

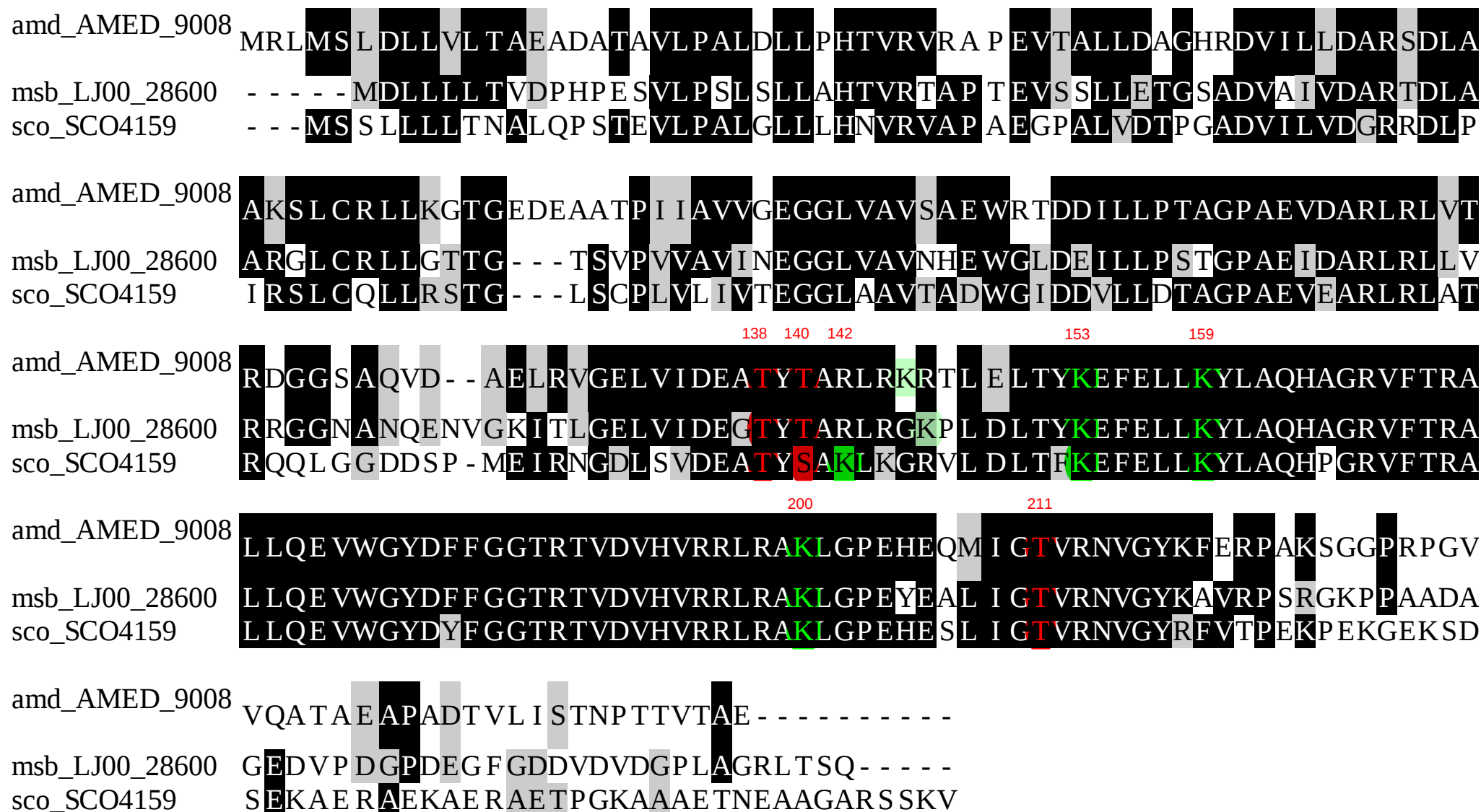


Fig. S4 Alignment of the GlnR homologous protein sequences from *S. coelicolor* (SCO4159), *M. smegmatis* (LJ00_28600) and *A. mediterranei* U32 (AMED_9008). Alignment of the GlnR-protein sequences (<http://www.genome.jp/kegg/>) was performed using Clustal W and Boxshade (<http://mobyle.pasteur.fr>). Conserved residues are shown as white letter on black background. Non-conserved residues are shown as black letters on a white background. Black letters on gray background indicate similar amino acids. Phosphorylated serine/threonine residues are highlighted in red. Acetylated lysine residues are highlighted in green. Positions of the modified residues are referred to GlnR-protein sequence from *S. coelicolor*.