## Chenglong Yu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Does genetic predisposition modify the effect of lifestyle-related factors on DNA methylation?. Epigenetics, 2022, 17, 1838-1847.	2.7	2
2	Rare Functional Variants Associated with Antidepressant Remission in Mexican-Americans. Journal of Affective Disorders, 2021, 279, 491-500.	4.1	3
3	VTRNA2-1: Genetic Variation, Heritable Methylation and Disease Association. International Journal of Molecular Sciences, 2021, 22, 2535.	4.1	15
4	Epigenetic Drift Association with Cancer Risk and Survival, and Modification by Sex. Cancers, 2021, 13, 1881.	3.7	9
5	Smoking Methylation Marks for Prediction of Urothelial Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2197-2206.	2.5	4
6	Biological Aging Measures Based on Blood DNA Methylation and Risk of Cancer: A Prospective Study. JNCI Cancer Spectrum, 2021, 5, pkaa109.	2.9	40
7	Repeatability of methylation measures using a QIAseq targeted methyl panel and comparison with the Illumina HumanMethylation450 assay. BMC Research Notes, 2021, 14, 394.	1.4	2
8	Association of FOXO3 Blood DNA Methylation with Cancer Risk, Cancer Survival, and Mortality. Cells, 2021, 10, 3384.	4.1	6
9	Detecting Genotype-Population Interaction Effects by Ancestry Principal Components. Frontiers in Genetics, 2020, 11, 379.	2.3	2
10	Investigation of short tandem repeats in major depression using whole-genome sequencing data. Journal of Affective Disorders, 2018, 232, 305-309.	4.1	10
11	Control effect of periodic variation on the growth of harmful algal bloom causative species. Communications in Nonlinear Science and Numerical Simulation, 2018, 54, 185-201.	3.3	3
12	Genetic clustering of depressed patients and normal controls based on single-nucleotide variant proportion. Journal of Affective Disorders, 2018, 227, 450-454.	4.1	7
13	On a two-dimensional risk model with time-dependent claim sizes and risky investments. Journal of Computational and Applied Mathematics, 2018, 344, 367-380.	2.0	4
14	Low-frequency and rare variants may contribute to elucidate the genetics of major depressive disorder. Translational Psychiatry, 2018, 8, 70.	4.8	25
15	Natural Vector Method for Virus Phylogenetic Classification: A Mini- Review. Current Bioinformatics, 2018, 13, 332-336.	1.5	1
16	Single-nucleotide variant proportion in genes: a new concept to explore major depression based on DNA sequencing data. Journal of Human Genetics, 2017, 62, 577-580.	2.3	11
17	Whole-genome single nucleotide variant distribution on genomic regions and its relationship to major depression. Psychiatry Research, 2017, 252, 75-79.	3.3	12
18	A latent genetic subtype of major depression identified by whole-exome genotyping data in a Mexican-American cohort. Translational Psychiatry, 2017, 7, e1134-e1134.	4.8	19

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19	A novel strategy for clustering major depression individuals using whole-genome sequencing variant data. Scientific Reports, 2017, 7, 44389.	3.3	14
20	The PHF21B gene is associated with major depression and modulates the stress response. Molecular Psychiatry, 2017, 22, 1015-1025.	7.9	56
21	Virus Database and Online Inquiry System Based on Natural Vectors. Evolutionary Bioinformatics, 2017, 13, 117693431774666.	1.2	7
22	Investigation of copy number variation in subjects with major depression based on whole-genome sequencing data. Journal of Affective Disorders, 2017, 220, 38-42.	4.1	9
23	Control of finite-time anti-synchronization for variable-order fractional chaotic systems with unknown parameters. Nonlinear Dynamics, 2016, 86, 1967-1980.	5.2	16
24	Clustering DNA sequences using the out-of-place measure with reduced n-grams. Journal of Theoretical Biology, 2016, 406, 61-72.	1.7	13
25	GENERALIZED WEIERSTRASS–MANDELBROT FUNCTION MODEL FOR ACTUAL STOCKS MARKETS INDEXES WITH NONLINEAR CHARACTERISTICS. Fractals, 2015, 23, 1550006.	3.7	15
26	A new method to cluster DNA sequences using Fourier power spectrum. Journal of Theoretical Biology, 2015, 372, 135-145.	1.7	67
27	Serum Uric Acid Levels and Risk of Metabolic Syndrome: A Dose-Response Meta-Analysis of Prospective Studies. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 4198-4207.	3.6	180
28	PuzzleCluster: A Novel Unsupervised Clustering Algorithm for Binning DNA Fragments in Metagenomics. Current Bioinformatics, 2015, 10, 231-252.	1.5	6
29	DFA7, a New Method to Distinguish between Intron-Containing and Intronless Genes. PLoS ONE, 2014, 9, e101363.	2.5	13
30	Control of Weierstrass–Mandelbrot Function Model with Morlet Wavelets. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2014, 24, 1450121.	1.7	2
31	Viral genome phylogeny based on Lempel–Ziv complexity and Hausdorff distance. Journal of Theoretical Biology, 2014, 348, 12-20.	1.7	17
32	Global comparison of multiple-segmented viruses in 12-dimensional genome space. Molecular Phylogenetics and Evolution, 2014, 81, 29-36.	2.7	32
33	Chaotic behaviour of nonlinear coupled reaction–diffusion system in four-dimensional space. Pramana - Journal of Physics, 2014, 82, 995-1009.	1.8	8
34	Control effects of Morlet wavelet term on Weierstrass–Mandelbrot function model. Indian Journal of Physics, 2014, 88, 867-874.	1.8	6
35	Protein sequence comparison based on K-string dictionary. Gene, 2013, 529, 250-256.	2.2	33
36	Protein space: A natural method for realizing the nature of protein universe. Journal of Theoretical Biology, 2013, 318, 197-204.	1.7	43

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37	Real Time Classification of Viruses in 12 Dimensions. PLoS ONE, 2013, 8, e64328.	2.5	59
38	Protein map: An alignment-free sequence comparison method based on various properties of amino acids. Gene, 2011, 486, 110-118.	2.2	43
39	A Novel Method of Characterizing Genetic Sequences: Genome Space with Biological Distance and Applications. PLoS ONE, 2011, 6, e17293.	2.5	89
40	DNA sequence comparison by a novel probabilistic method. Information Sciences, 2011, 181, 1484-1492.	6.9	47
41	A Novel Construction of Genome Space with Biological Geometry. DNA Research, 2010, 17, 155-168.	3.4	55
42	A Protein Map and Its Application. DNA and Cell Biology, 2008, 27, 241-250.	1.9	61