

Yann F Boucher

List of Publications by Year in descending order

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75
papers

5,306
citations

136885

32
h-index

91828

69
g-index

80
all docs

80
docs citations

80
times ranked

6147
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic Subspecies Population Structure of <i>Vibrio cholerae</i> in Dhaka, Bangladesh. <i>Microbial Ecology</i> , 2022, 84, 730-745.	1.4	1
2	Assay for Evaluating the Abundance of <i>Vibrio cholerae</i> and Its O1 Serogroup Subpopulation from Water without DNA Extraction. <i>Pathogens</i> , 2022, 11, 363.	1.2	4
3	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.	1.5	15
4	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.. <i>Frontiers in Microbiology</i> , 2021, 12, 683109.	1.5	263
5	Population Analysis of <i>Vibrio cholerae</i> in Aquatic Reservoirs Reveals a Novel Sister Species (<i>Vibrio</i>) Tj ETQq1 1 0.784314 rgBT /Over <i>Microbiology</i> , 2021, 87, e0042221.	1.4	15
6	Simultaneous Quantification of <i>Vibrio metoecus</i> and <i>Vibrio cholerae</i> with Its O1 Serogroup and Toxigenic Subpopulations in Environmental Reservoirs. <i>Pathogens</i> , 2020, 9, 1053.	1.2	8
7	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, .	1.0	16
8	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.	1.8	15
9	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> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
10	Draft Genome Sequences of Nine <i>Vibrio</i> sp. Isolates from across the United States Closely Related to <i>Vibrio cholerae</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	8
11	Sequential displacement of Type VI Secretion System effector genes leads to evolution of diverse immunity gene arrays in <i>Vibrio cholerae</i> . <i>Scientific Reports</i> , 2017, 7, 45133.	1.6	90
12	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. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
13	Emergence, ecology and dispersal of the pandemic generating <i>Vibrio cholerae</i> lineage. <i>International Microbiology</i> , 2017, 20, 106-115.	1.1	23
14	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.	1.4	24
15	Sustained Local Diversity of <i>Vibrio cholerae</i> O1 Biotypes in a Previously Cholera-Free Country. <i>MBio</i> , 2016, 7, .	1.8	10
16	Major <i>tdh</i> + <i>Vibrio parahaemolyticus</i> serotype changes temporally in the Bay of Bengal estuary of Bangladesh. <i>Infection, Genetics and Evolution</i> , 2016, 41, 153-159.	1.0	12
17	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.	1.6	40
18	Draft Genome Sequences of Seven Bacterial Strains Isolated from a Polymicrobial Culture of Coccolith-Bearing (C-Type) <i>Emiliana huxleyi</i> M217. <i>Genome Announcements</i> , 2016, 4, .	0.8	11

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19	Draft Genome Sequences of Four Bacterial Strains Isolated from a Polymicrobial Culture of Naked (N-Type) <i>Emiliana huxleyi</i> CCMP1516. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
20	Characterization of clinical and environmental isolates of <i>Vibrio cidicii</i> sp. nov., a close relative of <i>Vibrio navarrensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4148-4155.	0.8	21
21	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.	1.5	27
22	Ancient origin of the biosynthesis of lignin precursors. <i>Biology Direct</i> , 2015, 10, 23.	1.9	78
23	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.	1.1	33
24	Lateral Gene Transfer and Microbial Diversity. , 2015, , 347-352.		0
25	<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.	0.8	39
26	The 2010 Cholera Outbreak in Haiti: How Science Solved a Controversy. <i>PLoS Pathogens</i> , 2014, 10, e1003967.	2.1	99
27	Poster session abstracts for Genomics: the Power and the Promise 2014 / Les r�sum�s sur affiches La g�nominique : le pouvoir et la promesse 2014. <i>Genome</i> , 2014, 57, 373-410.	0.9	0
28	Evolutionary Dynamics of <i>Vibrio cholerae</i> O1 following a Single-Source Introduction to Haiti. <i>MBio</i> , 2013, 4, .	1.8	118
29	Integron Gene Cassettes: A Repository of Novel Protein Folds with Distinct Interaction Sites. <i>PLoS ONE</i> , 2013, 8, e52934.	1.1	11
30	Lateral Gene Transfer and Microbial Diversity. , 2013, , 1-7.		0
31	Integron associated mobile genes. <i>Mobile Genetic Elements</i> , 2012, 2, 13-18.	1.8	5
32	High Frequency of a Novel Filamentous Phage, VCY�, within an Environmental <i>Vibrio cholerae</i> Population. <i>Applied and Environmental Microbiology</i> , 2012, 78, 28-33.	1.4	27
33	Local Mobile Gene Pools Rapidly Cross Species Boundaries To Create Endemicity within Global <i>Vibrio cholerae</i> Populations. <i>MBio</i> , 2011, 2, .	1.8	97
34	Crystal Structure of an Integron Gene Cassette-Associated Protein from <i>Vibrio cholerae</i> Identifies a Cationic Drug-Binding Module. <i>PLoS ONE</i> , 2011, 6, e16934.	1.1	13
35	Metapopulation structure of <i>Vibrionaceae</i> among coastal marine invertebrates. <i>Environmental Microbiology</i> , 2011, 13, 265-275.	1.8	76
36	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.	4.4	37

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37	Molecular musings in microbial ecology and evolution. <i>Biology Direct</i> , 2011, 6, 58.	1.9	5
38	Integration of a laterally acquired gene into a cell network important for growth in a strain of <i>Vibrio rotiferianus</i> . <i>BMC Microbiology</i> , 2011, 11, 253.	1.3	4
39	Genome Sequence of <i>Vibrio rotiferianus</i> Strain DAT722. <i>Journal of Bacteriology</i> , 2011, 193, 3381-3382.	1.0	16
40	Clanistics: a multi-level perspective for harvesting unrooted gene trees. <i>Trends in Microbiology</i> , 2010, 18, 341-347.	3.5	16
41	ACID: annotation of cassette and integron data. <i>BMC Bioinformatics</i> , 2009, 10, 118.	1.2	53
42	Revisiting the concept of lineage in prokaryotes: a phylogenetic perspective. <i>BioEssays</i> , 2009, 31, 526-536.	1.2	25
43	Prokaryotic evolution and the tree of life are two different things. <i>Biology Direct</i> , 2009, 4, 34.	1.9	188
44	Epistemological Impacts of Horizontal Gene Transfer on Classification in Microbiology. <i>Methods in Molecular Biology</i> , 2009, 532, 55-72.	0.4	34
45	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.	1.1	46
46	Integron-associated gene cassettes in Halifax Harbour: assessment of a mobile gene pool in marine sediments. <i>Environmental Microbiology</i> , 2008, 10, 1024-1038.	1.8	59
47	Lateral gene transfer challenges principles of microbial systematics. <i>Trends in Microbiology</i> , 2008, 16, 200-207.	3.5	56
48	The Evolution of Class 1 Integrons and the Rise of Antibiotic Resistance. <i>Journal of Bacteriology</i> , 2008, 190, 5095-5100.	1.0	432
49	Structural Genomics of the Bacterial Mobile Metagenome: an Overview. <i>Methods in Molecular Biology</i> , 2008, 426, 589-595.	0.4	7
50	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.	0.7	41
51	Integrons: mobilizable platforms that promote genetic diversity in bacteria. <i>Trends in Microbiology</i> , 2007, 15, 301-309.	3.5	266
52	Use of 16S rRNA and rpoB Genes as Molecular Markers for Microbial Ecology Studies. <i>Applied and Environmental Microbiology</i> , 2007, 73, 278-288.	1.4	492
53	A putative housecleaning enzyme encoded within an integron array: 1.8Å... crystal structure defines a new MazG subtype. <i>Molecular Microbiology</i> , 2007, 66, 610-621.	1.2	20
54	Refuting phylogenetic relationships. <i>Biology Direct</i> , 2006, 1, 26.	1.9	16

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55	Improving protein solubility: The use of the Escherichia coli dihydrofolate reductase gene as a fusion reporter. <i>Protein Expression and Purification</i> , 2006, 47, 258-263.	0.6	31
56	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
57	Complex Histories of Genes Encoding 3-Hydroxy-3-methylglutaryl-CoenzymeA Reductase. <i>Molecular Biology and Evolution</i> , 2006, 23, 168-178.	3.5	14
58	Class 1 Integrons Potentially Predating the Association with Tn 402 -Like Transposition Genes Are Present in a Sediment Microbial Community. <i>Journal of Bacteriology</i> , 2006, 188, 5722-5730.	1.0	139
59	<i>Vibrio</i> 2005: the First International Conference on the Biology of <i>Vibrios</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4592-4596.	1.0	17
60	Lateral gene transfer and phylogenetic assignment of environmental fosmid clones. <i>Environmental Microbiology</i> , 2005, 7, 2011-2026.	1.8	33
61	Higher-level classification of the Archaea: evolution of methanogenesis and methanogens. <i>Archaea</i> , 2005, 1, 353-363.	2.3	218
62	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.	0.8	51
63	Origins and evolution of isoprenoid lipid biosynthesis in archaea. <i>Molecular Microbiology</i> , 2004, 52, 515-527.	1.2	145
64	Intragenomic Heterogeneity and Intergenomic Recombination among Haloarchaeal rRNA Genes. <i>Journal of Bacteriology</i> , 2004, 186, 3980-3990.	1.0	110
65	Phylogenetic reconstruction and lateral gene transfer. <i>Trends in Microbiology</i> , 2004, 12, 406-411.	3.5	124
66	Lateral Gene Transfer and the Origins of Prokaryotic Groups. <i>Annual Review of Genetics</i> , 2003, 37, 283-328.	3.2	357
67	Comparison of Bayesian and Maximum Likelihood Bootstrap Measures of Phylogenetic Reliability. <i>Molecular Biology and Evolution</i> , 2003, 20, 248-254.	3.5	460
68	Inferring functional constraints and divergence in protein families using 3D mapping of phylogenetic information. <i>Nucleic Acids Research</i> , 2003, 31, 790-797.	6.5	35
69	Something new under the sea. <i>Nature</i> , 2002, 417, 27-28.	13.7	24
70	Microbial genomes: dealing with diversity. <i>Current Opinion in Microbiology</i> , 2001, 4, 285-289.	2.3	85
71	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.	3.5	45
72	Defining the Core of Nontransferable Prokaryotic Genes: The Euryarchaeal Core. <i>Journal of Molecular Evolution</i> , 2001, 53, 340-350.	0.8	74

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73	The role of lateral gene transfer in the evolution of isoprenoid biosynthesis pathways. <i>Molecular Microbiology</i> , 2000, 37, 703-716.	1.2	247
74	Lipids: Biosynthesis, Function, and Evolution. , 0, , 341-353.		7
75	The Roles of Lateral Gene Transfer and Vertical Descent in <i>Vibrio</i> Evolution. , 0, , 84-94.		5