INTRODUCTION. Due to the emerging of bacterial drug resistance, new antimicrobial or antibiotics agents are needed. One of the strategies to obtain new antibiotics is the manipulation of biosynthetic pathways through synthetic biology in order to generate new derivatives of known molecules. In this context, aminoglycosides are biosynthesized by various enzymes that modify sugars or make the linkage between them. Sisomicin belongs to the 2-DOS class of aminoglycosides and have the purporosamin and garosamin aminosugars at the position C-4 and C-6, respectively. Sisomicin biosynthesis has four aminotransferases that catalyse the transamination at different positions of the purporosamin. The objective of this work is obtain the tridimensional structure of Sis5, an aminotransferase which acts at position C6’ of sisomicin intermediate.

MATERIAL AND METHODS. sis5 gene was cloned in pET28a and expressed in BL21(DE3) with selenomethionine supplementation. The purification was carried out using His-tag affinity and molecular exclusion columns. Sis5 incubated with pirodoxal-5-phosphate (PLP) was crystallized and data collection was executed at PETRA III and SLS. X-ray data analysis was performed using the programs XDS and CCP4. The Sis5 structure was determined by SAD. DISCUSSION AND RESULTS. Sis5 was crystallized in C2 space group and has two molecules in the asymmetric unit. The crystals diffract up to 1.4 Å of resolution. Sis5 has the similar folding of other aminotransferases, which belong the α-family of B6-dependent enzymes. The active site is in the interface of the two promoters and the PLP is bond to the Lys232 through of Schiff base. CONCLUSION. We solved the structure of the first aminotransferase from an aminoglycoside biosynthesis. This structure might reveals key details of the biosynthesis of aminoglycoside and could be useful start point to generate new aminoglycoside derivatives in vitro through enzymatic engineering or site direct mutagenesis.

Key words: aminoglycoside, aminotransferase, crystallography