Supplemental Figure 1A.
stk protein sequences from CV598 and CRO1

CV598 MIELGKKLNGRYQITGNIGSGGMANVFLAHDLILDRDVAVKVLRFDFQNDQTAIRRFQREALAATELVHPNIVSVYDVGEEDNMQYLVMEYVKGMDLKRYIQTHYPVPYETAVNI
CRO1 MIELGKKLNGRYQITGNIGSGGMANVFLAHDLILDRDVAVKVLRFDFQNDQTAIRRFQREALAATELVHPNIVSVYDVGEEDNMQYLVMEYVKGMDLKRYIQTHYPVPYETAVNI

CV598 MQQILSAISLAHNHQIIHRDLKPQNVLIDNEGVVKITDFGIAIALSETSITQTNTMLGSVHYLSPEQARGSMATKQSDIYALGIILYEMLTGSVPFDGESAVTIALKHFQDDLPSIKALD
CRO1 MQQILSAISLAHNHQIIHRDLKPQNVLIDNEGVVKITDFGIAIALSETSITQTNTMLGSVHYLSPEQARGSMATKQSDIYALGIILYEMLTGSVPFDGESAVTIALKHFQDDLPSIKALD

CV598 PNVPQALENVILRATAKEPADRYKSAE EMSDDLSTVLSPARANEEKWQPHVMDNETKVITPLTEDAPMPDTFKSMPLPKDKPENETLPEEEEVLPDPKKKGQKKWWLILLAILAVL
CRO1 PNVPQALENVILRATAKEPADRYKSAE EMSDDLSTVLSPARANEEKWQPHVMDNETKVITPLTEDAPMPDTFKSMPLPKDKPENETLPEEEEVLPDPKKKGQKKWWLILLAILAVL

CV598 GIGTAVFFASGGRGEVVVPDVSDLSEASARETLAKAKLEVATKTEEIADDKIEEGNVVKTDPAAGTTVKQKREVTLYISSGTKKI KLDDYSGKSYEDAEASLKELGFSADLIQKEEEFSSEV
CRO1 GIGTAVFFASGGRGEVVVPDVSDLSEASARETLAKAKLEVATKTEEIADDKIEEGNVVKTDPAAGTTVKQKREVTLYISSGTKKI KLDDYSGKSYEDAEASLKELGFSADLIQKEEEFSSEV

CV598 ESGMIISQSPSEDTEVDPKTDTITFTVSK GPETVTLSSH VGENYETVRNWLVTQGFNINNISATYDYSDTVPSGSIISQDPASGEVVAEETYINFVVSQ GTEPKL NDISGYTKSEAQSYL
CRO1 ESGMIISQSPSEDTEVDPKTDTITFTVSK GPETVTLSSH VGENYETVRNWLVTQGFNINNISATYDYSDTVPSGSIISQDPASGEVVAEETYINFVVSQ GTEPKL NDISGYTKSEAQSYL

CV598 ASVGAEYIGHETSEYSNTVDKDKVIRTVPGAGTTITKGMVVNVIYSK GPDPASSSSE KDSSDSSSSSSSSSSTSNSSKEESSSSTSSSASTSESSK.
CRO1 ASVGAEYIGHETSEYSNTVDKDKVIRTVPGAGTTITKGMVVNVIYSK GPDPASSSSE.

Ser/Thr kinase domain
T: Threonines that are predicted to be auto-phosphorylated in *E. faecalis* and important to regulation of activity
PASTA domain
Transmembrane helix

Missing in CRO mutant, predicted to be disordered