

# 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	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
2	Solubility-Weighted Index: fast and accurate prediction of protein solubility. <i>Bioinformatics</i> , 2020, 36, 4691-4698.	4.1	40
3	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
4	The exon-intron gene structure upstream of the initiation codon predicts translation efficiency. <i>Nucleic Acids Research</i> , 2018, 46, 4575-4591.	14.5	23
5	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
6	Hepatitis B virus nuclear export elements: RNA stem-loop $\hat{1}$ and $\hat{2}$ , key parts of the HBV post-transcriptional regulatory element. <i>RNA Biology</i> , 2016, 13, 743-747.	3.1	16
7	Quantitative analysis of the splice variants expressed by the major hepatitis B virus genotypes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	16
8	TISIGNER.com: web services for improving recombinant protein production. <i>Nucleic Acids Research</i> , 2021, 49, W654-W661.	14.5	15
9	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
10	On optimizing the blocking step of indirect enzyme-linked immunosorbent assay for Epstein-Barr virus serology. <i>Clinica Chimica Acta</i> , 2013, 415, 158-161.	1.1	8
11	R54C Mutation of NOTCH3 Gene in the First Rungus Family with CADASIL. <i>PLoS ONE</i> , 2015, 10, e0135470.	2.5	6
12	A crowdsourced set of curated structural variants for the human genome. <i>PLoS Computational Biology</i> , 2020, 16, e1007933.	3.2	6
13	Recombinant production of Epstein-Barr virus BZLF1 trans-activator and characterization of its DNA-binding specificity. <i>Protein Expression and Purification</i> , 2014, 95, 8-12.	1.3	2
14	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
15	Inclusion bodies of recombinant Epstein-Barr virus capsid antigen p18 as potential immobilized antigens in enzyme immunoassays for detection of nasopharyngeal carcinoma. <i>Clinica Chimica Acta</i> , 2015, 448, 206-210.	1.1	1
16	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
17	A new class of ribozyme from hepatitis B virus. <i>FEBS Journal</i> , 2017, 284, 1182-1183.	4.7	0
18	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0

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19	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
20	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
21	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0