

# Richard Allcock

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1806457/publications.pdf>

Version: 2024-02-01

15  
papers

569  
citations

1162889

8  
h-index

1199470

12  
g-index

15  
all docs

15  
docs citations

15  
times ranked

1216  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbial 16S rRNA Ion Tag and community metagenome sequencing using the Ion Torrent (PGM) Platform. <i>Journal of Microbiological Methods</i> , 2012, 91, 80-88.	0.7	187
2	Multiple Immune Factors Are Involved in Controlling Acute and Chronic Chikungunya Virus Infection. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3354.	1.3	145
3	Polymorphisms of the CRP gene inhibit inflammatory response and increase susceptibility to depression: The Health in Men Study. <i>International Journal of Epidemiology</i> , 2009, 38, 1049-1059.	0.9	70
4	Sporadic inclusion body myositis: HLA-DRB1 allele interactions influence disease risk and clinical phenotype. <i>Neuromuscular Disorders</i> , 2009, 19, 763-765.	0.3	48
5	A New Species of Mesonivirus from the Northern Territory, Australia. <i>PLoS ONE</i> , 2014, 9, e91103.	1.1	45
6	Detection of Arboviruses and Other Micro-Organisms in Experimentally Infected Mosquitoes Using Massively Parallel Sequencing. <i>PLoS ONE</i> , 2013, 8, e58026.	1.1	26
7	Genetic Characterization of Archived Bunyaviruses and their Potential for Emergence in Australia. <i>Emerging Infectious Diseases</i> , 2016, 22, 833-840.	2.0	11
8	Newly characterized arboviruses of northern Australia. <i>Virology Reports</i> , 2016, 6, 11-17.	0.4	11
9	Susceptibility to non-tuberculous mycobacterial disease is influenced by rs1518111 in IL10. <i>Human Immunology</i> , 2017, 78, 391-393.	1.2	10
10	A haplotype spanning P2X7R, P2X4R and CAMKK2 may mark susceptibility to pulmonary non-tuberculous mycobacterial disease. <i>Immunogenetics</i> , 2017, 69, 287-293.	1.2	8
11	Macroinvertebrates and Microbes (Archaea, Bacteria) Offer Complementary Insights into Mine-Pit Lake Ecology. <i>Mine Water and the Environment</i> , 2020, 39, 589-602.	0.9	5
12	Low-Pass Whole-Genome Sequencing as a Method of Determining Copy Number Variations in Uveal Melanoma Tissue Samples. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 429-434.	1.2	3
13	Genomic sequence and expression profile of murine Bat1a and Nfkbil1. <i>DNA Sequence</i> , 2006, 17, 292-299.	0.7	0
14	It infrastructure for genomic testing. <i>Pathology</i> , 2012, 44, S3-S4.	0.3	0
15	COMBINED WHOLE EXOME SEQUENCING AND LINKAGE ANALYSIS REVEALS LINKAGE TO 10Q11-10Q21 LOCUS WHICH IS NOT EXPLAINED BY GWAS-ASSOCIATED SNP OR RARE VARIANTS IN ANK3. <i>European Neuropsychopharmacology</i> , 2019, 29, S834-S835.	0.3	0