

Publication**A novel protein kinase that controls carbon catabolite repression in bacteria****JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 4615882**Author(s)** Reizer, Jonathan; Hoischen, Christian; Titgemeyer, Friedrich; Rivolta, Carlo; Rabus, Ralf; Stülke, Jörg; Karamata, Dimitri; Saier Jr, Milton H.; Hillen, Wolfgang**Author(s) at UniBasel** [Rivolta, Carlo](#) ;**Year** 1998**Title** A novel protein kinase that controls carbon catabolite repression in bacteria**Journal** Molecular microbiology**Volume** 27**Number** 6**Pages / Article-Number** 1157-1169**Mesh terms** Adenosine Triphosphate, pharmacology; Allosteric Regulation, physiology; Amino Acid Sequence; Bacillus subtilis, enzymology, metabolism; Bacterial Proteins, chemistry; Enzyme Activation, physiology; Enzyme Inhibitors; Escherichia coli, genetics; Fructosediphosphates, pharmacology; Genome, Bacterial; Molecular Sequence Data; Phosphoenolpyruvate Sugar Phosphotransferase System, metabolism; Phosphorylation; Protein Kinase Inhibitors; Protein Kinases, chemistry; Protein-Serine-Threonine Kinases; Recombinant Proteins, chemistry; Sequence Alignment; Sequence Analysis

HPr(Ser) kinase is the sensor in a multicomponent phosphorelay system that controls catabolite repression, sugar transport and carbon metabolism in gram-positive bacteria. Unlike most other protein kinases, it recognizes the tertiary structure in its target protein, HPr, a phosphocarrier protein of the bacterial phosphotransferase system and a transcriptional cofactor controlling the phenomenon of catabolite repression. We have identified the gene (ptsK) encoding this serine/threonine protein kinase and characterized the purified protein product. Orthologues of PtsK have been identified only in bacteria. These proteins constitute a novel family unrelated to other previously characterized protein phosphorylating enzymes. The Bacillus subtilis kinase is shown to be allosterically activated by metabolites such as fructose 1,6-bisphosphate and inhibited by inorganic phosphate. In contrast to wild-type B. subtilis, the ptsK mutant is insensitive to transcriptional regulation by catabolite repression. The reported results advance our understanding of phosphorylation-dependent carbon control mechanisms in Gram-positive bacteria.

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