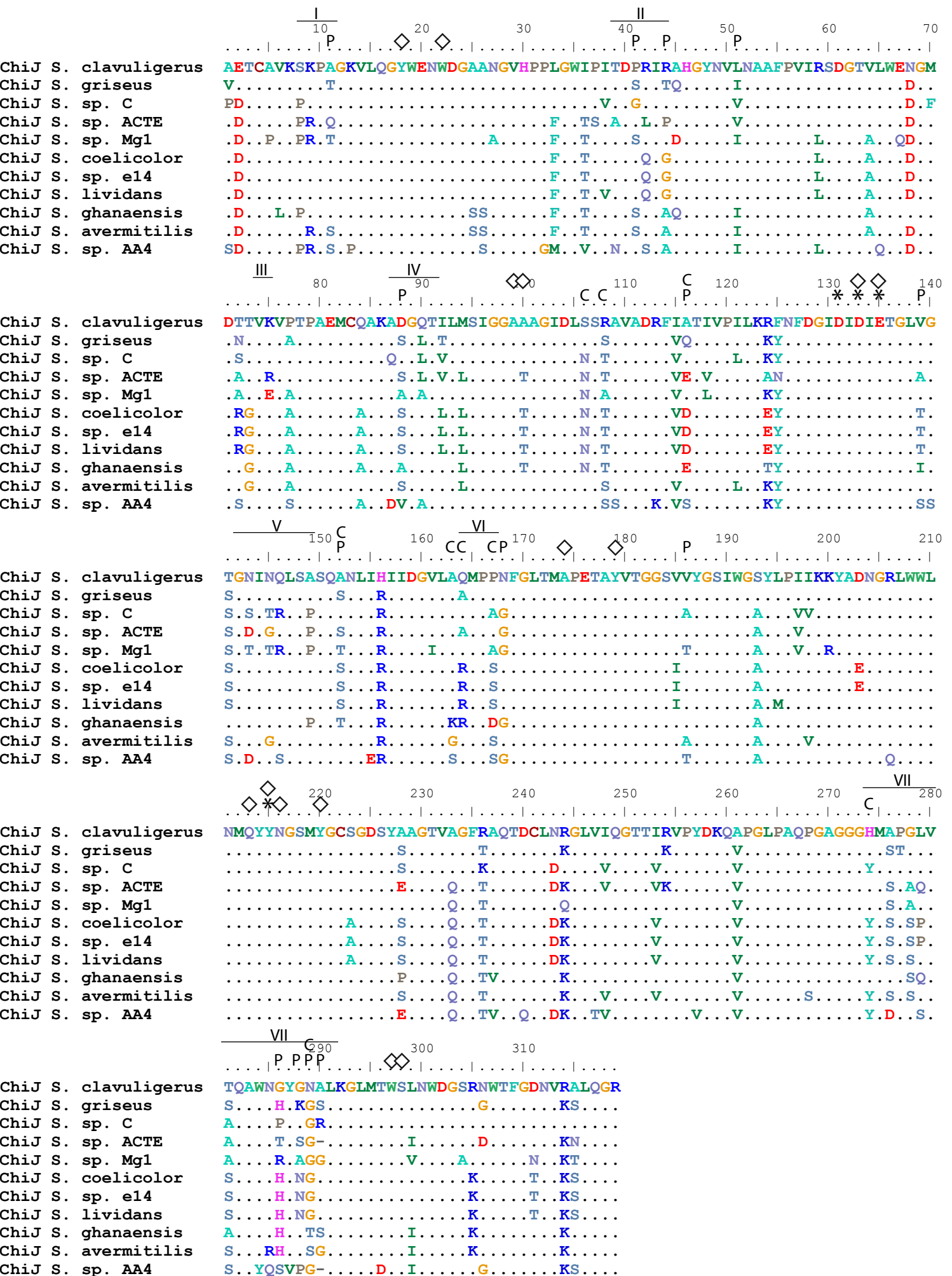


Additional file 2. Alignment of *Streptomyces* spp. ChiJ sequences, where a dot indicate an identical amino acid residue as in *S. clavuligerus* ChiJ and a dash indicate a gap.



As outlined in Fig. 3, asterisks (*) indicate positions of predicted catalytic residues, diamonds (◇) indicate predicted substrate-interacting residues, P indicate residues under positive selection, C indicate co-evolving residues. Positions of highly variable regions are indicated (I through VII).