```
(A).  KREPB6   35 WCSLCLEPLNSWSEHRGKRDHICLEMFYNAITQYGRRWSPSTLWWEVEEC     84
      KREPB7    7 WCDLCKEPVALWVNHHGRKDHALMDMHYTQMMEYPRRWNP-------EEV     49

                85 TLLRRHASPRLVLDGGEGFFSGCILDYVRDSTGKRGGLSLLMDYYDR-ME    133
                50 LV---------------AFFD---------------ELQLPVETYQRSYT     69

               134 HYKR--RLELYACIQHLID----------NGIVRTDRGSLGGGASFHGSL    171
                70 CYERAHRNELYSMLVELEEAKMLYFGEPRNTYLHRMQGGL-RGMDHQGAL    118

               172 VTFKELFPNLVNMFPFADAKEISALTQMIASTYNGETVFDLCNFQGL---    218
               119 VLHRYILGPFMRLYPNAHIQDFSNLVDFVTCAYNMETVYDLCGFYTLDKV    168

               219 ---------LPAGQG-GG---DTTGGKGNTSGCGNSQQ--RLAFNAEQKG    253
               169 ALKADYKPSSPAALGLGGIAVHSSPSHGFVQNAAESQQQSRRASSTASTG    218

               254 SEDSSVTASAEGVYSYHWKGMFCRGVMGQLRW-ALECDS--VACPLKRAD    300
               219 SR-SAADMDEE---AFSRKAVFVRQLLGQLRWLTLPCEEHPAGCKFPQ--    262

               301 GSKHVCDPYWQVLSEYTCRALLAEMVFCRVSEYIVRVEGVWRKCGQELAN    350
               263 --------HLMLLGEICLKYLVVEIIAARLCEYMVRVEPVWRDHGYERVK    304

               351 KHVSHGSQKEEEERAHP------PRTSNWGYIRYMGDHLYDDMFG    389
               305 LNVDKIMKQGRDILPEPIKYFYRPMSPNM-------DDLYSTKVG    342


(B).  KREPB6   27 RVWNETE-NWCSLCLEPLN-SWSEHRGKRDHICLEMFYNAITQYGRRWSP     74
      KREPB8   35 QAWLDLKTGWCHLCQEPLGATMGVHIGDRDHTNLQYFLFLYAAHGRRWS-     83

                75 STLWWEVEECTLLRRHASPRLVLDGGEGFFSGCIL------DYVRDSTGK    118
                84 -------------------------SEEVLRSCLATAPTVHNYATRHT--    106

               119 RGGLSLLMDYYDRMEHYKRRLELYACIQHLI---DNGIVRTDRGSLGGGA    165
               107 ------TWDHLHVMDDALRRAELEALLFHLTHPPQQALSHVLQGRSPLGF    150

               166 SFHGSLVTFKELFPNLVNMFPFADAKEISALTQMIASTYNGETVFDLCNF    215
               151 WYSGERMWKLRISRLVTQVFPPISAGMMTNFTQKCWGRSNGERMYDALRL    200

               216 Q------GLLPAGQGGGDTTGGKGNTSGCGNSQQRLAFNAEQKGSEDSSV    259
               201 QRIKAYYGWQP--------------------------YESKEK-------    217

               260 TASAEGVYSYHWKGMFCRGVMGQLRWAL-------ECDSVACPLKRADGS    302
               218 ------------KAFFVR----QLLWELLSVEVRDEVDEL---------T    242

               303 KHVCDPYWQVLSEYTCRALLAEMVFCRVSEYIVRVEGVWRKCGQ----EL    348
               243 KHMAD--------LALRRMAFEMIFLQSMEYMHKVQYVYDLMGRPTVDEL    284

               349 A    349
               285 A    285


(C).  KREPB7    7 WCDLCKEPVALWVN-HHGRKDHALMDMHYTQMMEYPRRWNPEEVLVAFFD     55
      KREPB8   44 WCHLCQEPLGATMGVHIGDRDHTNLQYFLFLYAAHGRRWSSEEVLRSCLA     93

                56 ELQLPVETYQRSYTCYERAH-------RNELYSMLVELEEAKMLYFGEPR     98
                94 TAP-TVHNYATRHTTWDHLHVMDDALRRAELEALLFHLTH-------PPQ    135

                99 NTYLHRMQG-GLRGMDHQGALVLHRYILGPFMRLYPNAHIQDFSNLVDFV    147
               136 QALSHVLQGRSPLGFWYSGERMWKLRISRLVTQVFPPISAGMMTNFTQKC    185

               148 TCAYNMETVYDLCGFYTLDKVALKADYKPSSPAALGLGGIAVHSSPSHGF    197
               186 WGRSNGERMYD----------------------ALRLQRIKAY----YGW    209

               198 VQNAAESQQQSRRASSTASTGSRSAADMDEEAFSRKAVFVRQLLGQLRWL    247
               210 ---------------------------QPYESKEKKAFFVRQLL----WE    228

               248 TLPCEEHPAGCKFPQHLMLLGEICLKYLVVEIIAARLCEYMVRVEPVW    295
               229 LLSVEVRDEVDELTKH---MADLALRRMAFEMIFLQSMEYMHKVQYVY    273
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Figure S1 Sequence comparison between KREPB6 and KREPB7 (A), KREPB6 and KREPB8 (B), and KREPB7 and KREPB8 (C). The sequences deleting mitochondrial targeting signal were aligned using the ClustalW algorithm (http://www.ebi.ac.uk). The amino acid alignments indicate conserved (|), semiconserved (:), partially conserved (.).