

pSEA1 : 71 DKEFDRIIRPIIHVIRYFMSLPASERHHHTDMSASLFFHSLQNTANIALAKYNS 124
ICE_Vnig : 71 DEQFNLIIRPILHHVIKYFMALPASERHHHTDMSASLFFHSLQNTANIALAKYNS 124
R391 : 60 QRDFQRLIQPCIDHLAAYVHLLPASEHHHSG-AGGLLRHSLEVAFWAAQAAEG 112
SXT : 60 QREFQRLIQPCIDHLAAYVHLLPASEHHHSG-AGGLLRHSLEVAFWAAQAAEG 112
pAsa4 : 65 IEDFNRLVLPVIHRYAAFVHLLPASEAHHHRG-AGGLFRHGLEVAFWAAQASES 117
pIP1202 : 72 VDDFNRLVLPVIQRYAAFVHLLPASESHHHRG-AGGLFRHGLEVAFWAAQASES 124
pAQU1 : 70 QEEYDRLVMPVIGRYAAFVHLLPASEAHHHRG-AGGLFRHGLEVAFWATQASES 122
Pls_Rhofe : 85 NDDFERRYLAPLERRAAELINLI PATRDKHHTG-AGGLFRFAATMAIRSAQSADG 137
Pls_Shesp : 99 VYNAQTLVRDVVANFLSYAHLL PASENHHHAA-VGGLARHSLEVALFSLRHMAS 151
Chr_Neigo : 79 DENWSKDALPFLEKYIAFVQRL PASESHHHAG-DGGLVRRHTLDVAALALVASTS 131
pKLC102 : 55 KQQFEEIYRRPLANYAELVQQL PASENHHHAH-PGGMIDHGLEIVAYALKVRQT 107
PAGI-4_C : 24 KQQFEEIYRRPLANYAELVQQL PASENHHHAH-PGGMIDHGLEIVAYALKVRQT 76
clc : 58 RKQFATLYRAPLERYAELVQRF PASEAHHHAY-PGGLMDHGLEIVAYALKLRQS 110
PAGI-3SG : 58 RQQTALYLAPLERYASLVQAF PASESHHHAY-SGGLMDHGLEIVAYALKLRQS 110
PAGI-2_C : 58 RKQFAVLYRAPLERYAELVQAF PASESHHHAY-PGGLMDHGLEIVAYALKLRQS 110
pCAR1 :139 ASDLKLYVEPILVNFAELAHML PASENHHHSG-PGGLLRHSLEVASLTLDGCLT 191
R478 :106 AYTFTNLVKLPLVEYVRWIHLL PASENHHHNG-IGGLLSHSLEVAIISLKNANH 158
R27 :104 AYTFTNLVKLPLIEYIRWIHLL PASENHHHNG-IGGLLSHSLEVAMISLKNANH 156
Rts1 : 76 DAEYDEYIQPMLTNFANFVHLL PASEFHHHRA-QGGLLRHTLEVVLYSIKIAKS 128
pMAQU02 : 51 EQVWNKHLYAIEQFAELVQEV PASEIHHHSE-SGGLIDHTLEALYAGVRISQG 103
Consensus_aa : PASE HHH GGL H L
Consensus_ss : hhhhhhhhhhhhhhhhhhhhhhhhh hhhhhhhhhhhhhhhhhhhhhhhhh

pSEA1 :132 IKIEHKNEYKHAAGVAVFLAALFHDAGKLFSDMSVYPSDEK 172
ICE_Vnig :132 IKIEHKNEYKHAASVAVFLAALFHDAGKLYSDMSVYPSDEK 172
R391 :119 GTPVEKKELEPRWRVAAALGGLFHDIGKPVSDLSITDEDGR 159
SXT :119 GTPVEKKELEPRWRVAAALGGLFHDIGKPVSDLSITDEDGR 159
pAsa4 :124 GTPKQRRDNEPRWRLASCFSGLLHDVGKPLADVSIITDKNGV 164
pIP1202 :131 GTPRERRDNEPRWRLASCFSGLLHDVGKPLSDVSIITDKDGS 171
pAQU1 :129 GSPRERRRNEPRWRLACCFSGLLHDVGKPLSDVVITNSDGS 169
Pls_Rhofe :144 EGIERRRQTEAAWRHAAFLTGLTCELFRLPT-EMMIFDPKGN 184
Pls_Shesp :158 KFTDELHGKKIRWQYAAWVIGLVHDIGKALHDMTVQADDS- 197
Chr_Neigo :138 AKTEEIAKKTAVWRYGIMCAALLHDVGKTVT-GFQVELFDSA 178
pKLC102 :114 AAPESQSAQTEAWSAAAAYGALAHDLGKIVVDLQVELQDGS 154
PAGI-4_C : 83 AAPESQSAQAEAWSAAAAYGALAHDLGKIVVDLQVELQDGS 123
clc :117 STPEDQAAQSEAWTAAVAYAALLHDVGKLAVDLHVELADGS 157
PAGI-3SG :117 TTPEDQVIQAEAWTAATAIYAALLHDIGKVAVDLHVEYGDGS 157
PAGI-2_C :117 ASPEDQAAQAEAWTAAVAYAALLHDIGKIAVDLHVELADGS 157
pCAR1 :198 ETPARRSMRLRRWYVAGIASGLLHDAGKPLTDIRATDFEGN 238
R478 :165 GYQDEEVVRRKVYLYAAFICGLVHDAGKVYDLDIVSLNLASP 206
R27 :163 GYQDEEVVRRKVYLYAAFICGLVHDAGKVYDLDIVSLNLSET 204
Rts1 :135 ESPVIKSDRALAWRIAVVVGAVMHDIGKPISDVDVWDKSGE 175
pMAQU02 :110 AEPESIAESADRWRFAMIAI LSHDLGKIVTDIEVVYRLPE 150
Consensus_aa : L HD GK D
Consensus_ss : hhhhhhhhhhhhhhhhhhhhhhhhh eeee eeeeeee

S3 Fig. Consensus sequence found in the secondary structure alignment of MOB_H family relaxase. Secondary structure alignment was generated using PROMAL3D. The plasmid sequenced in this study (pSEA1) is highlighted in light blue. Consensus_ss: consensus secondary structure: h, alpha-helix; e, beta-sheet.