

Yann F Boucher

List of Publications by Year in descending order

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75
papers

5,306
citations

136950

32
h-index

91884

69
g-index

80
all docs

80
docs citations

80
times ranked

6147
citing authors

#	ARTICLE	IF	CITATIONS
1	Use of 16S rRNA and rpoB Genes as Molecular Markers for Microbial Ecology Studies. Applied and Environmental Microbiology, 2007, 73, 278-288.	3.1	492
2	Comparison of Bayesian and Maximum Likelihood Bootstrap Measures of Phylogenetic Reliability. Molecular Biology and Evolution, 2003, 20, 248-254.	8.9	460
3	The Evolution of Class 1 Integrins and the Rise of Antibiotic Resistance. Journal of Bacteriology, 2008, 190, 5095-5100.	2.2	432
4	Lateral Gene Transfer and the Origins of Prokaryotic Groups. Annual Review of Genetics, 2003, 37, 283-328.	7.6	357
5	Integrins: mobilizable platforms that promote genetic diversity in bacteria. Trends in Microbiology, 2007, 15, 301-309.	7.7	266
6	Roseobacters in a Sea of Poly- and Paraphyly: Whole Genome-Based Taxonomy of the Family Rhodobacteraceae and the Proposal for the Split of the "Roseobacter Clade" into a Novel Family, Roseobacteraceae fam. nov.. Frontiers in Microbiology, 2021, 12, 683109.	3.5	263
7	The role of lateral gene transfer in the evolution of isoprenoid biosynthesis pathways. Molecular Microbiology, 2000, 37, 703-716.	2.5	247
8	Higher-level classification of the Archaea: evolution of methanogenesis and methanogens. Archaea, 2005, 1, 353-363.	2.3	218
9	Prokaryotic evolution and the tree of life are two different things. Biology Direct, 2009, 4, 34.	4.6	188
10	Origins and evolution of isoprenoid lipid biosynthesis in archaea. Molecular Microbiology, 2004, 52, 515-527.	2.5	145
11	Class 1 Integrins Potentially Predating the Association with Tn 402 -Like Transposition Genes Are Present in a Sediment Microbial Community. Journal of Bacteriology, 2006, 188, 5722-5730.	2.2	139
12	Phylogenetic reconstruction and lateral gene transfer. Trends in Microbiology, 2004, 12, 406-411.	7.7	124
13	Evolutionary Dynamics of Vibrio cholerae O1 following a Single-Source Introduction to Haiti. MBio, 2013, 4, .	4.1	118
14	Intragenomic Heterogeneity and Intergenomic Recombination among Haloarchaeal rRNA Genes. Journal of Bacteriology, 2004, 186, 3980-3990.	2.2	110
15	The 2010 Cholera Outbreak in Haiti: How Science Solved a Controversy. PLoS Pathogens, 2014, 10, e1003967.	4.7	99
16	Local Mobile Gene Pools Rapidly Cross Species Boundaries To Create Endemicity within Global Vibrio cholerae Populations. MBio, 2011, 2, .	4.1	97
17	Sequential displacement of Type VI Secretion System effector genes leads to evolution of diverse immunity gene arrays in Vibrio cholerae. Scientific Reports, 2017, 7, 45133.	3.3	90
18	Microbial genomes: dealing with diversity. Current Opinion in Microbiology, 2001, 4, 285-289.	5.1	85

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19	Ancient origin of the biosynthesis of lignin precursors. <i>Biology Direct</i> , 2015, 10, 23.	4.6	78
20	Metapopulation structure of <i>Vibrionaceae</i> among coastal marine invertebrates. <i>Environmental Microbiology</i> , 2011, 13, 265-275.	3.8	76
21	Defining the Core of Nontransferable Prokaryotic Genes: The Euryarchaeal Core. <i>Journal of Molecular Evolution</i> , 2001, 53, 340-350.	1.8	74
22	Integron-associated gene cassettes in Halifax Harbour: assessment of a mobile gene pool in marine sediments. <i>Environmental Microbiology</i> , 2008, 10, 1024-1038.	3.8	59
23	Lateral gene transfer challenges principles of microbial systematics. <i>Trends in Microbiology</i> , 2008, 16, 200-207.	7.7	56
24	ACID: annotation of cassette and integron data. <i>BMC Bioinformatics</i> , 2009, 10, 118.	2.6	53
25	Paradigm change in evolutionary microbiology. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2005, 36, 183-208.	1.3	51
26	Recovery and evolutionary analysis of complete integron gene cassette arrays from <i>Vibrio</i> . <i>BMC Evolutionary Biology</i> , 2006, 6, 3.	3.2	51
27	Integron Gene Cassettes and Degradation of Compounds Associated with Industrial Waste: The Case of the Sydney Tar Ponds. <i>PLoS ONE</i> , 2009, 4, e5276.	2.5	46
28	Bacterial Origin for the Isoprenoid Biosynthesis Enzyme HMG-CoA Reductase of the Archaeal Orders Thermoplasmatales and Archaeoglobales. <i>Molecular Biology and Evolution</i> , 2001, 18, 1378-1388.	8.9	45
29	Use of chromosomal integron arrays as a phylogenetic typing system for <i>Vibrio cholerae</i> pandemic strains. <i>Microbiology (United Kingdom)</i> , 2007, 153, 1488-1498.	1.8	41
30	A genomic island in <i>Vibrio cholerae</i> with VPI-1 site-specific recombination characteristics contains CRISPR-Cas and type VI secretion modules. <i>Scientific Reports</i> , 2016, 6, 36891.	3.3	40
31	<i>Vibrio metoecus</i> sp. nov., a close relative of <i>Vibrio cholerae</i> isolated from coastal brackish ponds and clinical specimens. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 3208-3214.	1.7	39
32	Coral-mucus-associated <i>Vibrio</i> integrons in the Great Barrier Reef: genomic hotspots for environmental adaptation. <i>ISME Journal</i> , 2011, 5, 962-972.	9.8	37
33	Inferring functional constraints and divergence in protein families using 3D mapping of phylogenetic information. <i>Nucleic Acids Research</i> , 2003, 31, 790-797.	14.5	35
34	Epistemological Impacts of Horizontal Gene Transfer on Classification in Microbiology. <i>Methods in Molecular Biology</i> , 2009, 532, 55-72.	0.9	34
35	Lateral gene transfer and phylogenetic assignment of environmental fosmid clones. <i>Environmental Microbiology</i> , 2005, 7, 2011-2026.	3.8	33
36	The Dynamics of Genetic Interactions between <i>Vibrio metoecus</i> and <i>Vibrio cholerae</i> , Two Close Relatives Co-Occurring in the Environment. <i>Genome Biology and Evolution</i> , 2015, 7, 2941-2954.	2.5	33

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37	Improving protein solubility: The use of the <i>Escherichia coli</i> dihydrofolate reductase gene as a fusion reporter. <i>Protein Expression and Purification</i> , 2006, 47, 258-263.	1.3	31
38	High Frequency of a Novel Filamentous Phage, VCY1, within an Environmental <i>Vibrio cholerae</i> Population. <i>Applied and Environmental Microbiology</i> , 2012, 78, 28-33.	3.1	27
39	The out-of-the-delta hypothesis: dense human populations in low-lying river deltas served as agents for the evolution of a deadly pathogen. <i>Frontiers in Microbiology</i> , 2015, 6, 1120.	3.5	27
40	Revisiting the concept of lineage in prokaryotes: a phylogenetic perspective. <i>BioEssays</i> , 2009, 31, 526-536.	2.5	25
41	Something new under the sea. <i>Nature</i> , 2002, 417, 27-28.	27.8	24
42	A Small Number of Phylogenetically Distinct Clonal Complexes Dominate a Coastal <i>Vibrio cholerae</i> Population. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5576-5586.	3.1	24
43	Emergence, ecology and dispersal of the pandemic generating <i>Vibrio cholerae</i> lineage. <i>International Microbiology</i> , 2017, 20, 106-115.	2.4	23
44	Characterization of clinical and environmental isolates of <i>Vibrio cideii</i> sp. nov., a close relative of <i>Vibrio nautica</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4148-4155.	1.7	21
45	A putative housekeeping enzyme encoded within an integron array: 1.8Å crystal structure defines a new MazG subtype. <i>Molecular Microbiology</i> , 2007, 66, 610-621.	2.5	20
46	<i>Vibrio</i> 2005: the First International Conference on the Biology of <i>Vibrios</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4592-4596.	2.2	17
47	Refuting phylogenetic relationships. <i>Biology Direct</i> , 2006, 1, 26.	4.6	16
48	Clanistics: a multi-level perspective for harvesting unrooted gene trees. <i>Trends in Microbiology</i> , 2010, 18, 341-347.	7.7	16
49	Genome Sequence of <i>Vibrio rotiferianus</i> Strain DAT722. <i>Journal of Bacteriology</i> , 2011, 193, 3381-3382.	2.2	16
50	A <i>Vibrio cholerae</i> Core Genome Multilocus Sequence Typing Scheme To Facilitate the Epidemiological Study of Cholera. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	16
51	Culture-independent tracking of <i>Vibrio cholerae</i> lineages reveals complex spatiotemporal dynamics in a natural population. <i>Environmental Microbiology</i> , 2020, 22, 4244-4256.	3.8	15
52	Modular Molecular Weaponry Plays a Key Role in Competition Within an Environmental <i>Vibrio cholerae</i> Population. <i>Frontiers in Microbiology</i> , 2021, 12, 671092.	3.5	15
53	Population Analysis of <i>Vibrio cholerae</i> in Aquatic Reservoirs Reveals a Novel Sister Species (<i>Vibrio</i>) Tj ETQq1 1 0.784314 rgBT /Overl <i>Microbiology</i> , 2021, 87, e0042221.	3.1	15
54	Complex Histories of Genes Encoding 3-Hydroxy-3-methylglutaryl-CoenzymeA Reductase. <i>Molecular Biology and Evolution</i> , 2006, 23, 168-178.	8.9	14

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55	Crystal Structure of an Integron Gene Cassette-Associated Protein from <i>Vibrio cholerae</i> Identifies a Cationic Drug-Binding Module. PLoS ONE, 2011, 6, e16934.	2.5	13
56	Major <i>tdh</i> + <i>Vibrio parahaemolyticus</i> serotype changes temporally in the Bay of Bengal estuary of Bangladesh. Infection, Genetics and Evolution, 2016, 41, 153-159.	2.3	12
57	Integron Gene Cassettes: A Repository of Novel Protein Folds with Distinct Interaction Sites. PLoS ONE, 2013, 8, e52934.	2.5	11
58	Draft Genome Sequences of Seven Bacterial Strains Isolated from a Polymicrobial Culture of Coccolith-Bearing (C-Type) <i>Emiliana huxleyi</i> M217. Genome Announcements, 2016, 4, .	0.8	11
59	Sustained Local Diversity of <i>Vibrio cholerae</i> O1 Biotypes in a Previously Cholera-Free Country. MBio, 2016, 7, .	4.1	10
60	Draft Genome Sequences of Nine <i>Vibrio</i> sp. Isolates from across the United States Closely Related to <i>Vibrio cholerae</i> . Microbiology Resource Announcements, 2018, 7, .	0.6	8
61	Simultaneous Quantification of <i>Vibrio metoecus</i> and <i>Vibrio cholerae</i> with Its O1 Serogroup and Toxigenic Subpopulations in Environmental Reservoirs. Pathogens, 2020, 9, 1053.	2.8	8
62	Structural Genomics of the Bacterial Mobile Metagenome: an Overview. Methods in Molecular Biology, 2008, 426, 589-595.	0.9	7
63	Lipids: Biosynthesis, Function, and Evolution. , 0, , 341-353.		7
64	Complete Genome Sequence of <i>Vibrio</i> sp. Strain 2521-89, a Close Relative of <i>Vibrio cholerae</i> Isolated from Lake Water in New Mexico, USA. Genome Announcements, 2017, 5, .	0.8	6
65	Molecular musings in microbial ecology and evolution. Biology Direct, 2011, 6, 58.	4.6	5
66	Integron associated mobile genes. Mobile Genetic Elements, 2012, 2, 13-18.	1.8	5
67	Draft Genome Sequences of Four Bacterial Strains Isolated from a Polymicrobial Culture of Naked (N-Type) <i>Emiliana huxleyi</i> CCMP1516. Genome Announcements, 2016, 4, .	0.8	5
68	Draft Genome Sequences of Eight <i>Vibrio</i> sp. Clinical Isolates from across the United States That Form a Basal Sister Clade to <i>Vibrio cholerae</i> . Microbiology Resource Announcements, 2019, 8, .	0.6	5
69	The Roles of Lateral Gene Transfer and Vertical Descent in <i>Vibrio</i> Evolution. , 0, , 84-94.		5
70	Integration of a laterally acquired gene into a cell network important for growth in a strain of <i>Vibrio rotiferianus</i> . BMC Microbiology, 2011, 11, 253.	3.3	4
71	Assay for Evaluating the Abundance of <i>Vibrio cholerae</i> and Its O1 Serogroup Subpopulation from Water without DNA Extraction. Pathogens, 2022, 11, 363.	2.8	4
72	Dynamic Subspecies Population Structure of <i>Vibrio cholerae</i> in Dhaka, Bangladesh. Microbial Ecology, 2022, 84, 730-745.	2.8	1

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73	Poster session abstracts for Genomics: the Power and the Promise 2014 / Les r�sum�s sur affiches La g�nomique : le pouvoir et la promesse 2014. Genome, 2014, 57, 373-410.	2.0	0
74	Lateral Gene Transfer and Microbial Diversity. , 2013, , 1-7.		0
75	Lateral Gene Transfer and Microbial Diversity. , 2015, , 347-352.		0