Jingwen Yan

List of Publications by Year
in descending order

63 papers	1,108 citations	471509 17 h-index	434195 31 g-index
69 all docs	69 docs citations	69 times ranked	1423 citing authors

#	Article	IF	Citations
1	Global Brain Functional Network Connectivity in Infants With Prenatal Opioid Exposure. Frontiers in Pediatrics, 2022, 10, 847037.	1.9	15
2	Gene co-expression changes underlying the functional connectomic alterations in Alzheimer's disease. BMC Medical Genomics, 2022, 15, 92.	1.5	0
3	Integrative analysis of eQTL and GWAS summary statistics reveals transcriptomic alteration in Alzheimer brains. BMC Medical Genomics, 2022, 15, 93.	1.5	2
4	Integrative-omics for discovery of network-level disease biomarkers: a case study in Alzheimer's disease. Briefings in Bioinformatics, 2021, 22, .	6.5	8
5	Deep Fusion of Brain Structure-Function in Mild Cognitive Impairment. Medical Image Analysis, 2021, 72, 102082.	11.6	37
6	MoNET: an R package for multi-omic network analysis. Bioinformatics, 2021, , .	4.1	2
7	Genetic Influence Underlying Brain Connectivity Phenotype: A Study on Two Age-Specific Cohorts. Frontiers in Genetics, 2021, 12, 782953.	2.3	0
8	Biomarker-based polygenic risk scores for profiling genetic susceptibility in Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, .	0.8	0
9	Integrative analysis of eQTL and GWAS summary statistics reveals novel genes related to Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, .	0.8	0
10	Integrative -omics for discovery of network-level disease biomarkers for Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, .	0.8	0
11	Regional imaging genetic enrichment analysis. Bioinformatics, 2020, 36, 2554-2560.	4.1	16
12	Identification of functionally connected multi-omic biomarkers for Alzheimer's disease using modularity-constrained Lasso. PLoS ONE, 2020, 15, e0234748.	2.5	6
13	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Metabolism in Alzheimer's Disease. Cell Reports Medicine, 2020, 1, 100138.	6.5	102
14	Endophenotype driven polygenic risk scores for Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e046766.	0.8	0
15	Differential co-expression analysis reveals early stage transcriptomic decoupling in alzheimer's disease. BMC Medical Genomics, 2020, 13, 53.	1.5	4
16	Genome-wide Network-assisted Association and Enrichment Study of Amyloid Imaging Phenotype in Alzheimer's Disease. Current Alzheimer Research, 2020, 16, 1163-1174.	1.4	11
17	Multivariate genome wide association and network analysis of subcortical imaging phenotypes in Alzheimer's disease. BMC Genomics, 2020, 21, 896.	2.8	11
18	Progress in Polygenic Composite Scores in Alzheimer's and Other Complex Diseases. Trends in Genetics, 2019, 35, 371-382.	6.7	52

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19	Network approaches to systems biology analysis of complex disease: integrative methods for multi-omics data. Briefings in Bioinformatics, 2018, 19, 1370-1381.	6.5	185
20	A novel SCCA approach via truncated *__ℓ__* 1-norm and truncated group lasso for brain imaging genetics. Bioinformatics, 2018, 34, 278-285.	4.1	31
21	P2–253: *EP300* IS ASSOCIATED WITH ALTERED BILE ACIDS IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P772.	0.8	0
22	IC–P–075: GENETIC FINDINGS USING ADNI MULTIMODAL QUANTITATIVE PHENOTYPES: A 2017 UPDATE. Alzheimer's and Dementia, 2018, 14, P66.	0.8	0
23	Quantitative trait loci identification for brain endophenotypes via new additive model with random networks. Bioinformatics, 2018, 34, i866-i874.	4.1	11
24	Longitudinal Genotype–Phenotype Association Study through Temporal Structure Auto-Learning Predictive Model. Journal of Computational Biology, 2018, 25, 809-824.	1.6	6
25	Heritability Estimation of Reliable Connectomic Features. Lecture Notes in Computer Science, 2018, 11083, 58-66.	1.3	8
26	Network-based genome wide study of hippocampal imaging phenotype in Alzheimer's Disease to identify functional interaction modules. , 2017, 2017, 6170-6174.		1
27	Tissue-specific network-based genome wide study of amygdala imaging phenotypes to identify functional interaction modules. Bioinformatics, 2017, 33, 3250-3257.	4.1	23
28	Mining Outcome-relevant Brain Imaging Genetic Associations via Three-way Sparse Canonical Correlation Analysis in Alzheimer's Disease. Scientific Reports, 2017, 7, 44272.	3.3	44
29	Genome-wide association and interaction studies of CSF T-tau/Aβ42 ratio in ADNI cohort. Neurobiology of Aging, 2017, 57, 247.e1-247.e8.	3.1	34
30	Genome-wide network-based pathway analysis of CSF t-tau/Aβ1-42 ratio in the ADNI cohort. BMC Genomics, 2017, 18, 421.	2.8	13
31	Two-dimensional enrichment analysis for mining high-level imaging genetic associations. Brain Informatics, 2017, 4, 27-37.	3.0	13
32	Pattern Discovery in Brain Imaging Genetics via SCCA Modeling with a Generic Non-convex Penalty. Scientific Reports, 2017, 7, 14052.	3.3	9
33	[P2–120]: INVESTIGATION OF GENETIC INFLUENCES ON ATROPHY RATE DURING THE MCI DISEASE STAGE USING A BOOTSTRAP–ENHANCED SPARSE ASSOCIATION MODEL. Alzheimer's and Dementia, 2017, 13, P653.	0.8	0
34	[P2–220]: GENETIC FINDINGS USING ADNI MULTIMODAL QUANTITATIVE PHENOTYPES: A 2016 UPDATE. Alzheimer's and Dementia, 2017, 13, P694.	0.8	0
35	[F1–02–04]: INTEGRATING MULTI–MODALITY IMAGING AND MULTI–LAYER –OMICS TO ADVANCE THE SYSTEMS BIOLOGY OF ALZHEIMER's DISEASE. Alzheimer's and Dementia, 2017, 13, P175.	0.8	0
36	IDENTIFICATION OF DISCRIMINATIVE IMAGING PROTEOMICS ASSOCIATIONS IN ALZHEIMER'S DISEASE VIA A NOVEL SPARSE CORRELATION MODEL. , 2017, 22, 94-104.		14

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37	Identification of associations between genotypes and longitudinal phenotypes via temporally-constrained group sparse canonical correlation analysis. Bioinformatics, 2017, 33, i341-i349.	4.1	42
38	Longitudinal Genotype-Phenotype Association Study via Temporal Structure Auto-learning Predictive Model. Lecture Notes in Computer Science, 2017, 10229, 287-302.	1.3	8
39	Predicting Interrelated Alzheimer's Disease Outcomes via New Self-learned Structured Low-Rank Model. Lecture Notes in Computer Science, 2017, 10265, 198-209.	1.3	4
40	Identifying Associations Between Brain Imaging Phenotypes and Genetic Factors via a Novel Structured SCCA Approach. Lecture Notes in Computer Science, 2017, 10265, 543-555.	1.3	12
41	Transcriptome-Guided Imaging Genetic Analysis via a Novel Sparse CCA Algorithm. Lecture Notes in Computer Science, 2017, 10551, 220-229.	1.3	5
42	Sparse Canonical Correlation Analysis via truncated ℓ_1-norm with application to brain imaging genetics. , 2016, 2016, 707-711.		6
43	DIAGNOSIS-GUIDED METHOD FOR IDENTIFYING MULTI-MODALITY NEUROIMAGING BIOMARKERS ASSOCIATED WITH GENETIC RISK FACTORS IN ALZHEIMER'S DISEASE. , 2016, , .		4
44	Structured sparse CCA for brain imaging genetics via graph OSCAR. BMC Systems Biology, 2016, 10, 68.	3.0	9
45	Identifying Multimodal Intermediate Phenotypes Between Genetic Risk Factors and Disease Status in Alzheimer's Disease. Neuroinformatics, 2016, 14, 439-452.	2.8	26
46	Network-based analysis of genetic variants associated with hippocampal volume in Alzheimer's disease: a study of ADNI cohorts. BioData Mining, 2016, 9, 3.	4.0	28
47	Structured sparse canonical correlation analysis for brain imaging genetics: an improved GraphNet method. Bioinformatics, 2016, 32, 1544-1551.	4.1	96
48	P4-002: Genome-wide network-based pathway analysis of CSF biomarker t-tau in the ADNI cohort. , 2015, 11, P765-P765.		0
49	Genetic Interactions Explain Variance in Cingulate Amyloid Burden: An AV-45 PET Genome-Wide Association and Interaction Study in the ADNI Cohort. BioMed Research International, 2015, 2015, 1-11.	1.9	24
50	P1-009: The nav2 (neuron navigator 2) gene as a common genetic influence across correlated episodic memory performances. , 2015, 11, P339-P340.		0
51	Cortical surface biomarkers for predicting cognitive outcomes using group l2,1 norm. Neurobiology of Aging, 2015, 36, S185-S193.	3.1	43
52	Hippocampal transcriptome-guided genetic analysis of correlated episodic memory phenotypes in Alzheimer's disease. Frontiers in Genetics, 2015, 6, 117.	2.3	23
53	GN-SCCA: GraphNet Based Sparse Canonical Correlation Analysis for Brain Imaging Genetics. Lecture Notes in Computer Science, 2015, 9250, 275-284.	1.3	14
54	Joint identification of imaging and proteomics biomarkers of Alzheimer's disease using network-guided sparse learning. , 2014, 2014, 665-668.		1

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55	Data synthesis and method evaluation for brain imaging genetics. , 2014, 2014, 1202-1205.		6
56	Transcriptome-guided amyloid imaging genetic analysis via a novel structured sparse learning algorithm. Bioinformatics, 2014, 30, i564-i571.	4.1	57
57	IC-P-172: GENOME-WIDE PROTEIN INTERACTION GUIDED EPISTATIC ANALYSIS ON MEMORY PERFORMANCE: AN ADNI STUDY. , 2014, 10, P95-P96.		0
58	IC-P-173: EFFECTS OF NEWLY IDENTIFIED TOP AD CANDIDATE GENES ON MEMORY PERFORMANCE: SNP, GENE, AND EPISTASIS ANALYSES IN ADNI. , 2014, 10, P96-P97.		0
59	P1-230: EFFECTS OF NEWLY IDENTIFIED TOP AD CANDIDATE GENES ON MEMORY PERFORMANCE: SNP, GENE, AND EPISTASIS ANALYSES IN ADNI. , 2014, 10, P388-P388.		0
60	P1-213: GENOME-WIDE PROTEIN INTERACTION-GUIDED EPISTATIC ANALYSIS ON MEMORY PERFORMANCE: AN ADNI STUDY. , 2014, 10, P381-P382.		0
61	A Novel Structure-Aware Sparse Learning Algorithm for Brain Imaging Genetics. Lecture Notes in Computer Science, 2014, 17, 329-336.	1.3	36
62	IC-O1-03: Hippocampal transcriptome-guided gene-gene interaction of memory phenotype in MCI and Alzheimer's disease. , 2013, 9, P4-P4.		0
63	Network-Guided Sparse Learning for Predicting Cognitive Outcomes from MRI Measures. Lecture Notes in Computer Science, 2013, 8159, 202-210.	1.3	5