

RA3	MAQ-AQLSLFGQ-NEAETVHDTSGARGFSSLLVQWP--TGKROSSFPLEQMPTVLINAVDHRIDTWLSQAEFMRPNRRVVNLIRIGLLFADLDITYKMPWAQGRKPEE	101
Rms149	MGQ-AQLRLFSPADEAGCYHDTARQGFFSLLMATGEGSGKKQDSYRLSQMPVVLMLDHSRDTWLSQAEFIKPNRRVVNLARIGLLFADLDITYREPWAQGRSPEQ	104
Plasmid2	MAADQQLSLFDRDEEARAYHDPQAGFFSILVNAK--GDKRQSSHRLIDMPTVLGLIDKNRDTWMTQAEFIRPNRRVVNLARVGLLFADLDITYKPPWASGRTPEQ	103
pAMTVIM-7	MAGQAQLALFEPADDEAGTYHDTARTGFFSLLVAVG--KDKRQDSYRLTDMPTILGLMVDQTRDTWLTQAEFMRPNRRVVNLARVGLLFADLDITYKPPWATGRTPEQ	103
pRSB105	MGQ-AQLRLFSPADEAGCYHDTARQGFFSLLMATGEGSGKKQDSYRLSQMPVVLMLDHSRDTWLSQAEFIKPNRRVVNLARIGLLFADLDITYREPWAQGRSPEQ	104
pRIO-5	MGQ-AQLRLFSPADEAGCYHDTARQGFFSLLMATGEGSGKKQDSYRLSQMPVVLMLDHSRDTWLSQAEFIKPNRRVVNLARIGLLFADLDITYREPWAQGRSPEQ	104
pAb5S9	MAAVEQLSLFDRDEEARAYHDPQAGFFSILVDVN--GDKRQSSHRLIEMPTVLELIDKSRDTWLTQAEFIRPNRRVVNLARVGLLFADLDITYKPPWAKGRTPEQ	103
pKBB4037	MAAVAQSLSLFDRDEEARAYHDPQSGFFSILVDVH--GDKRQSSHRLIEMPTVLELIDKTRDTWLTQAEFIRPNRRVVNLARIGLMFADLDITYKPPWATGRTPEQ	103
RA3	LAAAITTFVQSEGIPOPSIMVYSGRGIQAKWLLERPVPQALPRWNACQTHLINKLAELGADPAKADASRVLRVNTVNSKSGAVCRVVHVEE-GGLPIRYNFE	205
Rms149	LAAAVMFRFYDEGVPPPSILVFSGRGVQAKWLLDGTLPQALPRWNACQRYLIDRLAGLGADPAKADASRVLRVNTVNSKSGEVCRVHVEQGPDGEPYRYNFE	209
Plasmid2	LVDSVLYHCTQEGIPPPSILVFSGRGIQAKWLLDGTLPQALPRWNACQRYLIDRLAYLGADPAKADASRVLRVNTVNEKSGEICRVVHVQNEINQGPVRYNFE	208
pAMTVIM-7	LAAITVLYHCAQEGIPTFSLIVYSGRGIQAKWLLDGTLPQALPRWNACQRYLIDRLAGLGADPAKADASRVLRVNTVNTKSGDVCRVVHVEHQDQGPVRYGFE	208
pRSB105	LAAAVMFRFYDEGVPPPSILVFSGRGVQAKWLLDGTLPQALPRWNACQRYLIDRLAGLGADPAKADASRVLRVNTVNSKSGEVCRVHVEQGPDGEPYRYNFE	209
pRIO-5	LAAAVMFRFYDEGVPPPSILVFSGRGVQAKWLLDGTLPQALPRWNACQRYLIDRLAGLGADPAKADASRVLRVNTVNSKSGEVCRVHVEQGPDGEPYRYNFE	209
pAb5S9	LAAAVLYHCAQEGIPTFSLIFSGRGIQAKWLLDGTLPQALPRWNACQRYLIDRLRPVGADVAAKADASRVLRVNTVNSKSGEICRVVHVENGPDGPVRYSE	208
pKBB4037	LAAAVLYHCAQEGIPTFSLIFSGRGIQAKWLLDRVPQALPRWNACQRYLIDRLMAIGADVAAKADASRVLRVNTVNTKSGEICRVVHVETGADGPVRYGFE	208
RA3	YLAEMLLPVARWDIE--KQ-KAERQ-QARTIVVNGGKVGNLRTFSGRQLAWDRLEDRLKLGQLRGGINEGERMRHLFWRLNFFLLSGATNSAQMYHEAAALSSSEI	306
Rms149	YLAEALLPVARWDIEADRKARAD---RRQFKLLPGGQGTGNLRTLNGRQLAWDRLEDRLTAAALRGVVAEGERMQHLFWRLNFFLLSGATHGQMYHEAAALAREI	311
Plasmid2	YMAEILLPVARWTIEQQRQERKRAIRRQKLKLLPGDKTDNLRGFSGRQLAWHRLLEDRLTAEALRGGVQEGERMQHLFWRLNFFLLSGATNSRLMYEAKAITKEI	313
pAMTVIM-7	YLAEMLLPVARWDIEQQRDRDAE---RRQKLKLLPGGKADNLRGFSGRQLAWDRLEDRLKLGELRGGVREGERMQHLFWRLNFFLLSGATHSGQMYHEAAALAGEI	310
pRSB105	YLAEALLPVARWDIEADRKARAD---RRQFKLLPGGQGTGNLRTLNGRQLAWDRLEDRLTAAALRGVVAEGERMQHLFWRLNFFLLSGATHGQMYHEAAALAREI	311
pRIO-5	YLAEALLPVARWDIEADRKARAD---RRQFKLLPGGQGTGNLRTLNGRQLAWDRLEDRLTAAALRGVVAEGERMQHLFWRLNFFLLSGATHGQMYHEAAALAREI	311
pAb5S9	YLAEMLLPVARWTIEQQRQERAE---RRQKLKLLSGAKTDNLRGFSGRQLAWHRLLEDRLKATLRGGVSEGERMQHLFWRLNFFLLSGATHSGQMYEAKALAGEI	310
pKBB4037	YLAEMLLPVARWETIEQQRERAEER---RQQLKLLPGTKTDNLRGFSGRQLAWHRLLEDRLKATLRGGVQEGERMQHLFWRLNFFLLSGATHSGQMYHEAKALAREI	311
RA3	DTWVSYSKELMTLYSKAKSYEAGERVEFGGKSFAPLYTPKNDTLINLFIQSQQEQQLKTIISTDEAQKRRERDRRLDEERRRAAGQ---LEREAYEANSLS	407
Rms149	DPRWNYRSAELMTLYAKAKAHEAGEKVEFGGKFAPLYTPKNDTLISLFIHISDDEQKRLRTLISRDMAETERRDRDRKDEARRRAAGA---VDRATYEANSAS	412
Plasmid2	DPNWQENSKELMTLYSKAKAYEAGEKVSFGGREYAPLYTPRNDTLINLFIQITDDEQAQLRTIISRDMAKERDRAR---KEAVVRAAGA---VDRETYESQSLS	410
pAMTVIM-7	DPAWSYSKELMTLYAKAKAYEAGERVTLGGREFAPLYTPKNDTLISLFIQITDDEQKRLRTLISSDMAKERDRER---HTARRRAAGA---VDREYLYDAAEA	407
pRSB105	DPRWNYRSAELMTLYAKAKAHEAGEKVEFGGKFAPLYTPKNDTLISLFIHITDDEQKRLRTLISRDMAAERHSER---EKARRRAAGA---VDRASYLEAASA	408
pRIO-5	DPRWNYRSAELMTLYAKAKAHEAGEKVEFGGKFAPLYTPKNDTLISLFIHITDDEQKRLRTLISRDMAAERHSER---EKARRRAAGA---VDRASYLEAASA	408
pAb5S9	APTWAYRKELMTLYSKAKAYEAGEKISFAGREFAPLYTPKNDTLINLFIQITDDEQAQLRTIISKGMAGKDRAR---KEAARRAAGA---VDRETYLEAANA	407
pKBB4037	APDWOQNSKELMTLYSKAKAYEAGEKITFGGKEYAPLYTPRNDTLINLFIQITDDEQAQLRTIISRDMAAERRSA---TESATRPVGGPLVVRWIGKTYLEAANT	412
HTH		
RA3	RQKPWEAMGSRSAKWYRLGKPSPOQNSSETSPSPITNGEASAPPLQAARCAV-----	459
Rms149	RQKPWESLGMSRASWYRAGKPMPA--CETGSSPITASKVERKA-----	453
Plasmid2	RQKPWEALGMSRASWYRAGKPMPA-NSETSPSVLQKNGRFLV-----	452
pAMTVIM-7	KRAQAQALKAEGLSVRAIAQRMGISKSLAAMYAKEAAECP-----KSVR---ITADQAMPVASIAGSDEGGREGVQSPSVLIMAEPTGRGAV----	491
pRSB105	KQAQALALKAQGLSVRAIAAQMGIKTAAGRYIAEPGECF-----KSMR---ITGGEG-----	458
pRIO-5	KQAQALALKAQGLSVRAIAAQMGIKTAAGRYIAEPGECF-----KSMR---ITGGEG-----	458
pAb5S9	KQAQAQALRAQGLSIRAIQAQMGSVGSVSGYLKAAPGVQSPSVLQADLAGCSKSVR---ITNGEAHARFVGPAFE-----	480
pKBB4037	KQAQAQALREQGLSVRAIAAQMGSVGSVSGYLKAGASVQSGSPITGAVMEKSG-VQSPSPTNGEAYARFVGPAFE-----	488

Figure S1. Comparison of RepB homologs. Residues identical and similar in at least four proteins are shadowed in dark grey or light grey, respectively. The red arrow marks the putative Helix-Turn-Helix motif in RepB of RA3. RA3 (ABD64829); Rms149 of *Pseudomonas aeruginosa* (WP_011270176); Plasmid 2 of *Nitrosomonas eutropha* (WP_011630685); pAMTVIM-7 of *P. aeruginosa* (WP_011997473); pRSB105 (ABI20460); pRIO-5 of *Serratia marcescens* (WP_015060213); pAb5S9 of *Aeromonas bestiarum* (WP_011931113); pKBB4037 of *Bordetella bronchiseptica* (CAI47016).