Stephane Aris-Brosou

List of Publications by Year
in descending order

55 papers	**1,659** citations	361296 **20** h-index	315616 **38** g-index
69 all docs	**69** docs citations	**69** times ranked	**4937** citing authors

#	Article	IF	Citations
1	Extreme diversity in noncalcifying haptophytes explains a major pigment paradox in open oceans. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12803-12808.	3.3	263
2	Effects of Models of Rate Evolution on Estimation of Divergence Dates with Special Reference to the Metazoan 18S Ribosomal RNA Phylogeny. Systematic Biology, 2002, 51, 703-714.	2.7	203
3	Bayesian Models of Episodic Evolution Support a Late Precambrian Explosive Diversification of the Metazoa. Molecular Biology and Evolution, 2003, 20, 1947-1954.	3.5	141
4	Genome analyses suggest the presence of polyploidy and recent human€driven expansions in eight global populations of the honeybee pathogen <scp><i>N</i></scp><i>osema ceranae</i>. Environmental Microbiology, 2015, 17, 4443-4458.	1.8	66
5	The Metabolic Consequences of Hepatic AMP-Kinase Phosphorylation in Rainbow Trout. PLoS ONE, 2011, 6, e20228.	1.1	65
6	A Time line of the Environmental Genetics of the Haptophytes. Molecular Biology and Evolution, 2010, 27, 161-176.	3.5	64
7	Determinants of Adaptive Evolution at the Molecular Level: the Extended Complexity Hypothesis. Molecular Biology and Evolution, 2004, 22, 200-209.	3.5	56
8	Genetic Diversity as a Marker for Timing Infection in HIV-Infected Patients: Evaluation of a 6-Month Window and Comparison With BED. Journal of Infectious Diseases, 2012, 206, 756-764.	1.9	50
9	Microbial DNA records historical delivery of anthropogenic mercury. ISME Journal, 2015, 9, 2541-2550.	4.4	50
10	Physicochemical Drivers of Microbial Community Structure in Sediments of Lake Hazen, Nunavut, Canada. Frontiers in Microbiology, 2018, 9, 1138.	1.5	46
11	Microbial Community Structure in Lake and Wetland Sediments from a High Arctic Polar Desert Revealed by Targeted Transcriptomics. PLoS ONE, 2014, 9, e89531.	1.1	42
12	Dual foraging and pair-coordination during chick provisioning by Manx shearwaters: empirical evidence supported by a simple model. Journal of Experimental Biology, 2015, 218, 2116-23.	0.8	41
13	Spatial and temporal dynamics of rabies virus variants in big brown bat populations across Canada: footprints of an emerging zoonosis. Molecular Ecology, 2010, 19, 2120-2136.	2.0	36
14	Dating Phylogenies with Hybrid Local Molecular Clocks. PLoS ONE, 2007, 2, e879.	1.1	33
15	Comparative Dynamics and Distribution of Influenza Drug Resistance Acquisition to Protein M2 and Neuraminidase Inhibitors. Molecular Biology and Evolution, 2014, 31, 355-363.	3.5	31
16	The Essentials of Computational Molecular Evolution. Methods in Molecular Biology, 2012, 855, 111-152.	0.4	28
17	Breeding phenology and winter activity predict subsequent breeding success in a trans-global migratory seabird. Biology Letters, 2015, 11, .	1.0	27
18	Least and Most Powerful Phylogenetic Tests to Elucidate the Origin of the Seed Plants in the Presence of Conflicting Signals under Misspecified Models. Systematic Biology, 2003, 52, 781-793.	2.7	21

#	Article	IF	Citations
19	Large-scale analyses of synonymous substitution rates can be sensitive to assumptions about the process of mutation. Gene, 2006, 378, 58-64.	1.0	21
20	Incubation Patterns in a Central-Place Forager Affect Lifetime Reproductive Success: Scaling of Patterns from a Foraging Bout to a Lifetime. PLoS ONE, 2011, 6, e17760.	1.1	21
21	Habitat-specific type I polyketide synthases in soils and street sediments. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 75-85.	1.4	21
22	Microbial genomes retrieved from High Arctic lake sediments encode for adaptation to cold and oligotrophic environments. Limnology and Oceanography, 2020, 65, S233.	1.6	20
23	How Bayes tests of molecular phylogenies compare with frequentist approaches. Bioinformatics, 2003, 19, 618-624.	1.8	19
24	Both Epistasis and Diversifying Selection Drive the Structural Evolution of the Ebola Virus Glycoprotein Mucin-Like Domain. Journal of Virology, 2016, 90, 5475-5484.	1.5	18
25	Flight costs in volant vertebrates: A phylogenetically-controlled meta-analysis of birds and bats. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2019, 235, 193-201.	0.8	18
26	Swift evolutionary response of microbes to a rise in anthropogenic mercury in the Northern Hemisphere. ISME Journal, 2020, 14, 788-800.	4.4	18
27	Early Evolution of Ionotropic GABA Receptors and Selective Regimes Acting on the Mammalian-Specific Theta and Epsilon Subunits. PLoS ONE, 2007, 2, e894.	1.1	18
28	Viral outbreaks involve destabilized evolutionary networks: evidence from Ebola, Influenza and Zika. Scientific Reports, 2017, 7, 11881.	1.6	15
29	Flexible foraging strategies in a diving seabird with high flight cost. Marine Biology, 2014, 161, 2121-2129.	0.7	13
30	Foraging flexibility and search patterns are unlinked during breeding in a free-ranging seabird. Marine Biology, 2016, 163, 72.	0.7	13
31	Warming Climate Is Reducing the Diversity of Dominant Microbes in the Largest High Arctic Lake. Frontiers in Microbiology, 2020, 11, 561194.	1.5	13
32	Morphospecies<i>versus</i>Phylospecies Concepts for Evaluating Phytoplankton Diversity: The Case of the Coccolithophores. Cryptogamie, Algologie, 2014, 35, 353-377.	0.3	12
33	Widespread Historical Contingency in Influenza Viruses. Genetics, 2017, 205, 409-420.	1.2	12
34	Direct Evidence of an Increasing Mutational Load in Humans. Molecular Biology and Evolution, 2019, 36, 2823-2829.	3.5	12
35	Characterization and functional divergence of the α₁-adrenoceptor gene family: insights from rainbow trout (<i>Oncorhynchus mykiss</i>). Physiological Genomics, 2007, 32, 142-153.	1.0	11
36	The nonadaptive nature of the H1N1 2009 Swine Flu pandemic contrasts with the adaptive facilitation of transmission to a new host. BMC Evolutionary Biology, 2011, 11, 6.	3.2	10

#	ARTICLE	IF	CITATIONS
37	How the Central American Seaway and an Ancient Northern Passage Affected Flatfish Diversification. Molecular Biology and Evolution, 2018, 35, 1982-1989.	3.5	9
38	Geolocators link marine mercury with levels in wild seabirds throughout their annual cycle: Consequences for trans-ecosystem biotransport. Environmental Pollution, 2021, 284, 117035.	3.7	8
39	Phylogenetic Analyses: A Toolbox Expanding towards Bayesian Methods. International Journal of Plant Genomics, 2008, 2008, 1-16.	2.2	7
40	Fast Bayesian Choice of Phylogenetic Models: Prospecting Data Augmentationâ€"Based Thermodynamic Integration. Systematic Biology, 2011, 60, 881-887.	2.7	7
41	Predicting the Emergence of H3N2 Influenza Viruses Reveals Contrasted Modes of Evolution of HA and NA Antigens. Journal of Molecular Evolution, 2014, 78, 1-12.	0.8	7
42	Predictors of incubation costs in seabirds: an evolutionary perspective. Ibis, 2015, 157, 44-53.	1.0	7
43	Identifying genetic determinants of complex phenotypes from whole genome sequence data. BMC Genomics, 2019, 20, 470.	1.2	6
44	Identifying sites under positive selection with uncertain parameter estimates. Genome, 2006, 49, 767-776.	0.9	5
45	Adaptive Evolution of HIV at HLA Epitopes Is Associated with Ethnicity in Canada. PLoS ONE, 2012, 7, e36933.	1.1	5
46	Phylodynamics of the Emergence of Influenza Viruses after Cross-Species Transmission. PLoS ONE, 2013, 8, e82486.	1.1	5
47	A Not-So-Long Introduction to Computational Molecular Evolution. Methods in Molecular Biology, 2019, 1910, 71-117.	0.4	5
48	Predicting the Reasons of Customer Complaints: A First Step Toward Anticipating Quality Issues of In Vitro Diagnostics Assays with Machine Learning. JMIR Medical Informatics, 2018, 6, e34.	1.3	5
49	Least and most powerful phylogenetic tests to elucidate the origin of the seed plants in the presence of conflicting signals under misspecified models. Systematic Biology, 2003, 52, 781-93.	2.7	5
50	Inferring influenza global transmission networks without complete phylogenetic information. Evolutionary Applications, 2014, 7, 403-412.	1.5	4
51	Viral Long-Term Evolutionary Strategies Favor Stability over Proliferation. Viruses, 2019, 11, 677.	1.5	4
52	Identifying the drivers of computationally detected correlated evolution among sites under antibiotic selection. Evolutionary Applications, 2020, 13, 781-793.	1.5	3
53	Automatic detection of rate change in large data sets with an unsupervised approach: the case of influenza viruses. Genome, 2016, 59, 253-262.	0.9	2
54	A Simple Measure of the Dynamics of Segmented Genomes: An Application to Influenza. Lecture Notes in Computer Science, 2010, , 149-160.	1.0	2

#	Article	IF	Citations
55	Testing alternative hypotheses on the origin and speciation of Hawaiian katydids. Bmc Ecology and Evolution, 2022, 22, .	0.7	1