This section presents a collection of papers bringing together some of the latest research by leading international groups in this active and wide-ranging field. The collection was edited by H. F. Jenkinson, T. J. Mitchell, J. C. Paton, D. A. Morrison, S. Hammerschmidt and E. Garcia.

The pneumococcus: ‘old man’s friend’ and children’s foe

A. Finn and H. F. Jenkinson

Innate immunity and the pneumococcus

G. K. Paterson and T. J. Mitchell

Versatility of pneumococcal surface proteins

S. Bergmann and S. Hammerschmidt

Differential expression of key pneumococcal virulence genes in vivo

K. S. LeMessurier, A. D. Oggunyi and J. C. Paton

Zinc metalloproteinase genes in clinical isolates of Streptococcus pneumoniae: association of the full array with a clonal cluster comprising serotypes 8 and 11A

R. Camilli, E. Pettini, M. Del Grosso, G. Pozzi, A. Pantosti and M. R. Oggioni

Inhibition of competence development in Streptococcus pneumoniae by increased basal-level expression of the ComDE two-component regulatory system

S. Guiral, V. Hénard, C. Granadel, B. Martin and J.-P. Claverys

LuxS impacts on LytA-dependent autolysis and on competence in Streptococcus pneumoniae

S. Romao, G. Memmi, M. R. Oggioni and M.-C. Trombe

Construction and evaluation of a chromosomal expression platform (CEP) for ectopic, maltose-driven gene expression in Streptococcus pneumoniae

S. Guiral, V. Hénard, M.-H. Laaberki, C. Granadel, M. Prudhomme, B. Martin and J.-P. Claverys

To have neighbour’s fare: extending the molecular toolbox for Streptococcus pneumoniae

T. G. Kloosterman, J. J. E. Bijlsma, J. Kok and O. P. Kuipers

Distribution of epidemic antibiotic-resistant pneumococcal clones in Scottish pneumococcal isolates analysed by multilocus sequence typing


Identification, prevalence and population structure of non-typable Streptococcus pneumoniae in carriage samples isolated from preschoolers attending day-care centres

R. Sã-Leão, A. S. Simões, S. Nunes, N. G. Sousa, N. Frazão and H. de Lencastre

Dynamics of pneumococcal colonization in healthy Dutch children


Front cover illustration

Adherence of Streptococcus pneumoniae to human umbilical vein epithelial cells (HUVEC) 4 h after infection as seen by high-resolution field emission scanning electron microscopy. Image courtesy Manfred Rohde, German Research Centre for Biotechnology, Braunschweig, Germany.
The DNA-binding domain of the *Escherichia coli* CpxR two-component response regulator is constitutively active and cannot be fully attenuated by fused adjacent heterologous regulatory domains

C. Tapparel, A. Monod and W. L. Kelley

431–441

The *Sinorhizobium meliloti* chromosomal origin of replication

C. D. Sibley, S. R. MacLellan and T. Finan

443–455

Production and properties of the native *Chromobacterium violaceum* fucose-binding lectin (CV-Il) compared to homologous lectins of *Pseudomonas aeruginosa* (PA-Il) and *Ralstonia solanacearum* (RS-Il)

K. Zinger-Yosovich, D. Sudakevitz, A. Imberty, N. C. Garber and N. Gilboa-Garber

457–463

SoxV transfers electrons to the periplasm of *Paracoccus pantotrophus* – an essential reaction for chemotrophic sulfur oxidation

F. Bardischewsky, J. Fischer, B. Höller and C. G. Friedrich

465–472

Functional analysis of the competence transcription factor ComK of *Bacillus subtilis* by characterization of truncation variants


473–483

Regulation of *Serratia marcescens* ompF and ompC porin genes in response to osmotic stress, salicylate, temperature and pH

S. Begic and E. A. Worobec

485–491

The serine/threonine kinase PknB of *Mycobacterium tuberculosis* phosphorylates PBPA, a penicillin-binding protein required for cell division

A. Dasgupta, P. Datta, M. Kundu and J. Basu

493–504

**BIOCHEMISTRY AND MOLECULAR BIOLOGY**

Metagenomic analysis of mesopelagic Antarctic plankton reveals a novel deltaproteobacterial group

D. Moreira, F. Rodriguez-Valera and P. López-Garcia

505–517

**BIODIVERSITY AND EVOLUTION**

Biofilm formation in *Campylobacter jejuni*

G. W. P. Joshua, C. Guthrie-Irons, A. V. Karlyshev and B. W. Wren

387–396

Putative glycogen-accumulating organisms belonging to the *Alphaproteobacteria* identified through rRNA-based stable isotope probing

R. L. Meyer, A. M. Saunders and L. L. Blackall

419–429

**ENVIRONMENTAL MICROBIOLOGY**

Putative glycogen-accumulating organisms belonging to the *Alphaproteobacteria* identified through rRNA-based stable isotope probing

R. L. Meyer, A. M. Saunders and L. L. Blackall

419–429

**GENES AND GENOMES**

Influence of the regulatory protein RsmA on cellular functions in *Pseudomonas aeruginosa* PAO1, as revealed by transcriptome analysis

E. Burrowes, C. Baysse, C. Adams and F. O'Gara

405–418

Comparative analysis of antibiotic resistance gene markers in *Mycoplasma genitalium*: application to studies of the minimal gene complement


519–527

The structural proteome of *Pseudomonas aeruginosa* bacteriophage φKMV


529–534
PATHOGENS AND PATHOGENICITY

Phenol/water extract of *Treponema socranskii* subsp. *socranskii* as an antagonist of Toll-like receptor 4 signalling


*MfLIP1*, a gene encoding an extracellular lipase of the lipid-dependent fungus *Malassezia furfur*

S. Brunke and B. Hube 547–554

The uptake of a *Klebsiella pneumoniae* capsule polysaccharide mutant triggers an inflammatory response by human airway epithelial cells

V. Regueiro, M. A. Campos, J. Pons, S. Albertí and J. A. Bengoechea 555–566

Transcriptional and translational expression patterns associated with immobilized growth of *Campylobacter jejuni*


PHYSIOLOGY

Homocysteine accumulation causes a defect in purine biosynthesis: further characterization of *Schizosaccharomyces pombe* methionine auxotrophs