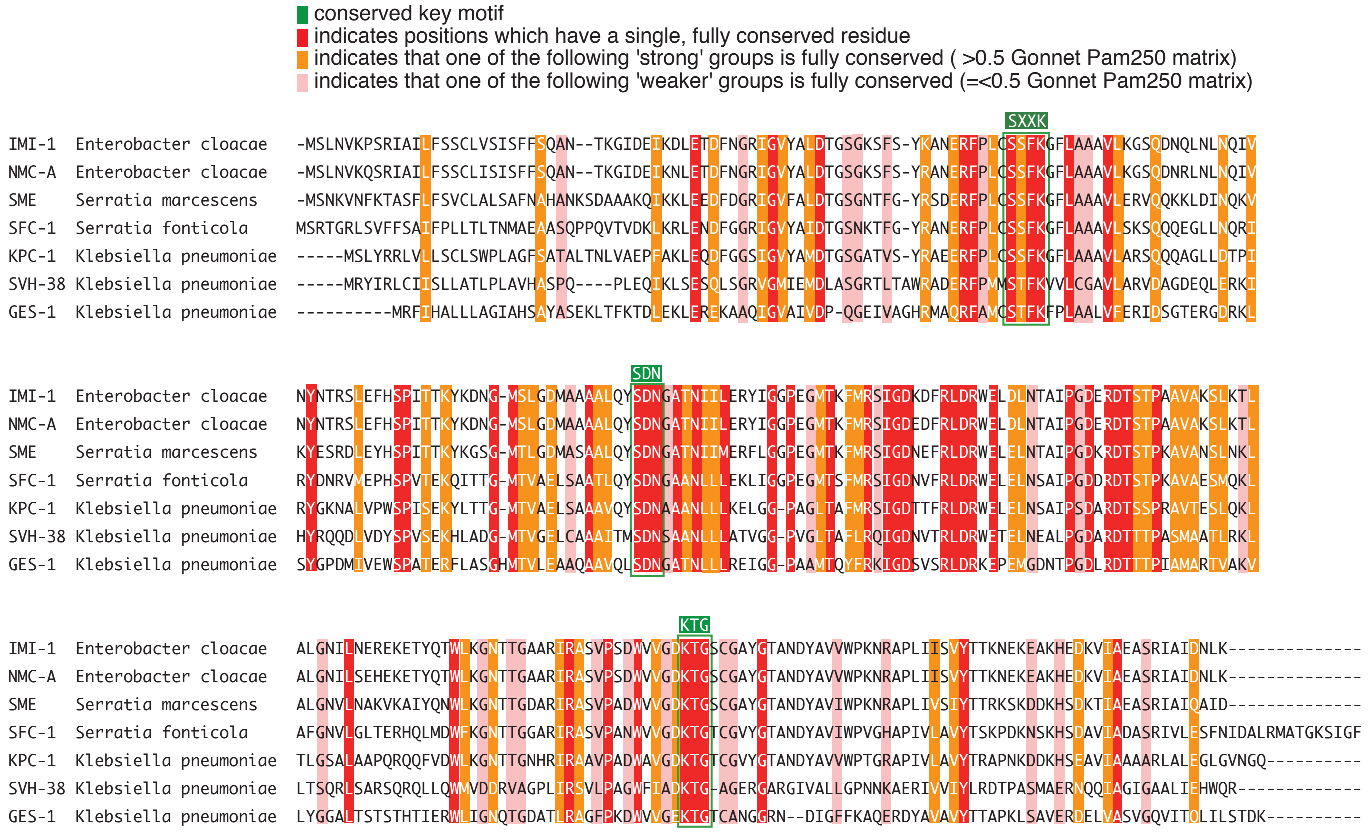

🟩 conserved key motif
🟥 indicates positions which have a single, fully conserved residue
🟧 indicates that one of the following 'strong' groups is fully conserved (>0.5 Gonnet Pam250 matrix)
▨ indicates that one of the following 'weaker' groups is fully conserved (=<0.5 Gonnet Pam250 matrix)

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IMI-1  Enterobacter cloacae    -MSLNVKPSRIAILFSSCLVSISFFSQAN--TKGIDEIKDLETDFNGRIGVYALDTGSGKSFS-YKANERFPLCSSFKGFLAAAVLKGSQDNQLNLNQIV
NMC-A  Enterobacter cloacae    -MSLNVKQSRIAILFSSCLISISFFSQAN--TKGIDEIKNLETDFNGRIGVYALDTGSGKSFS-YRANERFPLCSSFKGFLAAAVLKGSQDNRLNLNQIV
SME    Serratia marcescens     -MSNKVNFKTASFLFSVCLALSAFNAHANKSDAAAKQIKKLEEDFDGRIGVFALDTGSGNTFG-YRSDERFPLCSSFKGFLAAAVLERVQQKKLDINQKV
SFC-1  Serratia fonticola      MSRTGRLSVFFSAIFPLLTLTNMAEAASQPPQVTVDKLKRLENDFGGRIGVYAIDTGSNKTFG-YRANERFPLCSSFKGFLAAAVLSKSQQQEGLLNQRI
KPC-1  Klebsiella pneumoniae   -----MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVS-YRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPI
SVH-38 Klebsiella pneumoniae   -----MRYIRLCIISLLATLPLAVHASPQ----PLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDAGDEQLERKI
GES-1  Klebsiella pneumoniae   ----------MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDP-QGEIVAGHRMAQRFAMCSTFKFPLAALVFERIDSGTERGDRKL

IMI-1  Enterobacter cloacae    NYNTRSLEFHSPITTKYKDNG-MSLGDMAAAALQYSDNGATNIILERYIGGPEGMTKFMRSIGDKDFRLDRWELDLNTAIPGDERDTSTPAAVAKSLKTL
NMC-A  Enterobacter cloacae    NYNTRSLEFHSPITTKYKDNG-MSLGDMAAAALQYSDNGATNIILERYIGGPEGMTKFMRSIGDEDFRLDRWELDLNTAIPGDERDTSTPAAVAKSLKTL
SME    Serratia marcescens     KYESRDLEYHSPITTKYKGSG-MTLGDMASAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGDNEFRLDRWELELNTAIPGDKRDTSTPKAVANSLNKL
SFC-1  Serratia fonticola      RYDNRVMEPHSPVTEKQITTG-MTVAELSAATLQYSDNGAANLLLEKLIGGPEGMTSFMRSIGDNVFRLDRWELELNSAIPGDDRDTSTPKAVAESMQKL
KPC-1  Klebsiella pneumoniae   RYGKNALVPWSPISEKYLTTG-MTVAELSAAAVQYSDNAAANLLLKELGG-PAGLTAFMRSIGDTTFRLDRWELELNSAIPSDARDTSSPRAVTESLQKL
SVH-38 Klebsiella pneumoniae   HYRQQDLVDYSPVSEKHLADG-MTVGELCAAAITMSDNSAANLLLATVGG-PVGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPASMAATLRKL
GES-1  Klebsiella pneumoniae   SYGPDMIVEWSPATERFLASGHMTVLEAAQAAVQLSDNGATNLLLREIGG-PAAMTQYFRKIGDSVSRLDRKEPEMGDNTPGDLRDTTTPIAMARTVAKV

IMI-1  Enterobacter cloacae    ALGNILNEREKETYQTWLKGNTTGAARIRASVPSDWVVGDKTGSCGAYGTANDYAVVWPKNRAPLIISVYTTKNEKEAKHEDKVIAEASRIAIDNLK--------------
NMC-A  Enterobacter cloacae    ALGNILSEHEKETYQTWLKGNTTGAARIRASVPSDWVVGDKTGSCGAYGTANDYAVVWPKNRAPLIISVYTTKNEKEAKHEDKVIAEASRIAIDNLK--------------
SME    Serratia marcescens     ALGNVLNAKVKAIYQNWLKGNTTGDARIRASVPADWVVGDKTGSCGAYGTANDYAVIWPKNRAPLIVSIYTTRKSKDDKHSDKTIAEASRIAIQAID--------------
SFC-1  Serratia fonticola      AFGNVLGLTERHQLMDWFKGNTTGGARIRASVPANWVVGDKTGTCGVYGTANDYAVIWPVGHAPIVLAVYTSKPDKNSKHSDAVIADASRIVLESFNIDALRMATGKSIGF
KPC-1  Klebsiella pneumoniae   TLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAAARLALEGLGVNGQ----------
SVH-38 Klebsiella pneumoniae   LTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTG-AGERGARGIVALLGPNNKAERIVVIYLRDTPASMAERNQQIAGIGAALIEHWQR-------------
GES-1  Klebsiella pneumoniae   LYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVGEKTGTCANGGRN--DIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILSTDK----------
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Supplemental Fig. 2. The alignment of class A carbapenemases based on their primary sequences
Characteristic features of class A β-lactamases are the tetrad motif S-X-X-K, the S-D-N triad, and the K-T-G triad, which contain the serine in the enzyme active site in their primary sequences. Based on the primary sequences, the tree was generated using Clustal Omega [32, 33, 34] of GenomeNet at Kyoto University Bioinformatics Center (https://www.genome.jp/tools-bin/clustalw).