

Jingwen Yan

List of Publications by Year in descending order

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Version: 2024-02-01

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	Network approaches to systems biology analysis of complex disease: integrative methods for multi-omics data. <i>Briefings in Bioinformatics</i> , 2018, 19, 1370-1381.	6.5	185
2	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Metabolism in Alzheimer's Disease. <i>Cell Reports Medicine</i> , 2020, 1, 100138.	6.5	102
3	Structured sparse canonical correlation analysis for brain imaging genetics: an improved GraphNet method. <i>Bioinformatics</i> , 2016, 32, 1544-1551.	4.1	96
4	Transcriptome-guided amyloid imaging genetic analysis via a novel structured sparse learning algorithm. <i>Bioinformatics</i> , 2014, 30, i564-i571.	4.1	57
5	Progress in Polygenic Composite Scores in Alzheimer's and Other Complex Diseases. <i>Trends in Genetics</i> , 2019, 35, 371-382.	6.7	52
6	Mining Outcome-relevant Brain Imaging Genetic Associations via Three-way Sparse Canonical Correlation Analysis in Alzheimer's Disease. <i>Scientific Reports</i> , 2017, 7, 44272.	3.3	44
7	Cortical surface biomarkers for predicting cognitive outcomes using group l _{2,1} norm. <i>Neurobiology of Aging</i> , 2015, 36, S185-S193.	3.1	43
8	Identification of associations between genotypes and longitudinal phenotypes via temporally-constrained group sparse canonical correlation analysis. <i>Bioinformatics</i> , 2017, 33, i341-i349.	4.1	42
9	Deep Fusion of Brain Structure-Function in Mild Cognitive Impairment. <i>Medical Image Analysis</i> , 2021, 72, 102082.	11.6	37
10	A Novel Structure-Aware Sparse Learning Algorithm for Brain Imaging Genetics. <i>Lecture Notes in Computer Science</i> , 2014, 17, 329-336.	1.3	36
11	Genome-wide association and interaction studies of CSF T-tau/A β ²⁴² ratio in ADNI cohort. <i>Neurobiology of Aging</i> , 2017, 57, 247.e1-247.e8.	3.1	34
12	A novel SCCA approach via truncated ℓ_1 -norm and truncated group lasso for brain imaging genetics. <i>Bioinformatics</i> , 2018, 34, 278-285.	4.1	31
13	Network-based analysis of genetic variants associated with hippocampal volume in Alzheimer's disease: a study of ADNI cohorts. <i>BioData Mining</i> , 2016, 9, 3.	4.0	28
14	Identifying Multimodal Intermediate Phenotypes Between Genetic Risk Factors and Disease Status in Alzheimer's Disease. <i>Neuroinformatics</i> , 2016, 14, 439-452.	2.8	26
15	Genetic Interactions Explain Variance in Cingulate Amyloid Burden: An AV-45 PET Genome-Wide Association and Interaction Study in the ADNI Cohort. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	24
16	Hippocampal transcriptome-guided genetic analysis of correlated episodic memory phenotypes in Alzheimer's disease. <i>Frontiers in Genetics</i> , 2015, 6, 117.	2.3	23
17	Tissue-specific network-based genome wide study of amygdala imaging phenotypes to identify functional interaction modules. <i>Bioinformatics</i> , 2017, 33, 3250-3257.	4.1	23
18	Regional imaging genetic enrichment analysis. <i>Bioinformatics</i> , 2020, 36, 2554-2560.	4.1	16

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19	Global Brain Functional Network Connectivity in Infants With Prenatal Opioid Exposure. <i>Frontiers in Pediatrics</i> , 2022, 10, 847037.	1.9	15
20	IDENTIFICATION OF DISCRIMINATIVE IMAGING PROTEOMICS ASSOCIATIONS IN ALZHEIMER'S DISEASE VIA A NOVEL SPARSE CORRELATION MODEL. , 2017, 22, 94-104.		14
21	GN-SCCA: GraphNet Based Sparse Canonical Correlation Analysis for Brain Imaging Genetics. <i>Lecture Notes in Computer Science</i> , 2015, 9250, 275-284.	1.3	14
22	Genome-wide network-based pathway analysis of CSF t-tau/ β 1-42 ratio in the ADNI cohort. <i>BMC Genomics</i> , 2017, 18, 421.	2.8	13
23	Two-dimensional enrichment analysis for mining high-level imaging genetic associations. <i>Brain Informatics</i> , 2017, 4, 27-37.	3.0	13
24	Identifying Associations Between Brain Imaging Phenotypes and Genetic Factors via a Novel Structured SCCA Approach. <i>Lecture Notes in Computer Science</i> , 2017, 10265, 543-555.	1.3	12
25	Quantitative trait loci identification for brain endophenotypes via new additive model with random networks. <i>Bioinformatics</i> , 2018, 34, i866-i874.	4.1	11
26	Genome-wide Network-assisted Association and Enrichment Study of Amyloid Imaging Phenotype in Alzheimer's Disease. <i>Current Alzheimer Research</i> , 2020, 16, 1163-1174.	1.4	11
27	Multivariate genome wide association and network analysis of subcortical imaging phenotypes in Alzheimer's disease. <i>BMC Genomics</i> , 2020, 21, 896.	2.8	11
28	Structured sparse CCA for brain imaging genetics via graph OSCAR. <i>BMC Systems Biology</i> , 2016, 10, 68.	3.0	9
29	Pattern Discovery in Brain Imaging Genetics via SCCA Modeling with a Generic Non-convex Penalty. <i>Scientific Reports</i> , 2017, 7, 14052.	3.3	9
30	Integrative-omics for discovery of network-level disease biomarkers: a case study in Alzheimer's disease. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	8
31	Heritability Estimation of Reliable Connectomic Features. <i>Lecture Notes in Computer Science</i> , 2018, 11083, 58-66.	1.3	8
32	Longitudinal Genotype-Phenotype Association Study via Temporal Structure Auto-learning Predictive Model. <i>Lecture Notes in Computer Science</i> , 2017, 10229, 287-302.	1.3	8
33	Data synthesis and method evaluation for brain imaging genetics. , 2014, 2014, 1202-1205.		6
34	Sparse Canonical Correlation Analysis via truncated $\ell_{1/\alpha}$ -norm with application to brain imaging genetics. , 2016, 2016, 707-711.		6
35	Longitudinal Genotype-Phenotype Association Study through Temporal Structure Auto-Learning Predictive Model. <i>Journal of Computational Biology</i> , 2018, 25, 809-824.	1.6	6
36	Identification of functionally connected multi-omic biomarkers for Alzheimer's disease using modularity-constrained Lasso. <i>PLoS ONE</i> , 2020, 15, e0234748.	2.5	6

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37	Network-Guided Sparse Learning for Predicting Cognitive Outcomes from MRI Measures. Lecture Notes in Computer Science, 2013, 8159, 202-210.	1.3	5
38	Transcriptome-Guided Imaging Genetic Analysis via a Novel Sparse CCA Algorithm. Lecture Notes in Computer Science, 2017, 10551, 220-229.	1.3	5
39	DIAGNOSIS-GUIDED METHOD FOR IDENTIFYING MULTI-MODALITY NEUROIMAGING BIOMARKERS ASSOCIATED WITH GENETIC RISK FACTORS IN ALZHEIMER'S DISEASE. , 2016, , .		4
40	Differential co-expression analysis reveals early stage transcriptomic decoupling in alzheimerâ€™s disease. BMC Medical Genomics, 2020, 13, 53.	1.5	4
41	Predicting Interrelated Alzheimerâ€™s Disease Outcomes via New Self-learned Structured Low-Rank Model. Lecture Notes in Computer Science, 2017, 10265, 198-209.	1.3	4
42	MoNET: an R package for multi-omic network analysis. Bioinformatics, 2021, , .	4.1	2
43	Integrative analysis of eQTL and GWAS summary statistics reveals transcriptomic alteration in Alzheimer brains. BMC Medical Genomics, 2022, 15, 93.	1.5	2
44	Joint identification of imaging and proteomics biomarkers of Alzheimer's disease using network-guided sparse learning. , 2014, 2014, 665-668.		1
45	Network-based genome wide study of hippocampal imaging phenotype in Alzheimer's Disease to identify functional interaction modules. , 2017, 2017, 6170-6174.		1
46	IC-O1-03: Hippocampal transcriptome-guided gene-gene interaction of memory phenotype in MCI and Alzheimer's disease. , 2013, 9, P4-P4.		0
47	IC-P-172: GENOME-WIDE PROTEIN INTERACTION GUIDED EPISTATIC ANALYSIS ON MEMORY PERFORMANCE: AN ADNI STUDY. , 2014, 10, P95-P96.		0
48	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
49	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
50	P1-213: GENOME-WIDE PROTEIN INTERACTION-GUIDED EPISTATIC ANALYSIS ON MEMORY PERFORMANCE: AN ADNI STUDY. , 2014, 10, P381-P382.		0
51	P4-002: Genome-wide network-based pathway analysis of CSF biomarker t-tau in the ADNI cohort. , 2015, 11, P765-P765.		0
52	P1-009: The nav2 (neuron navigator 2) gene as a common genetic influence across correlated episodic memory performances. , 2015, 11, P339-P340.		0
53	[P2â€™120]: INVESTIGATION OF GENETIC INFLUENCES ON ATROPHY RATE DURING THE MCI DISEASE STAGE USING A BOOTSTRAPâ€™ENHANCED SPARSE ASSOCIATION MODEL. Alzheimer's and Dementia, 2017, 13, P653.	0.8	0
54	[P2â€™220]: GENETIC FINDINGS USING ADNI MULTIMODAL QUANTITATIVE PHENOTYPES: A 2016 UPDATE. Alzheimer's and Dementia, 2017, 13, P694.	0.8	0

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55	[F1â€“02â€“04]: INTEGRATING MULTIâ€“MODALITY IMAGING AND MULTIâ€“LAYER â€“OMICS TO ADVANCE THE SYSTEMS BIOLOGY OF ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2017, 13, P175.	0.8	0
56	P2â€“253: <i>EP300</i> IS ASSOCIATED WITH ALTERED BILE ACIDS IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P772.	0.8	0
57	ICâ€“Pâ€“075: GENETIC FINDINGS USING ADNI MULTIMODAL QUANTITATIVE PHENOTYPES: A 2017 UPDATE. Alzheimer's and Dementia, 2018, 14, P66.	0.8	0
58	Endophenotype driven polygenic risk scores for Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e046766.	0.8	0
59	Genetic Influence Underlying Brain Connectivity Phenotype: A Study on Two Age-Specific Cohorts. Frontiers in Genetics, 2021, 12, 782953.	2.3	0
60	Biomarkerâ€“based polygenic risk scores for profiling genetic susceptibility in Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, .	0.8	0
61	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
62	Integrative â€“omics for discovery of networkâ€“level disease biomarkers for Alzheimerâ€™s disease. Alzheimer's and Dementia, 2021, 17, .	0.8	0
63	Gene co-expression changes underlying the functional connectomic alterations in Alzheimerâ€™s disease. BMC Medical Genomics, 2022, 15, 92.	1.5	0