

Claire Hoede

List of Publications by Year in descending order

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17
papers

2,481
citations

759233

12
h-index

888059

17
g-index

17
all docs

17
docs citations

17
times ranked

6165
citing authors

#	ARTICLE	IF	CITATIONS
1	Intracellular <i>Salmonella Paratyphi A</i> is motile and differs in the expression of flagella-chemotaxis, SPI-1 and carbon utilization pathways in comparison to intracellular <i>S. Typhimurium</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010425.	4.7	4
2	Widely rhythmic transcriptome in <i>Calanus finmarchicus</i> during the high Arctic summer solstice period. <i>IScience</i> , 2021, 24, 101927.	4.1	7
3	Phylogenetic study of the conserved RNA structure encompassing the hemagglutinin cleavage site encoding region of H5 and H7 low pathogenic avian influenza viruses. <i>Virus Evolution</i> , 2021, 7, veab093.	4.9	7
4	Daily transcriptomes of the copepod <i>Calanus finmarchicus</i> during the summer solstice at high Arctic latitudes. <i>Scientific Data</i> , 2020, 7, 415.	5.3	6
5	A comparative transcriptomic approach to understanding the formation of cork. <i>Plant Molecular Biology</i> , 2018, 96, 103-118.	3.9	35
6	Remodeling of the cycling transcriptome of the oyster <i>Crassostrea gigas</i> by the harmful algae <i>Alexandrium minutum</i> . <i>Scientific Reports</i> , 2017, 7, 3480.	3.3	32
7	Human Adipose-Derived Stem Cells Expanded Under Ambient Oxygen Concentration Accumulate Oxidative DNA Lesions and Experience Procarcinogenic DNA Replication Stress. <i>Stem Cells Translational Medicine</i> , 2017, 6, 68-76.	3.3	15
8	Links between Transcription, Environmental Adaptation and Gene Variability in <i>Escherichia coli</i> : Correlations between Gene Expression and Gene Variability Reflect Growth Efficiencies. <i>Molecular Biology and Evolution</i> , 2016, 33, 2515-2529.	8.9	31
9	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015, 43, W589-W598.	14.5	682
10	PASTEC: An Automatic Transposable Element Classification Tool. <i>PLoS ONE</i> , 2014, 9, e91929.	2.5	285
11	RNAbrowse: RNA-Seq De Novo Assembly Results Browser. <i>PLoS ONE</i> , 2014, 9, e96821.	2.5	19
12	Animal and human pathogenic <i>Escherichia coli</i> strains share common genetic backgrounds. <i>Infection, Genetics and Evolution</i> , 2011, 11, 654-662.	2.3	169
13	A Module Located at a Chromosomal Integration Hot Spot Is Responsible for the Multidrug Resistance of a Reference Strain from <i>Escherichia coli</i> Clonal Group A. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2283-2288.	3.2	33
14	Organised Genome Dynamics in the <i>Escherichia coli</i> Species Results in Highly Diverse Adaptive Paths. <i>PLoS Genetics</i> , 2009, 5, e1000344.	3.5	1,005
15	aes, the gene encoding the esterase B in <i>Escherichia coli</i> , is a powerful phylogenetic marker of the species. <i>BMC Microbiology</i> , 2009, 9, 273.	3.3	9
16	Contribution of Recombination to the Evolution of Human Immunodeficiency Viruses Expressing Resistance to Antiretroviral Treatment. <i>Journal of Virology</i> , 2007, 81, 7620-7628.	3.4	103
17	Selection Acts on DNA Secondary Structures to Decrease Transcriptional Mutagenesis. <i>PLoS Genetics</i> , 2006, 2, e176.	3.5	39