## **Virus Report**

(Comparisons)

20-01-2015 11:06:47

Sequences

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

Secondary structure:

GC content HI-V: 45.0 HI-V: 45.0

Number of Proteins

HI-V: 3 HI-V: 3

Percentual similarity od domains: 100%

	Position in HI-V		Length in HI-V	Length in HI-V
DUF1319	534:632	534:632	98	98
zf-CCHC	2057:2074	2057:2074	17	17
RVP	2317:2434	2317:2434	117	117
RVT_1	2604:2765	2604:2765	161	161
MP	1357:1512	1357:1512	155	155