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1 **The use of structural modelling to infer structure and function in biocontrol agents**

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11 Key words:

12 Insecticidal toxins; *Bacillus thuringiensis*; structural modelling; P20; PirB

13

14 **Abstract:**

15 Homology modelling can provide important insights into the structures of proteins
16 when a related protein structure has already been solved. However, for many proteins,
17 including a number of invertebrate-active toxins and accessory proteins, no such templates
18 exist. In these cases, techniques of *ab initio*, template-independent modelling can be
19 employed to generate models that may give insight into structure and function. In this
20 overview, examples of both the problems and the potential benefits of *ab initio* techniques are
21 illustrated. Consistent modelling results may indicate useful approximations to actual protein
22 structures and can thus allow the generation of hypotheses regarding activity that can be
23 tested experimentally.

24

25

26 **1. Introduction**

27 Homology modelling permits the construction of modelled structures of proteins
28 where the actual structure of a member of the same protein family has been solved
29 experimentally. In order to initiate the production of a homology model, a level of primary
30 sequence identity between the solved template structure and the candidate protein of
31 approximately 20% or higher is required and modelling accuracy declines below 50% and
32 drops rapidly below 30% identity (Baker and Sali, 2001). Using this approach,
33 approximations of the molecular structures of insecticidal toxins can be developed, as shown
34 for the Cry48/Cry49 toxin pair that is active against *Culex* mosquito larvae (Jones et al., 2008;
35 Kelker et al., 2014). However, if no suitable templates exist in the protein structure database,
36 emerging computational solutions may allow us to develop structural models that are
37 template independent. Such *ab initio* models must be treated with some caution since there is
38 no direct experimental basis for their predictions, however, they can provide hypotheses
39 regarding toxin structure. In addition, in cases where predicted structures resemble known
40 toxins, hypotheses regarding mechanism of action can also be developed and these can
41 subsequently be tested.

42 *Ab initio* modelling has been applied to a range of insecticidal toxins and accessory
43 proteins as described below. The shortcomings of this methodology will be illustrated along
44 with examples where consistent predictions of structures have been derived, and, in some
45 cases subsequently been shown to mirror actual structures. Modelling of the Cry6Aa
46 structure *ab initio* and the similarity of the resulting prediction with the subsequent
47 crystallographic structure of the protein will be described elsewhere [Dementiev et al.
48 submitted for publication].

49

50 **2. Methods**

51 *2.1. Modelling software:* For the majority of cases described here the Rosetta software
52 (Bonneau et al., 2002) was used via the Robetta website (robett.bakerlab.org) with default
53 settings. After generating secondary structure predictions, the program continued to full
54 structure prediction using either *de novo* or database structure comparison methods. Each
55 method returned five best model structures, which were visualised using standard molecular
56 graphics software such as Pymol (DeLano, 2010). In the case of P20, the I-TASSER server
57 (Roy et al., 2010; Yang et al., 2015; Zhang, 2008) was also used (with default settings) to
58 compare predictions. Although it does not produce protein models, the HHPRED software
59 (Soding et al., 2005) is a powerful tool for the detection of remote homologs and can predict
60 structural homologies that simpler primary sequence comparisons such as Blast (Altschul et
61 al., 1990) will not identify. Thus, the use of HHPRED may also be valuable in predicting
62 structural classes to which proteins may belong and may contribute to the building of
63 hypotheses regarding their modes of action.

64

65 **3. Results and Discussion**

66 *3.1 Modelling outcomes and interpretations:*

67 *3.1.1. P19 protein:* The gene encoding the P19 accessory protein (accession number
68 AJ010753) is found in close association with the *cry11Aa* gene as the first in a 3-gene operon
69 (*p19-cry11Aa-p20*) on the *Bacillus thuringiensis* serovar. *israelensis* pBtoxis plasmid (Berry et
70 al., 2002; Dervyn et al., 1995). A closely-related protein is encoded by *orf1* in the operon
71 encoding Cry2Aa. The P19 protein does not appear to influence the crystallisation of Cry11Aa
72 or its toxicity, although it may influence toxin yield (Manasherob et al., 2001; Shi et al., 2006).

73 Modelling of the P19 protein using the Rosetta program returned 5 structure
74 predictions with no significant similarity to each other (Figure 1). The lack of consistency of
75 the models makes it extremely difficult to resolve which, if indeed any, of the models might

76 approximate to the real structure of the protein. I-TASSER was also inconsistent in the
77 models that it generated for this protein and HHPRED did not identify any clear homologs. As
78 a result, the example of P19 serves as a warning of the real limitations of *ab initio* modelling.
79 No hypotheses regarding the structure or function of this protein could be derived from the
80 modelling and resolution of these issues will require the application of classical structural
81 techniques such as X-ray crystallography.

82

83 *3.1.2. P20 protein:* The P20 protein is encoded by the third gene on the *cry11Aa*
84 operon. It appears to have a role in stabilising some Cry and Cyt toxins from *B. thuringiensis*.
85 It is able to enhance the accumulation of Cyt1Aa and Cyt2Ba toxins and protects bacterial cells
86 from the growth inhibition induced by production of Cyt toxins (Manasherob et al., 2006;
87 Manasherob et al., 2001; Nisnevitch et al., 2006; Wu and Federici, 1993). It is also able to
88 interact with and synergise the toxicity of Cry11Aa against *Aedes aegypti* although P20 itself
89 does not appear to be toxic to this insect (Xu et al., 2001).

90 *Ab initio* modelling of P20 using Rosetta, returned 5 models with remarkable similarity
91 to each other (Figure 2) and the I-TASSER predictions also produced very similar predictions
92 (not shown). These models show a 3-layer, α/β structure with the alpha helices contributed
93 from the N-terminal end of the protein and a central anti-parallel beta sheet structure lying
94 between two helix-turn-helix motifs with their helices running approximately parallel to the
95 beta strands. The overall fold predicted for the P20 protein shows a high degree of similarity
96 to the structure of *B. thuringiensis* Cyt toxins (Figure 2) with a root mean squared deviation
97 between 400 backbone atoms of 2.7 Å (model 1 compared to Cyt1Aa pdb accession number
98 3RON). The HHPRED program also identifies homologies to Cyt toxins and also to volvatoxin,
99 another toxin previously recognised as sharing the cytolysin fold (Cohen et al., 2011).

100 Although the mechanism by which P20 might interact with Cry and Cyt toxins is not entirely
101 clear from the predicted structure, it is interesting to note that Cyt toxins have been shown to

102 form dimers and Cyt and P20 co-immunoprecipitate (Visick and Whiteley, 1991). It is
103 possible that Cyt-P20 heterodimers may form and that this may assist in masking the
104 detrimental effects of Cyt toxin in producing bacteria. Interactions of Cyt with Cry11Aa may
105 occur (Couche et al., 1987; Perez et al., 2005) and Cyt1Aa synergises with Cry11Aa (Wu et al.,
106 1994). We may speculate that the known P20/Cry11Aa interactions and synergism may
107 mirror the Cyt1Aa/Cry11Aa interactions however, the specific residues in Cyt1Aa identified
108 as playing a role in the interaction with Cry11Aa (Perez et al., 2005) are not present in P20.
109 Further analysis of all of the above interactions will be necessary to resolve this possibility.

110

111 *3.1.3. PirB:* The PirB protein from *Photobacterium luminescens* (Waterfield et al., 2005)
112 and *Photobacterium asymbiotica* (Ahantarig et al., 2009) are the larger components of two part
113 toxins PirA/PirB. The proteins have been shown to be toxic against *Aedes* mosquitoes and
114 *Galleria mellonella* larvae and some small regions of similarity to 3-domain Cry toxins have
115 been noted (Ahantarig et al., 2009; Waterfield et al., 2005). This similarity, however, was
116 insufficient for homology modelling of the proteins.

117 Rosetta simulations for the PirA component returned inconsistent structures (not
118 shown), all of which were rich in beta sheets. PirB models, in contrast, showed significant
119 similarity to each other (Figure 3) and resembled domains I and II of the typical 3-domain Cry
120 toxin structure. This similarity is consistent with the I-TASSER model of the protein
121 generated by Maithri *et al.* (Maithri et al., 2012) and was validated by the recent publication of
122 the structure of the PirB ortholog from *Vibrio parahaemolyticus* (PDB 3X0U along with PirA
123 structure PDB 3X0T)(Lee et al., 2015). Structural alignments shows a high degree of
124 similarity with the *P. luminescens* PirB model 1 giving a root mean squared deviation between
125 1273 backbone atoms of 3.6 Å compared to the *V. parahaemolyticus* protein. This provides a
126 clear example of the predictive abilities of Rosetta and I-TASSER for this class of proteins.

127

128 3.2. *Summary:* In conclusion, it can be seen that *ab initio* modelling is able in some
129 instances to generate models with a good match to the actual structures of the proteins as
130 later validated by crystallographic methods (Cry6 and PirB). In other cases, such as P20, the
131 consistency of models both within the predictions of Rosetta and between predictive tools
132 (Rosetta and I_TASSER) enhance confidence in the models and allow us to speculate on the
133 roles of the proteins. Models must always be treated with caution and subjected to
134 experimental testing to validate their predictions. However, the modelling is powerful in
135 directing us to the best experiments to perform and it is to be hoped that they will help to
136 accelerate our understanding of the invertebrate-active toxins and their accessory proteins.

137

138 Figure Legends:

139 Figure 1: P19 models

140 The top 5 models of P19 generated by the Rosetta software are presented.

141

142 Figure 2: P20 models

143 The top 5 models of P20 generated by the Rosetta software are presented along with the
144 structure of Cyt1Aa (PBD accession 3RON).

145

146 Figure 3: PirB models

147 The top 5 models of *P. luminescens* PirB generated by the Rosetta software are presented
148 along with the structure of *V. parahaemolyticus* PirB (PBD accession 3X0U).

149

150

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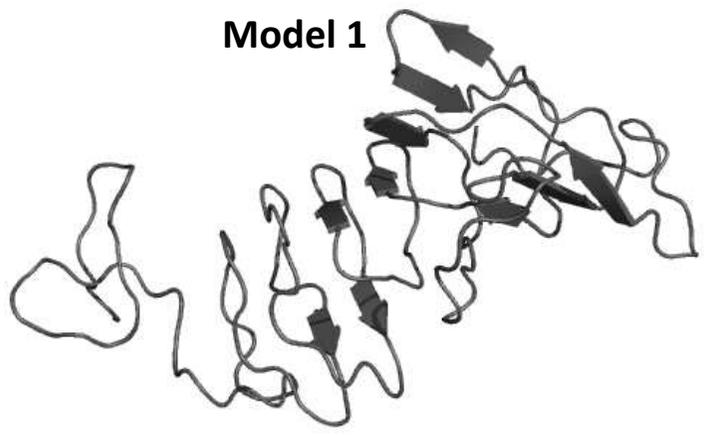
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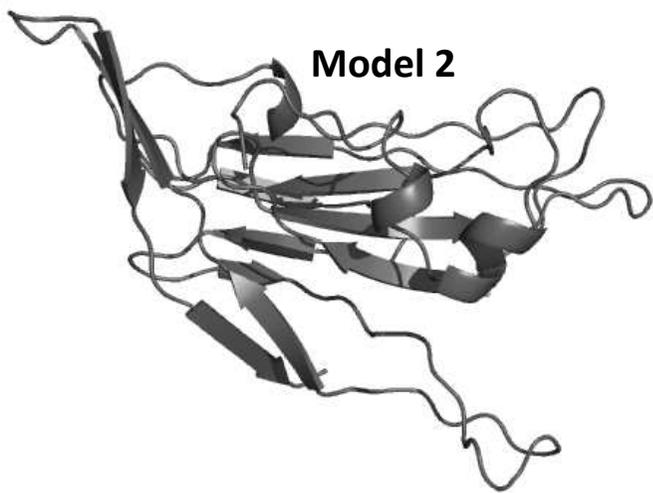
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Figure 1
Figure 1

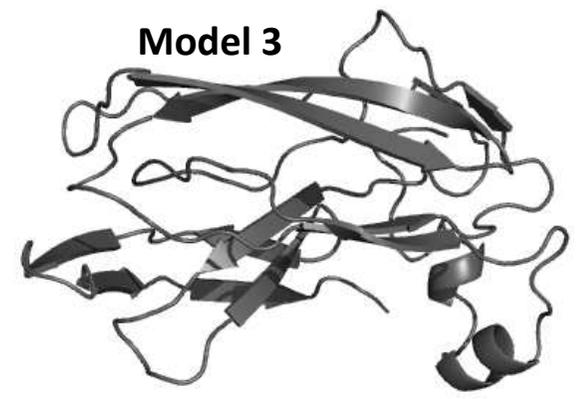
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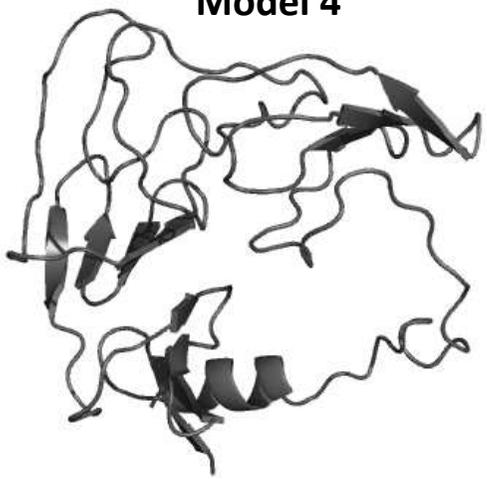
Model 2



Model 3



Model 4



Model 5

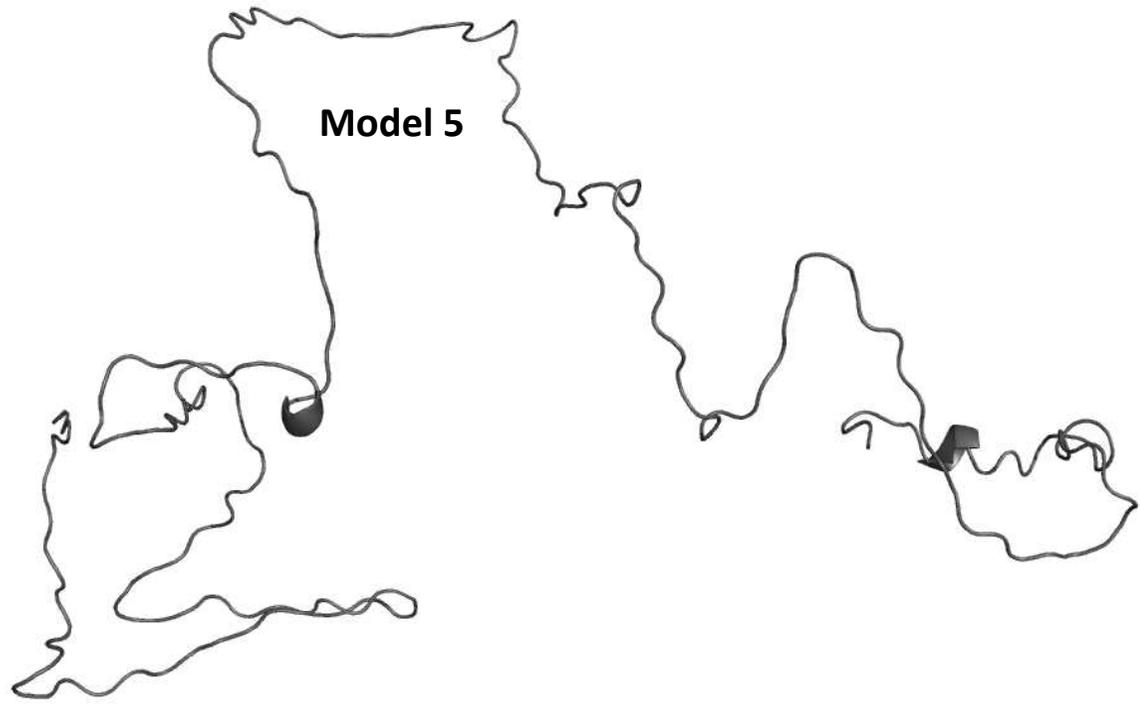
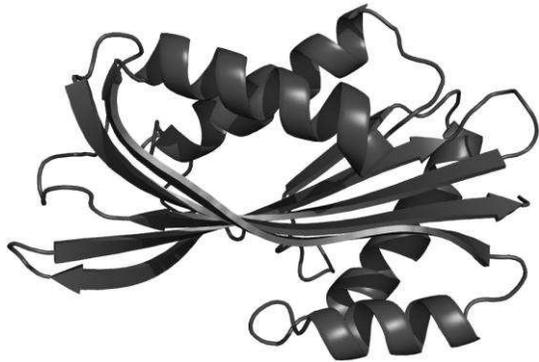
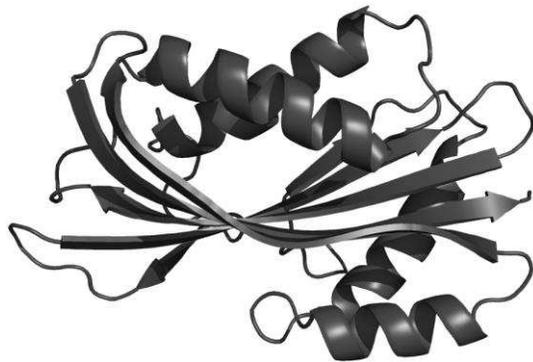


Figure 2
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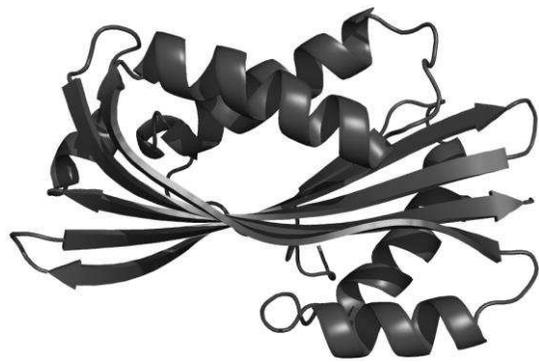
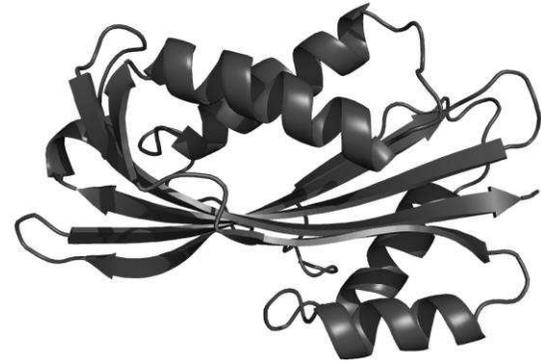
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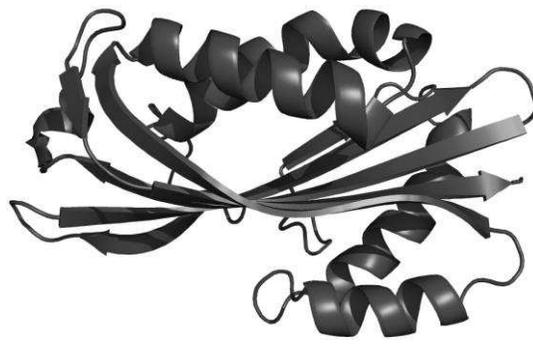
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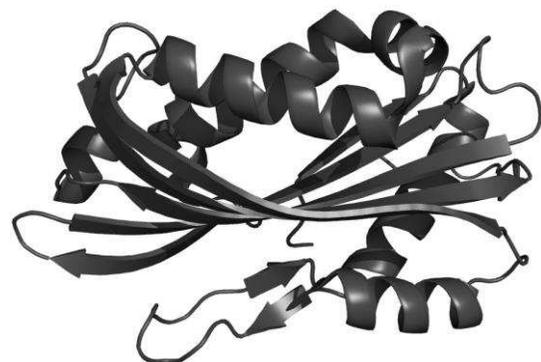
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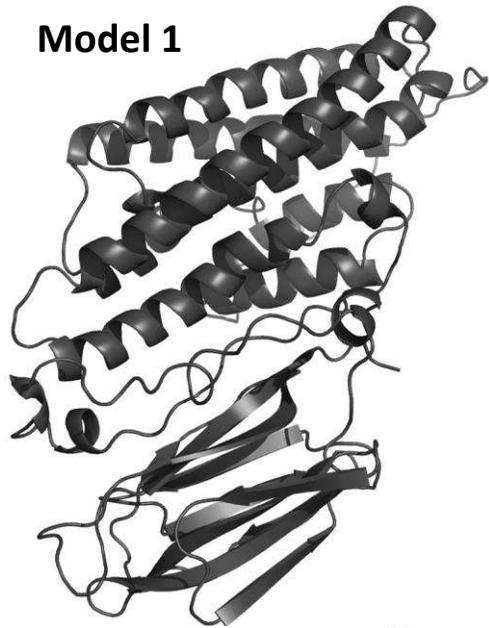
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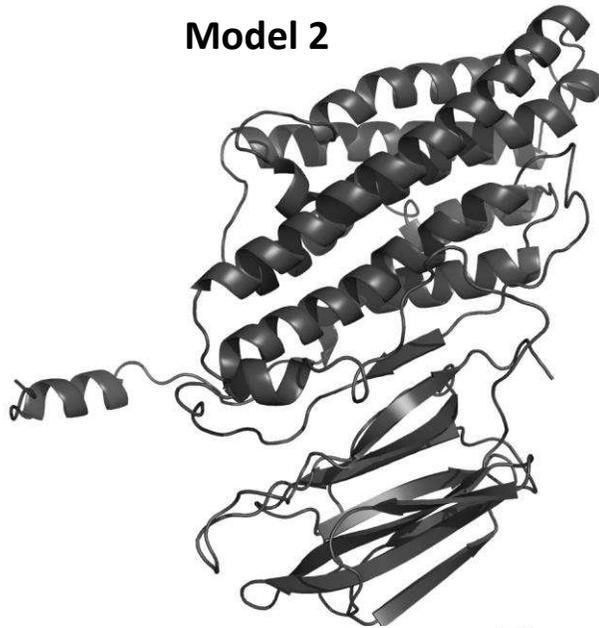
Cyt1Aa

Figure 3
Figure 3

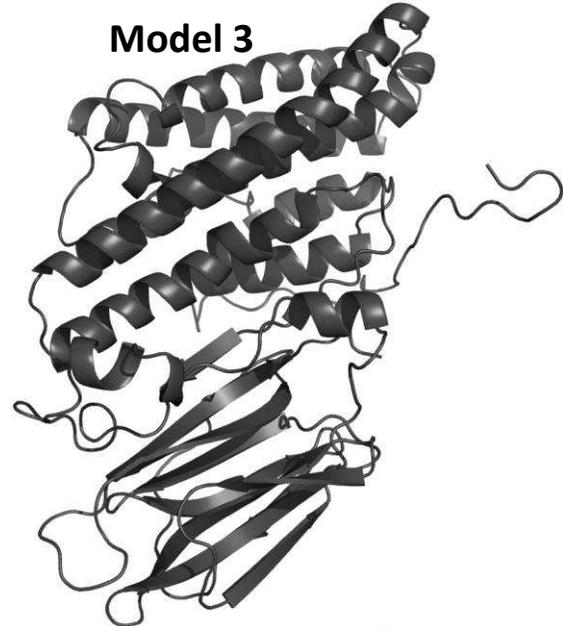
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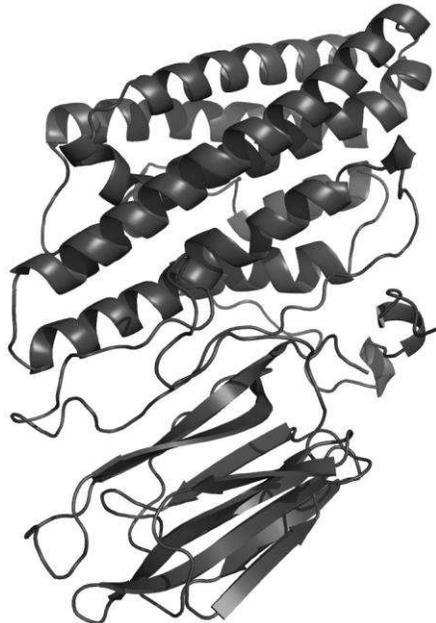
Model 2



Model 3



Model 4



Model 5



PirB

