

S4 Fig.

S.viridis
S.flavogriseus
S.clavuligerus
S.jumonjinensis
S.katsurahamanus

S. viridis
S. flavogriseus
S. clavuligerus
S. jumonjinensis
S. katsurahamanus

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S4 Fig. Multiple sequence alignment of different Cpe proteins described in the current study. Analysis was performed with Clustal Omega (ver 1.2.1) using translated Cpe amino acid sequences from *S. clavuligerus* (WP_003952519.1), *S. flavogriseus* (WP_014152684.1), *S. viridis* (WP_015787620), *S. jumonjinensis* and *S. katsurahamanus*. The DNA sequences of *cpe* from the latter two producers (*S. jumonjinensis* and *S. katsurahamanus*) were determined as part of the current study and are reported in S3 Fig. The boxes in black highlight the conserved SXXK, SDN and KTG/KAG motifs present in class A β -lactamases and the respective Cpe proteins, whereas the box in blue represents the N-terminus domain identified in Cpe^{Sc}. The arrows indicate amino acids from Cpe^{Sc} that were selected for mutagenesis and the ones highlighted in red were shown to be essential for *in vivo* clavulanic acid production in *S. clavuligerus*.