## Jae-Yoon Jung

List of Publications by Year in descending order

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840776 552781 46 931 11 26 citations h-index g-index papers 51 51 51 1767 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Inherited and De Novo Genetic Risk for Autism Impacts Shared Networks. Cell, 2019, 178, 850-866.e26.	28.9	326
2	Use of Artificial Intelligence to Shorten the Behavioral Diagnosis of Autism. PLoS ONE, 2012, 7, e43855.	2.5	145
3	Genotator: A disease-agnostic tool for genetic annotation of disease. BMC Medical Genomics, 2010, 3, 50.	1.5	47
4	Roundup 2.0: enabling comparative genomics for over 1800 genomes. Bioinformatics, 2012, 28, 715-716.	4.1	38
5	Indels in SARS-CoV-2 occur at template-switching hotspots. BioData Mining, 2021, 14, 20.	4.0	26
6	Evolutionary Design of Neural Network Architectures Using a Descriptive Encoding Language. IEEE Transactions on Evolutionary Computation, 2006, 10, 676-688.	10.0	25
7	Selection of trustworthy crowd workers for telemedical diagnosis of pediatric autism spectrum disorder. , 2020, , .		25
8	Comorbid Analysis of Genes Associated with Autism Spectrum Disorders Reveals Differential Evolutionary Constraints. PLoS ONE, 2016, 11, e0157937.	2.5	24
9	Improved Digital Therapy for Developmental Pediatrics Using Domain-Specific Artificial Intelligence: Machine Learning Study. JMIR Pediatrics and Parenting, 2022, 5, e26760.	1.6	24
10	COSMOS: Python library for massively parallel workflows. Bioinformatics, 2014, 30, 2956-2958.	4.1	23
11	Identification of Social Engagement Indicators Associated With Autism Spectrum Disorder Using a Game-Based Mobile App: Comparative Study of Gaze Fixation and Visual Scanning Methods. Journal of Medical Internet Research, 2022, 24, e31830.	4.3	23
12	Autworks: a cross-disease network biology application for Autism and related disorders. BMC Medical Genomics, 2012, 5, 56.	1.5	22
13	Scalable and cost-effective NGS genotyping in the cloud. BMC Medical Genomics, 2015, 8, 64.	1.5	19
14	Genetic Association of Attention-Deficit/Hyperactivity Disorder and Major Depression With Suicidal Ideation and Attempts in Children: The Adolescent Brain Cognitive Development Study. Biological Psychiatry, 2022, 92, 236-245.	1.3	17
15	Training Affective Computer Vision Models by Crowdsourcing Soft-Target Labels. Cognitive Computation, 2021, 13, 1363-1373.	5.2	16
16	Cross-Disorder Genomics Data Analysis Elucidates a Shared Genetic Basis Between Major Depression and Osteoarthritis Pain. Frontiers in Genetics, 2021, 12, 687687.	2.3	14
17	A literature search tool for intelligent extraction of disease-associated genes. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 399-405.	4.4	13
18	Cloud Computing for Comparative Genomics with Windows Azure Platform. Evolutionary Bioinformatics, 2012, 8, EBO.S9946.	1.2	9

#	Article	IF	Citations
19	Estimating sequencing error rates using families. BioData Mining, 2021, 14, 27.	4.0	9
20	Analysis of Sex and Recurrence Ratios in Simplex and Multiplex Autism Spectrum Disorder Implicates Sex-Specific Alleles as Inheritance Mechanism. , 2018, , .		8
21	Game theoretic centrality: a novel approach to prioritize disease candidate genes by combining biological networks with the Shapley value. BMC Bioinformatics, 2020, 21, 356.	2.6	8
22	Outgroup Machine Learning Approach Identifies Single Nucleotide Variants in Noncoding DNA Associated with Autism Spectrum Disorder. , 2018, , .		6
23	Genomewide alteration of histone H3K4 methylation underlies genetic vulnerability to psychopathology. Journal of Genetics, 2021, 100, 1.	0.7	6
24	A hierarchical ensemble model for automated assessment of stroke impairment. , 2008, , .		4
25	Coalitional Game Theory Facilitates Identification of Non-Coding Variants Associated With Autism. Biomedical Informatics Insights, 2019, 11, 117822261983285.	4.6	4
26	miR-92a Suppresses Mushroom Body-Dependent Memory Consolidation in Drosophila. ENeuro, 2020, 7, ENEURO.0224-20.2020.	1.9	4
27	Functionally Informative Tag SNP Selection Using a Pareto-Optimal Approach. Advances in Experimental Medicine and Biology, 2010, 680, 173-180.	1.6	4
28	Selection of trustworthy crowd workers for telemedical diagnosis of pediatric autism spectrum disorder. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2021, 26, 14-25.	0.7	4
29	Recombination of common sensory-motor impairment evaluation techniques using a committee of classifiers., 2009, 2009, 857-60.		3
30	Phylogenetically informed logic relationships improve detection of biological network organization. BMC Bioinformatics, 2011, 12, 476.	2.6	3
31	The Automated Design of Artificial Neural Networks Using Evolutionary Computation. Studies in Computational Intelligence, 2008, , 19-41.	0.9	3
32	Detecting biological network organization and functional gene orthologs. Bioinformatics, 2011, 27, 2919-2920.	4.1	2
33	COSMOS: cloud enabled NGS analysis. BMC Bioinformatics, 2015, 16, A2.	2.6	2
34	A Method for Localizing Non-Reference Sequences to the Human Genome. , 2021, , .		2
35	Causal Modeling to Mitigate Selection Bias and Unmeasured Confounding in Internet-Based Epidemiology of COVID-19: Model Development and Validation. JMIR Public Health and Surveillance, 2022, 8, e31306.	2.6	2
36	Trial map: A visualization approach for verification of stroke impairment assessment database. , 2008, , .		1

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37	Nested evolution of an autonomous agent using descriptive encoding. , 2008, , .		1
38	Evolving an autonomous agent for non-Markovian reinforcement learning. , 2009, , .		1
39	Coalitional game theory as a promising approach to identify candidate autism genes. , 2018, , .		1
40	Improved Digital Therapy for Developmental Pediatrics Using Domain-Specific Artificial Intelligence. SSRN Electronic Journal, $0, , .$	0.4	1
41	A Neural Network Model for Maximizing Prediction Accuracy in Haplotype Tagging SNP Selection. , 0, , .		O
42	A Neural Network Model for Maximizing Prediction Accuracy in Haplotype Tagging SNP Selection. , 2006, , .		0
43	Feature selection and classification for assessment of chronic stroke impairment. , 2008, , .		O
44	A maximum flow-based network approach for identification of stable noncoding biomarkers associated with the multigenic neurological condition, autism. BioData Mining, 2021, 14, 28.	4.0	0
45	12. Elucidating the Genetic Basis of H3-K4 Methylation in Schizophrenia and Bipolar Disorder. Biological Psychiatry, 2017, 81, S5-S6.	1.3	0
46	Genetic Networks of Complex Disorders: from a Novel Search Engine for PubMed Article Database. AMIA Summits on Translational Science Proceedings, 2013, 2013, 99.	0.4	O