

The lysine (K) residue at position 146 of MsrR of *S. aureus* Mu50 and Mu3 is indicated by a red box. The LytR-CpsA-Psr domain as defined in the PFAM database (PF03816) is shaded in grey, and conserved residues as determined in Figure 6 are highlighted in blue. Residues of the predicted transmembrane regions are printed in red. Sequences are labelled using UniProt entry names.

[illegible]