

BepA 1 MPRKAKARTKTEIISPRSEIVENTTTLRNKYGIKLNNAFLKESGHIITAKAMINLRRESIF 6C
 BepB 1 MPRKAKAK--NISTASPRNLIKDEGTQILRNKYGETDLKLLLEKLDREQAMNLRRESIF 5E
 BepC 1 -----MLSENNLAKNSNTLNRNKYGIKDPQLRYERCAHDTAR EVMNLRFEFPIF 4F
 Fic-1 1 MPRKAKERTKNIETSSEIVENTTTLRNKYGIITNFDAFTAKYTHITAKALINLRREAPLIF 6C

COG2184.1 consensus RMDLDFEG----RDE--LIMESEGVLRNLLRITTDQQLLEAEYELSLRIDEI--ESGPR

BepA 61 EY--RDTATLGHFHQLERKNTFEWAGHLEHIDFTSPGTTAAMRSPKRTGWNNAFAIGDEI 11S
 BepB 59 EY--RDCAVLYLTHQCLEKTFEWAGHLEHIDFTSPGSSIAAMRSPKRTGWNKDFAKSEKI 11T
 BepC 48 QR--SGLAVLKLHWLTHRSFEWAGHLEHIDFTSPGSSIAAMRSPKGRHVVFVAVGPCI 10G
 Fic-1 61 EK--RDSYVLSHGHQLERKNTFEWAGHLEHIDFTSPGSSIAAMRSPKRAEWNVVFANDEI 11S

COG2184.1 consensus KGGLDLHNRRAHTRQLRQDIFEWAGHLEHIDFTSPGSSIAAMRSPKRAEWNVVFANDEI

BepA 120 QEG--RHDQTLAEKNNLQGLAREEENSFALEIENSINLHPSREENRTRCRLESPENAKA 17S
 BepB 118 PEL--RQDQTLAEKNNLQGLAREEENKQTEIHYSEHKHLEPDIENHEEQHSPENAKA 17T
 BepC 107 QKE--RQDQTLAEKNNLQGLAREEENKQTEIHYSEHKHLEPDIENHEEQHSPENAKA 16E
 Fic-1 120 EEG--RHDQTLAEKNNLQGLAREEENSFALEIENSINLHPSREENRTRCRLESPENAKA 17S

COG2184.1 consensus ERADYVAQWMPQETY-----LSEVFRHAKIVEINIAHPSREENRTRCRLESPENAKA

BepA 180 AGHQLNFSYDTRKRMVAVSVAVAENGDLERMQHLEFEDDISNRRIRLLKREHMTTKNVE--R 23E
 BepB 178 AGHQLNFSYDTRKRMVAVSVAVAENGDLERMQHLEFEDDISNRRIRLLKREHMTTKNVE--R 23E
 BepC 167 AGYKILNFSYDTRKRMVAVSVAVAENGDLERMQHLEFEDDISNRRIRLLKREHMTTKNVE--R 22E
 Fic-1 180 AGHQLNFSYDTRKRMVAVSVAATQNDNLEEMQHLEFEDDISNRRIRLLKREHMTTKNVE--R 23E

COG2184.1 consensus LGRALIMQSTISKE---AYLQALRRG---ENAKALALIT-ALREIIRGIRIQAGEYI--E

BepA 239 NVNDRVAVVIRESETYVSRVRSAGLEGALNVKGYIIGDIDHLEPQLRIRKIKGKRT 29T
 BepB 237 NVNDCVAVVIRKSETYVSRVRSYSEAFVLDMQGTYIIGKIDDLLEPRLRSRIRKIGKRT 29S
 BepC 227 EINEHIVVIRKSETYVSRVRSYSEAFVLELEDGFVGHKIDDLLEPVRVLRQGRIV 28S
 Fic-1 239 DINDRVAVVIRESETYVSRVRSAGHDSLAFNVNGAYIIGDKELDLLEPQLRIRKIKGKRT 29T

COG2184.1 consensus -----

BepA 298 VTA PKAEIIRKKT 309
 BepB 296 VTA PKNKLENT 307
 BepC 286 VRKSNVLIIRKEI 297
 Fic-1 298 VTA SQTQLEIRNI 309

COG2184.1 consensus -----