Roy R Chaudhuri

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74	papers
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65	g-index
84	ext. papers
4,985	ext. citations
6.9	avg, IF
4.8	L-index

#	Paper	IF	Citations
74	The pangenome structure of Escherichia coli: comparative genomic analysis of E. coli commensal and pathogenic isolates. *Journal of Bacteriology*, **2008**, 190, 6881-93	3.5	607
73	Escherichia coli K-12: a cooperatively developed annotation snapshot--2005. *Nucleic Acids Research*, **2006**, 34, 1-9	20.1	525
72	The origins of acquired immune deficiency syndrome viruses: where and when?. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2001**, 356, 867-76	5.8	204
71	Comprehensive identification of essential Staphylococcus aureus genes using Transposon-Mediated Differential Hybridisation (TMDH). *BMC Genomics*, **2009**, 10, 291	4.5	194
70	A commensal gone bad: complete genome sequence of the prototypical enterotoxigenic Escherichia coli strain H10407. *Journal of Bacteriology*, **2010**, 192, 5822-31	3.5	141
69	Genomic analysis of secretion systems. *Current Opinion in Microbiology*, **2003**, 6, 519-27	7.9	139
68	Comprehensive assignment of roles for Salmonella typhimurium genes in intestinal colonization of food-producing animals. *PLoS Genetics*, **2013**, 9, e1003456	6	134
67	Complete genome sequence and comparative metabolic profiling of the prototypical enteroaggregative Escherichia coli strain 042. *PLoS ONE*, **2010**, 5, e8801	3.7	134
66	The evolution of the Escherichia coli phylogeny. *Infection, Genetics and Evolution*, **2012**, 12, 214-26	4.5	121
65	xBASE2: a comprehensive resource for comparative bacterial genomics. *Nucleic Acids Research*, **2008**, 36, D543-6	20.1	113
64	Bacterial FHA domains: neglected players in the phospho-threonine signalling game?. *Trends in Microbiology*, **2002**, 10, 556-63	12.4	94
63	The ETT2 gene cluster, encoding a second type III secretion system from Escherichia coli, is present in the majority of strains but has undergone widespread mutational attrition. *Journal of Bacteriology*, **2004**, 186, 3547-60	3.5	93
62	Genomic signatures of human and animal disease in the zoonotic pathogen Streptococcus suis. *Nature Communications*, **2015**, 6, 6740	17.4	89
61	Bacterial flagellar diversity in the post-genomic era. *Trends in Microbiology*, **2005**, 13, 143-9	12.4	85
60	Down-regulation of key virulence factors makes the Salmonella enterica serovar Typhimurium rfaH mutant a promising live-attenuated vaccine candidate. *Infection and Immunity*, **2006**, 74, 5914-25	3.7	82
59	Regulators encoded in the Escherichia coli type III secretion system 2 gene cluster influence expression of genes within the locus for enterocyte effacement in enterohemorrhagic E. coli O157:H7. *Infection and Immunity*, **2004**, 72, 7282-93	3.7	82
58	Structure and function of BamE within the outer membrane and the □barrel assembly machine. *EMBO Reports*, **2011**, 12, 123-8	6.5	79

57	Comprehensive identification of Salmonella enterica serovar typhimurium genes required for infection of BALB/c mice. *PLoS Pathogens*, **2009**, 5, e1000529	7.6	66
56	Sequencing and functional annotation of avian pathogenic Escherichia coli serogroup O78 strains reveal the evolution of E. coli lineages pathogenic for poultry via distinct mechanisms. *Infection and Immunity*, **2013**, 81, 838-49	3.7	64
55	coliBASE: an online database for Escherichia coli, Shigella and Salmonella comparative genomics. *Nucleic Acids Research*, **2004**, 32, D296-9	20.1	63
54	A novel strategy for the identification of genomic islands by comparative analysis of the contents and contexts of tRNA sites in closely related bacteria. *Nucleic Acids Research*, **2006**, 34, e3	20.1	62
53	Phylogenetic comparisons reveal multiple acquisitions of the toxin genes by enterotoxigenic Escherichia coli strains of different evolutionary lineages. *Journal of Clinical Microbiology*, **2006**, 44, 4528-36	9.7	61
52	xBASE, a collection of online databases for bacterial comparative genomics. *Nucleic Acids Research*, **2006**, 34, D335-7	20.1	60
51	A degenerate type III secretion system from septicemic Escherichia coli contributes to pathogenesis. *Journal of Bacteriology*, **2005**, 187, 8164-71	3.5	56
50	Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of Haemophilus parasuis. *Journal of Clinical Microbiology*, **2015**, 53, 3812-21	9.7	52
49	Genome sequencing shows that European isolates of Francisella tularensis subspecies tularensis are almost identical to US laboratory strain Schu S4. *PLoS ONE*, **2007**, 2, e352	3.7	41
48	Population genomics of the killer whale indicates ecotype evolution in sympatry involving both selection and drift. *Molecular Ecology*, **2014**, 23, 5179-92	5.7	40
47	Prevalence of pathogenicity island IICFT073 genes among extraintestinal clinical isolates of Escherichia coli. *Journal of Clinical Microbiology*, **2005**, 43, 2425-34	9.7	39
46	Phylogenomics of the killer whale indicates ecotype divergence in sympatry. *Heredity*, **2015**, 114, 48-55	3.6	38
45	Quantitative RNA-seq analysis of the Campylobacter jejuni transcriptome. *Microbiology (United Kingdom)*, **2011**, 157, 2922-2932	2.9	38
44	Genomic analysis of the protein secretion systems in Clostridium acetobutylicum ATCC 824. *Biochimica Et Biophysica Acta - Molecular Cell Research*, **2005**, 1745, 223-53	4.9	38
43	Retrospective application of transposon-directed insertion site sequencing to a library of signature-tagged mini-Tn5Km2 mutants of Escherichia coli O157:H7 screened in cattle. *Journal of Bacteriology*, **2011**, 193, 1771-6	3.5	35
42	Complete genome sequence of the Crohn's disease-associated adherent-invasive Escherichia coli strain HM605. *Journal of Bacteriology*, **2011**, 193, 4540	3.5	34
41	Gene content and diversity of the loci encoding biosynthesis of capsular polysaccharides of the 15 serovar reference strains of Haemophilus parasuis. *Journal of Bacteriology*, **2013**, 195, 4264-73	3.5	33
40	Activity of Bdellovibrio hit locus proteins, Bd0108 and Bd0109, links Type IVa pilus extrusion/retraction status to prey-independent growth signalling. *PLoS ONE*, **2013**, 8, e79759	3.7	32

39	Adding function to the genome of African Salmonella Typhimurium ST313 strain D23580. *PLoS Biology*, **2019**, 17, e3000059	9.7	32
38	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in. *Frontiers in Microbiology* , **2017**, 8, 311	5.7	31
37	A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium Myxococcus xanthus. *ISME Journal*, **2016**, 10, 2468-77	11.9	31
36	Multiplex PCR assay for unequivocal differentiation of Actinobacillus pleuropneumoniae serovars 1 to 3, 5 to 8, 10, and 12. *Journal of Clinical Microbiology*, **2014**, 52, 2380-5	9.7	30
35	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in Haemophilus parasuis. *BMC Genomics*, **2014**, 15, 1179	4.5	29
34	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in Actinobacillus pleuropneumoniae. *Veterinary Microbiology*, **2015**, 178, 279-82	3.3	27
33	Genome-wide DNA methylation patterns in wild samples of two morphotypes of threespine stickleback (Gasterosteus aculeatus). *Molecular Biology and Evolution*, **2015**, 32, 888-95	8.3	25
32	Identification of dfrA14 in two distinct plasmids conferring trimethoprim resistance in Actinobacillus pleuropneumoniae. *Journal of Antimicrobial Chemotherapy*, **2015**, 70, 2217-22	5.1	23
31	An analysis of type-III secretion gene clusters in Chromobacterium violaceum. *Trends in Microbiology*, **2004**, 12, 476-82	12.4	23
30	Sequencing a piece of history: complete genome sequence of the original strain. *Microbial Genomics* , **2017**, 3, mgen000106	4.4	23
29	Single-step selection of bivalent aptamers validated by comparison with SELEX using high-throughput sequencing. *PLoS ONE*, **2014**, 9, e100572	3.7	22
28	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. *PeerJ*, **2021**, 9, e10941	3.1	21
27	Proteomic Profiling, Transcription Factor Modeling, and Genomics of Evolved Tolerant Strains Elucidate Mechanisms of Vanillin Toxicity in Escherichia coli. *MSystems*, **2019**, 4,	7.6	18
26	Whole genome investigation of a divergent clade of the pathogen Streptococcus suis. *Frontiers in Microbiology*, **2015**, 6, 1191	5.7	18
25	Supramolecular structure in the membrane of Staphylococcus aureus. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 15725-30	11.5	17
24	Genome-wide high-throughput screening to investigate essential genes involved in methicillin-resistant Staphylococcus aureus Sequence Type 398 survival. *PLoS ONE*, **2014**, 9, e89018	3.7	17
23	Genes Required for the Fitness of Salmonella enterica Serovar Typhimurium during Infection of Immunodeficient gp91-/- phox Mice. *Infection and Immunity*, **2016**, 84, 989-997	3.7	16
22	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of Actinobacillus pleuropneumoniae. *Genome Announcements*, **2016**, 4,		16

21	ICEApl1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen Actinobacillus pleuropneumoniae. *Frontiers in Microbiology*, **2016**, 7, 810	5.7	16
20	"Pathotyping" Multiplex PCR Assay for Haemophilus parasuis: a Tool for Prediction of Virulence. *Journal of Clinical Microbiology*, **2017**, 55, 2617-2628	9.7	15
19	Retrospective application of transposon-directed insertion-site sequencing to investigate niche-specific virulence of Salmonella Typhimurium in cattle. *BMC Genomics*, **2019**, 20, 20	4.5	13
18	Generation of a Tn5 transposon library in Haemophilus parasuis and analysis by transposon-directed insertion-site sequencing (TraDIS). *Veterinary Microbiology*, **2013**, 166, 558-66	3.3	11
17	Use of Proteins Identified through a Functional Genomic Screen To Develop a Protein Subunit Vaccine That Provides Significant Protection against Virulent Streptococcus suis in Pigs. *Infection and Immunity*, **2018**, 86,	3.7	10
16	Two Unrelated 8-Vinyl Reductases Ensure Production of Mature Chlorophylls in Acaryochloris marina. *Journal of Bacteriology*, **2016**, 198, 1393-400	3.5	10
15	The fitness landscape of the African Salmonella Typhimurium ST313 strain D23580 reveals unique properties of the pBT1 plasmid. *PLoS Pathogens*, **2019**, 15, e1007948	7.6	9
14	ArrayOme: a program for estimating the sizes of microarray-visualized bacterial genomes. *Nucleic Acids Research*, **2005**, 33, e3	20.1	9
13	The Evolution of Primate Lentiviruses and the Origins of AIDS **2002**, 65-96		9
12	Draft Genome Sequences of Three Clinical Isolates of Tannerella forsythia Isolated from Subgingival Plaque from Periodontitis Patients in the United States. *Genome Announcements*, **2016**, 4,		8
11	Increasing prevalence of a fluoroquinolone resistance mutation amongst Campylobacter jejuni isolates from four human infectious intestinal disease studies in the United Kingdom. *PLoS ONE*, **2020**, 15, e0227535	3.7	7
10	Transcriptome and proteome analysis of Salmonella enterica serovar Typhimurium systemic infection of wild type and immune-deficient mice. *PLoS ONE*, **2017**, 12, e0181365	3.7	6
9	MycoDB: an online database for comparative genomics of the mycobacteria and related organisms. *Methods in Molecular Biology*, **2009**, 465, 419-31	1.4	3
8	Architecture and Self-Assembly of Clostridium sporogenes and Clostridium botulinum Spore Surfaces Illustrate a General Protective Strategy across Spore Formers. *MSphere*, **2020**, 5,	5	2
7	Characterization of ISBth4, a functional new IS231 variant from Bacillus thuringiensis MEX312. *Plasmid*, **2010**, 63, 46-52	3.3	2
6	Rationally designed mariner vectors to allow functional genomic analysis of Actinobacillus pleuropneumoniae and other bacteria by transposon-directed insertion-site sequencing (TraDIS)		2
5	Understanding the Model and the Menace: a Postgenomic View of Escherichia Coli21-48		1
4	Rationally designed vectors for functional genomic analysis of and other species by transposon-directed insertion-site sequencing (TraDIS). *Animal Diseases*, **2021**, 1, 29		1

3 The fitness landscape of the African Salmonella Typhimurium ST313 strain D23580 reveals unique properties of the pBT1 plasmid **2019**, 15, e1007948

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1 The fitness landscape of the African Salmonella Typhimurium ST313 strain D23580 reveals unique properties of the pBT1 plasmid **2019**, 15, e1007948