



Sequence alignment using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo>). Strictly conserved and highly conserved residues are highlighted with red boxes and red lettering, respectively. Secondary-structure elements are shown on top as spirals and arrows for α -helices and β -strands, respectively. Solid stars indicate the active-site residues that are conserved. The GenBank accession numbers are as follows: CaMan5_18 (AEE72695); CaGH5_18 from *Cutibacterium avidum* 44067 (AGJ77370); KfGH5_18 from *Kribbella flavida* DSM 17836 (ADB34475); BlGH5_18 from *Bifidobacterium longum* subsp. infantis 157F (BAJ71452); SkGH5_18 from *Sanguibacter keddiei* DSM 10542 (ACZ21418); ScGH5_18 from *Streptomyces coelicolor* A3(2) (CAB61915) and AhGH5_18 from *Arcanobacterium haemolyticum* DSM 20595 ADH91800). The figure was prepared with ESPript3 (<http://esript.ibcp.fr/ESPript/ESPript/>).