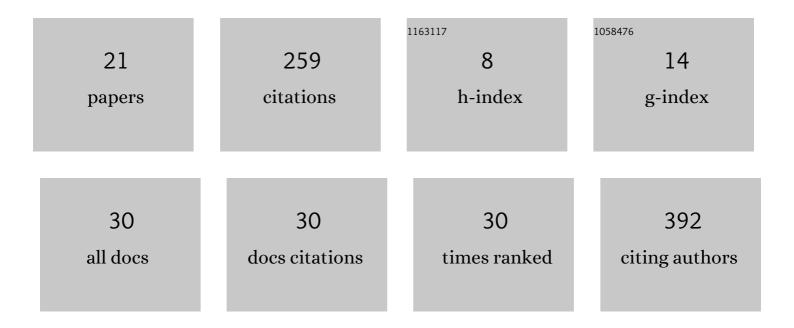
Chun Shen Lim

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/964216/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Quantitative analysis of the splice variants expressed by the major hepatitis B virus genotypes. Microbial Genomics, 2021, 7, .	2.0	16
2	Lysine modification of human serum albumin and its effect on protein conformation and nalidixic acid binding. Journal of the Indian Chemical Society, 2021, 98, 100031.	2.8	1
3	TISIGNER.com: web services for improving recombinant protein production. Nucleic Acids Research, 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. Molecular Biology and Evolution, 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. PLoS Computational Biology, 2021, 17, e1009461.	3.2	9
6	Systematic comparison of plasma EBV DNA, anti‣BV antibodies and miRNA levels for early detection and prognosis of nasopharyngeal carcinoma. International Journal of Cancer, 2020, 146, 2336-2347.	5.1	53
7	Solubility-Weighted Index: fast and accurate prediction of protein solubility. Bioinformatics, 2020, 36, 4691-4698.	4.1	40
8	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 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. Neuroscience Research Notes, 2019, 2, 1-11.	0.8	2
14	The exon–intron gene structure upstream of the initiation codon predicts translation efficiency. Nucleic Acids Research, 2018, 46, 4575-4591.	14.5	23
15	A new class of ribozyme from hepatitis B virus. FEBS Journal, 2017, 284, 1182-1183.	4.7	0
16	Know Your Enemy: Successful Bioinformatic Approaches to Predict Functional RNA Structures in Viral RNAs. Frontiers in Microbiology, 2017, 8, 2582.	3.5	26
17	Hepatitis B virus nuclear export elements: RNA stem-loop α and β, key parts of the HBV post-transcriptional regulatory element. RNA Biology, 2016, 13, 743-747.	3.1	16
18	R54C Mutation of NOTCH3 Gene in the First Rungus Family with CADASIL. PLoS ONE, 2015, 10, e0135470.	2.5	6

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#	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