Josep CasadesÃºs

List of Publications by Year
in descending order

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127	7,419	53794 45	64796 79
papers	citations	h-index	g-index

137	137	137	6879
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Pervasive transcription enhances the accessibility of H-NSâ€“silenced promoters and generates bistability in Salmonella virulence gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	15
2	Evidence for Involvement of the Salmonella enterica Z-Ring Assembly Factors ZapA and ZapB in Resistance to Bile. Frontiers in Microbiology, 2021, 12, 647305.	3.5	0
3	Redox controls RecA protein activity via reversible oxidation of its methionine residues. ELife, 2021, 10, .	6.0	18
4	Genome-Wide Identification and Expression Analysis of SOS Response Genes in Salmonella enterica Serovar Typhimurium. Cells, 2021, 10, 943.	4.1	9
5	Waddingtonâ€™s Landscapes in the Bacterial World. Frontiers in Microbiology, 2021, 12, 685080.	3.5	15
6	Single Cell Analysis of Bistable Expression of Pathogenicity Island 1 and the Flagellar Regulon in Salmonella enterica. Microorganisms, 2021, 9, 210.	3.6	13
7	The bacterial epigenome. Nature Reviews Microbiology, 2020, 18, 7-20.	28.6	160
8	Contribution of DNA adenine methylation to gene expression heterogeneity inSalmonella enterica. Nucleic Acids Research, 2020, 48, 11857-11867.	14.5	21
9	Copy Number Heterogeneity in the Virulence Plasmid of Salmonella enterica. Frontiers in Microbiology, 2020, 11, 599931.	3.5	8
10	Epigenetic biosensors for bacteriophage detection and phage receptor discrimination. Environmental Microbiology, 2020, 22, 3126-3142.	3.8	7
11	A portable epigenetic switch for bistable gene expression in bacteria. Scientific Reports, 2019, 9, 11261.	3.3	15
12	Regulation of bistability in the std fimbrial operon of Salmonella enterica by DNA adenine methylation and transcription factors HdfR, StdE and StdF. Nucleic Acids Research, 2019, 47, 7929-7941.	14.5	21
13	Std fimbriae-fucose interaction increases Salmonella-induced intestinal inflammation and prolongs colonization. PLoS Pathogens, 2019, 15, e1007915.	4.7	49
14	Mutational and non mutational adaptation of Salmonella enterica to the gall bladder. Scientific Reports, 2019, 9, 5203.	3.3	11
15	Bistability and phase variation in Salmonella enterica. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 752-758.	1.9	19
16	Transcriptional regulation of the Salmonella enterica std fimbrial operon by the RcsCDB system. Microbiology (United Kingdom), 2019, 165, 1245-1250.	1.8	0
17	Adaptation of Salmonella enterica to bile: essential role of AcrABâ€mediated efflux. Environmental Microbiology, 2018, 20, 1405-1418.	3.8	20
18	Contribution of SPI-1 bistability to Salmonella enterica cooperative virulence: insights from single cell analysis. Scientific Reports, 2018, 8, 14875.	3.3	30

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19	Formation of phenotypic lineages in Salmonella enterica by a pleiotropic fimbrial switch. PLoS Genetics, 2018, 14, e1007677.	3.5	17
20	The UbiK protein is an accessory factor necessary for bacterial ubiquinone (UQ) biosynthesis and forms a complex with the UQ biogenesis factor UbiJ. Journal of Biological Chemistry, 2017, 292, 11937-11950.	3.4	35
21	Interactions between Bacteria and Bile Salts in the Gastrointestinal and Hepatobiliary Tracts. Frontiers in Medicine, 2017, 4, 163.	2.6	289
22	Pseudomonas syringae Differentiates into Phenotypically Distinct Subpopulations During Colonization of a Plant Host. Environmental Microbiology, 2016, 18, 3593-3605.	3.8	41
23	Bacterial DNA Methylation and Methylomes. Advances in Experimental Medicine and Biology, 2016, 945, 35-61.	1.6	51
24	OxyR-dependent formation of DNA methylation patterns in OpvAB^{OFF}and OpvAB^{ON}cell lineages ofSalmonella enterica. Nucleic Acids Research, 2016, 44, 3595-3609.	14.5	35
25	Formation of Bacterial Lineages in Salmonella enterica by Epigenetic Mechanisms. Epigenetics and Human Health, 2016, , 1-17.	0.2	1
26	Epigenetic Control of Salmonella enterica O-Antigen Chain Length: A Tradeoff between Virulence and Bacteriophage Resistance. PLoS Genetics, 2015, 11, e1005667.	3.5	88
27	Virulence Gene Regulation by l-Arabinose in Salmonella enterica. Genetics, 2015, 200, 807-819.	2.9	24
28	DNA methylation in bacteria: from the methyl group to the methylome. Current Opinion in Microbiology, 2015, 25, 9-16.	5.1	267
29	Small RNA-based feedforward loop with AND-gate logic regulates extrachromosomal DNA transfer in Salmonella. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4772-E4781.	7.1	83
30	Bileâ€induced peptidoglycan remodelling in <scp>S</scp>almonella enterica. Environmental Microbiology, 2015, 17, 1081-1089.	3.8	29
31	Regulation of <scp>S</scp>almonella enterica pathogenicity island 1 (<scp>SPI</scp>â€1) by the <scp>LysR</scp>â€type regulator <scp>LeuO</scp>. Molecular Microbiology, 2014, 91, 1057-1069.	2.5	30
32	A eukaryotic-like 3â€² untranslated region in Salmonella enterica hilD mRNA. Nucleic Acids Research, 2014, 42, 5894-5906.	14.5	50
33	Contribution of phenotypic heterogeneity to adaptive antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 355-360.	7.1	177
34	Dormant Intracellular Salmonella enterica Serovar Typhimurium Discriminates among Salmonella Pathogenicity Island 2 Effectors To Persist inside Fibroblasts. Infection and Immunity, 2014, 82, 221-232.	2.2	27
35	Intestinal invasion of Salmonella enterica serovar Typhimurium in the avian host is dose dependent and does not depend on motility and chemotaxis. Veterinary Microbiology, 2013, 165, 373-377.	1.9	7
36	The role of flagella and chemotaxis genes in host pathogen interaction of the host adapted Salmonella enterica serovar Dublin compared to the broad host range serovar S. Typhimurium. BMC Microbiology, 2013, 13, 67.	3.3	68

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37	Programmed Heterogeneity: Epigenetic Mechanisms in Bacteria. Journal of Biological Chemistry, 2013, 288, 13929-13935.	3.4	193
38	Genome Expression Analysis of Nonproliferating Intracellular Salmonella enterica Serovar Typhimurium Unravels an Acid pH-Dependent PhoP-PhoQ Response Essential for Dormancy. Infection and Immunity, 2013, 81, 154-165.	2.2	58
39	Increased bile resistance in Salmonella enterica mutants lacking Prc periplasmic protease. International Microbiology, 2013, 16, 87-92.	2.4	9
40	Adaptation and Preadaptation of Salmonella enterica to Bile. PLoS Genetics, 2012, 8, e1002459.	3.5	118
41	Crosstalk between Virulence Loci: Regulation of Salmonella enterica Pathogenicity Island 1 (SPI-1) by Products of the std Fimbrial Operon. PLoS ONE, 2012, 7, e30499.	2.5	24
42	The importance of motility and chemotaxis for extra-animal survival of Salmonella enterica serovar Typhimurium and Dublin. Journal of Applied Microbiology, 2012, 113, 560-568.	3.1	11
43	LeuO is a global regulator of gene expression in Salmonella enterica serovar Typhimurium. Molecular Microbiology, 2012, 85, 1072-1089.	2.5	68
44	STM2209-STM2208 (opvAB): A Phase Variation Locus of Salmonella enterica Involved in Control of O-Antigen Chain Length. PLoS ONE, 2012, 7, e36863.	2.5	55
45	Regulation at multiple levels: themes and variations. Current Opinion in Microbiology, 2011, 14, 115-117.	5.1	0
46	Intestinal and chronic infections: Salmonella lifestyles in hostile environments. Environmental Microbiology Reports, 2011, 3, 508-517.	2.4	28
47	Virulence plasmid interchange between strains ATCC 14028, LT2, and SL1344 of Salmonella enterica serovar Typhimurium. Plasmid, 2011, 65, 169-175.	1.4	24
48	Recognition of heptameric seed sequence underlies multiâ€target regulation by RybB small RNA in Salmonella enterica. Molecular Microbiology, 2010, 78, 380-394.	2.5	86
49	Identification of the Salmonella enterica damX Gene Product, an Inner Membrane Protein Involved in Bile Resistance. Journal of Bacteriology, 2010, 192, 893-895.	2.2	33
50	Regulation of Bacterial Conjugation in Microaerobiosis by Host-Encoded Functions ArcAB and SdhABCD. Genetics, 2010, 184, 947-958.	2.9	29
51	Regulation ofSalmonella entericaPathogenicity Island 1 by DNA Adenine Methylation. Genetics, 2010, 184, 637-649.	2.9	38
52	The DamX protein ofEscherichia coliandSalmonella enterica. Gut Microbes, 2010, 1, 285-288.	9.8	10
53	Roles of the Outer Membrane Protein AsmA of Salmonella enterica in the Control of marRAB Expression and Invasion of Epithelial Cells. Journal of Bacteriology, 2009, 191, 3615-3622.	2.2	33
54	Regulation ofigaAand the Rcs System by the MviA Response Regulator inSalmonella enterica. Journal of Bacteriology, 2009, 191, 2743-2752.	2.2	8

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55	Construction of genetically defined aroA mutant of a native E. coli O78:K80 isolated from avian colibacillosis, in Iran. Comparative Clinical Pathology, 2009, 18, 69-75.	0.7	3
56	Roles of DNA adenine methylation in hostâ€“pathogen interactions: mismatch repair, transcriptional regulation, and more. FEMS Microbiology Reviews, 2009, 33, 488-503.	8.6	268
57	Microbial DNA metabolism, genome dynamics and human disease. FEMS Microbiology Reviews, 2009, 33, 451-452.	8.6	0
58	Clocks and switches: bacterial gene regulation by DNA adenine methylation. Current Opinion in Microbiology, 2008, 11, 106-112.	5.1	109
59	Regulation of the Salmonella enterica std Fimbrial Operon by DNA Adenine Methylation, SeqA, and HdfR. Journal of Bacteriology, 2008, 190, 7406-7413.	2.2	60
60	Conjugal Transfer of the Salmonella enterica Virulence Plasmid in the Mouse Intestine. Journal of Bacteriology, 2008, 190, 1922-1927.	2.2	56
61	Insertion Hot Spot for Horizontally Acquired DNA within a Bidirectional Small-RNA Locus inSalmonella enterica. Journal of Bacteriology, 2008, 190, 4075-4078.	2.2	22
62	The GATC-Binding Protein SeqA Is Required for Bile Resistance and Virulence in Salmonella enterica Serovar Typhimurium. Journal of Bacteriology, 2007, 189, 8496-8502.	2.2	28
63	Rcs and PhoPQ Regulatory Overlap in the Control ofSalmonella entericaVirulence. Journal of Bacteriology, 2007, 189, 6635-6644.	2.2	54
64	YhdJ, a Nonessential CcrM-Like DNA Methyltransferase of Escherichia coli and Salmonella enterica. Journal of Bacteriology, 2007, 189, 4325-4327.	2.2	32
65	Bacterial L-forms require peptidoglycan synthesis for cell division. BioEssays, 2007, 29, 1189-1191.	2.5	12
66	Epigenetic Gene Regulation in the Bacterial World. Microbiology and Molecular Biology Reviews, 2006, 70, 830-856.	6.6	539
67	Loss of Hfq activates the ÏƒEâ€dependent envelope stress response inSalmonella enterica. Molecular Microbiology, 2006, 62, 838-852.	2.5	121
68	N6-methyl-adenine: an epigenetic signal for DNAâ€“protein interactions. Nature Reviews Microbiology, 2006, 4, 183-192.	28.6	485
69	DNA Adenine Methylation Regulates Virulence Gene Expression in Salmonella enterica Serovar Typhimurium. Journal of Bacteriology, 2006, 188, 8160-8168.	2.2	110
70	Bile-Induced Curing of the Virulence Plasmid in Salmonella enterica Serovar Typhimurium. Journal of Bacteriology, 2006, 188, 7963-7965.	2.2	39
71	Repair of DNA Damage Induced by Bile Salts in Salmonella enterica. Genetics, 2006, 174, 575-584.	2.9	105
72	The origin and evolution of human pathogens. Molecular Microbiology, 2005, 56, 1-7.	2.5	41

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73	Regulation oftraJtranscription in the Salmonella virulence plasmid by strand-specific DNA adenine hemimethylation. Molecular Microbiology, 2005, 57, 1700-1718.	2.5	67
74	Virulence attenuation in Salmonella enterica rcsC mutants with constitutive activation of the Rcs system. Microbiology (United Kingdom), 2005, 151, 579-588.	1.8	49
75	Regulation of finP Transcription by DNA Adenine Methylation in the Virulence Plasmid of Salmonella enterica. Journal of Bacteriology, 2005, 187, 5691-5699.	2.2	45
76	Regulation of conjugal transfer by Lrp and Dam methylation in plasmid R100. International Microbiology, 2005, 8, 279-85.	2.4	14
77	Bile-Induced DNA Damage in Salmonella enterica. Genetics, 2004, 168, 1787-1794.	2.9	104
78	Repression of the RcsC-YojN-RcsB phosphorelay by the IgaA protein is a requisite for Salmonella virulence. Molecular Microbiology, 2004, 53, 1437-1449.	2.5	85
79	Use of mixed infections to study cell invasion and intracellular proliferation of Salmonella enterica in eukaryotic cell cultures. Journal of Microbiological Methods, 2004, 56, 83-91.	1.6	45
80	IS200: an old and still bacterial transposon. International Microbiology, 2004, 7, 3-12.	2.4	47
81	Selection of Small-Colony Variants of Salmonella enterica Serovar Typhimurium in Nonphagocytic Eucaryotic Cells. Infection and Immunity, 2003, 71, 3690-3698.	2.2	53
82	Role for Salmonella enterica Enterobacterial Common Antigen in Bile Resistance and Virulence. Journal of Bacteriology, 2003, 185, 5328-5332.	2.2	111
83	Genetic Mapping in Salmonella enterica. , 2003, , 10-21.		0
84	Role of the RecBCD Recombination Pathway in Salmonella Virulence. Journal of Bacteriology, 2002, 184, 592-595.	2.2	53
85	Memory in bacteria and phage. BioEssays, 2002, 24, 512-518.	2.5	103
86	Conjugal transfer of the virulence plasmid of Salmonella enterica is regulated by the leucine-responsive regulatory protein and DNA adenine methylation. Molecular Microbiology, 2002, 44, 1589-1598.	2.5	80
87	Regulation of Capsule Synthesis and Cell Motility in Salmonella enterica by the Essential Gene igaA. Genetics, 2002, 162, 1513-1523.	2.9	107
88	Envelope instability in DNA adenine methylase mutants of Salmonella enterica. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	76
89	Salmonella enterica Serovar Typhimurium Response Involved in Attenuation of Pathogen Intracellular Proliferation. Infection and Immunity, 2001, 69, 6463-6474.	2.2	135
90	Genetic Mapping by Duplication Segregation in Salmonella enterica. Genetics, 2001, 157, 491-502.	2.9	11

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91	Host adapted serotypes of Salmonella enterica. Epidemiology and Infection, 2000, 125, 229-255.	2.1	377
92	Regulation of septation: a novel role for SerC/PdxF in Salmonella?. Molecular Genetics and Genomics, 2000, 264, 184-192.	2.4	4
93	Repression of IS200 transposase synthesis by RNA secondary structures. Nucleic Acids Research, 1999, 27, 3690-3695.	14.5	20
94	DNA adenine methylase mutants of Salmonella typhimurium show defects in protein secretion, cell invasion, and M cell cytotoxicity. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 11578-11583.	7.1	195
95	Lack of hotspot targets: a constraint for IS30 transposition in Salmonella. Gene, 1999, 238, 231-239.	2.2	5
96	Synthesis of FinP RNA by Plasmids F and pSLT Is Regulated by DNA Adenine Methylation. Genetics, 1999, 152, 31-45.	2.9	53
97	Underground metabolism. BioEssays, 1998, 20, 181-186.	2.5	126
98	The P22 Erf protein and host RecA provide alternative functions for transductional segregation of plasmid-borne duplications. Molecular Genetics and Genomics, 1998, 259, 39-45.	2.4	1
99	The sfiX, rfe and metN genes of Salmonella typhimurium and their involvement in the Hisc pleiotropic response. Molecular Genetics and Genomics, 1998, 259, 46-53.	2.4	15
100	Cell Division Inhibition in Salmonella typhimurium Histidine-Constitutive Strains: an ftsI -Like Defect in the Presence of Wild-Type Penicillin-Binding Protein 3 Levels. Journal of Bacteriology, 1998, 180, 5231-5234.	2.2	14
101	Conserved structure of IS200 elements in Salmonella. Nucleic Acids Research, 1997, 25, 1355-1361.	14.5	38
102	Cloning with Mud-P22 hybrid prophages: mapping of IS200 elements on the chromosome of Salmonella typhimurium LT2. Molecular Genetics and Genomics, 1997, 256, 586-588.	2.4	1
103	A possible relationship between vsp mismatch repair and gene expression level. Journal of Molecular Evolution, 1996, 43, 161-163.	1.8	2
104	recB recJ mutants ofSalmonella typhimurium are deficient in transductional recombination, DNA repair and plasmid maintenance. Molecular Genetics and Genomics, 1996, 250, 570-580.	2.4	18
105	DNA Adenine Methylase Mutants of Salmonella typhimurium and a Novel Dam-Regulated Locus. Genetics, 1996, 144, 15-26.	2.9	69
106	Strain typing with IS200 fingerprints in Salmonella abortusovis. Applied and Environmental Microbiology, 1996, 62, 2375-2380.	3.1	30
107	recB recJ. Molecular Genetics and Genomics, 1996, 250, 570.	2.4	2
108	Suppression of the pleiotropic effects of HisH and HisF overproduction identifies four novel loci on the Salmonella typhimurium chromosome: osmH, sfiW, sfiX, and sfiY. Journal of Bacteriology, 1995, 177, 4841-4850.	2.2	20

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109	Compositional heterogeneity of the Escherichia coli genome: A role for VSP repair?. Journal of Molecular Evolution, 1994, 39, 340-346.	1.8	23
110	Changes of ploidy during the Azotobacter vinelandii growth cycle. Journal of Bacteriology, 1994, 176, 3911-3919.	2.2	79
111	The pleiotropic effects of his overexpression in Salmonella typhimurium do not involve AICAR-induced mutagenesis. Molecular Genetics and Genomics, 1993, 240, 360-364.	2.4	11
112	Host RecJ is required for growth of P22 erf bacteriophage. Journal of Bacteriology, 1993, 175, 288-290.	2.2	7
113	The Salmonella typbimurium RecJ function permits growth of P22 abc phage on recBCD + hosts. Molecular Genetics and Genomics, 1992, 232, 470-478.	2.4	15
114	Detection of salmonellas by DNA hybridization with a fluorescent alkaline phosphatase substrate. Journal of Applied Bacteriology, 1992, 72, 393-399.	1.1	26
115	Tn5 mutagenesis and insertion replacement in Azotobacter vinelandii. Plasmid, 1991, 25, 76-80.	1.4	12
116	IS200is not a member of the IS600family of insertion sequences. Nucleic Acids Research, 1991, 19, 1343-1343.	14.5	40
117	sulA-independent division inhibition in his-constitutive strains of Salmonella typhimurium. FEMS Microbiology Letters, 1990, 69, 205-210.	1.8	13
118	Transcriptional occlusion of transposon targets. Molecular Genetics and Genomics, 1989, 216, 204-209.	2.4	34
119	Absence of insertions among spontaneous mutants of Salmonella typhimurium. Molecular Genetics and Genomics, 1989, 216, 210-216.	2.4	44
120	An Altruistic Model of the Rhizobiumâ€“Legume Association. Journal of Heredity, 1989, 80, 335-337.	2.4	63
121	Tn 10 mutagenesis in Azotobacter vinelandii. Molecular Genetics and Genomics, 1987, 209, 276-282.	2.4	23
122	Transposition of Tn 1 to the Rhizobium meliloti genome. Molecular Genetics and Genomics, 1980, 180, 405-410.	2.4	14
123	Method for Testing Degree of Infectivity of Rhizobium meliloti Strains. Applied and Environmental Microbiology, 1980, 39, 967-970.	3.1	72
124	Rough and fine linkage mapping of the Rhizobium meliloti chromosome. Molecular Genetics and Genomics, 1979, 174, 203-209.	2.4	81
125	General transduction in Rhizobium meliloti by a thermosensitive mutant of bacteriophage DF2. Journal of Bacteriology, 1979, 139, 316-317.	2.2	23
126	Of Bacteria and Bile. , 0, , 153-162.		0

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127	Covert Operations: the Adaptable Plan of Attack Deployed by Pathogenic Bacteria. , 0, , 185-200.		0