Anne-Laure BaÃ±uls

List of Publications by Year
in descending order

120 papers	5,962 citations	101543 36 h-index	79698 73 g-index
121 all docs	121 docs citations	121 times ranked	7575 citing authors

#	Article	IF	Citations
1	TreeDyn: towards dynamic graphics and annotations for analyses of trees. BMC Bioinformatics, 2006, 7, 439.	2.6	910
2	High-resolution minisatellite-based typing as a portable approach to global analysis of Mycobacterium tuberculosis molecular epidemiology. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 1901-1906.	7.1	393
3	Genetic diversity, clonality and sexuality in Toxoplasma gondii. International Journal for Parasitology, 2004, 34, 1185-1196.	3.1	312
4	Leishmania and the Leishmaniases: A Parasite Genetic Update and Advances in Taxonomy, Epidemiology and Pathogenicity in Humans. Advances in Parasitology, 2007, 64, 1-458.	3.2	245
5	Microsatellite analysis of Toxoplasma gondii shows considerable polymorphism structured into two main clonal groups. International Journal for Parasitology, 2002, 32, 27-38.	3.1	236
6	Linkage disequilibrium between minisatellite loci supports clonal evolution of Mycobacterium tuberculosis in a high tuberculosis incidence area. Molecular Microbiology, 2003, 47, 529-538.	2.5	171
7	Extreme inbreeding in Leishmania braziliensis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10224-10229.	7.1	158
8	Seasonal Dynamics of Phlebotomine Sand Fly Species Proven Vectors of Mediterranean Leishmaniasis Caused by Leishmania infantum. PLoS Neglected Tropical Diseases, 2016, 10, e0004458.	3.0	152
9	Bedaquiline Resistance: Its Emergence, Mechanism, and Prevention. Clinical Infectious Diseases, 2018, 66, 1625-1630.	5.8	131
10	Visceral Leishmaniasis in a German Child Who Had Never Entered a Known Endemic Area: Case Report and Review of the Literature. Clinical Infectious Diseases, 2001, 32, 302-306.	5.8	125
11	Additional Haplogroups of Toxoplasma gondii out of Africa: Population Structure and Mouse-Virulence of Strains from Gabon. PLoS Neglected Tropical Diseases, 2010, 4, e876.	3.0	117
12	Study of Leishmania pathogenesis in mice: experimental considerations. Parasites and Vectors, 2016, 9, 144.	2.5	110
13	Clinical pleiomorphism in human leishmaniases, with special mention of asymptomatic infection. Clinical Microbiology and Infection, 2011, 17, 1451-1461.	6.0	101
14	Mycobacterium tuberculosis: ecology and evolution of a human bacterium. Journal of Medical Microbiology, 2015, 64, 1261-1269.	1.8	97
15	Putative Leishmania hybrids in the Eastern Andean valley of Huanuco, Peru. Acta Tropica, 1995, 59, 293-307.	2.0	96
16	Unusual cutaneous lesions in two patients with visceral leishmaniasis and HIV infection. Journal of the American Academy of Dermatology, 1999, 41, 847-850.	1.2	90
17	Genetic Evolution of Mycobacterium bovis Causing Tuberculosis in Livestock and Wildlife in France since 1978. PLoS ONE, 2015, 10, e0117103.	2.5	85
18	Evidence for Hybridization by Multilocus Enzyme Electrophoresis and Random Amplified Polymorphic DNA Between Leishmania braziliensis and Leishmania panamensis/guyanensis in Ecuador. Journal of Eukaryotic Microbiology, 1997, 44, 408-411.	1.7	81

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19	Molecular Diagnosis of Drug-Resistant Tuberculosis; A Literature Review. Frontiers in Microbiology, 2019, 10, 794.	3.5	80
20	American tegumentary leishmaniasis: antigen-gene polymorphism, taxonomy and clinical pleomorphism. Infection, Genetics and Evolution, 2005, 5, 109-116.	2.3	75
21	A phylogenetic analysis of the Trypanosoma cruzi genome project CL Brener reference strain by multilocus enzyme electrophoresis and multiprimer random amplified polymorphic DNA fingerprinting. Molecular and Biochemical Parasitology, 1998, 92, 253-263.	1.1	72
22	First Molecular Epidemiology Study of Mycobacterium tuberculosis in Burkina Faso. Journal of Clinical Microbiology, 2007, 45, 921-927.	3.9	71
23	Identification of phlebotomine sand flies using one MALDI-TOF MS reference database and two mass spectrometer systems. Parasites and Vectors, 2015, 8, 266.	2.5	66
24	Pulmonary tuberculosis due to Mycobacterium microti: a study of six recent cases in France. Journal of Medical Microbiology, 2010, 59, 984-989.	1.8	62
25	â€œEverything You Always Wanted to Know about Sex (but Were Afraid to Ask)â€•in Leishmania after Two Decades of Laboratory and Field Analyses. PLoS Pathogens, 2010, 6, e1001004.	4.7	60
26	<scp>iDNA</scp> screening: Disease vectors as vertebrate samplers. Molecular Ecology, 2017, 26, 6478-6486.	3.9	57
27	Species-specific PCR assay for L. infantum/L. donovani discrimination. Acta Tropica, 2006, 100, 241-245.	2.0	55
28	Emergence and spread of antibiotic resistance in West AfricaÂ: contributing factors and threat assessment. Medecine Et Sante Tropicales, 2017, 27, 147-154.	0.3	53
29	Sampling strategies for phlebotomine sand flies (Diptera: Psychodidae) in Europe. Bulletin of Entomological Research, 2015, 105, 664-678.	1.0	52
30	Molecular epidemiology and evolutionary genetics of Leishmania parasites. International Journal for Parasitology, 1999, 29, 1137-1147.	3.1	51
31	Insights into the processes that drive the evolution of drug resistance in Mycobacterium tuberculosis. Evolutionary Applications, 2018, 11, 1498-1511.	3.1	51
32	Genetic heterogeneity and phylogenetic status of Leishmania (Leishmania) infantum zymodeme MON-1: epidemiological implications. Parasitology, 2001, 123, 425-432.	1.5	47
33	Ecology of Phlebotomine Sand Flies in the Rural Community of Mont Rolland (ThiÃ¨s Region, Senegal): Area of Transmission of Canine Leishmaniasis. PLoS ONE, 2011, 6, e14773.	2.5	39
34	Ecology and spatiotemporal dynamics of sandflies in the Mediterranean Languedoc region (Roquedur) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.5	39
35	Cryptosporidium Population Genetics: Evidence of Clonality in Isolates from France and Haiti. Journal of Eukaryotic Microbiology, 2006, 53, S33-S36.	1.7	38
36	High prevalence and characterization of extended-spectrum ÃŸ-lactamase producing Enterobacteriaceae in Chadian hospitals. BMC Infectious Diseases, 2019, 19, 205.	2.9	38

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37	Is Leishmania (Viannia) peruviana a Distinct Species? A MLEE/RAPD Evolutionary Genetics Answer. Journal of Eukaryotic Microbiology, 2000, 47, 197-207.	1.7	37
38	Reproductive strategies and population structure in Leishmania: substantial amount of sex in Leishmania Viannia guyanensis. Molecular Ecology, 2011, 20, 3116-3127.	3.9	37
39	Transmission of Leishmania infantum in the Canine Leishmaniasis Focus of Mont-Rolland, Senegal: Ecological, Parasitological and Molecular Evidence for a Possible Role of Sergentomyia Sand Flies. PLoS Neglected Tropical Diseases, 2016, 10, e0004940.	3.0	37
40	Molecular Evidence that Nasal Carriage of Staphylococcus aureus Plays a Role in Respiratory Tract Infections of Critically Ill Patients. Journal of Clinical Microbiology, 2005, 43, 3491-3493.	3.9	35
41	Fecal carriage of extended-spectrum Î²-lactamase-producing Enterobacteriaceae in hospital and community settings in Chad. Antimicrobial Resistance and Infection Control, 2019, 8, 169.	4.1	34
42	Genetic diversity, population structure and drug resistance of Mycobacterium tuberculosis in Peru. Infection, Genetics and Evolution, 2012, 12, 577-585.	2.3	33
43	Mycobacterium tuberculosis lineages and anti-tuberculosis drug resistance in reference hospitals across Viet Nam. BMC Microbiology, 2016, 16, 167.	3.3	33
44	Evaluation of short mitochondrial metabarcodes for the identification of Amazonian mammals. Methods in Ecology and Evolution, 2017, 8, 1276-1283.	5.2	33
45	Vector soup: highâ€throughput identification of Neotropical phlebotomine sand flies using metabarcoding. Molecular Ecology Resources, 2017, 17, 172-182.	4.8	31
46	Epidemiology and prevalence of extended-spectrum Î²-lactamase- and carbapenemase-producing Enterobacteriaceae in humans, animals and the environment in West and Central Africa. International Journal of Antimicrobial Agents, 2021, 57, 106203.	2.5	31
47	A primer for Leishmania population genetic studies. Trends in Parasitology, 2015, 31, 52-59.	3.3	30
48	Delamanid Resistance: Update and Clinical Management. Clinical Infectious Diseases, 2020, 71, 3252-3259.	5.8	30
49	Specific cpb copies within the Leishmania donovani complex: evolutionary interpretations and potential clinical implications in humans. Parasitology, 2007, 134, 379.	1.5	29
50	The promastigote surface antigen gene family of the Leishmania parasite: differential evolution by positive selection and recombination. BMC Evolutionary Biology, 2008, 8, 292.	3.2	27
51	Canine visceral leishmaniasis caused by Leishmania infantum in Senegal: risk of emergence in humans?. Microbes and Infection, 2010, 12, 1219-1225.	1.9	26
52	Wing size and shape variation of Phlebotomus papatasi (Diptera: Psychodidae) populations from the south and north slopes of the Atlas Mountains in Morocco. Journal of Vector Ecology, 2012, 37, 137-147.	1.0	26
53	Ecology and morphological variations in wings of Phlebotomus ariasi (Diptera: Psychodidae) in the region of Roquedur (Gard, France): a geometric morphometrics approach. Parasites and Vectors, 2016, 9, 578.	2.5	26
54	Fluorogenic Assay for Molecular Typing of theLeishmania donovaniComplex: Taxonomic and Clinical Applications. Journal of Infectious Diseases, 2005, 192, 685-692.	4.0	25

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55	Identification of Old World Leishmania spp. by specific polymerase chain reaction amplification of cysteine proteinase B genes and rapid dipstick detection. Diagnostic Microbiology and Infectious Disease, 2009, 63, 173-181.	1.8	24
56	DNAGear- a free software for spa type identification in Staphylococcus aureus. BMC Research Notes, 2012, 5, 642.	1.4	24
57	Of parasites and men. Infection, Genetics and Evolution, 2013, 20, 61-70.	2.3	24
58	Mycobacterium bovis in Burkina Faso: Epidemiologic and Genetic Links between Human and Cattle Isolates. PLoS Neglected Tropical Diseases, 2014, 8, e3142.	3.0	24
59	High Prevalence of Beijing and EAI4-VNM Genotypes among M. tuberculosis Isolates in Northern Vietnam: Sampling Effect, Rural and Urban Disparities. PLoS ONE, 2012, 7, e45553.	2.5	24
60	High-throughput sequencing of kDNA amplicons for the analysis ofLeishmaniaminicircles and identification of Neotropical species. Parasitology, 2018, 145, 585-594.	1.5	23
61	Evolutionary genetics and molecular diagnosis of Leishmania species. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2002, 96, S9-S13.	1.8	22
62	Genetic Diversity and Population Structure of Mycobacterium tuberculosis in Casablanca, a Moroccan City with High Incidence of Tuberculosis. Journal of Clinical Microbiology, 2004, 42, 461-466.	3.9	22
63	Methicillin-SensitiveStaphylococcus aureusCC398 in Intensive Care Unit, France. Emerging Infectious Diseases, 2014, 20, 1511-1515.	4.3	22
64	Broader Geographical Distribution of Toscana Virus in the Mediterranean Region Suggests the Existence of Larger Varieties of Sand Fly Vectors. Microorganisms, 2020, 8, 114.	3.6	22
65	Multifaceted Population Structure and Reproductive Strategy in Leishmania donovani Complex in One Sudanese Village. PLoS Neglected Tropical Diseases, 2011, 5, e1448.	3.0	21
66	Polymerase chain reaction-based identification of New World Leishmania species complexes by specific kDNA probes. Acta Tropica, 1999, 73, 283-293.	2.0	20
67	Unusual case of spondylodiscitis due to Staphylococcus saccharolyticus. Joint Bone Spine, 2005, 72, 91-93.	1.6	19
68	Parasitic genotypes appear to differ in leishmaniasis patients compared with asymptomatic related carriers. International Journal for Parasitology, 2013, 43, 389-397.	3.1	19
69	Predominant clonal evolution leads to a close parity between gene expression profiles and subspecific phylogeny in Trypanosoma cruzi. Molecular and Biochemical Parasitology, 2004, 137, 133-141.	1.1	18
70	Genetic Diversity and Population Structure of Mycobacterium marinum: New Insights into Host and Environmental Specificities. Journal of Clinical Microbiology, 2012, 50, 3627-3634.	3.9	18
71	Biodiversity and vectorâ€borne diseases: Host dilution and vector amplification occur simultaneously for Amazonian leishmaniases. Molecular Ecology, 2023, 32, 1817-1831.	3.9	18
72	A microculture technique for isolating live Leishmania parasites from peripheral blood of visceral leishmaniasis patients. Acta Tropica, 2007, 102, 197-200.	2.0	17

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73	Tuberculosis transmission in a high incidence area: A retrospective molecular epidemiological study of Mycobacterium tuberculosis in Casablanca, Morocco. Infection, Genetics and Evolution, 2007, 7, 636-644.	2.3	17
74	A battery of 12 microsatellite markers for genetic analysis of theLeishmania(Viannia)guyanensiscomplex. Parasitology, 2010, 137, 1879-1884.	1.5	17
75	Reproduction in Leishmania : A focus on genetic exchange. Infection, Genetics and Evolution, 2017, 50, 128-132.	2.3	17
76	Molecular analysis of pyrazinamide resistance in Mycobacterium tuberculosis in Vietnam highlights the high rate of pyrazinamide resistance-associated mutations in clinical isolates. Emerging Microbes and Infections, 2017, 6, 1-7.	6.5	17
77	PERMANENT GENETIC RESOURCES: A set of 12 microsatellite loci for genetic studies of Leishmania braziliensis. Molecular Ecology Resources, 2008, 8, 351-353.	4.8	16
78	Clonal propagation and the fast generation of karyotype diversity: anin vitro Leishmaniamodel. Parasitology, 2007, 134, 33-39.	1.5	15
79	Evaluation of the SLOMYCO SensititreÂ® panel for testing the antimicrobial susceptibility of Mycobacterium marinum isolates. Annals of Clinical Microbiology and Antimicrobials, 2016, 15, 30.	3.8	15
80	High Nasal Carriage Rate of Staphylococcus aureus Containing Panton-Valentine leukocidin- and EDIN-Encoding Genes in Community and Hospital Settings in Burkina Faso. Frontiers in Microbiology, 2016, 7, 1406.	3.5	14
81	Lower mgpB diversity in macrolide-resistant Mycoplasma genitalium infecting men visiting two sexually transmitted infection clinics in Montpellier, France. Journal of Antimicrobial Chemotherapy, 2021, 76, 43-47.	3.0	13
82	Population structure of colonizing and invasive Staphylococcus aureus strains in northern Vietnam. Journal of Medical Microbiology, 2016, 65, 298-305.	1.8	13
83	Intrafamilial Cluster of Pulmonary Tuberculosis Due to Mycobacterium bovis of the African 1 Clonal Complex. Journal of Clinical Microbiology, 2010, 48, 4680-4683.	3.9	12
84	Complete mitochondrial genome of Lutzomyia (Nyssomyia) umbratilis (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Mapping, Sequencing, and Analysis, 2016, 27, 4219-4221.	0.7	12
85	Spread of NDM-5 and OXA-181 Carbapenemase-Producing Escherichia coli in Chad. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	12
86	Expansion of KPCâ€“producing Enterobacterales in four large hospitals in Hanoi, Vietnam. Journal of Global Antimicrobial Resistance, 2021, 27, 200-211.	2.2	12
87	Evaluation of the GenoType NTM-DR assay performance for the identification and molecular detection of antibiotic resistance in Mycobacterium abscessus complex. PLoS ONE, 2020, 15, e0239146.	2.5	11
88	Genetic Diversity and Population Structure of Leishmania infantum from Southeastern France: Evaluation Using Multi-Locus Microsatellite Typing. PLoS Neglected Tropical Diseases, 2016, 10, e0004303.	3.0	10
89	Leishmania major and Trypanosoma lewisi infection in invasive and native rodents in Senegal. PLoS Neglected Tropical Diseases, 2018, 12, e0006615.	3.0	10
90	Comparison of Leishmania killicki (syn. L. tropica) and Leishmania tropica Population Structure in Maghreb by Microsatellite Typing. PLoS Neglected Tropical Diseases, 2015, 9, e0004204.	3.0	10

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91	Multilocus microsatellite typing ofLeishmaniaand clinical applications: a review. Parasite, 2015, 22, 16.	2.0	9
92	Reduced turn-around time for Mycobacterium tuberculosis drug susceptibility testing with a proportional agar microplate assay. Clinical Microbiology and Infection, 2015, 21, 1084-1092.	6.0	9
93	Genetic diversity and population structure of Mycobacterium tuberculosis in HIV-1-infected compared with uninfected individuals in Burkina Faso. Aids, 2007, 21, 248-250.	2.2	8
94	Highly structured genetic diversity of the Mycobacterium tuberculosis population in Djibouti. Clinical Microbiology and Infection, 2010, 16, 1023-1026.	6.0	8
95	Spatio-temporal Genetic Structuring of Leishmania major in Tunisia by Microsatellite Analysis. PLoS Neglected Tropical Diseases, 2015, 9, e0004017.	3.0	8
96	Incubation Period for Neuroinvasive Toscana Virus Infections. Emerging Infectious Diseases, 2021, 27, 3147-3150.	4.3	8
97	First insights into the genetic diversity and origin of Leishmania infantum in Mont Rolland (ThiÃ¨s) Tj ETQq1 1 0.784314 rgBT /Overloc	1.9	7
98	Quadruple-first line drug resistance in Mycobacterium tuberculosis in Vietnam: What can we learn from genes?. Infection, Genetics and Evolution, 2017, 50, 55-61.	2.3	7
99	Phlebotomus (Paraphlebotomus) chabaudi and Phlebotomus riouxi: closely related species or synonyms?. Parasite, 2017, 24, 47.	2.0	7
100	A single amino acid substitution (H451Y) in Leishmania calcium-dependent kinase SCAMK confers high tolerance and resistance to antimony. Journal of Antimicrobial Chemotherapy, 2019, 74, 3231-3239.	3.0	7
101	A first insight into genetic diversity of Mycobacterium bovis isolated from extrapulmonary tuberculosis patients in South Tunisia assessed by spoligotyping and MIRU VNTR. PLoS Neglected Tropical Diseases, 2019, 13, e0007707.	3.0	7
102	Metabarcoding: A Powerful Yet Still Underestimated Approach for the Comprehensive Study of Vector-Borne Pathogen Transmission Cycles and Their Dynamics. , 0, , .		7
103	Population Structure of Trypanosoma brucei s. l. in Cote D'Ivoire Assayed by Multilocus Enzyme Electrophoresis: Epidemiological and Taxonomical Considerations. Journal of Parasitology, 1997, 83, 19.	0.7	6
104	Pulmonary Tuberculosis andMycobacterium Tuberculosis: Modern Molecular Epidemiology and Perspectives. , 0, , 1-29.		6
105	Comparative Study of Promastigote- and Amastigote-Initiated Infection of Leishmania infantum (Kinetoplastida: Trypanosomatidae) in Phlebotomus perniciosus (Diptera: Psychodidae) Conducted in Different Biosafety Level Laboratories. Journal of Medical Entomology, 2020, 57, 601-607.	1.8	6
106	Resistance to Second-Line Anti-TB Drugs in Cambodia: A Phenotypic and Genetic Study. Infection and Drug Resistance, 2021, Volume 14, 1089-1104.	2.7	6
107	Rifampin-ResistantMycobacterium bovisBCGâ€“Induced Disease in HIV-Infected Infant, Vietnam. Emerging Infectious Diseases, 2013, 19, 1168-1168.	4.3	5
108	Response to Tibayrenc et al.: can recombination in Leishmania parasites be so rare?. Trends in Parasitology, 2015, 31, 280-281.	3.3	5

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109	New microsatellite markers for multi-scale genetic studies on Phlebotomus ariasi Tonnoir, vector of Leishmania infantum in the Mediterranean area. Acta Tropica, 2015, 142, 79-85.	2.0	5
110	Rocking the curve. Trends in Microbiology, 2004, 12, 534-536.	7.7	4
111	Sacroiliitis secondary to catheter-related bacteremia due to Mycobacterium abscessus (sensu) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.8	4
112	Diversity and Ecology of Sand Flies (Diptera: Psychodidae), Potential Vectors of Leishmania in the Quang Ninh Province, Vietnam. Journal of Medical Entomology, 2020, 57, 259-265.	1.8	4
113	Resistance mechanisms and genetic relatedness among carbapenem-resistant Pseudomonas aeruginosa isolates from three major hospitals in Hanoi, Vietnam (2011â€“15). JAC-Antimicrobial Resistance, 2021, 3, dlab103.	2.1	4
114	Taxonomical insights and ecology of sandfly (Diptera, Psychodidae) species in six provinces of Northern Vietnam. Parasite, 2021, 28, 85.	2.0	4
115	First insights into the genetic characteristics and drug resistance of Mycobacterium tuberculosis population collected during the first national tuberculosis prevalence survey of Lao PDR (2010â€“2011). BMC Infectious Diseases, 2019, 19, 851.	2.9	3
116	Altitude and hillside orientation shapes the population structure of the Leishmania infantum vector Phlebotomus ariasi. Scientific Reports, 2020, 10, 14443.	3.3	3
117	Evaluation of Loopamp Assay for the Diagnosis of Pulmonary Tuberculosis in Cambodia. BioMed Research International, 2020, 2020, 1-7.	1.9	2
118	Rifampin-ResistantMycobacterium bovisBCGâ€“Induced Disease in HIV-Infected Infant, Vietnam. Emerging Infectious Diseases, 2013, 19, 1168-1168.	4.3	2
119	Multilocus microsatellite typing of Leishmania infantum isolates in monitored Leishmania/HIV coinfected patients. Parasites and Vectors, 2015, 8, 386.	2.5	1
120	Un cas inhabituel de spondylodiscite Ã Staphylococcus saccharolyticus. Revue Du Rhumatisme (Edition) Tj ETQq0 0 0 rgBT /Overlock 10	0.0	0