```
Secondary structure predicted by PSIPRED      ChHHHHHHHHHHHHHHhCCeeEeccC------CCCCeEEEEEEEecCCCCeEEEEEEEcHHHHHHHHH-HHcCCCC-CCh
C. jejuni CheX                              1 MLKILEYSITHFCEHILRLRIEAAQD------ISGELYGASIPIMGKSEGECNFYLFFPKEFLKKIAE-ILINDEK-FKE 72 (140)
Consensus                                   1 ~~~~~~~s~~~~~~~~~~~~~~~~~~------~~~~~~~~~i~~~g~~~~~g~~~l~~~~~~~~~l~~-~~~g~~~-~~~ 72 (140)
                                              +.+.+.+++.++|+++++.+++....      .....+.+.+.+.|+.  +|.+.+.++++.+.++++ .|.|.+. +.+
Consensus                                   5 ~~~~~~~~~~~~l~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~~~~~~~G~~--~G~~~l~~~~~~~~~i~~~~~~g~~~~~~~ 82 (155)
T. maritima CheX(1SQU_B)                    5 IVNALIGSVYETIRDVLGIEPKTGKPSTVSHIEIPHSLVTVIGITGGI--EGSLIYSFSSETALKVVSAMMGGMEYNQLD 82 (155)
Secondary structure                           HHHHHHHHHHHHHHHHhCCCCeeCCcccccccCCCceEEEEEEeeccc--EEEEEEEeCHHHHHHHHHHHhCCCCccccC

Secondary structure predicted by PSIPRED      hHHHHHHHHHHHHHhHHHhhccccCCCCCcEEeeCCeEeCCCCc---ccceeceeEEEEECC-EEEEEEEe
C. jejuni CheX                             73 DDWCDLTKECANQIIGYAKNLLNDAKGDDEYKLGIPEYLGKVDF---SEIVLDEALTYKFEN-CYFRIGYC 139 (140)
Consensus                                  73 ~~~~D~~~El~Nii~G~~~~~l~~~~~~~~~~~~~P~~~~~~~~---~~~~~~~~~~f~~~~-~~~~v~i~ 139 (140)
                                              ++..|+++|++|+++|++.+.+.+.+  ....+++|.+..+...   ..- ....++|.+++ +.+.+.+.
Consensus                                  83 ~~~~d~l~Ei~n~i~g~~~~~l~~~~--~~~~~~~P~~~~~~~~~~~~~~~~-~~~~i~f~~~~~g~~~~~~~ 150 (155)
T. maritima CheX(1SQU_B)                   83 ELALSAIGELGNMTAGKLAMKLEHLG--KHVDITPPTVVSGRDLKIKSFG-VILKLPISVFSEEDFDLHLS 150 (155)
Secondary structure                           HHHHHHHHHHHHHHHHHHHHHHHHcC--CceEecCCeEEecCCeEeeecC-cEEEEEeecCCCCceEEEEEE
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**S3 Fig.** Pairwise sequence and secondary structural comparison of CheX from *Campylobacter jejuni* and *Thermotoga maritima*. The ([DS]xxxExxNx(22)P) motif is highlighted in red.