Changchuan Yin

List of Publications by Year
in descending order

42 papers	1,687 citations	430874 18 h-index	345221 36 g-index
46 all docs	46 docs citations	46 times ranked	2370 citing authors

#	Article	IF	Citations
1	Genotyping coronavirus SARS-CoV-2: methods and implications. Genomics, 2020, 112, 3588-3596.	2.9	244
2	Mutations on COVID-19 diagnostic targets. Genomics, 2020, 112, 5204-5213.	2.9	164
3	Prediction of protein coding regions by the 3-base periodicity analysis of a DNA sequence. Journal of Theoretical Biology, 2007, 247, 687-694.	1.7	146
4	Analysis of SARS-CoV-2 mutations in the United States suggests presence of four substrains and novel variants. Communications Biology, 2021, 4, 228.	4.4	126
5	Decoding SARS-CoV-2 Transmission and Evolution and Ramifications for COVID-19 Diagnosis, Vaccine, and Medicine. Journal of Chemical Information and Modeling, 2020, 60, 5853-5865.	5.4	91
6	A Fourier Characteristic of Coding Sequences: Origins and a Non-Fourier Approximation. Journal of Computational Biology, 2005, 12, 1153-1165.	1.6	81
7	A measure of DNA sequence similarity by Fourier Transform with applications on hierarchical clustering. Journal of Theoretical Biology, 2014, 359, 18-28.	1.7	70
8	Host Immune Response Driving SARS-CoV-2 Evolution. Viruses, 2020, 12, 1095.	3.3	68
9	A new method to cluster DNA sequences using Fourier power spectrum. Journal of Theoretical Biology, 2015, 372, 135-145.	1.7	67
10	Numerical encoding of DNA sequences by chaos game representation with application in similarity comparison. Genomics, 2016, 108, 134-142.	2.9	67
11	Decoding Asymptomatic COVID-19 Infection and Transmission. Journal of Physical Chemistry Letters, 2020, 11, 10007-10015.	4.6	61
12	Emerging Vaccine-Breakthrough SARS-CoV-2 Variants. ACS Infectious Diseases, 2022, 8, 546-556.	3.8	59
13	UMAP-assisted K-means clustering of large-scale SARS-CoV-2 mutation datasets. Computers in Biology and Medicine, 2021, 131, 104264.	7.0	57
14	A Novel Construction of Genome Space with Biological Geometry. DNA Research, 2010, 17, 155-168.	3.4	55
15	An improved model for whole genome phylogenetic analysis by Fourier transform. Journal of Theoretical Biology, 2015, 382, 99-110.	1.7	38
16	Virus classification in 60-dimensional protein space. Molecular Phylogenetics and Evolution, 2016, 99, 53-62.	2.7	31
17	Two Dimensional Yau-Hausdorff Distance with Applications on Comparison of DNA and Protein Sequences. PLoS ONE, 2015, 10, e0136577.	2.5	27
18	Ebolavirus Classification Based on Natural Vectors. DNA and Cell Biology, 2015, 34, 418-428.	1.9	22

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19	Analysis of the Hosts and Transmission Paths of SARS-CoV-2 in the COVID-19 Outbreak. Genes, 2020, 11, 637.	2.4	21
20	A coevolution analysis for identifying protein-protein interactions by Fourier transform. PLoS ONE, 2017, 12, e0174862.	2.5	20
21	A new method to cluster genomes based on cumulative Fourier power spectrum. Gene, 2018, 673, 239-250.	2.2	17
22	A Novel Method for Comparative Analysis of DNA Sequences by Ramanujan-Fourier Transform. Journal of Computational Biology, 2014, 21, 867-879.	1.6	14
23	Encoding and Decoding DNA Sequences by Integer Chaos Game Representation. Journal of Computational Biology, 2019, 26, 143-151.	1.6	13
24	Splice sites detection using chaos game representation and neural network. Genomics, 2020, 112, 1847-1852.	2.9	13
25	Numerical representation of DNA sequences based on genetic code context and its applications in periodicity analysis of genomes. , 2008, , .		12
26	Geometric construction of viral genome space and its applications. Computational and Structural Biotechnology Journal, 2021, 19, 4226-4234.	4.1	11
27	Periodic power spectrum with applications in detection of latent periodicities in DNA sequences. Journal of Mathematical Biology, 2016, 73, 1053-1079.	1.9	9
28	kmer2vec: A Novel Method for Comparing DNA Sequences by word2vec Embedding. Journal of Computational Biology, 2022, 29, 1001-1021.	1.6	8
29	Virus Database and Online Inquiry System Based on Natural Vectors. Evolutionary Bioinformatics, 2017, 13, 117693431774666.	1.2	7
30	Representation of DNA sequences in genetic codon context with applications in exon and intron prediction. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550004.	0.8	6
31	Identification of repeats in DNA sequences using nucleotide distribution uniformity. Journal of Theoretical Biology, 2017, 412, 138-145.	1.7	6
32	Tracking the 3-Base Periodicity of Protein-Coding Regions by the Nonlinear Tracking-Differentiator. , 2006, , .		5
33	A New Method Based on Coding Sequence Density to Cluster Bacteria. Journal of Computational Biology, 2020, 27, 1688-1698.	1.6	2
34	Inverted repeats in coronavirus SARS-CoV-2 genome and implications in evolution. Communications in Information and Systems, 2021, 21, 125-145.	0.5	2
35	A Fast Algorithm for Computing the Fourier Spectrum of a Fractional Period. Journal of Computational Biology, 2021, 28, 269-282.	1.6	2
36	Inverted repeats in coronavirus SARS-CoV-2 genome manifest the evolution events. Journal of Theoretical Biology, 2021, 530, 110885.	1.7	2

#	ARTICLE	IF	CITATIONS
37	Whole genome single nucleotide polymorphism genotyping of <i>Staphylococcus aureus</i>. Communications in Information and Systems, 2019, 19, 57-80.	0.5	1
38	A Workflow to Improve Variant Calling Accuracy in Molecular Barcoded Sequencing Reads. Journal of Computational Biology, 2019, 26, 96-103.	1.6	0
39	Latent periodicity-2 in coronavirus SARS-CoV-2 genome: Evolutionary implications. Journal of Theoretical Biology, 2021, 515, 110604.	1.7	0
40	Indian perspective Architecture for Advancement of Biomedical Telemedicine and mHealth System. Journal of Medical and Bioengineering, 2013, 2, 80-83.	0.5	0
41	Whole-genome phylogeny of giant viruses by Fourier transform. Communications in Information and Systems, 2020, 20, 61-76.	0.5	0
42	Full Chromosomal Relationships Between Populations and the Origin of Humans. Frontiers in Genetics, 2021, 12, 828805.	2.3	0