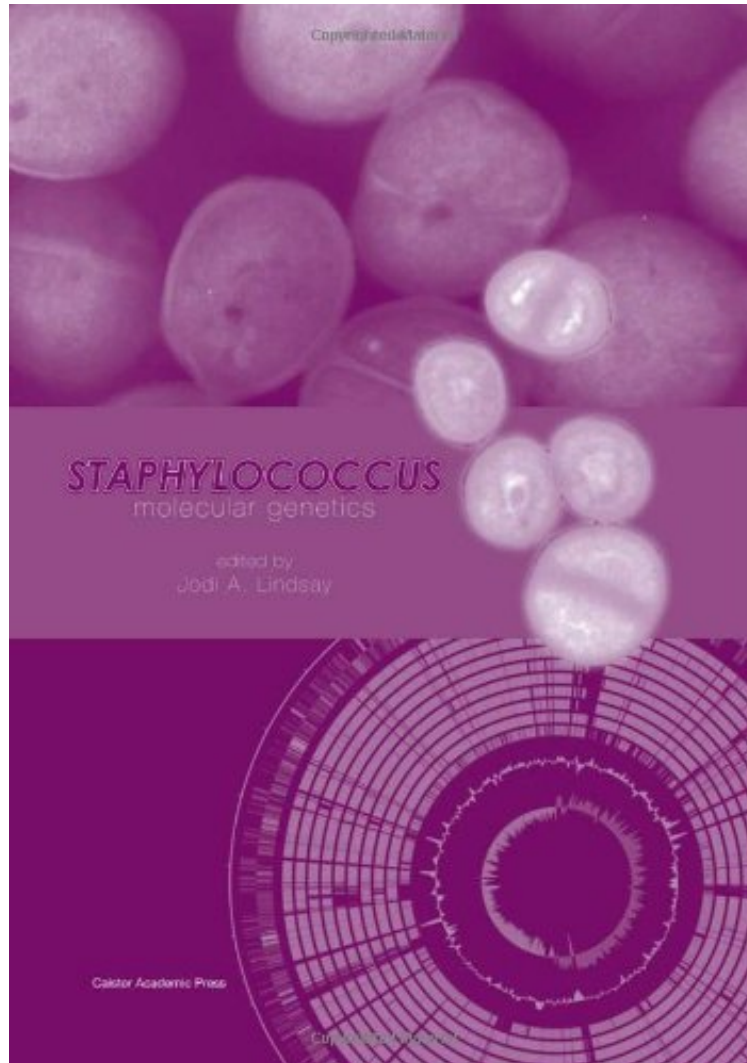


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The staphylococci are important pathogenic bacteria responsible for a variety of diseases in humans and other animals. They are the most common cause of hospital-acquired infection. Antibiotic resistant strains (MRSA) have become endemic in hospitals in most countries, causing major public health issues. In addition, the incidence of new strains

that cause severe community-acquired infections in healthy people is increasing and MRSA strains are emerging in agricultural and domestic animals. In the race to understand staphylococcal pathogenesis, the focus has been on genetics, as a bacterium can only do what its genes allow. The publication of the first staphylococcal whole genome sequence in 2001 paved the way for a greater understanding of the molecular basis of its virulence, evolution, epidemiology, and drug resistance. Since then, the available genomic data has mushroomed and this, coupled with the major advances in genetic know-how and the availability of better genetic tools, has allowed significant advances to be made. This volume on staphylococcal genetics brings together the expertise and enthusiasm of an international panel of leading staphylococcal researchers to provide a state-of-the art overview of the field. Topics include the sequencing projects (including spin-off microarray and systems biology tools), epidemiology, evolution, manipulation of the genome, diagnostics, gene expression due to global regulators and environmental triggers, cell-wall synthesis, coagulase-negative species, and animal pathogens. The book is designed for two major audiences: first, as an introduction on the subject for new researchers, including those unfamiliar with genetics; and for established researchers, for whom the book will serve as an invaluable reference and summary of this large field.