Addendum to "Enhanced functional and structural domain assignments using remote similarity detection procedures for proteins encoded in the genome of *Mycobacterium tuberculosis* H37Rv" (*J. Biosci.* **29** (3) 245–259, 2004) by *Seema Namboori*, *Natasha Mhatre*, *Sentivel Sujatha*, *Narayanaswamy Srinivasan and Shashi Bhushan Pandit*

The three-dimensional structure and subcellular localization of various domains and sub-domains of Rv1318c, a putative cyclase from *Mycobacterium tubercolosis*, are currently unknown from experimental studies. We have predicted that Rv1318c consists of five transmembrane helices (Namboori *et al* 2004). However, depending upon the algorithm for prediction and the parameters used, the predicted number of helices can vary. We have also suggested that the C-terminal cyclase domain of Rv1318c is located intracellularly; this is a conserved feature in the family of adenylyl/guanylyl cyclases. Recently it has been shown experimentally that Rv1318c is an adenylyl cyclase (Linder *et al* 2004; *Eur. J. Biochem*. **271** 2446–2451).