

Romilio T Espejo

List of Publications by Year in descending order

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72
papers

4,262
citations

117625

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118850

62
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73
docs citations

73
times ranked

2896
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple Ribosomal RNA Operons in Bacteria; Their Concerted Evolution and Potential Consequences on the Rate of Evolution of Their 16S rRNA. <i>Frontiers in Microbiology</i> , 2018, 9, 1232.	3.5	67
2	Gene expression of <i>Vibrio parahaemolyticus</i> growing in laboratory isolation conditions compared to those common in its natural ocean environment. <i>BMC Microbiology</i> , 2017, 17, 118.	3.3	6
3	Insight Into the Origin and Evolution of the <i>Vibrio parahaemolyticus</i> Pandemic Strain. <i>Frontiers in Microbiology</i> , 2017, 8, 1397.	3.5	27
4	Comparative Genome Analysis Provides Insights into the Pathogenicity of <i>Flavobacterium psychrophilum</i> . <i>PLoS ONE</i> , 2016, 11, e0152515.	2.5	41
5	Role of Non-coding Regulatory RNA in the Virulence of Human Pathogenic Vibrios. <i>Frontiers in Microbiology</i> , 2016, 7, 2160.	3.5	24
6	Amplification of <i>tlh</i> gene in other Vibrionaceae specie by specie-specific multiplex PCR of <i>Vibrio parahaemolyticus</i> . <i>Electronic Journal of Biotechnology</i> , 2015, 18, 459-463.	2.2	19
7	Inactivated <i>E. coli</i> transformed with plasmids that produce dsRNA against infectious salmon anemia virus hemagglutinin show antiviral activity when added to infected ASK cells. <i>Frontiers in Microbiology</i> , 2015, 6, 300.	3.5	7
8	Genome diversification within a clonal population of pandemic <i>Vibrio parahaemolyticus</i> seems to depend on the life circumstances of each individual bacteria. <i>BMC Genomics</i> , 2015, 16, 176.	2.8	18
9	Complete Genome Sequence of <i>Vibrio anguillarum</i> Phage CHOED Successfully Used for Phage Therapy in Aquaculture. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
10	Diversity and Geographical Distribution of <i>Flavobacterium psychrophilum</i> Isolates and Their Phages: Patterns of Susceptibility to Phage Infection and Phage Host Range. <i>Microbial Ecology</i> , 2014, 67, 748-757.	2.8	25
11	Genomic structure of bacteriophage 6H and its distribution as prophage in <i>Flavobacterium psychrophilum</i> strains. <i>FEMS Microbiology Letters</i> , 2014, 351, 51-58.	1.8	37
12	Recently discovered <i>Vibrio anguillarum</i> phages can protect against experimentally induced vibriosis in Atlantic salmon, <i>Salmo salar</i> . <i>Aquaculture</i> , 2013, 392-395, 128-133.	3.5	92
13	Rise and fall of pandemic <i>Vibrio parahaemolyticus</i> serotype O3:K6 in southern Chile. <i>Environmental Microbiology</i> , 2013, 15, 527-534.	3.8	23
14	Short-term effects of dietary soybean meal and lactic acid bacteria on the intestinal morphology and microbiota of Atlantic salmon (<i>Salmo salar</i>). <i>Aquaculture Nutrition</i> , 2013, 19, 827-836.	2.7	55
15	Reduction of Soybean Meal Non-Starch Polysaccharides and β -Galactosides by Solid-State Fermentation Using Cellulolytic Bacteria Obtained from Different Environments. <i>PLoS ONE</i> , 2012, 7, e44783.	2.5	30
16	Microevolution of Pandemic <i>Vibrio parahaemolyticus</i> Assessed by the Number of Repeat Units in Short Sequence Tandem Repeat Regions. <i>PLoS ONE</i> , 2012, 7, e30823.	2.5	11
17	Diversity of <i>Flavobacterium psychrophilum</i> and the potential use of its phages for protection against bacterial cold water disease in salmonids. <i>Journal of Fish Diseases</i> , 2012, 35, 193-201.	1.9	68
18	PCR-TTGE Analysis of 16S rRNA from Rainbow Trout (<i>Oncorhynchus mykiss</i>) Gut Microbiota Reveals Host-Specific Communities of Active Bacteria. <i>PLoS ONE</i> , 2012, 7, e31335.	2.5	160

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19	Effect of <i>Thymus vulgaris</i> essential oil on intestinal bacterial microbiota of rainbow trout, <i>Oncorhynchus mykiss</i> (Walbaum) and bacterial isolates. <i>Aquaculture Research</i> , 2010, 41, no-no.	1.8	34
20	Origins and colonization history of pandemic <i>Vibrio parahaemolyticus</i> in South America. <i>Molecular Ecology</i> , 2010, 19, 3924-3937.	3.9	20
21	A new group of cosmopolitan bacteriophages induce a carrier state in the pandemic strain of <i>Vibrio parahaemolyticus</i> . <i>Environmental Microbiology</i> , 2010, 12, 990-1000.	3.8	43
22	Multiple-Locus Variable-Number Tandem-Repeat Analysis for Clonal Identification of <i>Vibrio parahaemolyticus</i> Isolates by Using Capillary Electrophoresis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4079-4088.	3.1	20
23	The Linear Plasmid Prophage Vp58.5 of <i>Vibrio parahaemolyticus</i> Is Closely Related to the Integrating Phage VHML and Constitutes a New Incompatibility Group of Telomere Phages. <i>Journal of Virology</i> , 2009, 83, 9313-9320.	3.4	33
24	Epidemiology of <i>Vibrio parahaemolyticus</i> Outbreaks, Southern Chile. <i>Emerging Infectious Diseases</i> , 2009, 15, 163-168.	4.3	80
25	Dynamics of Clinical and Environmental <i>Vibrio parahaemolyticus</i> Strains during Seafood-Related Summer Diarrhea Outbreaks in Southern Chile. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7482-7487.	3.1	72
26	Molecular Analysis of Microbiota Along the Digestive Tract of Juvenile Atlantic Salmon (<i>Salmo salar</i>)	2.8	141
27	Enhancement of UV Light Sensitivity of a <i>Vibrio parahaemolyticus</i> O3:K6 Pandemic Strain Due to Natural Lysogenization by a Telomeric Phage. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1697-1702.	3.1	17
28	Oxytetracycline Treatment Reduces Bacterial Diversity of Intestinal Microbiota of Atlantic Salmon. <i>Journal of Aquatic Animal Health</i> , 2008, 20, 177-183.	1.4	130
29	Determination of Molecular Phylogenetics of <i>Vibrio parahaemolyticus</i> Strains by Multilocus Sequence Typing. <i>Journal of Bacteriology</i> , 2008, 190, 2831-2840.	2.2	191
30	Intragenomic heterogeneity and intergenomic recombination among <i>Vibrio parahaemolyticus</i> 16S rRNA genes. <i>Microbiology (United Kingdom)</i> , 2007, 153, 2640-2647.	1.8	23
31	<i>Vibrio parahaemolyticus</i> strains isolated during investigation of the summer 2006 seafood related diarrhea outbreaks in two regions of Chile. <i>International Journal of Food Microbiology</i> , 2007, 117, 270-275.	4.7	54
32	<i>Vibrio parahaemolyticus</i> O3:K6 Epidemic Diarrhea, Chile, 2005. <i>Emerging Infectious Diseases</i> , 2007, 13, 655-656.	4.3	25
33	Quantitative reverse transcription polymerase chain reaction analysis of <i>Vibrio cholerae</i> cells entering the viable but non-culturable state and starvation in response to cold shock. <i>Environmental Microbiology</i> , 2006, 8, 658-666.	3.8	102
34	<i>Vibrio parahaemolyticus</i> in shellfish and clinical samples during two large epidemics of diarrhoea in southern Chile. <i>Environmental Microbiology</i> , 2006, 8, 675-683.	3.8	91
35	Variation in the 16S rRNA intergenic spacer regions in <i>Vibrio parahaemolyticus</i> strains are due to indels nearby their tRNA ^{Leu} . <i>FEMS Microbiology Letters</i> , 2006, 256, 38-43.	1.8	9
36	Polymorphism and gene conversion of the 16S rRNA genes in the multiple rRNA operons of <i>Vibrio parahaemolyticus</i> . <i>FEMS Microbiology Letters</i> , 2005, 246, 213-219.	1.8	32

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37	Tracing <i>Vibrio parahaemolyticus</i> in oysters (<i>Tiostrea chilensis</i>) using a Green Fluorescent Protein tag. <i>Journal of Experimental Marine Biology and Ecology</i> , 2005, 327, 157-166.	1.5	25
38	<i>Vibrio parahaemolyticus</i> Diarrhea, Chile, 1998 and 2004. <i>Emerging Infectious Diseases</i> , 2005, 11, 129-131.	4.3	156
39	Comprehensive detection of bacterial populations by PCR amplification of the 16S rRNA spacer region. <i>Journal of Microbiological Methods</i> , 2003, 55, 91-97.	1.6	22
40	Characterization and identification of an iron-oxidizing, <i>Leptospirillum</i> -like bacterium, present in the high sulfate leaching solution of a commercial bioleaching plant. <i>Research in Microbiology</i> , 2003, 154, 353-359.	2.1	19
41	Effect of Associated Bacteria on the Growth and Toxicity of <i>Alexandrium catenella</i> . <i>Applied and Environmental Microbiology</i> , 2003, 69, 659-662.	3.1	72
42	Polymorphism in repeated 16S rRNA genes is a common property of type strains and environmental isolates of the genus <i>Vibrio</i> . The GenBank accession numbers for the sequences reported in this paper are AF388386 (Vp23), AF388387 (Vp16), AF388388 (F44), AF388389 (Vp27), AF388390 (F6), AF388391 (3d2), AF388392 (3d4), AF388393 (3d7) and AF388394 (3d8). <i>Microbiology (United Kingdom)</i> , 2002, 148, 1233-1239.	1.8	143
43	Bacterial 16S rRNA Gene Analysis Revealed That Bacteria Related to <i>Arcobacter</i> spp. Constitute an Abundant and Common Component of the Oyster Microbiota (<i>Tiostrea chilensis</i>). <i>Microbial Ecology</i> , 2002, 44, 365-371.	2.8	99
44	Marine <i>Pseudoalteromonas</i> sp. Composes Most of the Bacterial Population Developed in Oysters (<i>Tiostrea chilensis</i>) Spoiled During Storage. <i>Journal of Food Science</i> , 2002, 67, 2300-2303.	3.1	16
45	RIBOSOMAL RNA HETEROGENEITY AND IDENTIFICATION OF TOXIC DINOFLAGELLATE CULTURES BY HETERODUPLEX MOBILITY ASSAY. <i>Journal of Phycology</i> , 1999, 35, 884-888.	2.3	11
46	Detection by polymerase chain reaction-amplification and sequencing of an archaeon in a commercial-scale copper bioleaching plant. <i>FEMS Microbiology Letters</i> , 1999, 173, 183-187.	1.8	21
47	Detection by polymerase chain reaction-amplification and sequencing of an archaeon in a commercial-scale copper bioleaching plant. <i>FEMS Microbiology Letters</i> , 1999, 173, 183-187.	1.8	12
48	PAGE analysis of the heteroduplexes formed between PCR-amplified 16S rRNA genes: estimation of sequence similarity and rDNA complexity. <i>Microbiology (United Kingdom)</i> , 1998, 144, 1611-1617.	1.8	55
49	Bacterial populations in samples of bioleached copper ore as revealed by analysis of DNA obtained before and after cultivation. <i>Applied and Environmental Microbiology</i> , 1996, 62, 1323-1328.	3.1	89
50	Detection of HIV1 DNA by a simple procedure of polymerase chain reaction, using primer-dimer formation as an internal control of amplification. <i>Research in Virology</i> , 1993, 144, 243-246.	0.7	18
51	HIV Infection in Brazil. <i>New England Journal of Medicine</i> , 1989, 321, 830-832.	27.0	9
52	Oxidation of Ferrous Iron and Elemental Sulfur by <i>Thiobacillus ferrooxidans</i> . <i>Applied and Environmental Microbiology</i> , 1988, 54, 1694-1699.	3.1	41
53	Growth of free and attached <i>Thiobacillus ferrooxidans</i> in ore suspension. <i>Biotechnology and Bioengineering</i> , 1987, 30, 586-592.	3.3	26
54	Growth of <i>Thiobacillus ferrooxidans</i> on Elemental Sulfur. <i>Applied and Environmental Microbiology</i> , 1987, 53, 1907-1912.	3.1	56

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55	Conservation in rotaviruses of the protein region containing the two sites associated with trypsin enhancement of infectivity. <i>Virology</i> , 1986, 154, 224-227.	2.4	53
56	Heterogeneity in base sequence among different DNA clones containing equivalent sequences of rotavirus double-stranded RNA. <i>Journal of Virology</i> , 1986, 57, 1207-1209.	3.4	11
57	Primary structure of the cleavage site associated with trypsin enhancement of rotavirus SA11 infectivity. <i>Virology</i> , 1985, 144, 11-19.	2.4	130
58	Shifts in the electrophoretic pattern on the RNA genome of rota viruses under different electrophoretic conditions. <i>Journal of Virological Methods</i> , 1984, 8, 293-299.	2.1	13
59	Distinctive ribonucleic acid patterns of human rotavirus subgroups 1 and 2. <i>Infection and Immunity</i> , 1981, 33, 958-961.	2.2	171
60	Shift in the prevalent human rotavirus detected by ribonucleic acid segment differences. <i>Infection and Immunity</i> , 1980, 27, 351-354.	2.2	116
61	Different polypeptide composition of two human rotavirus types. <i>Infection and Immunity</i> , 1980, 28, 230-237.	2.2	39
62	Presence of Two Distinct Types of Rotavirus in Infants and Young Children Hospitalized with Acute Gastroenteritis in Mexico City, 1977. <i>Journal of Infectious Diseases</i> , 1979, 139, 474-477.	4.0	102
63	Stimulation of \hat{I}^2 -galactoside transport in pseudomonas BAL-31 by infection with bacteriophage PM2. <i>FEBS Letters</i> , 1977, 81, 289-293.	2.8	0
64	The process of infection with bacteriophage \hat{I}^2 X174. <i>Journal of Molecular Biology</i> , 1976, 102, 723-741.	4.2	5
65	A simple electrophoretic method for the determination of superhelix density of closed circular DNAs and for observation of their superhelix density heterogeneity. <i>Analytical Biochemistry</i> , 1976, 72, 95-103.	2.4	83
66	A difference between intracellular and viral supercoiled PM2 DNA. <i>Journal of Molecular Biology</i> , 1971, 56, 623-626.	4.2	18
67	Replication of bacteriophage PM2 deoxyribonucleic acid: A closed circular double-stranded molecule. <i>Journal of Molecular Biology</i> , 1971, 56, 597-621.	4.2	63
68	The DNA of Bacteriophage PM 2. Ultracentrifugal evidence for a circular structure. <i>Virology</i> , 1969, 37, 495-498.	2.4	22
69	DNA OF BACTERIOPHAGE PM2: A CLOSED CIRCULAR DOUBLE-STRANDED MOLECULE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1969, 63, 1164-1168.	7.1	241
70	Properties of bacteriophage PM2: A lipid-containing bacterial virus. <i>Virology</i> , 1968, 34, 738-747.	2.4	355
71	Properties and Characterization of the Host Bacterium of Bacteriophage PM2. <i>Journal of Bacteriology</i> , 1968, 95, 1887-1891.	2.2	78
72	Origin of Phospholipid in Bacteriophage PM2. <i>Journal of Virology</i> , 1968, 2, 1235-1240.	3.4	23