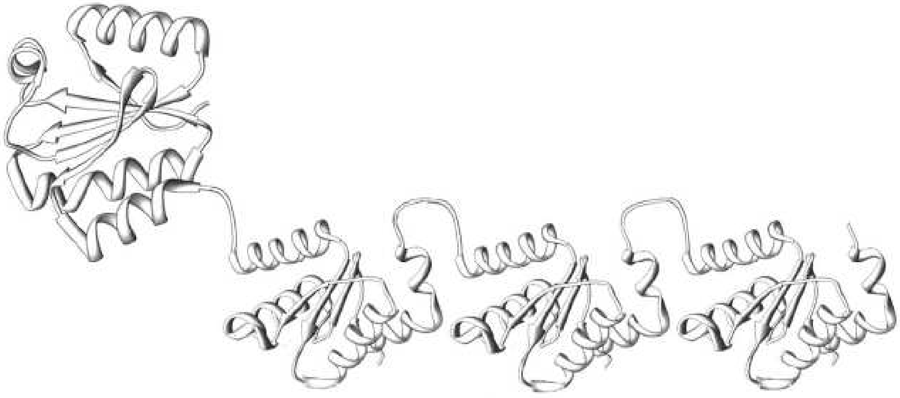
Figure S8



```
M2   MLFMKGIPEEPRCGFSRKVVDILKEVNVDFGSFDILSDNEVREGLKKFSNWPTFPQLYCN 226
M3   MLFMKGRPEEPKCGFSGKVVEILNQEKIEFGSFDILLDDEVRQGLKVYSNWSSYPQLYVK 356
M4   MLFMKGSPDEPKCGFSSKVVKALRGENVSFGSFDILTDEEVRQGIKNFSNWPTFPQLYYK 463
     ****** *:**:**** ***. *.  ::.******* *:***:*:* :***.::**** :
M2   GELLGGADIAIAMHESGELKDAFKD 251
M3   GELMGGSDIVLEMQKSGELKKVLTE 381
M4   GELIGGCDIIMELSESGDLKATLSE 488
     ***:**.** : : :**:** .:.:
```

Figure S8. Hypothetical structure of GRXS17 and amino acid alignment of the three GRX domains M2, M3 and M4 from *A. thaliana*. The structures of the single domains were generated from 1XFL and 3L4N pdb entries for TRX and GRX proteins, respectively, and are not experimentally confirmed. The linker regions and the relative positions of the TRX domain are speculative.