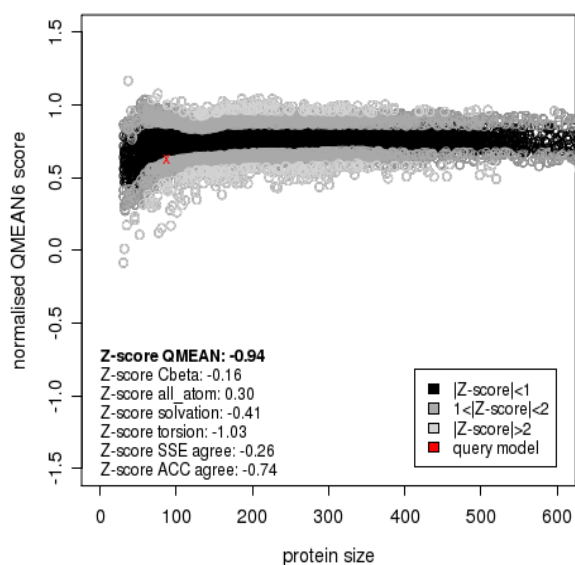


## SUPPLEMENTARY MATERIAL

### Homology modelling, bioinformatics analysis and insilico functional annotation of an antitoxin protein from *Streptomyces coelicolor* A3 (2)

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**Figure S1:** Graphical presentation of estimation of absolute quality of model by Qmean6 server. Here the red star indicates the position of the model.

**Table S1:** Ramachandran plot statistics of the predicted three-dimensional model for the target protein SCO2235

<b>Ramachandran plot statistics</b>	<b>Number of amino acid residues</b>	<b>Percentage (%)</b>
Residues in most favoured regions [A,B,L]	76	96.2%
Residues in additional allowed regions [a,b,l,p]	3	3.8
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0
Residues in disallowed regions	0	0.0
Number of non-glycine and non-proline residues	79	100.0
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	2	
Number of proline residues	4	
Total number of residues	87	