

# Roy R Chaudhuri

## List of Publications by Year in descending order

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78  
papers

5,473  
citations

101496

36  
h-index

85498

71  
g-index

84  
all docs

84  
docs citations

84  
times ranked

7513  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Pangenome Structure of <i>Escherichia coli</i> : Comparative Genomic Analysis of <i>E. coli</i> Commensal and Pathogenic Isolates. <i>Journal of Bacteriology</i> , 2008, 190, 6881-6893.	1.0	763
2	<i>Escherichia coli</i> K-12: a cooperatively developed annotation snapshot--2005. <i>Nucleic Acids Research</i> , 2006, 34, 1-9.	6.5	606
3	The origins of acquired immune deficiency syndrome viruses: where and when?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2001, 356, 867-876.	1.8	263
4	Comprehensive identification of essential <i>Staphylococcus aureus</i> genes using Transposon-Mediated Differential Hybridisation (TMDH). <i>BMC Genomics</i> , 2009, 10, 291.	1.2	253
5	Comprehensive Assignment of Roles for <i>Salmonella</i> Typhimurium Genes in Intestinal Colonization of Food-Producing Animals. <i>PLoS Genetics</i> , 2013, 9, e1003456.	1.5	176
6	A Commensal Gone Bad: Complete Genome Sequence of the Prototypical Enterotoxigenic <i>Escherichia coli</i> Strain H10407. <i>Journal of Bacteriology</i> , 2010, 192, 5822-5831.	1.0	168
7	The evolution of the <i>Escherichia coli</i> phylogeny. <i>Infection, Genetics and Evolution</i> , 2012, 12, 214-226.	1.0	167
8	Complete Genome Sequence and Comparative Metabolic Profiling of the Prototypical Enteroadhesive <i>Escherichia coli</i> Strain O42. <i>PLoS ONE</i> , 2010, 5, e8801.	1.1	165
9	Genomic analysis of secretion systems. <i>Current Opinion in Microbiology</i> , 2003, 6, 519-527.	2.3	150
10	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015, 6, 6740.	5.8	124
11	xBASE2: a comprehensive resource for comparative bacterial genomics. <i>Nucleic Acids Research</i> , 2007, 36, D543-D546.	6.5	119
12	The ETT2 Gene Cluster, Encoding a Second Type III Secretion System from <i>Escherichia coli</i> , Is Present in the Majority of Strains but Has Undergone Widespread Mutational Attrition. <i>Journal of Bacteriology</i> , 2004, 186, 3547-3560.	1.0	117
13	Bacterial flagellar diversity in the post-genomic era. <i>Trends in Microbiology</i> , 2005, 13, 143-149.	3.5	103
14	Bacterial FHA domains: neglected players in the phospho-threonine signalling game?. <i>Trends in Microbiology</i> , 2002, 10, 556-563.	3.5	102
15	Regulators Encoded in the <i>Escherichia coli</i> Type III Secretion System 2 Gene Cluster Influence Expression of Genes within the Locus for Enterocyte Effacement in Enterohemorrhagic <i>E. coli</i> O157:H7. <i>Infection and Immunity</i> , 2004, 72, 7282-7293.	1.0	89
16	Down-Regulation of Key Virulence Factors Makes the <i>Salmonella enterica</i> Serovar Typhimurium <i>rfaH</i> Mutant a Promising Live-Attenuated Vaccine Candidate. <i>Infection and Immunity</i> , 2006, 74, 5914-5925.	1.0	88
17	Structure and function of BamE within the outer membrane and the $\beta$ -barrel assembly machine. <i>EMBO Reports</i> , 2011, 12, 123-128.	2.0	88
18	Sequencing and Functional Annotation of Avian Pathogenic <i>Escherichia coli</i> Serogroup O78 Strains Reveal the Evolution of <i>E. coli</i> Lineages Pathogenic for Poultry via Distinct Mechanisms. <i>Infection and Immunity</i> , 2013, 81, 838-849.	1.0	82

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19	Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of <i>Haemophilus parasuis</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 3812-3821.	1.8	80
20	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
21	Comprehensive Identification of <i>Salmonella enterica</i> Serovar Typhimurium Genes Required for Infection of BALB/c Mice. <i>PLoS Pathogens</i> , 2009, 5, e1000529.	2.1	75
22	Phylogenetic Comparisons Reveal Multiple Acquisitions of the Toxin Genes by Enterotoxigenic <i>Escherichia coli</i> Strains of Different Evolutionary Lineages. <i>Journal of Clinical Microbiology</i> , 2006, 44, 4528-4536.	1.8	74
23	A novel strategy for the identification of genomic islands by comparative analysis of the contents and contexts of tRNA sites in closely related bacteria. <i>Nucleic Acids Research</i> , 2006, 34, e3-e3.	6.5	67
24	coliBASE: an online database for <i>Escherichia coli</i> , <i>Shigella</i> and <i>Salmonella</i> comparative genomics. <i>Nucleic Acids Research</i> , 2004, 32, 296D-299.	6.5	65
25	A Degenerate Type III Secretion System from Septicemic <i>Escherichia coli</i> Contributes to Pathogenesis. <i>Journal of Bacteriology</i> , 2005, 187, 8164-8171.	1.0	62
26	xBASE, a collection of online databases for bacterial comparative genomics. <i>Nucleic Acids Research</i> , 2006, 34, D335-D337.	6.5	62
27	Adding function to the genome of African <i>Salmonella</i> Typhimurium ST313 strain D23580. <i>PLoS Biology</i> , 2019, 17, e3000059.	2.6	62
28	A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium <i>Myxococcus xanthus</i> . <i>ISME Journal</i> , 2016, 10, 2468-2477.	4.4	52
29	Genome Sequencing Shows that European Isolates of <i>Francisella tularensis</i> Subspecies <i>tularensis</i> Are Almost Identical to US Laboratory Strain Schu S4. <i>PLoS ONE</i> , 2007, 2, e352.	1.1	51
30	Complete Genome Sequence of the Crohn's Disease-Associated Adherent-Invasive <i>Escherichia coli</i> Strain HM605. <i>Journal of Bacteriology</i> , 2011, 193, 4540-4540.	1.0	50
31	Population genomics of the killer whale indicates ecotype evolution in sympatry involving both selection and drift. <i>Molecular Ecology</i> , 2014, 23, 5179-5192.	2.0	48
32	Phylogenomics of the killer whale indicates ecotype divergence in sympatry. <i>Heredity</i> , 2015, 114, 48-55.	1.2	47
33	Prevalence of Pathogenicity Island II CFT073 Genes among Extraintestinal Clinical Isolates of <i>Escherichia coli</i> . <i>Journal of Clinical Microbiology</i> , 2005, 43, 2425-2434.	1.8	45
34	Quantitative RNA-seq analysis of the <i>Campylobacter jejuni</i> transcriptome. <i>Microbiology (United Kingdom)</i> , 2010, 154, 107-114.	0.7	44
35	Genome-Wide DNA Methylation Patterns in Wild Samples of Two Morphotypes of Threespine Stickleback ( <i>Gasterosteus aculeatus</i> ). <i>Molecular Biology and Evolution</i> , 2015, 32, 888-895.	3.5	43
36	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 311.	1.5	42

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37	Genomic analysis of the protein secretion systems in <i>Clostridium acetobutylicum</i> ATCC 824. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2005, 1745, 223-253.	1.9	40
38	Retrospective Application of Transposon-Directed Insertion Site Sequencing to a Library of Signature-Tagged Mini-Tn <i>km2</i> Mutants of <i>Escherichia coli</i> O157:H7 Screened in Cattle. <i>Journal of Bacteriology</i> , 2011, 193, 1771-1776.	1.0	40
39	Activity of <i>Bdellovibrio</i> Hit Locus Proteins, Bd0108 and Bd0109, Links Type IVa Pilus Extrusion/Retraction Status to Prey-Independent Growth Signalling. <i>PLoS ONE</i> , 2013, 8, e79759.	1.1	40
40	Gene Content and Diversity of the Loci Encoding Biosynthesis of Capsular Polysaccharides of the 15 Serovar Reference Strains of <i>Haemophilus parasuis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 4264-4273.	1.0	37
41	Multiplex PCR Assay for Unequivocal Differentiation of <i>Actinobacillus pleuropneumoniae</i> Serovars 1 to 3, 5 to 8, 10, and 12. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2380-2385.	1.8	36
42	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in <i>Haemophilus parasuis</i> . <i>BMC Genomics</i> , 2014, 15, 1179.	1.2	34
43	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , 2015, 178, 279-282.	0.8	34
44	Sequencing a piece of history: complete genome sequence of the original <i>Escherichia coli</i> strain. <i>Microbial Genomics</i> , 2017, 3, mgen000106.	1.0	33
45	Identification of <i>dfrA14</i> in two distinct plasmids conferring trimethoprim resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2217-2222.	1.3	30
46	Proteomic Profiling, Transcription Factor Modeling, and Genomics of Evolved Tolerant Strains Elucidate Mechanisms of Vanillin Toxicity in <i>Escherichia coli</i> . <i>MSystems</i> , 2019, 4, .	1.7	28
47	Whole genome investigation of a divergent clade of the pathogen <i>Streptococcus suis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1191.	1.5	27
48	Supramolecular structure in the membrane of <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15725-15730.	3.3	26
49	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of <i>Actinobacillus pleuropneumoniae</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	26
50	Single-Step Selection of Bivalent Aptamers Validated by Comparison with SELEX Using High-Throughput Sequencing. <i>PLoS ONE</i> , 2014, 9, e100572.	1.1	25
51	An analysis of type-III secretion gene clusters in <i>Chromobacterium violaceum</i> . <i>Trends in Microbiology</i> , 2004, 12, 476-482.	3.5	24
52	Genome-Wide High-Throughput Screening to Investigate Essential Genes Involved in Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398 Survival. <i>PLoS ONE</i> , 2014, 9, e89018.	1.1	23
53	ICEAp1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 810.	1.5	20
54	Genes Required for the Fitness of <i>Salmonella enterica</i> Serovar Typhimurium during Infection of Immunodeficient <i>gp91</i> Mice. <i>Infection and Immunity</i> , 2016, 84, 989-997.	1.0	20

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55	The fitness landscape of the African Salmonella Typhimurium ST313 strain D23580 reveals unique properties of the pBT1 plasmid. <i>PLoS Pathogens</i> , 2019, 15, e1007948.	2.1	20
56	â€œPathotypingâ€•Multiplex PCR Assay for Haemophilus parasuis: a Tool for Prediction of Virulence. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2617-2628.	1.8	18
57	Retrospective application of transposon-directed insertion-site sequencing to investigate niche-specific virulence of Salmonella Typhimurium in cattle. <i>BMC Genomics</i> , 2019, 20, 20.	1.2	17
58	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. <i>Infection and Immunity</i> , 2018, 86, .	1.0	16
59	Generation of a Tn5 transposon library in Haemophilus parasuis and analysis by transposon-directed insertion-site sequencing (TraDIS). <i>Veterinary Microbiology</i> , 2013, 166, 558-566.	0.8	15
60	Architecture and Self-Assembly of Clostridium sporogenes and Clostridium botulinum Spore Surfaces Illustrate a General Protective Strategy across Spore Formers. <i>MSphere</i> , 2020, 5, .	1.3	12
61	Genome-enabled discovery of candidate virulence loci in <i>Striga hermonthica</i> , a devastating parasite of African cereal crops. <i>New Phytologist</i> , 2022, 236, 622-638.	3.5	12
62	ArrayOme: a program for estimating the sizes of microarray-visualized bacterial genomes. <i>Nucleic Acids Research</i> , 2005, 33, e3-e3.	6.5	11
63	Two Unrelated 8-Vinyl Reductases Ensure Production of Mature Chlorophylls in Acaryochloris marina. <i>Journal of Bacteriology</i> , 2016, 198, 1393-1400.	1.0	11
64	The Evolution of Primate Lentiviruses and the Origins of AIDS. , 2002, , 65-96.		10
65	Draft Genome Sequences of Three Clinical Isolates of Tannerella forsythia Isolated from Subgingival Plaque from Periodontitis Patients in the United States. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
66	Increasing prevalence of a fluoroquinolone resistance mutation amongst Campylobacter jejuni isolates from four human infectious intestinal disease studies in the United Kingdom. <i>PLoS ONE</i> , 2020, 15, e0227535.	1.1	9
67	MycnoDB: An Online Database for Comparative Genomics of the Mycobacteria and Related Organisms. <i>Methods in Molecular Biology</i> , 2009, 465, 419-431.	0.4	6
68	Transcriptome and proteome analysis of Salmonella enterica serovar Typhimurium systemic infection of wild type and immune-deficient mice. <i>PLoS ONE</i> , 2017, 12, e0181365.	1.1	6
69	Characterization of ISBth4, a functional new IS231 variant from Bacillus thuringiensis MEX312. <i>Plasmid</i> , 2010, 63, 46-52.	0.4	2
70	Probabilistic identification of bacterial essential genes via insertion density using TraDIS data with Tn5 libraries. <i>Bioinformatics</i> , 2021, 37, 4343-4349.	1.8	2
71	Draft Whole-Genome Sequences of 10 <i>Aeromonas</i> Strains from Clinical and Environmental Sources. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
72	Understanding the Model and the Menace: a Postgenomic View of Escherichia Coli. , 0, , 21-48.		1

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73	Rationally designed mariner vectors for functional genomic analysis of <i>Actinobacillus pleuropneumoniae</i> and other Pasteurellaceae species by transposon-directed insertion-site sequencing (TraDIS). <i>Animal Diseases</i> , 2021, 1, 29.	0.6	1
74	Looking through the FOG: microbiome characterization and lipolytic bacteria isolation from a fatberg site. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	1
75	Corrigendum to: Probabilistic identification of bacterial essential genes via insertion density using TraDIS data with Tn5 libraries. <i>Bioinformatics</i> , 2021, 37, 3387-3387.	1.8	0
76	Title is missing!. , 2019, 15, e1007948.		0
77	Title is missing!. , 2019, 15, e1007948.		0
78	Title is missing!. , 2019, 15, e1007948.		0