107-116.	2.6	4
61	GeMSTONE: orchestrated prioritization of human germline mutations in the cloud. <i>Nucleic Acids Research</i> , 2017, 45, W207-W214.	14.5	2
62	A full-proteome, interaction-specific characterization of mutational hotspots across human cancers. <i>Genome Research</i> , 2022, 32, 135-149.	5.5	2
63	GRAM: A GeneRALized Model to predict the molecular effect of a non-coding variant in a cell-type specific manner. <i>PLoS Genetics</i> , 2019, 15, e1007860.	3.5	1
64	Advancing discovery of risk-altering variants for complex diseases by functionally informed fine-mapping. <i>Neuron</i> , 2022, 110, 905-907.	8.1	1
65	Studying Autism in Context. <i>Cell Systems</i> , 2015, 1, 312-313.	6.2	0
66	Combining views for newly sequenced organisms. <i>Nature Machine Intelligence</i> , 2021, 3, 1011-1012.	16.0	0