The phosphoenolpyruvate-dependent glucose-phosphotransferase system (PTSs) of enteric bacteria constitute a complex transport and sensory system. Such a PTS usually consists of two cytoplasmic energy-coupling proteins, Enzyme I (EI) and HPr, and one of more than 20 different carbohydrate-specific membrane proteins named Enzyme II (EII), which catalyze the uptake and concomitant phosphorylation of numerous carbohydrates. The most prominent representative is the glucose-PTS, which uses a PTS-typical phosphorylation cascade to transport and phosphorylate glucose. All components of the glucose-PTS interact with a large number of non-PTS proteins to regulate the carbohydrate flux in the bacterial cell. Several aspects of the glucose-PTS have been intensively investigated in various research projects of many groups. In this article we will review our recent findings on a Glc-PTS-dependent metalloprotease, on the interaction of EIIICB(Glc) with the regulatory peptide SgrT, on the structure of the membrane spanning C-domain of the glucose transporter and on the modeling approaches of ptsG regulation, respectively, and discuss them in context of general PTS research.