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The Crystal Structure of YaeQ from *Xanthomonas axonopodis* pv. *Citri*. J.A.R.G. Barbosa¹, C.R. Guzzo², R.A.P. Nagem³, L.M.P. Galvão-Botton², C.S. Farah², ¹Laboratório Nacional de Luz Síncrotron (LNLS), Campinas, SP, Brazil, ²Univ. de São Paulo (USP), São Paulo, SP, Brazil, ³Univ. Federal de Minas Gerais (UFMG), Belo Horizonte, MG, Brazil. *Xanthomonas axonopodis* pv. *citri* (Xac) YaeQ (XAC2396) is a member of a hypothetical proteins' family conserved in several gram negative pathogens. This protein was been cloned, expressed, purified and crystallized. Initial trials to get heavy atoms derivatives were unsuccessful, leading to the expression, purification and crystallization of recombinant YaeQ containing selenomethionine for MAD experiments. The crystals of space group P2₁ diffracted up to 1.9 Å resolution at a synchrotron source. The unit cell parameters are a = 39.75, b = 91.88, c = 48.03 Å and $\beta = 108.37^\circ$. The MAD data was used with SHELXD and autoSHARP to solve the crystal structure, which has two molecules in the asymmetric unit. The YaeQ structure reveals a novel protein fold characterized by a helix located inside an incomplete β -barrel. This barrel is open in one side where the internal helix is slightly exposed. The conserved residues are clustered on two loops located on the top of the barrel and on the exposed face of the central helix. Analysis of the YaeQ structure may provide leads through which information regarding its function may be gained.