

*Sau\_CsoR/1-97* 1 MT - - - - EQDNAHH - - - - SEQIKTNLKSRLNR I EGQVRA I NRM I EEDVYCDVLT 46  
*Sau\_CstR/1-86* 1 MN - - - - - - - - - - - - - - - YDK - - - KMINR I NR I QGQLNG I I KMMEEGK DCKDVI T 36  
*MTb\_Rv0190/1-96* 1 MT - - - - - - - - AAHG - - - - - YTQQKDN YAKRLRR VEGQVRG I ARM I EEDK YC I DVL T 43  
*Bsu\_CsoR/1-101* 1 ME - - - - - KHNEHKTLN HKSSKEKDQ I TNRLKR I EGQVRG I QNMVENDRYCVD I L V 50  
*GNTG\_1533/1-105* 1 MTHPSQEEHVL HGTMI PR TKEE I EN I MKRLKR I EGQVRGVQK MVEDNRYC I D I L V 55

*Sau\_CsoR/1-97* 47 QIRATRSALNSVAIKLLEQHMKSCIMNKVNQGG - - AQEEAMEEELL - VTFQKL IKD - 97  
*Sau\_CstR/1-86* 37 QISASKSSLQRLMGI I I SENL I ECVKAAADD - - - - - EESSQELINEAVNLLVKS SK 86  
*MTb\_Rv0190/1-96* 44 QISAVTSALRSVALNLLDEHLSHCVTRAVAE GGP GADGKLAEAS - AA I ARLVRS - 96  
*Bsu\_CsoR/1-101* 51 QISAVQAAMKNVALHLL EDHAHHC VADA I KSG - - DGEQA I SELL - DVFKKFTKS - 101  
*GNTG\_1533/1-105* 56 QISA I QAALRQVGMQLLERHANHCVAKA I REG - - SGEQSLRELM - DV I KQFAK - - 105