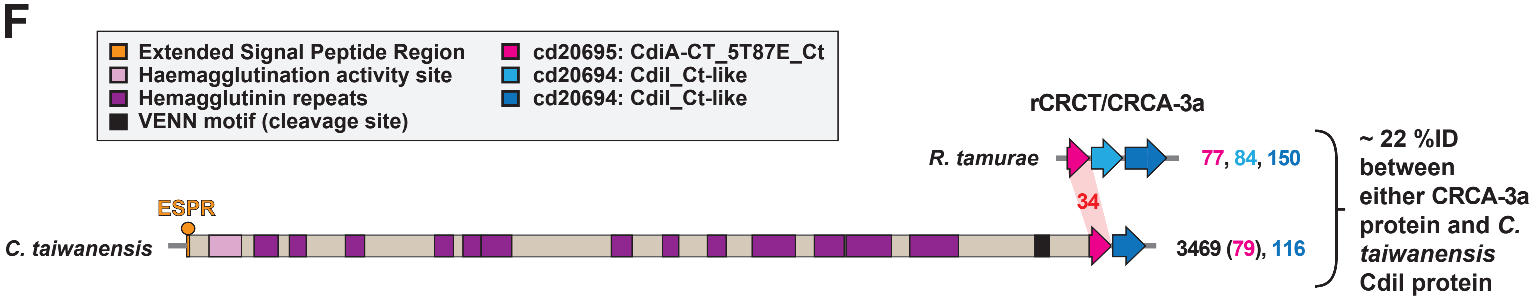
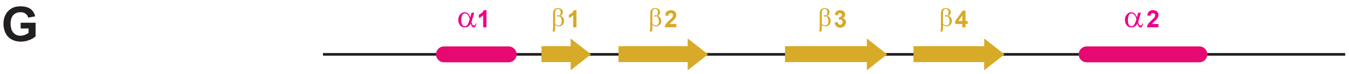
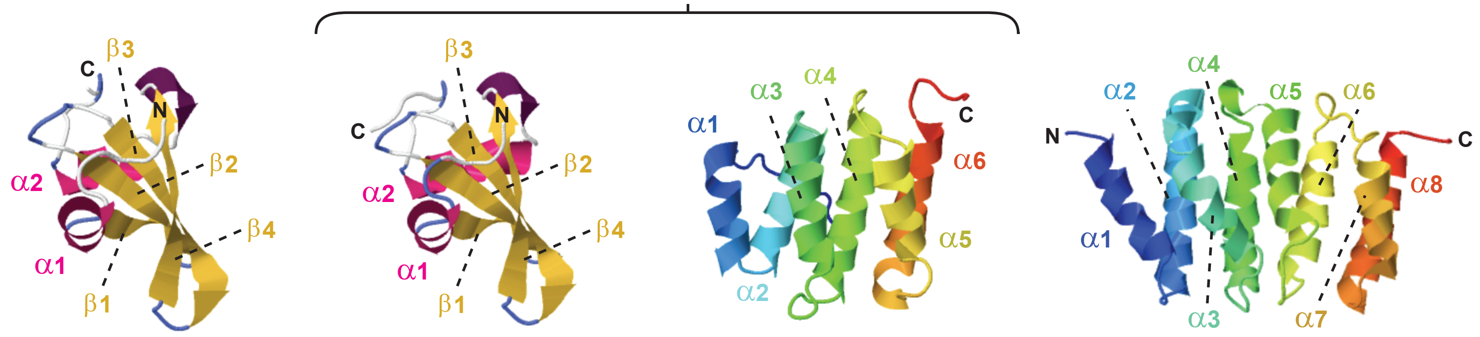




```
C. taiwanensis [3390] AVKSRGPSNGQSVLENSVQVKETSPRRVSVDPQTGEFVVFDRTLGDVYHGHVRAWKDLTSDMQNALVRGGYVDRKGN-PK 3469
R. tamurae            MVKNPASKDPKAALKNAYKISNDTERLIAVDIKNDQFVIFDNTSGNVYHGHIRTYKEIE---RNAVLKNNLIKTNGKIIK   77
REIP                  MVKNPASKDPKAALKNAYKISNDTERLIAVDIKNDQFVIFDNTSGNVYNGHIRTYKEIE---RDAVLKNNLIKTNGKIIK   77
                       **. ...: ::.*:*: ::.: : * ::** :..:**:**.* *:**:**:*::*::    .:*::... :. :*:  *
```

rCRCT-3a NCBI acc. #s: *R. tamurae* (WP_051965318) and REIP (KJW03590).

Solved as a toxin-antidote complex



rCRCT-3a (*R. tamurae*) modeled to PDB:5T87 *C. taiwanensis* CdiA-CT

PDB:5T87 *C. taiwanensis* CdiA-CT

PDB:5T87 *C. taiwanensis* CdiI

Fused rCRCA-3a proteins (*R. tamurae*) modeled to *D. melanogaster* MAST/Orbit N-terminal domain PDB:4G3A

Toxins in these diverse TA modules are 34 %ID

Antidotes in these diverse TA modules are too divergent for modeling; however, rCRCA-3a modeling to 4G3A indicates a similar helical bundle and possible similar topology as *C. taiwanensis* CdiI

Fig. S4