Ohad Gal-Mor

List of Publications by Year
in descending order

50 papers	2,874 citations	218592 26 h-index	206029 48 g-index
52 all docs	52 docs citations	52 times ranked	3714 citing authors

#	Article	IF	Citations
1	Meta-analysis defines predominant shared microbial responses in various diseases and a specific inflammatory bowel disease signal. Genome Biology, 2022, 23, 61.	3.8	13
2	Intracellular Salmonella Paratyphi A is motile and differs in the expression of flagella-chemotaxis, SPI-1 and carbon utilization pathways in comparison to intracellular S. Typhimurium. PLoS Pathogens, 2022, 18, e1010425.	2.1	4
3	The ancestral stringent response potentiator, DksA has been adapted throughout <i>Salmonella</i> evolution to orchestrate the expression of metabolic, motility, and virulence pathways. Gut Microbes, 2022, 14, 1997294.	4.3	8
4	Profiling of Secreted Type 3 Secretion System Substrates by Salmonella enterica. Methods in Molecular Biology, 2022, , 47-54.	0.4	1
5	In Vivo Tracking of Bacterial Colonization in Different Murine Models Using Bioluminescence: The Example of Salmonella. Methods in Molecular Biology, 2022, , 235-248.	0.4	3
6	The emergence of a multidrug resistant Salmonella Muenchen in Israel is associated with horizontal acquisition of the epidemic pESI plasmid. Clinical Microbiology and Infection, 2022, 28, 1499.e7-1499.e14.	2.8	14
7	Pathoadaptation of the passerine-associated Salmonella enterica serovar Typhimurium lineage to the avian host. PLoS Pathogens, 2021, 17, e1009451.	2.1	24
8	Emergence of new variants of antibiotic resistance genomic islands among multidrugâ€resistantSalmonella entericain poultry. Environmental Microbiology, 2020, 22, 413-432.	1.8	30
9	Genome Sequence of an Emerging Salmonella enterica Serovar Infantis and Genomic Comparison with Other S. Infantis Strains. Genome Biology and Evolution, 2020, 12, 223-228.	1.1	36
10	Std fimbriae-fucose interaction increases Salmonella-induced intestinal inflammation and prolongs colonization. PLoS Pathogens, 2019, 15, e1007915.	2.1	49
11	Differences in the expression of SPI-1 genes pathogenicity and epidemiology between the emerging Salmonella enterica serovar Infantis and the model Salmonella enterica serovar Typhimurium. Journal of Infectious Diseases, 2019, 220, 1071-1081.	1.9	15
12	Western Blotting Against Tagged Virulence Determinants to Study Bacterial Pathogenicity. Methods in Molecular Biology, 2018, 1734, 47-54.	0.4	3
13	Real-Time Reverse Transcription PCR as a Tool to Study Virulence Gene Regulation in Bacterial Pathogens. Methods in Molecular Biology, 2018, 1734, 23-32.	0.4	5
14	Usage of a Bioluminescence Reporter System to Image Promoter Activity During Host Infection. Methods in Molecular Biology, 2018, 1734, 33-38.	0.4	0
15	lacZ Reporter System as a Tool to Study Virulence Gene Regulation in Bacterial Pathogens. Methods in Molecular Biology, 2018, 1734, 39-45.	0.4	11
16	Persistent Infection and Long-Term Carriage of Typhoidal and Nontyphoidal Salmonellae. Clinical Microbiology Reviews, 2018, 32, .	5.7	105
17	Sink traps as the source of transmission of OXA-48â€“producing <i>Serratia marcescens</i> in an intensive care unit. Infection Control and Hospital Epidemiology, 2018, 39, 1307-1315.	1.0	46
18	The Typhi colonization factor (Tcf) is encoded by multiple non-typhoidal <i>Salmonella</i> serovars but exhibits a varying expression profile and interchanging contribution to intestinal colonization. Virulence, 2017, 8, 1791-1807.	1.8	16

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19	The plasmid-encoded Ipf and Klf fimbriae display different expression and varying roles in the virulence of Salmonella enterica serovar Infantis in mouse vs. avian hosts. PLoS Pathogens, 2017, 13, e1006559.	2.1	30
20	Travel- and Community-Based Transmission of Multidrug-ResistantShigellasonneiLineage among International Orthodox Jewish Communities. Emerging Infectious Diseases, 2016, 22, 1545-1553.	2.0	23
21	Genetic and Phenotypic Characterization of a Salmonella enterica serovar Enteritidis Emerging Strain with Superior Intra-macrophage Replication Phenotype. Frontiers in Microbiology, 2016, 7, 1468.	1.5	5
22	Reply to Yue. Clinical Infectious Diseases, 2016, 62, 1326-1327.	2.9	1
23	Horizontal Transfer of the Salmonella enterica Serovar Infantis Resistance and Virulence Plasmid pESI to the Gut Microbiota of Warm-Blooded Hosts. MBio, 2016, 7, .	1.8	92
24	Differences in Host Cell Invasion and Salmonella Pathogenicity Island 1 Expression between Salmonella enterica Serovar Paratyphi A and Nontyphoidal <i>S</i> . Typhimurium. Infection and Immunity, 2016, 84, 1150-1165.	1.0	29
25	Persistent Infections by Nontyphoidal<i>Salmonella</i>in Humans: Epidemiology and Genetics. Clinical Infectious Diseases, 2016, 62, 879-886.	2.9	98
26	The Stringent Response Regulator DksA Is Required for Salmonella enterica Serovar Typhimurium Growth in Minimal Medium, Motility, Biofilm Formation, and Intestinal Colonization. Infection and Immunity, 2016, 84, 375-384.	1.0	53
27	Travel- and Community-Based Transmission of Multidrug-ResistantShigellasonneiLineage among International Orthodox Jewish Communities. Emerging Infectious Diseases, 2016, 22, 1545-1553.	2.0	5
28	Flagellin Is Required for Host Cell Invasion and Normal Salmonella Pathogenicity Island 1 Expression by Salmonella enterica Serovar Paratyphi A. Infection and Immunity, 2015, 83, 3355-3368.	1.0	57
29	Feverlike Temperature is a Virulence Regulatory Cue Controlling the Motility and Host Cell Entry of Typhoidal Salmonella. Journal of Infectious Diseases, 2015, 212, 147-156.	1.9	22
30	Same species, different diseases: how and why typhoidal and non-typhoidal Salmonella enterica serovars differ. Frontiers in Microbiology, 2014, 5, 391.	1.5	349
31	A unique megaplasmid contributes to stress tolerance and pathogenicity of an emergent <scp><i>S</i></scp><i>almonella enterica</i> serovar Infantis strain. Environmental Microbiology, 2014, 16, 977-994.	1.8	172
32	Integrative Analysis of Salmonellosis in Israel Reveals Association of Salmonella enterica Serovar 9,12:l,v:â˘ with Extraintestinal Infections, Dissemination of Endemic S. enterica Serovar Typhimurium DT104 Biotypes, and Severe Underreporting of Outbreaks. Journal of Clinical Microbiology, 2014, 52, 2078-2088.	1.8	14
33	Isolation of Genetically Unrelated <i>bla</i> _{NDM-1} -Positive Providencia rettgeri Strains in Israel. Journal of Clinical Microbiology, 2013, 51, 1642-1643.	1.8	27
34	Virulence Gene Profiling and Pathogenicity Characterization of Non-Typhoidal Salmonella Accounted for Invasive Disease in Humans. PLoS ONE, 2013, 8, e58449.	1.1	143
35	Molecular and Cellular Characterization of a Salmonella enterica Serovar Paratyphi A Outbreak Strain and the Human Immune Response to Infection. Vaccine Journal, 2012, 19, 146-156.	3.2	30
36	Outcome of carbapenem resistant Klebsiella pneumoniae bloodstream infections. Clinical Microbiology and Infection, 2012, 18, 54-60.	2.8	284

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37	The Salmonella enterica PhoP Directly Activates the Horizontally Acquired SPI-2 Gene sseL and Is Functionally Different from a S. bongori Ortholog. PLoS ONE, 2011, 6, e20024.	1.1	14
38	Salmonella Phage ST64B Encodes a Member of the SseK/NleB Effector Family. PLoS ONE, 2011, 6, e17824.	1.1	66
39	Multidrug-Resistant<i>Salmonella enterica</i>Serovar Infantis, Israel. Emerging Infectious Diseases, 2010, 16, 1754-1757.	2.0	73
40	A Novel Secretion Pathway of Salmonella enterica Acts as an Antivirulence Modulator during Salmonellosis. PLoS Pathogens, 2008, 4, e1000036.	2.1	52
41	SseL Is a Salmonella -Specific Translocated Effector Integrated into the SsrB-Controlled Salmonella Pathogenicity Island 2 Type III Secretion System. Infection and Immunity, 2007, 75, 574-580.	1.0	69
42	Pathogens on aspirin: promising research and therapeutic applications. Nature Methods, 2007, 4, 893-894.	9.0	2
43	Pathogenicity islands: a molecular toolbox for bacterial virulence. Cellular Microbiology, 2006, 8, 1707-1719.	1.1	299
44	The temperature-sensing protein TlpA is repressed by PhoP and dispensable for virulence of Salmonella enterica serovar Typhimurium in mice. Microbes and Infection, 2006, 8, 2154-2162.	1.0	22
45	SseK1 and SseK2 Are Novel Translocated Proteins of Salmonella enterica Serovar Typhimurium. Infection and Immunity, 2004, 72, 5115-5125.	1.0	83
46	The Legionella pneumophila GacA homolog (LetA) is involved in the regulation of icm virulence genes and is required for intracellular multiplication in Acanthamoeba castellanii. Microbial Pathogenesis, 2003, 34, 187-194.	1.3	89
47	Identification of CpxR as a Positive Regulator of icm and dot Virulence Genes of Legionella pneumophila. Journal of Bacteriology, 2003, 185, 4908-4919.	1.0	121
48	Characterization of a Legionella pneumophila relA Insertion Mutant and Roles of RelA and RpoS in Virulence Gene Expression. Journal of Bacteriology, 2002, 184, 67-75.	1.0	99
49	Analysis of DNA Regulatory Elements Required for Expression of the Legionella pneumophila icm and dot Virulence Genes. Journal of Bacteriology, 2002, 184, 3823-3833.	1.0	48
50	Gene organization in the trxA/Bâ€"oriC region of the Streptomyces coelicolor chromosome and comparison with other eubacteria. Gene, 1998, 217, 83-90.	1.0	20