

Xf MSAVHPIPHPICESSIRIIEETHRNVYWIYMAHL---ARTTGAAAYFSLKLI DDIMNYQS
 Pa MTVIN---QATCRLFTEVGNTTQLVAYYEEGRRTMWMMLRAQPRPSENHელიEEIMN---

Xf VLRQRLKEQTVQLPFVVLAS-DSNVFN LGGDLQLFCDLIRRKEREALLDYACRCVIRGAYA
 Pa -LSYAAQRSGLPIDFWVTGSLVPMFNAGGDLRFFVFCIRNNRREALRAYARACVDCIHS

Xf FHAGLNANVHSTIALIQGNALGGGF EAALCCHTIVAEEGVMMGFPEVLFDFLPGMGAYSFM
 Pa AARGFDTGAVTLAMIEGSALGGGF EAALAHFILAQNARMGFPEIAFNLFPGMGGYSLV

Xf RQRISPKLAERLILEGNLYSSEELLAIGLIDKVVPRGKGI EAVEQIIRDSKRRQYTWAAM
 Pa ARRSGMKLAELICEGESHSAEWYETRGLVDKVFQPGDSYRATRTRFIDTLRPKLNGVRAM

Xf QEVKKIAHEVSLEEMIRITELWVDSALKLSNKSLRTMERLIRAQOTHKNTALK-N
 Pa LKARQRVLQLSRAELMDITEDWVDYAFTIEPKDIAYMERLVQLQNRHSASLRKAG

Figure S3. Sequence identity (shade in black) and similarity (shade in grey) of *X. fastidiosa* Tem1 RpfF and *P. agglomerans* 299R F385_3254. F385_3254, encoding a protein with 37% identity to that of *X. fastidiosa* RpfF.