

```

>tr|A9M500|A9M500_9VIBR SubName: Full=Phage integrase family
protein;
Length = 380

Score = 186 bits (471), Expect = 5e-45, Method: Compositional matrix adjust.
Identities = 122/302 (40%), Positives = 170/302 (56%), Gaps = 16/302 (5%)

Scre: 78 NTWRALMSRWAKFESWCLTNNLTPLPATPEVV-ATFIEYYQASSYTTLSQYAWAINSFHV 136
      NT R L S W F WCL N+ LPATP+ V A FIE + TLS Y WAI+ H
VCre: 61 NTLRRLAESAWTCFVDWCLANHRHSLPATPDPTVEAFFIERAEELHRNTLSVYRWAI SRVHR 120

Scre: 137 ECGLLSPVSSKTVQDKQNEIRIVKLESGGLAQEQATPPRLHHLQMLIESYGESERLLDKR 196
      G P V+D+ I K+ G A +QA+PF HL L + S++LL +R
VCre: 121 VAGCPDPCLDIYVEDRLKAIARKKVREGE-AVKQASPFNEQHLLKLTSLWYRS DKLLRR 179

Scre: 197 NLALLNIAYESLLRESELLRIKVGHLKSTFEGDYVLSVPYTKTNDSGEEVVNITPLGFK 256
      NLALL +AYES+LR SEL I+V ++ +G +L++P TKTN SGE + ++
VCre: 180 NLALLAVAYESMLRASELANIRVSDMELAGDGTAILTIPITKTNHSGEPDTCILSQDVVS 239

Scre: 257 LIQRYIQGAGL--TKEDYLFQPIGRSNKV-----SVQAKPMSTRTVDRVFLWAFE 304
      L+ Y + L + + +LF + + N V KP++T+TV+ VF A+E
VCre: 240 LLM DYTEAGKLDMSDGLFVGVSKHNTCIKPKKDKQTGEVLHKPITTKTVEGVFYS AWE 299

Scre: 305 SLGIDRHS A--WSGHSARIGAAQDLLAAGYSIAQIQENGRWKS PMMVLRYGKDIKAKESA 362
      +L + R ++ HSAR+GAAQDLL GY+ QIQ++GRW S MV RYG+ I A++ A
VCre: 300 TLDLGRQGVKPFHTAHSARVGAQDLLKKGYNLTIQIQSGRWSSGAMVARYGRAILARDGA 359

Scre: 363 MA 364
      MA
VCre: 360 MA 361

```

Figure S4