

# Roy R Chaudhuri

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

74  
papers

4,331  
citations

33  
h-index

65  
g-index

84  
ext. papers

4,985  
ext. citations

6.9  
avg, IF

4.8  
L-index

| #  | Paper   | IF  | Citations |
|----|---|-----|-----------|
| 74 | Rationally designed vectors for functional genomic analysis of and other species by transposon-directed insertion-site sequencing (TraDIS). <i>Animal Diseases</i> , <b>2021</b> , 1, 29  |     | 1         |
| 73 | Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , <b>2021</b> , 9, e10941  | 3.1 | 21        |
| 72 | Architecture and Self-Assembly of Clostridium sporogenes and Clostridium botulinum Spore Surfaces Illustrate a General Protective Strategy across Spore Formers. <i>MSphere</i> , <b>2020</b> , 5,                                      | 5   | 2         |
| 71 | 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> , <b>2020</b> , 15, e0227535          | 3.7 | 7         |
| 70 | The fitness landscape of the African Salmonella Typhimurium ST313 strain D23580 reveals unique properties of the pBT1 plasmid. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007948   | 7.6 | 9         |
| 69 | Retrospective application of transposon-directed insertion-site sequencing to investigate niche-specific virulence of Salmonella Typhimurium in cattle. <i>BMC Genomics</i> , <b>2019</b> , 20, 20                                      | 4.5 | 13        |
| 68 | Proteomic Profiling, Transcription Factor Modeling, and Genomics of Evolved Tolerant Strains Elucidate Mechanisms of Vanillin Toxicity in Escherichia coli. <i>MSystems</i> , <b>2019</b> , 4,  | 7.6 | 18        |
| 67 | Adding function to the genome of African Salmonella Typhimurium ST313 strain D23580. <i>PLoS Biology</i> , <b>2019</b> , 17, e3000059   | 9.7 | 32        |
| 66 | The fitness landscape of the African Salmonella Typhimurium ST313 strain D23580 reveals unique properties of the pBT1 plasmid <b>2019</b> , 15, e1007948  |     |           |
| 65 | The fitness landscape of the African Salmonella Typhimurium ST313 strain D23580 reveals unique properties of the pBT1 plasmid <b>2019</b> , 15, e1007948  |     |           |
| 64 | The fitness landscape of the African Salmonella Typhimurium ST313 strain D23580 reveals unique properties of the pBT1 plasmid <b>2019</b> , 15, e1007948  |     |           |
| 63 | 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> , <b>2018</b> , 86, | 3.7 | 10        |
| 62 | "Pathotyping" Multiplex PCR Assay for Haemophilus parasuis: a Tool for Prediction of Virulence. <i>Journal of Clinical Microbiology</i> , <b>2017</b> , 55, 2617-2628   | 9.7 | 15        |
| 61 | Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 311  | 5.7 | 31        |
| 60 | Transcriptome and proteome analysis of Salmonella enterica serovar Typhimurium systemic infection of wild type and immune-deficient mice. <i>PLoS ONE</i> , <b>2017</b> , 12, e0181365  | 3.7 | 6         |
| 59 | Sequencing a piece of history: complete genome sequence of the original strain. <i>Microbial Genomics</i> , <b>2017</b> , 3, mgen000106   | 4.4 | 23        |
| 58 | Genes Required for the Fitness of Salmonella enterica Serovar Typhimurium during Infection of Immunodeficient gp91-/- phox Mice. <i>Infection and Immunity</i> , <b>2016</b> , 84, 989-997  | 3.7 | 16        |

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|----|--|------|----|
| 57 | Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of <i>Actinobacillus pleuropneumoniae</i> . <i>Genome Announcements</i> , <b>2016</b> , 4,                                |      | 16 |
| 56 | ICEApl1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 810                 | 5.7  | 16 |
| 55 | Two Unrelated 8-Vinyl Reductases Ensure Production of Mature Chlorophylls in <i>Acaryochloris marina</i> . <i>Journal of Bacteriology</i> , <b>2016</b> , 198, 1393-400  | 3.5  | 10 |
| 54 | Draft Genome Sequences of Three Clinical Isolates of <i>Tannerella forsythia</i> Isolated from Subgingival Plaque from Periodontitis Patients in the United States. <i>Genome Announcements</i> , <b>2016</b> , 4, |      | 8  |
| 53 | A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium <i>Myxococcus xanthus</i> . <i>ISME Journal</i> , <b>2016</b> , 10, 2468-77                                      | 11.9 | 31 |
| 52 | Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , <b>2015</b> , 178, 279-82             | 3.3  | 27 |
| 51 | Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 6740   | 17.4 | 89 |
| 50 | Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of <i>Haemophilus parasuis</i> . <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 3812-21   | 9.7  | 52 |
| 49 | Identification of <i>dfrA14</i> in two distinct plasmids conferring trimethoprim resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 2217-22   | 5.1  | 23 |
| 48 | Phylogenomics of the killer whale indicates ecotype divergence in sympatry. <i>Heredity</i> , <b>2015</b> , 114, 48-55   | 3.6  | 38 |
| 47 | 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> , <b>2015</b> , 112, 15725-30                    | 11.5 | 17 |
| 46 | Whole genome investigation of a divergent clade of the pathogen <i>Streptococcus suis</i> . <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1191   | 5.7  | 18 |
| 45 | Genome-wide DNA methylation patterns in wild samples of two morphotypes of threespine stickleback ( <i>Gasterosteus aculeatus</i> ). <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 888-95             | 8.3  | 25 |
| 44 | 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> , <b>2014</b> , 52, 2380-5              | 9.7  | 30 |
| 43 | Single-step selection of bivalent aptamers validated by comparison with SELEX using high-throughput sequencing. <i>PLoS ONE</i> , <b>2014</b> , 9, e100572   | 3.7  | 22 |
| 42 | The use of genome wide association methods to investigate pathogenicity, population structure and serovar in <i>Haemophilus parasuis</i> . <i>BMC Genomics</i> , <b>2014</b> , 15, 1179                            | 4.5  | 29 |
| 41 | Population genomics of the killer whale indicates ecotype evolution in sympatry involving both selection and drift. <i>Molecular Ecology</i> , <b>2014</b> , 23, 5179-92   | 5.7  | 40 |
| 40 | 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> , <b>2014</b> , 9, e89018          | 3.7  | 17 |

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|----|---|------|-----|
| 39 | Generation of a Tn5 transposon library in Haemophilus parasuis and analysis by transposon-directed insertion-site sequencing (TraDIS). <i>Veterinary Microbiology</i> , <b>2013</b> , 166, 558-66   | 3.3  | 11  |
| 38 | Comprehensive assignment of roles for Salmonella typhimurium genes in intestinal colonization of food-producing animals. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003456   | 6    | 134 |
| 37 | 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. <i>Infection and Immunity</i> , <b>2013</b> , 81, 838-49 | 3.7  | 64  |
| 36 | Gene content and diversity of the loci encoding biosynthesis of capsular polysaccharides of the 15 serovar reference strains of Haemophilus parasuis. <i>Journal of Bacteriology</i> , <b>2013</b> , 195, 4264-73                                 | 3.5  | 33  |
| 35 | Activity of Bdellovibrio hit locus proteins, Bd0108 and Bd0109, links Type IVa pilus extrusion/retraction status to prey-independent growth signalling. <i>PLoS ONE</i> , <b>2013</b> , 8, e79759   | 3.7  | 32  |
| 34 | The evolution of the Escherichia coli phylogeny. <i>Infection, Genetics and Evolution</i> , <b>2012</b> , 12, 214-26  | 4.5  | 121 |
| 33 | Structure and function of BamE within the outer membrane and the $\beta$ barrel assembly machine. <i>EMBO Reports</i> , <b>2011</b> , 12, 123-8   | 6.5  | 79  |
| 32 | 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. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 1771-6        | 3.5  | 35  |
| 31 | Complete genome sequence of the Crohn's disease-associated adherent-invasive Escherichia coli strain HM605. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4540  | 3.5  | 34  |
| 30 | Quantitative RNA-seq analysis of the Campylobacter jejuni transcriptome. <i>Microbiology (United Kingdom)</i> , <b>2011</b> , 157, 2922-2932  | 2.9  | 38  |
| 29 | Complete genome sequence and comparative metabolic profiling of the prototypical enteroaggregative Escherichia coli strain 042. <i>PLoS ONE</i> , <b>2010</b> , 5, e8801  | 3.7  | 134 |
| 28 | A commensal gone bad: complete genome sequence of the prototypical enterotoxigenic Escherichia coli strain H10407. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 5822-31  | 3.5  | 141 |
| 27 | Characterization of ISBth4, a functional new IS231 variant from Bacillus thuringiensis MEX312. <i>Plasmid</i> , <b>2010</b> , 63, 46-52   | 3.3  | 2   |
| 26 | Comprehensive identification of Salmonella enterica serovar typhimurium genes required for infection of BALB/c mice. <i>PLoS Pathogens</i> , <b>2009</b> , 5, e1000529  | 7.6  | 66  |
| 25 | Comprehensive identification of essential Staphylococcus aureus genes using Transposon-Mediated Differential Hybridisation (TMDH). <i>BMC Genomics</i> , <b>2009</b> , 10, 291  | 4.5  | 194 |
| 24 | MycnoDB: an online database for comparative genomics of the mycobacteria and related organisms. <i>Methods in Molecular Biology</i> , <b>2009</b> , 465, 419-31   | 1.4  | 3   |
| 23 | The pangenome structure of Escherichia coli: comparative genomic analysis of E. coli commensal and pathogenic isolates. <i>Journal of Bacteriology</i> , <b>2008</b> , 190, 6881-93   | 3.5  | 607 |
| 22 | xBASE2: a comprehensive resource for comparative bacterial genomics. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D543-6   | 20.1 | 113 |

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|----|--|------|-----|
| 21 | 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> , <b>2007</b> , 2, e352   | 3.7  | 41  |
| 20 | 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> , <b>2006</b> , 44, 4528-36  | 9.7  | 61  |
| 19 | Down-regulation of key virulence factors makes the <i>Salmonella enterica</i> serovar Typhimurium rfaH mutant a promising live-attenuated vaccine candidate. <i>Infection and Immunity</i> , <b>2006</b> , 74, 5914-25   | 3.7  | 82  |
| 18 | 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> , <b>2006</b> , 34, e3  | 20.1 | 62  |
| 17 | <i>Escherichia coli</i> K-12: a cooperatively developed annotation snapshot--2005. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 1-9   | 20.1 | 525 |
| 16 | xBASE, a collection of online databases for bacterial comparative genomics. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D335-7   | 20.1 | 60  |
| 15 | ArrayOme: a program for estimating the sizes of microarray-visualized bacterial genomes. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, e3  | 20.1 | 9   |
| 14 | Prevalence of pathogenicity island IICFT073 genes among extraintestinal clinical isolates of <i>Escherichia coli</i> . <i>Journal of Clinical Microbiology</i> , <b>2005</b> , 43, 2425-34   | 9.7  | 39  |
| 13 | A degenerate type III secretion system from septicemic <i>Escherichia coli</i> contributes to pathogenesis. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 8164-71  | 3.5  | 56  |
| 12 | Bacterial flagellar diversity in the post-genomic era. <i>Trends in Microbiology</i> , <b>2005</b> , 13, 143-9   | 12.4 | 85  |
| 11 | Genomic analysis of the protein secretion systems in <i>Clostridium acetobutylicum</i> ATCC 824. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , <b>2005</b> , 1745, 223-53   | 4.9  | 38  |
| 10 | 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> , <b>2004</b> , 72, 7282-93 | 3.7  | 82  |
| 9  | 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> , <b>2004</b> , 186, 3547-60                     | 3.5  | 93  |
| 8  | coliBASE: an online database for <i>Escherichia coli</i> , <i>Shigella</i> and <i>Salmonella</i> comparative genomics. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D296-9  | 20.1 | 63  |
| 7  | An analysis of type-III secretion gene clusters in <i>Chromobacterium violaceum</i> . <i>Trends in Microbiology</i> , <b>2004</b> , 12, 476-82   | 12.4 | 23  |
| 6  | Genomic analysis of secretion systems. <i>Current Opinion in Microbiology</i> , <b>2003</b> , 6, 519-27  | 7.9  | 139 |
| 5  | The Evolution of Primate Lentiviruses and the Origins of AIDS <b>2002</b> , 65-96  |      | 9   |
| 4  | Bacterial FHA domains: neglected players in the phospho-threonine signalling game?. <i>Trends in Microbiology</i> , <b>2002</b> , 10, 556-63   | 12.4 | 94  |

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|---|--|-----|-----|
| 3 | The origins of acquired immune deficiency syndrome viruses: where and when?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2001</b> , 356, 867-76   | 5.8 | 204 |
| 2 | Understanding the Model and the Menace: a Postgenomic View of Escherichia Coli21-48  |     | 1   |
| 1 | Rationally designed mariner vectors to allow functional genomic analysis of Actinobacillus pleuropneumoniae and other bacteria by transposon-directed insertion-site sequencing (TraDIS) |     | 2   |