```
F. tularensis LVS (FTL_0724)       MDKNQIRRELLNIRDSL--INKTYLSEQISSKLISYIQANFTNPKIGSFA 48
M. pneumoniae FH (MPNE_0404)       MDKNALRKQILQKRMALSTIEKSHLDQKINQKLVAFLTPKPCIKTIALYE 50
                                   **** :*:::*: * :*  *:*::*.::*..**:::: .:    .*. :

F. tularensis LVS (FTL_0724)       SLKNEIDTQTINNHFENIYLPIVHPFIKHGLWFARDSKKYYLNKYKIKEP 98
M. pneumoniae FH (MPNE_0404)       PIKNEVT--FVDFFFEFLKINQIRAVYPK---VISDTEIIFIDQ------ 89
                                   .:***:    :: .** : :  ::..  :   .  *::  ::::

F. tularensis LVS (FTL_0724)       VYCVKDVVTAWELDIIIVPMVGFTSDKFRMGMGGGFYDYNLSFKKIHKWP 148
M. pneumoniae FH (MPNE_0404)       ---ETNTFEPNQIDCFLIPLVGFNKDNYRLGFGKGYYDR--YLMQLTRQQ 134
                                       .:.. . ::* :::*:***..*::*:*:* *:**    : :: :

F. tularensis LVS (FTL_0724)       LTIGIAFDEQQNNAIIIDKHDIKLDLIITPTRIL 182
M. pneumoniae FH (MPNE_0404)       PKIGIAYSFQKG-DFLADPWDVQLDLIINDE--- 164
                                    .****:. *:.  :: *  *::*****.

Key:
* = Identical residue
: = Conserved substitution
. = Semi-conserved substitution
  = Non-conserved substitution
```

Supplementary Figure 1. Alignment of the 5-formyltetrahydrofolate cycloligase protein sequence from *F. tularensis* LVS (FTL_0724) and *M. pneumonia* FH (MPNE_0404).