

# Chenglong Yu

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

1,096  
citations

586496

16  
h-index

488211

31  
g-index

49  
all docs

49  
docs citations

49  
times ranked

1270  
citing authors

#	ARTICLE	IF	CITATIONS
1	Does genetic predisposition modify the effect of lifestyle-related factors on DNA methylation?. <i>Epigenetics</i> , 2022, 17, 1838-1847.	1.3	2
2	Rare Functional Variants Associated with Antidepressant Remission in Mexican-Americans. <i>Journal of Affective Disorders</i> , 2021, 279, 491-500.	2.0	3
3	VTRNA2-1: Genetic Variation, Heritable Methylation and Disease Association. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2535.	1.8	15
4	Epigenetic Drift Association with Cancer Risk and Survival, and Modification by Sex. <i>Cancers</i> , 2021, 13, 1881.	1.7	9
5	Smoking Methylation Marks for Prediction of Urothelial Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 2197-2206.	1.1	4
6	Biological Aging Measures Based on Blood DNA Methylation and Risk of Cancer: A Prospective Study. <i>JNCI Cancer Spectrum</i> , 2021, 5, pkaa109.	1.4	40
7	Repeatability of methylation measures using a QIaseq targeted methyl panel and comparison with the Illumina HumanMethylation450 assay. <i>BMC Research Notes</i> , 2021, 14, 394.	0.6	2
8	Association of FOXO3 Blood DNA Methylation with Cancer Risk, Cancer Survival, and Mortality. <i>Cells</i> , 2021, 10, 3384.	1.8	6
9	Detecting Genotype-Population Interaction Effects by Ancestry Principal Components. <i>Frontiers in Genetics</i> , 2020, 11, 379.	1.1	2
10	Investigation of short tandem repeats in major depression using whole-genome sequencing data. <i>Journal of Affective Disorders</i> , 2018, 232, 305-309.	2.0	10
11	Control effect of periodic variation on the growth of harmful algal bloom causative species. <i>Communications in Nonlinear Science and Numerical Simulation</i> , 2018, 54, 185-201.	1.7	3
12	Genetic clustering of depressed patients and normal controls based on single-nucleotide variant proportion. <i>Journal of Affective Disorders</i> , 2018, 227, 450-454.	2.0	7
13	On a two-dimensional risk model with time-dependent claim sizes and risky investments. <i>Journal of Computational and Applied Mathematics</i> , 2018, 344, 367-380.	1.1	4
14	Low-frequency and rare variants may contribute to elucidate the genetics of major depressive disorder. <i>Translational Psychiatry</i> , 2018, 8, 70.	2.4	25
15	Natural Vector Method for Virus Phylogenetic Classification: A Mini- Review. <i>Current Bioinformatics</i> , 2018, 13, 332-336.	0.7	1
16	Single-nucleotide variant proportion in genes: a new concept to explore major depression based on DNA sequencing data. <i>Journal of Human Genetics</i> , 2017, 62, 577-580.	1.1	11
17	Whole-genome single nucleotide variant distribution on genomic regions and its relationship to major depression. <i>Psychiatry Research</i> , 2017, 252, 75-79.	1.7	12
18	A latent genetic subtype of major depression identified by whole-exome genotyping data in a Mexican-American cohort. <i>Translational Psychiatry</i> , 2017, 7, e1134-e1134.	2.4	19

#	ARTICLE	IF	CITATIONS
19	A novel strategy for clustering major depression individuals using whole-genome sequencing variant data. <i>Scientific Reports</i> , 2017, 7, 44389.	1.6	14
20	The PHF21B gene is associated with major depression and modulates the stress response. <i>Molecular Psychiatry</i> , 2017, 22, 1015-1025.	4.1	56
21	Virus Database and Online Inquiry System Based on Natural Vectors. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431774666.	0.6	7
22	Investigation of copy number variation in subjects with major depression based on whole-genome sequencing data. <i>Journal of Affective Disorders</i> , 2017, 220, 38-42.	2.0	9
23	Control of finite-time anti-synchronization for variable-order fractional chaotic systems with unknown parameters. <i>Nonlinear Dynamics</i> , 2016, 86, 1967-1980.	2.7	16
24	Clustering DNA sequences using the out-of-place measure with reduced n-grams. <i>Journal of Theoretical Biology</i> , 2016, 406, 61-72.	0.8	13
25	GENERALIZED WEIERSTRASSâ€™MANDELBROT FUNCTION MODEL FOR ACTUAL STOCKS MARKETS INDEXES WITH NONLINEAR CHARACTERISTICS. <i>Fractals</i> , 2015, 23, 1550006.	1.8	15
26	A new method to cluster DNA sequences using Fourier power spectrum. <i>Journal of Theoretical Biology</i> , 2015, 372, 135-145.	0.8	67
27	Serum Uric Acid Levels and Risk of Metabolic Syndrome: A Dose-Response Meta-Analysis of Prospective Studies. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015, 100, 4198-4207.	1.8	180
28	PuzzleCluster: A Novel Unsupervised Clustering Algorithm for Binning DNA Fragments in Metagenomics. <i>Current Bioinformatics</i> , 2015, 10, 231-252.	0.7	6
29	DFA7, a New Method to Distinguish between Intron-Containing and Intronless Genes. <i>PLoS ONE</i> , 2014, 9, e101363.	1.1	13
30	Control of Weierstrassâ€™Mandelbrot Function Model with Morlet Wavelets. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 2014, 24, 1450121.	0.7	2
31	Viral genome phylogeny based on Lempelâ€™Ziv complexity and Hausdorff distance. <i>Journal of Theoretical Biology</i> , 2014, 348, 12-20.	0.8	17
32	Global comparison of multiple-segmented viruses in 12-dimensional genome space. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 29-36.	1.2	32
33	Chaotic behaviour of nonlinear coupled reactionâ€™diffusion system in four-dimensional space. <i>Pramana - Journal of Physics</i> , 2014, 82, 995-1009.	0.9	8
34	Control effects of Morlet wavelet term on Weierstrassâ€™Mandelbrot function model. <i>Indian Journal of Physics</i> , 2014, 88, 867-874.	0.9	6
35	Protein sequence comparison based on K-string dictionary. <i>Gene</i> , 2013, 529, 250-256.	1.0	33
36	Protein space: A natural method for realizing the nature of protein universe. <i>Journal of Theoretical Biology</i> , 2013, 318, 197-204.	0.8	43

#	ARTICLE	IF	CITATIONS
37	Real Time Classification of Viruses in 12 Dimensions. PLoS ONE, 2013, 8, e64328.	1.1	59
38	Protein map: An alignment-free sequence comparison method based on various properties of amino acids. Gene, 2011, 486, 110-118.	1.0	43
39	A Novel Method of Characterizing Genetic Sequences: Genome Space with Biological Distance and Applications. PLoS ONE, 2011, 6, e17293.	1.1	89
40	DNA sequence comparison by a novel probabilistic method. Information Sciences, 2011, 181, 1484-1492.	4.0	47
41	A Novel Construction of Genome Space with Biological Geometry. DNA Research, 2010, 17, 155-168.	1.5	55
42	A Protein Map and Its Application. DNA and Cell Biology, 2008, 27, 241-250.	0.9	61