

Chun Shen Lim

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/964216/publications.pdf>

Version: 2024-02-01

21
papers

259
citations

1163117

8
h-index

1058476

14
g-index

30
all docs

30
docs citations

30
times ranked

392
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative analysis of the splice variants expressed by the major hepatitis B virus genotypes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	16
2	Lysine modification of human serum albumin and its effect on protein conformation and nalidixic acid binding. <i>Journal of the Indian Chemical Society</i> , 2021, 98, 100031.	2.8	1
3	TISIGNER.com: web services for improving recombinant protein production. <i>Nucleic Acids Research</i> , 2021, 49, W654-W661.	14.5	15
4	Analysis of Fungal Genomes Reveals Commonalities of Intron Gain or Loss and Functions in Intron-Poor Species. <i>Molecular Biology and Evolution</i> , 2021, 38, 4166-4186.	8.9	19
5	Analysis of 11,430 recombinant protein production experiments reveals that protein yield is tunable by synonymous codon changes of translation initiation sites. <i>PLoS Computational Biology</i> , 2021, 17, e1009461.	3.2	9
6	Systematic comparison of plasma EBV DNA, anti-EBV antibodies and miRNA levels for early detection and prognosis of nasopharyngeal carcinoma. <i>International Journal of Cancer</i> , 2020, 146, 2336-2347.	5.1	53
7	Solubility-Weighted Index: fast and accurate prediction of protein solubility. <i>Bioinformatics</i> , 2020, 36, 4691-4698.	4.1	40
8	A crowdsourced set of curated structural variants for the human genome. <i>PLoS Computational Biology</i> , 2020, 16, e1007933.	3.2	6
9	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
10	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
11	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
12	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
13	Genotypic and phenotypic variation of CADASIL among Chinese, Indians and Rungus in Malaysia. <i>Neuroscience Research Notes</i> , 2019, 2, 1-11.	0.8	2
14	The exonâ€intron gene structure upstream of the initiation codon predicts translation efficiency. <i>Nucleic Acids Research</i> , 2018, 46, 4575-4591.	14.5	23
15	A new class of ribozyme from hepatitis B virus. <i>FEBS Journal</i> , 2017, 284, 1182-1183.	4.7	0
16	Know Your Enemy: Successful Bioinformatic Approaches to Predict Functional RNA Structures in Viral RNAs. <i>Frontiers in Microbiology</i> , 2017, 8, 2582.	3.5	26
17	Hepatitis B virus nuclear export elements: RNA stem-loop $\hat{1}$ and $\hat{1}^2$, key parts of the HBV post-transcriptional regulatory element. <i>RNA Biology</i> , 2016, 13, 743-747.	3.1	16
18	R54C Mutation of NOTCH3 Gene in the First Rungus Family with CADASIL. <i>PLoS ONE</i> , 2015, 10, e0135470.	2.5	6

#	ARTICLE	IF	CITATIONS
19	Inclusion bodies of recombinant Epstein-Barr virus capsid antigen p18 as potential immobilized antigens in enzyme immunoassays for detection of nasopharyngeal carcinoma. Clinica Chimica Acta, 2015, 448, 206-210.	1.1	1
20	Recombinant production of Epstein-Barr virus BZLF1 trans-activator and characterization of its DNA-binding specificity. Protein Expression and Purification, 2014, 95, 8-12.	1.3	2
21	On optimizing the blocking step of indirect enzyme-linked immunosorbent assay for Epstein-Barr virus serology. Clinica Chimica Acta, 2013, 415, 158-161.	1.1	8