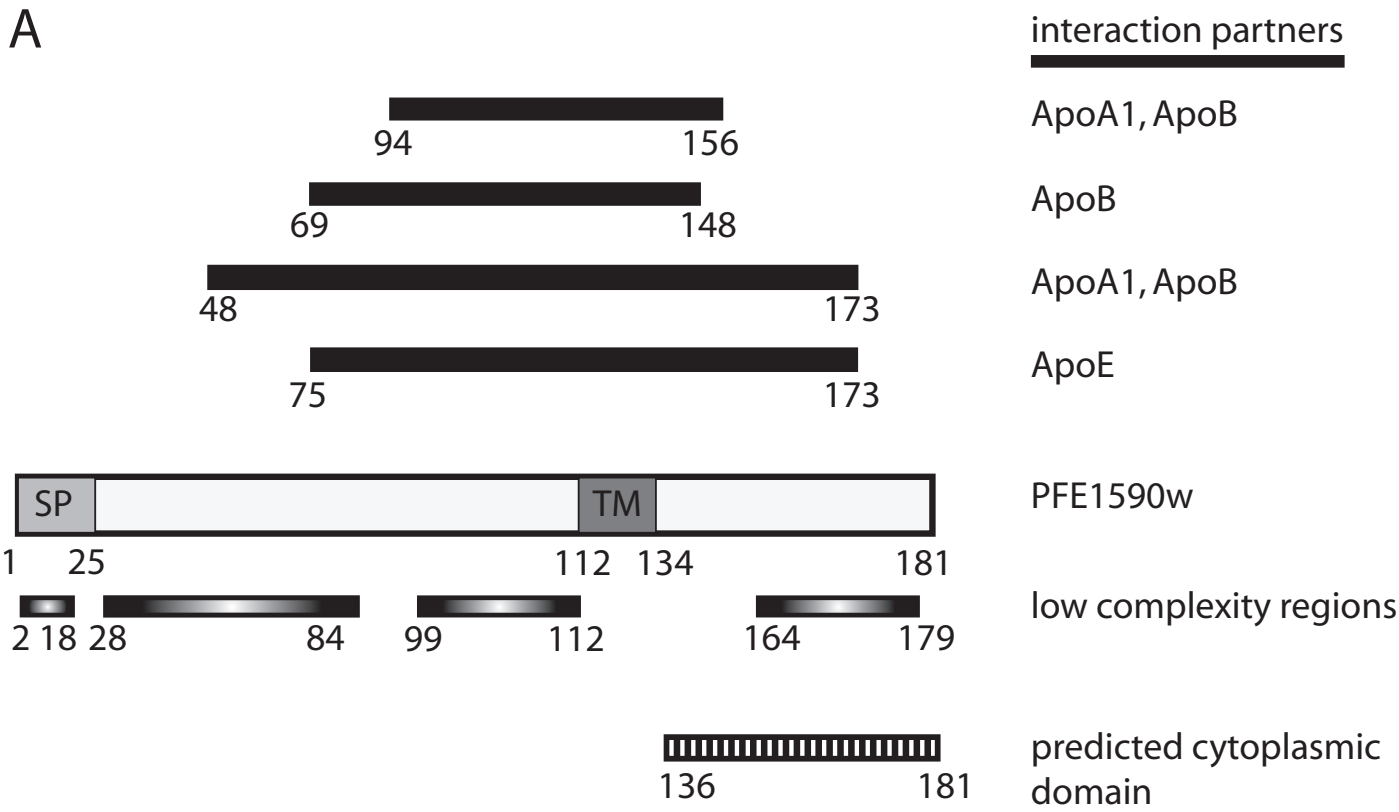
A



B

```
AMAP (2.0) multiple sequence alignment

ApoA1aa29to195       -------QSPWDRVKDLATVYVDVLKDSGRDYVSQFEG-SALGKQLNLKLLDNWDSVTST 52
ApoA1aa76to165       ----------------------------------------------------SVTST 5
ApoA1aa100to265      ------------------------------------------------------------
ApoA1aa127to265      ------------------------------------------------------------
ApoA1aa129to258      ------------------------------------------------------------
ApoEaa139to309       EVQAMLGQSTEELRVRLASHLRKLRKRLLRD-------ADDLQKRLAVYQAGAR------ 47
                            ..       ..             .                    . ...

ApoA1aa29to195       FSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYR 112
ApoA1aa76to165       FSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYR 65
ApoA1aa100to265      ------------------EKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYR 41
ApoA1aa127to265      ----------------------------------------------DFQKKWQEEMELYR 14
ApoA1aa129to258      ---------------------------------------------QKKWQEEMELYR 12
ApoEaa139to309       ------------------------------------------------------------
                      .      . .         .      .      .   .

ApoA1aa29to195       QKVEPLRAELQEGARQKLHELQEKLSPLGEEMRD---------------RARAHVDALRT 157
ApoA1aa76to165       QKVEPLRAELQEGARQKLHELQEKL---------------------------------- 90
ApoA1aa100to265      QKVEPLRAELQEGARQKLHELQEKLSPLGEEMRD---------------RARAHVDALRT 86
ApoA1aa127to265      QKVEPLRAELQEGARQKLHELQEKLSPLGEEMRD---------------RARAHVDALRT 59
ApoA1aa129to258      QKVEPLRAELQEGARQKLHELQEKLSPLGEEMRD---------------RARAHVDALRT 57
ApoEaa139to309       ----------EGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAW------ 90
                         . .   ***.: *  ::*:* .                      . .   . .

ApoA1aa29to195       HLAPYSDELR---------------------------------------------------- 167
ApoA1aa76to165       ------------------------------------------------------------
ApoA1aa100to265      HLAPYSDELRQRLAARLEALKENGGAR-------LAEYHAKATEHLSTLSEKAKPALEDL 139
ApoA1aa127to265      HLAPYSDELRQRLAARLEALKENGGAR-------LAEYHAKATEHLSTLSEKAKPALEDL 112
ApoA1aa129to258      HLAPYSDELRQRLAARLEALKENGGAR-------LAEYHAKATEHLSTLSEKAKPALEDL 110
ApoEaa139to309       ---------GERLRARMEEMGSRTRDRLDEVKEQVAEVRAKLEEQAQQIRLQAEAFQARL 141
                       .. .

ApoA1aa29to195       ------------------------------
ApoA1aa76to165       ------------------------------
ApoA1aa100to265      RQGLLPVLESFKVSFLSALEEYTKKLN--- 166
ApoA1aa127to265      RQGLLPVLESFKVSFLSALEEYTKKLN--- 139
ApoA1aa129to258      RQGLLPVLESFKVSFLSALE---------- 130
ApoEaa139to309       KSWFEPLVEDMQRQWAGLVEKVQAAVGTSA 171
```