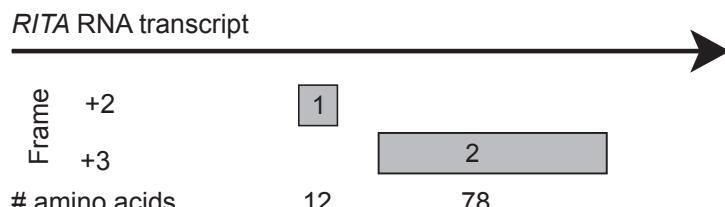
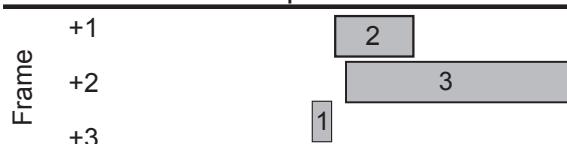


**A**

## BLAST P results for ORF2

| Accession     | Description  | Total Score | Query Coverage | E value |
|---------------|--|-------------|----------------|---------|
| XP_846961.1   | hypothetical protein [ <i>Trypanosoma brucei</i> TREU927]>gb AAX70328.1                          | 33.5        | 63%            | 8.2     |
| ZP_01463987.1 | phosphoribosylformylglycinamide synthase [ <i>Stigmatella aurantiaca</i> DW4/3-1]>gb EAU65257.1T | 33.1        | 70%            | 10.0    |

**B***MRD1* RNA transcript →

ORF1 - 5 amino acids - MERVW

ORF2- 32 amino acids - MGNYDSRRRQQIWWISSLVSSRRYLSSDEPPW

ORF3 - 120 amino acids

## BLAST P results for ORF3

| Accession      | Description  | Total Score | Query Coverage | E value |
|----------------|--|-------------|----------------|---------|
| XP_002887100.1 | hypothetical protein ARAYLDRAFT_475803 [ <i>Arabidopsis lyrata</i> subsp. <i>lyrata</i> ] >gb EFH63359.1 | 130         | 100%           | 7e-29   |
| NP_195929.1    | hypothetical protein [ <i>Arabidopsis thaliana</i> ]>emb CAB 86076.1                                     | 122         | 65%            | 2e-26   |
| ZP_08108626.1  | hypothetical protein HMPREF9475_03490 [ <i>Clostridium symbiosum</i> WAL-14673] >gb EGB 17427.1          | 37          | 68%            | 0.88    |
| ZP_08092817.1  | hypothetical protein HMPREF9474_04568 [ <i>Clostridium symbiosum</i> WAL-14163] >gb EGA91609.1           | 37          | 68%            | 0.89    |
| ZP_08176587.1  | adenine specific DNA methylase Mod [ <i>Xanthomonas vesicatoria</i> ATCC 35937] >gb EEGD11138.1          | 36.2        | 60%            | 1.3     |
| NP_636443.1    | DNA methylase [ <i>Xanthomonas campestris</i> pv. <i>campestris</i> str ATCC 33913] >gb AAM40367.1       | 35.8        | 60%            | 1.8     |
| ZP_02389774.1  | putative modification methylase [ <i>Burkholderia thailandensis</i> Bt4]                                 | 35.4        | 60%            | 2.5     |
| ZP_02353897.1  | putative modification methylase [ <i>Burkholderia oklahomenensis</i> EO147]                              | 35.4        | 60%            | 2.5     |
| YP_703251.1    | aspartate aminotransferase [ <i>Rhodococo justii</i> RHA1]>gb ABG95093.1                                 | 35          | 36%            | 3.0     |
| NP_881682.1    | putative modification methylase [ <i>Bordetella pertussis</i> Tohama I]>emb CAE43384.1                   | 34.3        | 60%            | 6.1     |
| YP_002780024.1 | aspartate aminotransferase [ <i>Rhodococo opacus</i> B4]>dbj BAH51079.1                                  | 33.9        | 36%            | 7.9     |