Virus Report

(Comparisons)

18-01-2015 15:05:45

Sequences

 $\begin{array}{ll} \text{HI-V:} & \text{TGGTATCAGAGCAAGGTTAAACATGGTCATGTCCGGCTAAAAACCTAGTGTTAGGTTCGG} \\ \text{HI-V:} & \text{TGGTATCAGAGCAAGGTTTTCTGTAAGTAATTTATGGCTTTCATGGGGTAAAACCCTTAGA} \end{array}$

Secondary structure:

GC content HI-V: 45.0

HI-V: 37.7049180328 Number of Proteins

HI-V: 1 HI-V: 1

Percentual similarity: 100%

referenced Similarity. 100%					
Common domains	Position in HI-V	Position in HI-V	Length in HI-V	Length in HI-V	
SH2	551:640	551:640	89	89	
SH3_1	798:844	798:844	46	46	
EF-hand_like	246:319	246:319	73	73	
C2	1091:1178	1091:1178	87	87	
PI-PLC-X	323:466	323:466	143	143	
PI-PLC-Y	953:1071	953:1071	118	118	
PI-PLC-Y	953:1071	953:1071	118	118	