

# Hifzur Rahman Ansari

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2704104/publications.pdf>

Version: 2024-02-01

25  
papers

1,600  
citations

567281

15  
h-index

677142

22  
g-index

28  
all docs

28  
docs citations

28  
times ranked

2487  
citing authors

#	ARTICLE	IF	CITATIONS
1	VE1 immunohistochemistry is an adjunct tool for detection of <i>BRAF</i> <sup>V600E</sup> mutation: Validation in thyroid cancer patients. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e23628.	2.1	9
2	Cover Image: Novel tumour suppressor roles for GZMA and RASGRP1 in <i>Theileria annulata</i> -transformed macrophages and human B lymphoma cells ( <i>Cellular Microbiology</i> 12/2020). <i>Cellular Microbiology</i> , 2020, 22, e13285.	2.1	0
3	Novel tumour suppressor roles for <i>GZMA</i> and <i>RASGRP1</i> in <i>Theileria annulata</i> -transformed macrophages and human B lymphoma cells. <i>Cellular Microbiology</i> , 2020, 22, e13255.	2.1	9
4	Malaria parasites regulate intra-erythrocytic development duration via serpentine receptor 10 to coordinate with host rhythms. <i>Nature Communications</i> , 2020, 11, 2763.	12.8	41
5	The Impact of Natural Antioxidants on the Regenerative Potential of Vascular Cells. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 6, 28.	2.4	30
6	<i>Theileria</i> highjacks JNK2 into a complex with the macroschizont GPI (GlycosylPhosphatidylinositol)-anchored surface protein p104. <i>Cellular Microbiology</i> , 2019, 21, e12973.	2.1	7
7	miR-126-5p by direct targeting of JNK-interacting protein-2 (JIP-2) plays a key role in <i>Theileria</i> -infected macrophage virulence. <i>PLoS Pathogens</i> , 2018, 14, e1006942.	4.7	18
8	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017, 18, 33.	2.8	11
9	In silico analysis to identify vaccine candidates common to multiple serotypes of <i>Shigella</i> and evaluation of their immunogenicity. <i>PLoS ONE</i> , 2017, 12, e0180505.	2.5	26
10	Genome-scale comparison of expanded gene families in <i>Plasmodium ovale wallikeri</i> and <i>Plasmodium ovale curtisi</i> with <i>Plasmodium malariae</i> and with other <i>Plasmodium</i> species. <i>International Journal for Parasitology</i> , 2016, 46, 685-696.	3.1	59
11	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical <i>Salmonella enterica</i> Serovar Senftenberg Variant in China. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2014-2022.	3.9	14
12	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. <i>Scientific Reports</i> , 2015, 5, 15443.	3.3	78
13	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>eLife</i> , 2015, 4, e06974.	6.0	198
14	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.	5.5	176
15	In Silico Models for B-Cell Epitope Recognition and Signaling. <i>Methods in Molecular Biology</i> , 2013, 993, 129-138.	0.9	7
16	Recruitment of EB1, a Master Regulator of Microtubule Dynamics, to the Surface of the <i>Theileria annulata</i> Schizont. <i>PLoS Pathogens</i> , 2013, 9, e1003346.	4.7	51
17	Identification of B-cell epitopes in an antigen for inducing specific class of antibodies. <i>Biology Direct</i> , 2013, 8, 27.	4.6	91
18	Improved Method for Linear B-Cell Epitope Prediction Using Antigen's Primary Sequence. <i>PLoS ONE</i> , 2013, 8, e62216.	2.5	269

#	ARTICLE	IF	CITATIONS
19	On the Development of Vaccine Antigen Databases: Progress, Opportunity, and Challenge. , 2013, , 117-130.		0
20	Vaccine Antigen Databases. , 2013, , 2331-2335.		0
21	Machine learning competition in immunology â€“ Prediction of HLA class I binding peptides. Journal of Immunological Methods, 2011, 374, 1-4.	1.4	53
22	Identification of NAD interacting residues in proteins. BMC Bioinformatics, 2010, 11, 160.	2.6	71
23	Identification of conformational B-cell Epitopes in an antigen from its primary sequence. Immunome Research, 2010, 6, 6.	0.1	264
24	AntigenDB: an immunoinformatics database of pathogen antigens. Nucleic Acids Research, 2010, 38, D847-D853.	14.5	58
25	Prediction of guide strand of microRNAs from its sequence and secondary structure. BMC Bioinformatics, 2009, 10, 105.	2.6	58