Figure S2.

```
BsaP    MSSIIGGASAA-RRGFSIDGTGSAAN---RLDAEPSLDDAPQTGAAGAADVQAQLAGVDE
InvE    ---MIPGSTSGISFSRILSRQTSHQDATQHTDAQQAEIQQAAEDSSPGAEVQKFVQSTDE
MxiC    ---MLDVKNTGVFSSAFIDKLNAMTNSD------DGDETADAELDSGLANSKYIDSSDE
             ::    .:.   .  :.   :  :             :     .   . :. **

BsaP    EAANAAAQFGR-FRASERKGRRSDELERILDTDADEKLDELAALLGG----RADLATLLR
InvE    -MSAALAQFRNRRDYEKKSSNLSNSFERVLEDEALPKAKQILKLISV---HGGALEDFLR
MxiC    -MASALSSFINRRDLEKLKGTNSDSQERILDGEEDEINHKIFDLKRTLKDNLPLDQDFID
          : * :.* .     .: .. *:. **:*: :     .::  *          ::

BsaP    DARERFRDESDLLLALRELRRRRRLDGESVDALERAIDELLAGDGAKRIKAGINAALKAK
InvE    QARSLFPDPSDLVLVLRELLRRKDLEEIVRKKLESLLKHVEEQTDPKTLKAGINCALKAR
MxiC    RLKRYFKDPSDQVLALRELLNEKDLTAEQVESLTKIINEII-SGSEKSVNAGINSAIQAK
           :   * * ** :*.**** ..: *      . *   :..:    * ::.****.*::*:

BsaP    VFGARMQLDARRLRELYRQFLEFDGSHLVIYEDWIEQFGASRRKRILDYVSAALSYDMQS
InvE    LFGKTLSLKPGLLRASYRQFIQSESHEVEIYSDWIASYGYQRRLVVLDFIEGSLLTDIDA
MxiC    LFGNKMKLEPQLLRACYRGFIMGNISTTDQYIEWLGNFGFNHRHTIVNFVEQSLIVDMDS
         :**   :.*.   **  ** *:  :        * :*: ..:* .:*  ::::::. :*  *:::

BsaP    HDPSCGCAAEFGPLLGTLHRARMLASADEQFVGRLLDDALARDCGLTEARALATMLGGLQ
InvE    NDASCS-RLEFGQLLRRLTQLKMLRSADLLFVSTLLSYSFTKAFNAEESSWLLLMLSLLQ
MxiC    EKPSCN-AYEFGFVLSKLIAIKMIRTSDVIFMKKLESSSLLKDGSLSAEQLLLTLLYIFQ
         .. **     *** :*   *   :*: ::*   *:  *  . :: :          *    :*    :*

BsaP    RPFSVADVLLGTLGDLLEPLAPARRSQLLQLALRAFAGVPIALYGDADARRAALGALEEL
InvE    QPHEVDSLLADIIGLNALLLSHKEHASFLQIFYQVCKAIPSSLFYEEYWQEELLMALRSM
MxiC    YPSESEQILTSVIDVSRA--SH-EDSVVYQTYLSSVNESPHDIFKSESEREIAINILREL
          *  .   .:*   :        :    .: . *        *   ::  .    :.  :    *..:

BsaP    IGATYARERRQARPRAD---
InvE    TDIAYKHEMAEQRRTIEKLS
MxiC    VTSAYKKELSR--------
           :* :*   .
```

Figure S2. Amino acid alignment of *B. pseudomallei* K96243 BsaP with *Salmonella* InvE and *Shigella* MxiC 'gatekeeper' proteins.

Amino acid sequences (BsaP, YP_111550.1; InvE, NP_461818.1; MxiC, NP_085309.1) were aligned using Clustal Omega software (Sievers et al. 2011. Mol. Syst. Biol. 7: 539). Amino acid conservation is indicated as fully conserved (*), or having strongly similar (:) or weakly similar properties (.).