

Joshua Faskowitz

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

2,942
citations

394421

19
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330143

37
g-index

66
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66
docs citations

66
times ranked

5193
citing authors

#	ARTICLE	IF	CITATIONS
1	Uncovering individual differences in fine-scale dynamics of functional connectivity. <i>Cerebral Cortex</i> , 2023, 33, 2375-2394.	2.9	15
2	Edges in brain networks: Contributions to models of structure and function. <i>Network Neuroscience</i> , 2022, 6, 1-28.	2.6	30
3	Multitask brain network reconfiguration is inversely associated with human intelligence. <i>Cerebral Cortex</i> , 2022, 32, 4172-4182.	2.9	19
4	Effects of diffusion signal modeling and segmentation approaches on subthalamic nucleus parcellation. <i>NeuroImage</i> , 2022, 250, 118959.	4.2	3
5	Cortico-subcortical interactions in overlapping communities of edge functional connectivity. <i>NeuroImage</i> , 2022, 250, 118971.	4.2	14
6	Individualized event structure drives individual differences in whole-brain functional connectivity. <i>NeuroImage</i> , 2022, 252, 118993.	4.2	46
7	Local structure-function relationships in human brain networks across the lifespan. <i>Nature Communications</i> , 2022, 13, 2053.	12.8	58
8	Edge-centric analysis of stroke patients: An alternative approach for biomarkers of lesion recovery. <i>NeuroImage: Clinical</i> , 2022, 35, 103055.	2.7	15
9	Dynamic expression of brain functional systems disclosed by fine-scale analysis of edge time series. <i>Network Neuroscience</i> , 2021, 5, 405-433.	2.6	54
10	Collegiate athlete brain data for white matter mapping and network neuroscience. <i>Scientific Data</i> , 2021, 8, 56.	5.3	4
11	Subject identification using edge-centric functional connectivity. <i>NeuroImage</i> , 2021, 238, 118204.	4.2	24
12	Mapping individual differences across brain network structure to function and behavior with connectome embedding. <i>NeuroImage</i> , 2021, 242, 118469.	4.2	23
13	Association of Immunosuppression and Viral Load With Subcortical Brain Volume in an International Sample of People Living With HIV. <i>JAMA Network Open</i> , 2021, 4, e2031190.	5.9	16
14	Modularity maximization as a flexible and generic framework for brain network exploratory analysis. <i>NeuroImage</i> , 2021, 244, 118607.	4.2	22
15	The diversity and multiplexity of edge communities within and between brain systems. <i>Cell Reports</i> , 2021, 37, 110032.	6.4	25
16	Ageing relates to a disproportionately weaker functional architecture of brain networks during rest and task states. <i>NeuroImage</i> , 2020, 209, 116521.	4.2	29
17	Mapping the community structure of the rat cerebral cortex with weighted stochastic block modeling. <i>Brain Structure and Function</i> , 2020, 225, 71-84.	2.3	13
18	Edge-centric functional network representations of human cerebral cortex reveal overlapping system-level architecture. <i>Nature Neuroscience</i> , 2020, 23, 1644-1654.	14.8	167

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19	High-amplitude fluctuations in cortical activity drive functional connectivity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28393-28401.	7.1	159
20	The reliability and heritability of cortical folds and their genetic correlations across hemispheres. Communications Biology, 2020, 3, 510.	4.4	42
21	The modular organization of brain cortical connectivity across the human lifespan. NeuroImage, 2020, 218, 116974.	4.2	52
22	Multi-Site Meta-Analysis of Morphometry. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1508-1514.	3.0	7
23	Age differences in specific neural connections within the Default Mode Network underlie theory of mind. NeuroImage, 2019, 191, 269-277.	4.2	26
24	Reply to: New Meta- and Mega-analyses of Magnetic Resonance Imaging Findings in Schizophrenia: Do They Really Increase Our Knowledge About the Nature of the Disease Process?. Biological Psychiatry, 2019, 85, e35-e39.	1.3	5
25	Systemic inflammation as a predictor of brain aging: Contributions of physical activity, metabolic risk, and genetic risk. NeuroImage, 2018, 172, 118-129.	4.2	82
26	Widespread white matter microstructural differences in schizophrenia across 4322 individuals: results from the ENIGMA Schizophrenia DTI Working Group. Molecular Psychiatry, 2018, 23, 1261-1269.	7.9	522
27	Weighted Stochastic Block Models of the Human Connectome across the Life Span. Scientific Reports, 2018, 8, 12997.	3.3	70
28	Multisite Metaanalysis of Image-Wide Genome-Wide Associations With Morphometry. , 2018, , 1-23.		1
29	Genetic Connectivityâ€“Correlated Genetic Control of Cortical Thickness, Brain Volume, and White Matter. , 2018, , 25-43.		1
30	Cortical Brain Abnormalities in 4474 Individuals With Schizophrenia and 5098 Control Subjects via the Enhancing Neuro Imaging Genetics Through Meta Analysis (ENIGMA) Consortium. Biological Psychiatry, 2018, 84, 644-654.	1.3	627
31	Voxelwise meta-analysis of brain structural associations with genome-wide polygenic risk for Alzheimerâ€™s disease. , 2018, , .		4
32	Sulcal-based morphometry in Parkinsonâ€™s disease: a study of reliability and disease effects. , 2018, , .		1
33	Cortical connectome registration using spherical demons. , 2017, , .		0
34	Continuous representations of brain connectivity using spatial point processes. Medical Image Analysis, 2017, 41, 32-39.	11.6	16
35	Utilizing brain measures for large-scale classification of autism applying EPIC. Proceedings of SPIE, 2017, , .	0.8	0
36	Relationship of a common OXTR gene variant to brain structure and default mode network function in healthy humans. NeuroImage, 2017, 147, 500-506.	4.2	21

#	ARTICLE	IF	CITATIONS
37	Classifying Phenotypes Based on the Community Structure of Human Brain Networks. Lecture Notes in Computer Science, 2017, , 3-11.	1.3	8
38	Diverging volumetric trajectories following pediatric traumatic brain injury. NeuroImage: Clinical, 2017, 15, 125-135.	2.7	28
39	A comparison of network definitions for detecting sex differences in brain connectivity using Support Vector Machines. , 2017, 2017, 961-965.		0
40	Structural connectome validation using pairwise classification. , 2017, , .		0
41	Partitioning heritability analysis reveals a shared genetic basis of brain anatomy and schizophrenia. Molecular Psychiatry, 2016, 21, 1680-1689.	7.9	69
42	Population learning of structural connectivity by white matter encoding and decoding. , 2016, , .		1
43	The heritability of the functional connectome is robust to common nonlinear registration methods. Proceedings of SPIE, 2016, , .	0.8	0
44	Embedded sparse representation of fMRI data via group-wise dictionary optimization. Proceedings of SPIE, 2016, , .	0.8	0
45	Comparison of template registration methods for multi-site meta-analysis of brain morphometry. Proceedings of SPIE, 2016, , .	0.8	0
46	Subcortical volumetric abnormalities in bipolar disorder. Molecular Psychiatry, 2016, 21, 1710-1716.	7.9	400
47	Heritability and reliability of automatically segmented human hippocampal formation subregions. NeuroImage, 2016, 128, 125-137.	4.2	107
48	A Continuous Model of Cortical Connectivity. Lecture Notes in Computer Science, 2016, 9900, 157-165.	1.3	7
49	Multi-modal Registration Improves Group Discrimination in Pediatric Traumatic Brain Injury. Lecture Notes in Computer Science, 2016, 10154, 32-42.	1.3	0
50	Blockmodels for connectome analysis. Proceedings of SPIE, 2015, , .	0.8	11
51	Genetic analysis of structural brain connectivity using DICCCOL models of diffusion MRI in 522 twins. , 2015, 2015, 1167-1171.		2