

Leandro R Jones

List of Publications by Year in descending order

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840776

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#	ARTICLE	IF	CITATIONS
1	Abundant microbes of surface sea waters of the uncharted Engaño Bay at the Atlantic Patagonian Coast: relevance of bacteria-sized photosynthetic eukaryotes. <i>Aquatic Ecology</i> , 2022, 56, 1217-1230.	1.5	1
2	Quantitative phylogenomic evidence reveals a spatially structured SARS-CoV-2 diversity. <i>Virology</i> , 2020, 550, 70-77.	2.4	6
3	Rare unclassified 16S rRNA operational taxonomic units from the uncharted Engaño Bay (Argentinean) Tj ETQq1 1.0.784314 rgBT /C	1.7	1
4	Are ocean currents too slow to counteract SARS11 evolution? A next-generation sequencing, phylogeographic analysis. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 324-337.	2.7	11
5	Nuisance <i>Didymosphenia geminata</i> blooms in the Argentinean Patagonia: Status and current research trends. <i>Aquatic Ecosystem Health and Management</i> , 2017, 20, 361-368.	0.6	6
6	Phylogenetic Diversity in Core Region of Hepatitis C Virus Genotype 1a as a Factor Associated with Fibrosis Severity in HIV-1-Coinfected Patients. <i>BioMed Research International</i> , 2017, 2017, 1-12.	1.9	3
7	Genomic characterization and molecular evolution analysis of subtype B and BF recombinant HIV-1 strains among Argentinean men who have sex with men reveal a complex scenario. <i>PLoS ONE</i> , 2017, 12, e0189705.	2.5	6
8	Hepatitis B virus resistance substitutions: long-term analysis by next-generation sequencing. <i>Archives of Virology</i> , 2016, 161, 2885-2891.	2.1	9
9	Evolution of hepatitis C virus in HIV coinfecting patients under antiretroviral therapy. <i>Infection, Genetics and Evolution</i> , 2016, 43, 186-196.	2.3	1
10	Virus evolution during chronic hepatitis B virus infection as revealed by ultradeep sequencing data. <i>Journal of General Virology</i> , 2016, 97, 435-444.	2.9	5
11	Molecular Characterization of the First Bovine Herpesvirus 4 (BoHV-4) Strains Isolated from In Vitro Bovine Embryos production in Argentina. <i>PLoS ONE</i> , 2015, 10, e0132212.	2.5	10
12	The peril of PCR inhibitors in environmental samples: the case of <i>Didymosphenia geminata</i> . <i>Biodiversity and Conservation</i> , 2015, 24, 1541-1548.	2.6	11
13	HIV-1 Tropism Dynamics and Phylogenetic Analysis from Longitudinal Ultra-Deep Sequencing Data of CCR5- and CXCR4-Using Variants. <i>PLoS ONE</i> , 2014, 9, e102857.	2.5	15
14	Phylogenetic analysis of <i>Ostreococcus</i> virus sequences from the Patagonian Coast. <i>Virus Genes</i> , 2012, 45, 316-326.	1.6	7
15	Effects of UV radiation on the taxonomic composition of natural bacterioplankton communities from Bahía Engaño (Patagonia, Argentina). <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2012, 117, 171-178.	3.8	20
16	A clustering phenomenon among HCVa1a strains among patients coinfecting with HIV from Buenos Aires, Argentina. <i>Journal of Medical Virology</i> , 2012, 84, 570-581.	5.0	6
17	Analysis of HIV Type 1 BF Recombinant Sequences from South America Dates the Origin of CRF12_BF to a Recombination Event in the 1970s. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 569-578.	1.1	13
18	Glycoprotein gene sequence variation in rhesus monkey rhadinovirus. <i>Virology</i> , 2010, 400, 175-186.	2.4	19

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19	Stable human T-cell lymphotropic virus type 1 (HTLV-1) subtype a/subgroup a endemicity in Amerindians from Northwest Argentina: A health problem to be resolved. <i>Journal of Medical Virology</i> , 2010, 82, 2116-2122.	5.0	12
20	The human fungal pathogen <i>Paracoccidioides brasiliensis</i> (Onygenales: Ajellomycetaceae) is a complex of two species: phylogenetic evidence from five mitochondrial markers. <i>Cladistics</i> , 2010, 26, 613-624.	3.3	37
21	In-Depth Analysis of the Origins of HIV Type 1 Subtype C in South America. <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 951-959.	1.1	12
22	Bovine leukemia virus can be classified into seven genotypes: evidence for the existence of two novel clades. <i>Journal of General Virology</i> , 2009, 90, 2788-2797.	2.9	76
23	Simple procedures to obtain exogenous internal controls for use in RT-PCR detection of bovine pestiviruses. <i>Molecular and Cellular Probes</i> , 2008, 22, 212-214.	2.1	2
24	Divergent Strains of Human T-Lymphotropic Virus Type 1 (HTLV-1) within the Cosmopolitan Subtype in Argentina. <i>AIDS Research and Human Retroviruses</i> , 2008, 24, 1237-1244.	1.1	9
25	A long distance RT-PCR able to amplify the Pestivirus genome. <i>Journal of Virological Methods</i> , 2006, 134, 197-204.	2.1	11
26	Genetic typing of bovine viral diarrhea virus isolates from Argentina. <i>Veterinary Microbiology</i> , 2001, 81, 367-375.	1.9	71
27	Application of Single-Strand Conformation Polymorphism to the Study of Bovine Viral Diarrhea Virus Isolates. <i>Journal of Veterinary Diagnostic Investigation</i> , 2001, 13, 50-56.	1.1	12