

Biochemistry**Data on Biochemistry Described by Researchers at Syracuse University**

2011 JUL 19 -- According to the authors of recent research from Syracuse, New York, "OpdK is an outer membrane protein of the pathogenic bacterium *Pseudomonas aeruginosa*. The recent crystal structure of this protein revealed a monomeric, 18-stranded beta-barrel with a kidney-shaped pore, whose constriction features a diameter of 8 angstrom." "Using systematic single-channel electrical recordings of this protein pore reconstituted into planar lipid bilayers under a broad range of ion concentrations, we were able to probe its discrete gating kinetics involving three major and functionally distinct conformations, in which a dominant open substate O-2 is accompanied by less thermodynamically stable substates O-1 and O-3. Single-channel electrical data enabled us to determine the alterations in the energetics and kinetics of the OpdK protein when experimental conditions were changed," wrote B.R. Cheneke and colleagues, Syracuse University. The researchers concluded: "In the future, such a semiquantitative analysis might provide a better understanding on the dynamics of current fluctuations of other beta-barrel membrane protein channels." Cheneke and colleagues published their study in *Biochemistry* (Analysis of Gating Transitions among the Three Major Open States of the OpdK Channel. *Biochemistry*, 2011;50(22):4987-4997). For additional information, contact L. Movileanu, Syracuse University, Dept. of Physics, 201 Physics Bldg, Syracuse, NY 13244, United States. Publisher contact information for the journal *Biochemistry* is: American Chemical Society, 1155 16th St., NW, Washington, DC 20036, USA. Keywords: City:Syracuse, State:New York, Country:United States, Region:North and Central America This article was prepared by Life Science Weekly editors from staff and other reports. Copyright 2011, Life Science Weekly via NewsRx.com.