

a

```
XacFhaB      ATRDTAMGRAATGLGGINAWRSNGPGRRYLIETDPRFVNYDNFISDDFLLDKLGVDPEWT 3120
Fha1         -----MGRAANGLGGINAWRSNGPGRRYLIETDPRFVNYDNFISDDFLLDKLGVDPEWT 54
          *****

XacFhaB      QTRLGDGFYEQRVLVDQITQLTGRRYLGNADGVAQYRALLESGVAAAGQLQLSMGVGLT 3180
Fha1         QTRLGDGFYEQRVLVDQITQLTGRRYLGNADGVAQYRALLESGVAAAGQLQLSMGVGLT 114
          *****

XacFhaB      AAQAAALTQDIVVMVEQEQYQGQTVLVPVVYLASNSLQLRNGALIAGGNVELNATNTLSN 3240
Fha1         AAQAAALTQDIVVMVEQDYQGQKVLVPVVYLASNSLQLRNGALIAGGNVELNAANAMSN 174
          *****

XacFhaB      QGVIAGADVSIAGNLLNQGRISGTGSVALEARNDLLNQGIQGRDVALVAGNNLVSEAS 3300
Fha1         QGVIAGADVSVTAGNLLNQGRISGTGTVLEARNLLNQGIQGRDVALVAGNNLVSEAA 234
          *****

XacFhaB      KAINGVGLSGISASNTLQLMAGNDMTLTGTRVQAGGSAALIAGNNLSLTPSALRDDNGL 3360
Fha1         KAINGVGLSGITASNTLQLMAGNDMTLTGTRVQAGGSAALIAGNNLSLTPSALRDDNGL 294
          *****

XacFhaB      LRGGDAVSVTGKDLIVSAGNDLQLHGVTIAAGGSAALQAGNDLSLTPPTGLDGKVATRT 3420
Fha1         LRGGDAVSVTGKDLIVSAGNDLQLHGVTIAAGGSAALQAGNNLSLTPITIGLDGKVATRT 354
          *****

XacFhaB      SLSTGDSLQLTAGNDLIRQAEVKAGGDLIAAGNNLNVEVSVNDSQSNDSNRNGKTRV 3480
Fha1         SISTGDSLQLTAGNDLIRQAEVKAGGDLIAAGNNLNVEVSLNDSNTRNYSNRNGKTRV 414
          *****

XacFhaB      TTTTTTQTIDQQALTAGNLIILSAGNDVNLVAAKLDAGKGLGISAGNDINASTLTTVDTS 3540
Fha1         TTTTTTQSIDQQALAAAGNLIILSAGNDVNP----- 444
          *****
```

b

```
AR2          SVALSSQAMQLDGVVAAATALQASAGGDLQQAGSLKAQSIALQAGQDLTANGSLQSAST 60
AR2'         TVLTSQGDMTLQGVVAAASTLHADAGGDLQQAGSLKAQSIALQAGRDLTAAAGSLQSASG 60
          :*:*:* * * :***** :*:* * *****

AR2          LDLQSQRTLALNGQASSAADATLNGATIAASAAAVLQSGASITLAGDSIESRGALDAAND 120
AR2'         LDLQAQRVLTALNGQAVSAANATLRGMQIATGQAAVLQSGAAISLDGAAIDSRGALGAVTD 120
          ***:*:* * :***** ***:*:* * ** : *****:*:* * * :*:*:* * :* *

AR2          LTLRSAGDLTLGGVAQAGRDIALTATGNLNGAQVVAARDLGVQAASATNASDATLGAKR 180
AR2'         IDLRSTGDLAVAGVVQADRNVLVATGALTNAAQVVAGDGLTATATSANTATGVLLAQG 180
          : ***:*:* :*:* * :*:* * * :*:* * * :* * :*:* * :* * *

AR2          DLRVDVAGGLDNLGSLHGERGLSLTSGSLLQRGRVYSGDALSIASNGAFENAGQLVSGKA 240
AR2'         NATLSIAGLLDNAGAVRAGHQLSLGVGSLRQTGQAYGLQRLGVSASGAVDNRGDLIGGNA 240
          : :*:* * * * :*:* * :* * * * * :* * :* * :* * :* * :* *

AR2          LSITAGSIVSNQGLGVTGALTLTSQNDIALQGVVSAATTLQATAGGDLAQAGTLTSAQ-T 299
AR2'         LRVEAAQLSSSGQLGSEKGDVALISRGNLQLDGRLASAGALTAQADGALTQNGNLSAAST 300
          * : * : * : * : * * * * * : * * : * * : * * : * * : * * * *

AR2          VALQAGRDLVAGGTLQASSTLDVQAQRVLSLNGQAQAGTDASLHGNRIATGRDAVLKSGG 359
AR2'         LDLRSKGDLTAVAG-QVAGQQLTLVSDAVVRQQG-TVSGTTVDVQGARIE--AGQTTAAG 356
          : * : * * * * * : * * * : * : * : * * : * * : * * * * * : * : *

AR2          AITLDGAAIDSRGTLDAQT--DLAVRSTGDLALAGVAQAGDVLVLSASGALGN-ASQVFA 416
AR2'         NLSLRAGEIGITGTGAGINADGSLGSGSMLSLVADRQLAASGTLLAGGNLTAQGSQQLQL 416
          :* * * * * :*:* * * :* * * * * * * * * * * * * * * * *

AR2          GRDLSLQAGSINNAAGALAAAGVTLATG--TLQNVGSLQSSGDLRITAASMDQSGTAV 474
AR2'         AGATTRATGNVALTSGGALDHRGGNLLAGGTLTVQAIGAIN-GRLNNVGGQLQANQLSI 475
          . : * : * : * * * * * * * * * * * * * * * * * * * * * *

AR2          AGKALTATVTGTLDNRGLI 494
AR2'         DGGSLSN-VGGGLVQSGTGA 494
          * : * : * * * * * :
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Fig. S1. XacFhaB sequence alignments. The sequences of XacFhaB and Fha1 from Xcv (a) and AR2 and AR2' (b) were aligned with ClustalW2.