

# Dongdong Lin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/308752/publications.pdf>

Version: 2024-02-01

43  
papers

1,685  
citations

331670

21  
h-index

345221

36  
g-index

47  
all docs

47  
docs citations

47  
times ranked

3048  
citing authors

#	ARTICLE	IF	CITATIONS
1	Interaction among subsystems within default mode network diminished in schizophrenia patients: A dynamic connectivity approach. <i>Schizophrenia Research</i> , 2016, 170, 55-65.	2.0	197
2	Multimodal neuromarkers in schizophrenia via cognition-guided MRI fusion. <i>Nature Communications</i> , 2018, 9, 3028.	12.8	127
3	Dynamic functional connectivity impairments in early schizophrenia and clinical high-risk for psychosis. <i>NeuroImage</i> , 2018, 180, 632-645.	4.2	125
4	Correspondence between fMRI and SNP data by group sparse canonical correlation analysis. <i>Medical Image Analysis</i> , 2014, 18, 891-902.	11.6	123
5	Identifying dynamic functional connectivity biomarkers using GIG-ICA: Application to schizophrenia, schizoaffective disorder, and psychotic bipolar disorder. <i>Human Brain Mapping</i> , 2017, 38, 2683-2708.	3.6	111
6	Predicting individualized clinical measures by a generalized prediction framework and multimodal fusion of MRI data. <i>NeuroImage</i> , 2017, 145, 218-229.	4.2	95
7	Gender Differences in Connectome-based Predictions of Individualized Intelligence Quotient and Sub-domain Scores. <i>Cerebral Cortex</i> , 2020, 30, 888-900.	2.9	92
8	Group sparse canonical correlation analysis for genomic data integration. <i>BMC Bioinformatics</i> , 2013, 14, 245.	2.6	91
9	Connectome-based individualized prediction of temperament trait scores. <i>NeuroImage</i> , 2018, 183, 366-374.	4.2	73
10	Characterization of cross-tissue genetic-epigenetic effects and their patterns in schizophrenia. <i>Genome Medicine</i> , 2018, 10, 13.	8.2	51
11	SMRI Biomarkers Predict Electroconvulsive Treatment Outcomes: Accuracy with Independent Data Sets. <i>Neuropsychopharmacology</i> , 2018, 43, 1078-1087.	5.4	49
12	Sparse models for correlative and integrative analysis of imaging and genetic data. <i>Journal of Neuroscience Methods</i> , 2014, 237, 69-78.	2.5	45
13	Transplanting Fecal Virus-Like Particles Reduces High-Fat Diet-Induced Small Intestinal Bacterial Overgrowth in Mice. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 348.	3.9	40
14	Identifying functional network changing patterns in individuals at clinical high-risk for psychosis and patients with early illness schizophrenia: A group ICA study. <i>NeuroImage: Clinical</i> , 2018, 17, 335-346.	2.7	35
15	A Schizophrenia-Related Genetic-Brain-Cognition Pathway Revealed in a Large Chinese Population. <i>EBioMedicine</i> , 2018, 37, 471-482.	6.1	31
16	Adaptive sparse multiple canonical correlation analysis with application to imaging (epi)genomics study of schizophrenia. <i>IEEE Transactions on Biomedical Engineering</i> , 2017, 65, 1-1.	4.2	30
17	An integrative imputation method based on multi-omics datasets. <i>BMC Bioinformatics</i> , 2016, 17, 247.	2.6	29
18	Comparison of statistical methods for subnetwork detection in the integration of gene expression and protein interaction network. <i>BMC Bioinformatics</i> , 2017, 18, 149.	2.6	29

#	ARTICLE	IF	CITATIONS
19	Neural correlates of cognitive function and symptoms in attention-deficit/hyperactivity disorder in adults. <i>NeuroImage: Clinical</i> , 2018, 19, 374-383.	2.7	29
20	Cross-Tissue Exploration of Genetic and Epigenetic Effects on Brain Gray Matter in Schizophrenia. <i>Schizophrenia Bulletin</i> , 2018, 44, 443-452.	4.3	29
21	Structural Brain Architectures Match Intrinsic Functional Networks and Vary across Domains: A Study from 15â€™000+ Individuals. <i>Cerebral Cortex</i> , 2020, 30, 5460-5470.	2.9	28
22	Association between the oral microbiome and brain resting state connectivity in smokers. <i>NeuroImage</i> , 2019, 200, 121-131.	4.2	25
23	Integrating fMRI and SNP data for biomarker identification for schizophrenia with a sparse representation based variable selection method. <i>BMC Medical Genomics</i> , 2013, 6, S2.	1.5	24
24	Integrative analysis of multiple diverse omics datasets by sparse group multitask regression. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 62.	3.7	23
25	Parallel group ICA+ICA: Joint estimation of linked functional network variability and structural covariation with application to schizophrenia. <i>Human Brain Mapping</i> , 2019, 40, 3795-3809.	3.6	23
26	Comparison of IVA and GIG-ICA in Brain Functional Network Estimation Using fMRI Data. <i>Frontiers in Neuroscience</i> , 2017, 11, 267.	2.8	22
27	Fast and Accurate Detection of Complex Imaging Genetics Associations Based on Greedy Projected Distance Correlation. <i>IEEE Transactions on Medical Imaging</i> , 2018, 37, 860-870.	8.9	17
28	Variability in Resting State Network and Functional Network Connectivity Associated With Schizophrenia Genetic Risk: A Pilot Study. <i>Frontiers in Neuroscience</i> , 2018, 12, 114.	2.8	17
29	Opposite Epigenetic Associations With Alcohol Use and Exercise Intervention. <i>Frontiers in Psychiatry</i> , 2018, 9, 594.	2.6	15
30	Brain function, structure and genomic data are linked but show different sensitivity to duration of illness and disease stage in schizophrenia. <i>NeuroImage: Clinical</i> , 2019, 23, 101887.	2.7	14
31	An improved sparse representation model with structural information for Multicolour Fluorescence In-Situ Hybridization (M-FISH) image classification. <i>BMC Systems Biology</i> , 2013, 7, S5.	3.0	8
32	A Systemic Analysis of Transcriptomic and Epigenomic Data To Reveal Regulation Patterns for Complex Disease. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2271-2279.	1.8	7
33	Exploring different impaired speed of genetic-related brain function and structures in schizophrenic progress using multimodal analysis*. , 2018, 2018, 4126-4129.		4
34	Genetics Modulate Gray Matter Variation Beyond Disease Burden in Prodromal Huntingtonâ€™s Disease. <i>Frontiers in Neurology</i> , 2018, 9, 190.	2.4	4
35	CHOmics: A web-based tool for multi-omics data analysis and interactive visualization in CHO cell lines. <i>PLoS Computational Biology</i> , 2020, 16, e1008498.	3.2	4
36	Editorial: Identifying Neuroimaging-Based Markers for Distinguishing Brain Disorders. <i>Frontiers in Neuroscience</i> , 2020, 14, 327.	2.8	1

#	ARTICLE	IF	CITATIONS
37	Segmentation of multicolor fluorescence in situ hybridization images using an improved fuzzy C-means clustering algorithm by incorporating both spatial and spectral information. Journal of Medical Imaging, 2017, 4, 1.	1.5	1
38	Title is missing!. , 2020, 16, e1008498.		0
39	Title is missing!. , 2020, 16, e1008498.		0
40	Title is missing!. , 2020, 16, e1008498.		0
41	Title is missing!. , 2020, 16, e1008498.		0
42	Title is missing!. , 2020, 16, e1008498.		0
43	Title is missing!. , 2020, 16, e1008498.		0