Bert Ely

List of Publications by Year in descending order

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218677 197818 2,753 71 26 49 citations h-index g-index papers 2102 74 74 74 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Plasmids Bring Additional Capabilities to Caulobacter Isolates. Current Microbiology, 2022, 79, 45.	2.2	O
2	S2B, a Temperate Bacteriophage That Infects Caulobacter Crescentus Strain CB15. Current Microbiology, 2022, 79, 98.	2.2	4
3	Genes related to redox and cell curvature facilitate interactions between Caulobacter strains and Arabidopsis. PLoS ONE, 2021, 16, e0249227.	2.5	5
4	Genomic GC content drifts downward in most bacterial genomes. PLoS ONE, 2021, 16, e0244163.	2.5	7
5	Evolutionary history of Caulobacter toxin–antitoxin systems. Current Microbiology, 2021, 78, 2899-2904.	2.2	2
6	Identification of proteins associated with two diverse Caulobacter phicbkvirus particles. Archives of Virology, 2020, 165, 1995-2002.	2.1	0
7	Novel Caulobacter bacteriophages illustrate the diversity of the podovirus genus Rauchvirus. Archives of Virology, 2020, 165, 2549-2554.	2.1	O
8	Plant growth enhancement is not a conserved feature in the Caulobacter genus. Plant and Soil, 2020, 449, 81-95.	3.7	17
9	Recombination and gene loss occur simultaneously during bacterial horizontal gene transfer. PLoS ONE, 2020, 15, e0227987.	2.5	15
10	The Isolation and Characterization of Kronos, a Novel Caulobacter Rhizosphere Phage that is Similar to Lambdoid Phages. Current Microbiology, 2019, 76, 558-565.	2.2	9
11	Genome Comparisons of Wild Isolates of Caulobacter crescentus Reveal Rates of Inversion and Horizontal Gene Transfer. Current Microbiology, 2019, 76, 159-167.	2.2	11
12	Analyses of four new Caulobacter Phicbkviruses indicate independent lineages. Journal of General Virology, 2019, 100, 321-331.	2.9	10
13	A Genome Comparison of T7-like Podoviruses That Infect Caulobacter crescentus. Current Microbiology, 2018, 75, 760-765.	2.2	4
14	Complete Genome Sequence of a Wild-Type Isolate of Caulobacter vibrioides Strain CB1. Microbiology Resource Announcements, 2018, 7, .	0.6	1
15	Complete Genome Sequence of a Wild-Type Isolate of Caulobacter vibrioides Strain CB2. Microbiology Resource Announcements, 2018, 7, .	0.6	0
16	Achieving Accurate Sequence and Annotation Data for Caulobacter vibrioides CB13. Current Microbiology, 2018, 75, 1642-1648.	2.2	6
17	Genomic Diversity of Type B3 Bacteriophages of Caulobacter crescentus. Current Microbiology, 2017, 74, 779-786.	2.2	12
18	Conservation of the Essential Genome Among Caulobacter and Brevundimonas Species. Current Microbiology, 2016, 72, 503-510.	2.2	13

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19	Characterization of the Proteins Associated with Caulobacter crescentus Bacteriophage CbK Particles. Current Microbiology, 2016, 72, 75-80.	2.2	5
20	Genome Sequence and Phenotypic Characterization of Caulobacter segnis. Current Microbiology, 2015, 70, 355-363.	2.2	13
21	The Caulobacter crescentus Transducing Phage Cr30 is a Unique Member of the T4-Like Family of Myophages. Current Microbiology, 2015, 70, 854-858.	2.2	11
22	Comparison of Genome Sequencing Technology and Assembly Methods for the Analysis of a GC-Rich Bacterial Genome. Current Microbiology, 2015, 70, 338-344.	2.2	24
23	A comparison of the Caulobacter NA1000 and K31 genomes reveals extensive genome rearrangements and differences in metabolic potential. Open Biology, 2014, 4, 140128.	3.6	16
24	Correction of the Caulobacter crescentus NA1000 Genome Annotation. PLoS ONE, 2014, 9, e91668.	2.5	7
25	Codon Usage Methods for Horizontal Gene Transfer Detection Generate an Abundance of False Positive and False Negative Results. Current Microbiology, 2012, 65, 639-642.	2.2	19
26	Across Bacterial Phyla, Distantly-Related Genomes with Similar Genomic GC Content Have Similar Patterns of Amino Acid Usage. PLoS ONE, 2011, 6, e17677.	2.5	71
27	Alternative mechanism for bacteriophage adsorption to the motile bacterium <i>Caulobacter crescentus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9963-9968.	7.1	114
28	Evaluating African-Derived mtDNA Haplotype Diversity Via Independent Sample Collections. Journal of the Canadian Society of Forensic Science, 2010, 43, 65-74.	0.9	2
29	Racial differences in the incidence of breast cancer subtypes defined by combined histologic grade and hormone receptor status. Cancer Causes and Control, 2010, 21, 399-409.	1.8	40
30	Evolution of an MHC class la gene fragment in four North American (i) Morone (i) species. Journal of Fish Biology, 2010, 76, 1984-1994.	1.6	1
31	Sibship reconstruction demonstrates the extremely low effective population size of striped bass <i>Morone saxatilis</i> in the Santee–Cooper system, South Carolina, USA. Molecular Ecology, 2009, 18, 4112-4120.	3.9	23
32	Complex evolution of a highly conserved microsatellite locus in several fish species. Journal of Fish Biology, 2009, 75, 442-447.	1.6	2
33	African-American mitochondrial DNAs often match mtDNAs found in multiple African ethnic groups. BMC Biology, 2006, 4, 34.	3.8	45
34	Comparative phylogeography of Atlantic bluefin tuna and swordfish: the combined effects of vicariance, secondary contact, introgression, and population expansion on the regional phylogenies of two highly migratory pelagic fishes. Molecular Phylogenetics and Evolution, 2005, 36, 169-187.	2.7	194
35	Consequences of the historical demography on the global population structure of two highly migratory cosmopolitan marine fishes: the yellowfin tuna (Thunnus albacares) and the skipjack tuna (Katsuwonus pelamis). BMC Evolutionary Biology, 2005, 5, 19.	3.2	106
36	Mitochondrial DNA genetic diversity among four ethnic groups in Sierra Leone. American Journal of Physical Anthropology, 2005, 128, 156-163.	2.1	40

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37	Amphitrite ornata dehaloperoxidase: enhanced activity for the catalytically active globin using MCPBA. Biochemical and Biophysical Research Communications, 2004, 324, 1194-1198.	2.1	47
38	Genetic Variation and Management of Striped Bass Populations in the Coastal Rivers of South Carolina. North American Journal of Fisheries Management, 2004, 24, 1322-1329.	1.0	4
39	Use of AFLP Analyses to Assess Genetic Variation in Morone and Thunnus Species. Marine Biotechnology, 2002, 4, 141-145.	2.4	23
40	Analyses of Nuclear IdhA Gene and mtDNA Control Region Sequences of Atlantic Northern Bluefin Tuna Populations. Marine Biotechnology, 2002, 4, 583-588.	2.4	26
41	Amphitrite ornata, a Marine Worm, Contains Two Dehaloperoxidase Genes. Marine Biotechnology, 2001, 3, 287-292.	2.4	48
42	Effect of Harvest and Effective Population Size on Genetic Diversity in a Striped Bass Population. Transactions of the American Fisheries Society, 2000, 129, 1367-1372.	1.4	10
43	A Family of Six Flagellin Genes Contributes to the Caulobacter crescentus Flagellar Filament. Journal of Bacteriology, 2000, 182, 5001-5004.	2.2	26
44	Isolation and Characterization of Microsatellite Loci for Striped Bass (Morone saxatilis). Marine Biotechnology, 2000, 2, 405-408.	2.4	17
45	FlbT Couples Flagellum Assembly to Gene Expression in <i>Caulobacter crescentus</i> Bacteriology, 1999, 181, 6160-6170.	2.2	52
46	Characterization of a Highly Repetitive Sequence Conserved Among the North American Morone Species. Marine Biotechnology, 1999, 1, 122-130.	2.4	9
47	Regulation of <i>podJ</i> Expression during the <i>Caulobacter crescentus</i> Cell Cycle. Journal of Bacteriology, 1999, 181, 3967-3973.	2.2	40
48	A Polymerase Chain Reaction–Restriction Fragment Length Polymorphism (PCR–RFLP) Assay for the Discrimination of Mitochondrial DNA from the Florida and Northern Subspecies of Largemouth Bass. Transactions of the American Fisheries Society, 1998, 127, 507-511.	1.4	8
49	A New Class of <i>Caulobacter crescentus</i> Flagellar Genes. Journal of Bacteriology, 1998, 180, 5010-5019.	2.2	53
50	Global population structure of the swordfish (Xiphias gladius L.) as revealed by analysis of the mitochondrial DNA control region. Journal of Experimental Marine Biology and Ecology, 1996, 197, 295-310.	1.5	80
51	Evidence for genetic purity of captive and domestic striped bass broodstocks. Aquaculture, 1995, 137, 41-44.	3.5	6
52	[17] Genetics of Caulobacter crescentus. Methods in Enzymology, 1991, 204, 372-384.	1.0	443
53	Nucleotide sequence of the Caulobacter crescents flaF and flbt genes and analysis of codon usage in organisms with G+C-rich genomes. Gene, 1990, 93, 17-25.	2.2	28
54	Use of transmissible plasmids as cloning vectors in Caulobacter crescentus. Gene, 1988, 70, 321-329.	2.2	23

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55	Use of pulsed-field-gradient gel electrophoresis to construct a physical map of the Caulobacter crescentus genome. Gene, 1988, 68, 323-333.	2.2	79
56	Separation of temporal control and trans-acting modulation of flagellin and chemotaxis genes in Caulobacter. Molecular Genetics and Genomics, 1987, 206, 300-306.	2.4	17
57	GENERAL NONCHEMOTACTIC MUTANTS OF <i>CAULOBACTER CRESCENTUS</i> . Genetics, 1986, 114, 717-730.	2.9	41
58	Vectors for transposon mutagenesis of non-enteric bacteria. Molecular Genetics and Genomics, 1985, 200, 302-304.	2.4	42
59	GENETIC MAPPING OF GENES REQUIRED FOR MOTILITY IN <i>CAULOBACTER CRESCENTUS</i> . Genetics, 1984, 108, 523-532.	2.9	63
60	Plasmids and Bacteriocins in <i>Caulobacter</i> Species. Journal of Bacteriology, 1983, 153, 1092-1094.	2.2	10
61	Resistance to amino acid inhibition in Caulobacter crescentus. Molecular Genetics and Genomics, 1982, 187, 446-452.	2.4	12
62	Transposition of Tn7 Occurs at a Single Site on the <i>Caulobacter crescentus</i> Chromosome. Journal of Bacteriology, 1982, 151, 1056-1058.	2.2	35
63	Plasmid-mediated antibiotic resistance in a changing hospital environment: Efficacy of control measures. American Journal of Infection Control, 1980, 8, 65-71.	2.3	13
64	TRANSFER OF DRUG RESISTANCE FACTORS TO THE DIMORPHIC BACTERIUM <i>CAULOBACTER CRESCENTUS </i> /i>. Genetics, 1979, 91, 371-380.	2.9	74
65	ISOLATION OF SPONTANEOUSLY DERIVED MUTANTS OF <i>CAULOBACTER CRESCENTUS</i> . Genetics, 1977, 86, 25-32.	2.9	193
66	GENERALIZED TRANSDUCTION IN <i>CAULOBACTER CRESCENTUS</i> . Genetics, 1977, 87, 391-399.	2.9	130
67	SOME IMPROVED METHODS IN P22 TRANSDUCTION. Genetics, 1974, 76, 625-631.	2.9	83
68	PHYSIOLOGICAL STUDIES OF SALMONELLA HISTIDINE OPERATOR-PROMOTER MUTANTS. Genetics, 1974, 78, 593-606.	2.9	44
69	A FINE STRUCTURE MAP OF THE SALMONELLA HISTIDINE OPERATOR-PROMOTER. Genetics, 1974, 78, 607-631.	2.9	46
70	Histidyl-Transfer Ribonucleic Acid Synthetase in Positive Control of the Histidine Operon in Salmonella typhimurium. Journal of Bacteriology, 1974, 117, 708-716.	2.2	42
71	Internal Promoter P2 of the Histidine Operon of <i>Salmonella typhimurium</i> Journal of Bacteriology, 1974, 120, 984-986.	2.2	31