PTS50 - The Prokaryotic Phosphoenolpyruvate: Sugar Phosphotransferase System
50 Years After Its Discovery

Editor
Milton H. Saier

A valuable update on the multifaceted functions of the PTS

In 1964 Saul Roseman first described the phosphotransferase system (PTS) – a novel sugar-phosphorylating system in Escherichia coli. This compendium results from an international meeting held in Göttingen, Germany, during the summer of 2014 to commemorate the 50th anniversary of his discovery. A number of active researchers with a focus on the PTS reported their most recent findings concerning the structures, functions, mechanisms of action and physiological consequences of this complex system. The numerous aspects of the PTS, including a discussion regarding its impact on bacterial physiology, pathogenesis and ecology, are presented in this up-to-date compendium, which will provide a valuable source of information for many years to come.

Researchers, students and teachers of the physiology of archaea and bacteria will find this compendium an essential source of reference. Additionally, biochemists and geneticists interested in the functions and mechanisms of complex enzymes, transport or regulatory systems in microbes will be fascinated by the complexity of the PTS.

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At the beginning of the 21st century, a microorganism which was visible under the microscope, could be Gram-stained and had been considered a bacterium for several years was identified as Mimivirus, the largest virus known at the time. This opened up the world of giant viruses which are today considered to represent a fourth domain of microbes.

In this special issue of Intervirology, recent findings on two new families of giant viruses, Marseilleviridae and Mimiviridae, are presented. The data confirm that both groups of viruses may be found in the environment (soil, water, insects) and in humans (blood, stool). New techniques to culture, purify and isolate these viruses are also reported. These new findings show that the world of giant viruses is expanding, and challenge the traditional classification of microbes into three domains (bacteria, archaea and eukaryotes) based on size and ribosomal genes. A new classification of microbes into four branches – giant viruses (Megavirales), bacteria, archaea and eukaryotes – is postulated which reflects more realistically our current knowledge of the microbial world.

Anyone interested in this revolution in virology should read this publication which may contribute to the discovery of further giant viruses that are as yet unknown.

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An in-depth compendium of current knowledge of chromosome dynamics and arrangement in bacteria and archaea

Bacterial Chromosomal Segregation

Editor
Peter L. Graumann

All cellular life depends on the accurate duplication and partitioning of the genome. It has become clear in recent years that the chromosomes of many bacterial species show a well-defined arrangement, and their layout, integrity and segregation is supported by a variety of conserved proteins. The architecture of the chromosome also has a large impact on global transcription, and proteins involved in the topology of the DNA play major roles in chromosome segregation and compaction. In this special issue, the molecular biological principles of these fundamental processes are described in several model and non-model bacteria.

Providing an in-depth compendium of our current knowledge of chromosome dynamics and arrangement in bacteria and archaea, this publication is a must-read for any researcher studying or teaching bacterial genetics or physiology.

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