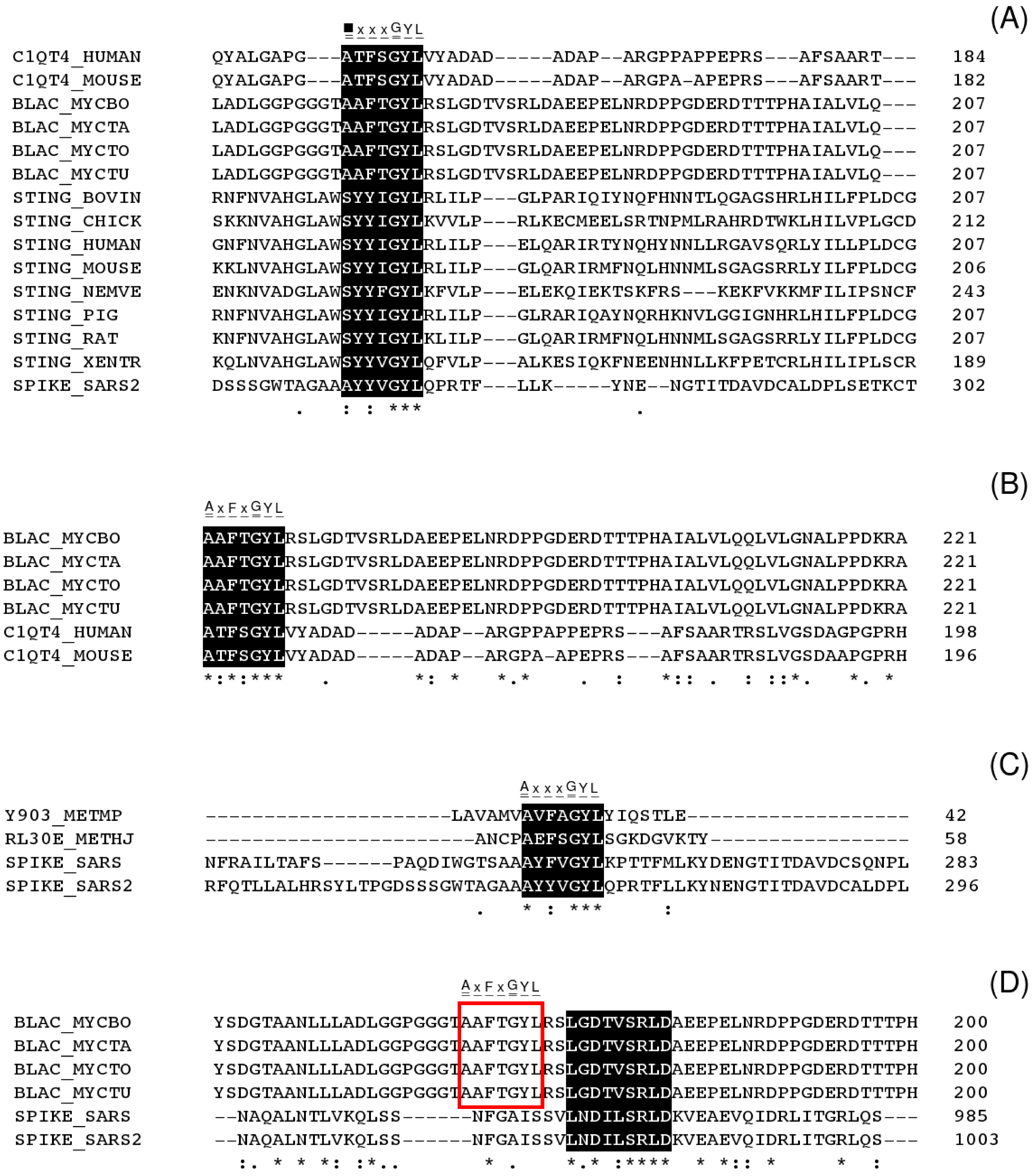

(A)

```
                            ■xxxGYL
C1QT4_HUMAN      QYALGAPG---ATFSGYLVYADAD-----ADAP--ARGPPAPPEPRS---AFSAART---  184
C1QT4_MOUSE      QYALGAPG---ATFSGYLVYADAD-----ADAP--ARGPA-APEPRS---AFSAART---  182
BLAC_MYCBO       LADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQ---  207
BLAC_MYCTA       LADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQ---  207
BLAC_MYCTO       LADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQ---  207
BLAC_MYCTU       LADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQ---  207
STING_BOVIN      RNFNVAHGLAWSYYIGYLRLILP---GLPARIQIYNQFHNNTLQGAGSHRLHILFPLDCG  207
STING_CHICK      SKKNVAHGLAWSYYIGYLKVVLP---RLKECMEELSRTNPMLRAHRDTWKLHILVPLGCD  212
STING_HUMAN      GNFNVAHGLAWSYYIGYLRLILP---ELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCG  207
STING_MOUSE      KKLNVAHGLAWSYYIGYLRLILP---GLQARIRMFNQLHNNMLSGAGSRRLYILFPLDCG  206
STING_NEMVE      ENKNVADGLAWSYYFGYLKFVLP---ELEKQIEKTSKFRS---KEKFVKKMFILIPSNCF  243
STING_PIG        RNFNVAHGLAWSYYIGYLRLILP---GLRARIQAYNQRHKNVLGGIGNHRLHILFPLDCG  207
STING_RAT        KNFNVAHGLAWSYYIGYLKLILP---GLQARIRMFNQLHNNMLSGAGSRRLYILFPLDCG  207
STING_XENTR      KQLNVAHGLAWSYYVGYLQFVLP---ALKESIQKFNEENHNLLKFPETCRLHILIPLSCR  189
SPIKE_SARS2      DSSSGWTAGAAAYYVGYLQPRTF---LLK-----YNE--NGTITDAVDCALDPLSETKCT  302
                        .   : : ***                  .
```

(B)

```
                 AxFxGYL
BLAC_MYCBO       AAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQLVLGNALPPDKRA  221
BLAC_MYCTA       AAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQLVLGNALPPDKRA  221
BLAC_MYCTO       AAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQLVLGNALPPDKRA  221
BLAC_MYCTU       AAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQLVLGNALPPDKRA  221
C1QT4_HUMAN      ATFSGYLVYADAD-----ADAP--ARGPPAPPEPRS---AFSAARTRSLVGSDAGPGPRH  198
C1QT4_MOUSE      ATFSGYLVYADAD-----ADAP--ARGPA-APEPRS---AFSAARTRSLVGSDAAPGPRH  196
                 *:*:***   .       *: *   *.*    .  :   *:: .  : ::*.   *. *
```

(C)

```
                                            AxxxGYL
Y903_METMP       ---------------------LAVAMVAVFAGYLYIQSTLE-------------------  42
RL30E_METHJ      -----------------------ANCPAEFSGYLSGKDGVKTY-----------------  58
SPIKE_SARS       NFRAILTAFS------PAQDIWGTSAAAYFVGYLKPTTFMLKYDENGTITDAVDCSQNPL  283
SPIKE_SARS2      RFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPL  296
                                        .   * : ***     :
```

(D)

```
                                      AxFxGYL
BLAC_MYCBO       YSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPH  200
BLAC_MYCTA       YSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPH  200
BLAC_MYCTO       YSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPH  200
BLAC_MYCTU       YSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPH  200
SPIKE_SARS       --NAQALNTLVKQLSS------NFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQS---  985
SPIKE_SARS2      --NAQALNTLVKQLSS------NFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQS---  1003
                   :. * * *: :*..       * .    *.* :****  * *:: *     *  :
```