

## Expression, Characterization and Identification of SODs genes from *Streptomyces peucetius* ACTCC 27952

Bashistha Kumar Kanth<sup>a</sup>, Sailesh Malla<sup>a</sup>, Kwangkyoung Liou<sup>a,c</sup>  
and Jae Kyung Sohng<sup>a</sup>

<sup>a</sup>Institute of Biomolecule Reconstruction (iBR), Department of Chemistry,  
Sun Moon University,

#100, Kalsan-ri, Tangeong-myeon, Asansi, Chungnam 336-708, South Korea

### Abstract

The complete genome of *Streptomyces peucetius* ACTCC 27952 has been sequenced that covers 8.1 Mb. The analysis of whole genome of *Streptomyces peucetius* ACTCC 27952 render two superoxide dismutase (*sp*SODs) named *sp*SOD1 & *sp*SOD2. The deduced amino acid sequences of *sp*SOD1 shows high similarity to SODs from *Streptomyces coelicolor* A3(2) and *Streptomyces avermitilis* MA-4680 (85% identity) whereas *sp*SOD2 shows high similarity to SODs from *Streptomyces avermitilis* MA-4680 and *Streptomyces coelicolor* A3(2) (94% identity, and 93% identity respectively). Out of two *sp*SODs, *sp*SOD1 has been cloned and expressed into *E. coli* BL21 (DE3) and characterized. It was also cloned into pIBR25, a *Streptomyces* expression vector and transformed into different *Streptomyces sp.* to study its effects in the production of secondary metabolites.

**Key words** : Genome, Superoxide dismutase, Secondary metabolites,