Figure S1

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>tr|A9M500|A9M500_9VIBR Phage integrase family protein.
         Length = 380

 Score =  115 bits (288), Expect = 5e-24,   Method: Compositional matrix adjust.

 Identities = 94/321 (29%), Positives = 155/321 (48%), Gaps = 15/321 (4%)

Cre : 25  KNLMDMFRDRQA-FSEHTWKMLLSVCRSWAAWCKLNNRKWFPAEPEDVRDYLLYLQARGL 83
          ++L++ F+ R+  +S +T + L S    + WC  N+R   PA P+ V + +  +A  L
VCre: 45  EHLLNEFKKREERYSPNTLRRLESAWTCFVDWCLANHRHSLPATPDTVEAFFIE-RAEEL 103

Cre : 84  AVKTIQQHLGQLNMLHRRSGLPRPSDSNAVSLVMRRIRKENVDAGERAKQALAFERTDFD 143
            T+  +   ++ +HR +G P P     V   ++ I ++ V  GE  KQA  F
VCre: 104 HRNTLSVYRWAISRVHRVAGCPDPCLDIYVEDRLKAIARKKVREGEAVKQASPFNEQHLL 163

Cre : 144 QVRSLMENSDRCQDIRNLAFLGIAYNTLLRIAEIARIRVKDISRTDGGRMLIHIGRTKTL 203
          ++ SL    SD+    RNLA L +AY ++LR +E+A IRV D+      G  ++ I  TKT
VCre: 164 KLTSLWYRSDKLLLRRNLALLAVAYESMLRASELANIRVSDMELAGDGTAILTIPITKTN 223

Cre : 204 VSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRK-NGVAAPSATSQ------- 255
           S        LS  V L+ +    +    + +LF  V K N    P    Q
VCre: 224 HSGEPDTCILSQDVVSLLMDYTEAGKLDMSSDGFLFVGVSKHNTCIKPKKDKQTGEVLHK 283

Cre : 256 -LSTRALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGG 314
           ++T+ +EG+F +  +     +    D   Q  ++ HSARVGAA+D+ + G +  +I Q+G
VCre: 284 PITTKTVEGVFYSAWETL----DLGRQGVKPFTAHSARVGAAQDLLKKGYNTLQIQQSGR 339

Cre : 315 WTNVNIVMNYIRNLDSETGAM 335
          W++  +V  Y R + +  GAM
VCre: 340 WSSGAMVARYGRAILARDGAM 360
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