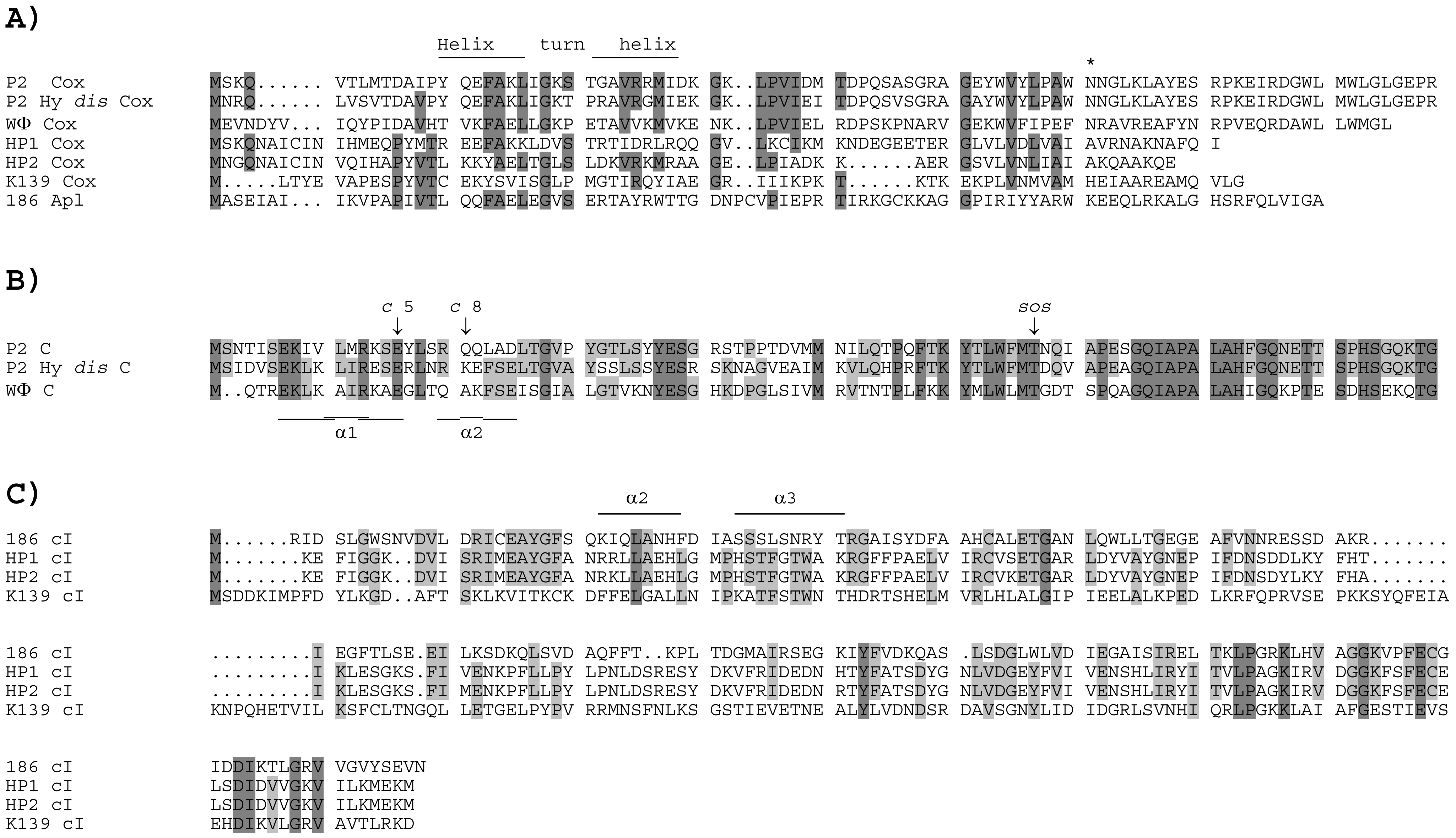
Fig. 25-8. Alignments of amino acid sequences using the CLUSTAL X program (58). *A.* Cox proteins. The location of the α-turn-α helix structure believed to be involved in DNA binding is indicated. The location of a P2 *cox* mutant, defective in dimerization, is indicated by a star. Amino acids present in at least 4 proteins are indicated by gray shades. *B.* Immunity C proteins of P2 and P2-like phages. The two α-helices presumed to contain the DNA binding motif are indicated. The mutations discussed in the text are indicated above the sequence. Amino acids common to all three proteins are shaded in dark gray, those present in two are shaded in light gray. C. Immunity cI proteins of 186 and the 186-like proteins. Amino acids common to at least four proteins are shaded in dark gray, those present in three are shaded in light gray. The location of the two α-helices, involved in DNA binding, are indicated.



A)

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                                   Helix     turn   helix
                                                                                     *
P2   Cox           MSKQ......  VTLMTDAIPY  QEFAKLIGKS  TGAVRRMIDK  GK..LPVIDM  TDPQSASGRA  GEYWVYLPAW  NNGLKLAYES  RPKEIRDGWL  MWLGLGEPR
P2 Hy dis Cox      MNRQ......  LVSVTDAVPY  QEFAKLIGKT  PRAVRGMIEK  GK..LPVIEI  TDPQSVSGRA  GAYWVYLPAW  NNGLKLAYES  RPKEIRDGWL  MWLGLGEPR
WΦ Cox             MEVNDYV...  IQYPIDAVHT  VKFAELLGKP  ETAVVKMVKE  NK..LPVIEL  RDPSKPNARV  GEKWVFIPEF  NRAVREAFYN  RPVEQRDAWL  LWMGL
HP1 Cox            MSKQNAICIN  IHMEQPYMTR  EEFAKKLDVS  TRTIDRLRQQ  GV..LKCIKM  KNDEGEETER  GLVLVDLVAI  AVRNAKNAFQ  I
HP2 Cox            MNGQNAICIN  VQIHAPYVTL  KKYAELTGLS  LDKVRKMRAA  GE..LPIADK  K......AER  GSVLVNLIAI  AKQAAKQE
K139 Cox           M.....LTYE  VAPESPYVTC  EKYSVISGLP  MGTIRQYIAE  GR..IIIKPK  T......KTK  EKPLVNMVAM  HEIAAREAMQ  VLG
186 Apl            MASEIAI...  IKVPAPIVTL  QQFAELEGVS  ERTAYRWTTG  DNPCVPIEPR  TIRKGCKKAG  GPIRIYYARW  KEEQLRKALG  HSRFQLVIGA
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B)

```
                           c 5    c 8                                                              sos
                              ↓      ↓                                                                ↓
P2 C               MSNTISEKIV  LMRKSEYLSR  QQLADLTGVP  YGTLSYYESG  RSTPPTDVMM  NILQTPQFTK  YTLWFMTNQI  APESGQIAPA  LAHFGQNETT  SPHSGQKTG
P2 Hy dis C        MSIDVSEKLK  LIRESERLNR  KEFSELTGVA  YSSLSSYESR  SKNAGVEAIM  KVLQHPRFTK  YTLWFMTDQV  APEAGQIAPA  LAHFGQNETT  SPHSGQKTG
WΦ C               M..QTREKLK  AIRKAEGLTQ  AKFSEISGIA  LGTVKNYESG  HKDPGLSIVM  RVTNTPLFKK  YMLWLMTGDT  SPQAGQIAPA  LAHIGQKPTE  SDHSEKQTG
                        ____________    _______
                             α1          α2
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C)

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                                                   α2          α3
                                                 ________    __________
186 cI             M......RID  SLGWSNVDVL  DRICEAYGFS  QKIQLANHFD  IASSSLSNRY  TRGAISYDFA  AHCALETGAN  LQWLLTGEGE  AFVNNRESSD  AKR.......
HP1 cI             M.......KE  FIGGK..DVI  SRIMEAYGFA  NRRLLAEHLG  MPHSTFGTWA  KRGFFPAELV  IRCVSETGAR  LDYVAYGNEP  IFDNSDDLKY  FHT.......
HP2 cI             M.......KE  FIGGK..DVI  SRIMEAYGFA  NRKLLAEHLG  MPHSTFGTWA  KRGFFPAELV  IRCVKETGAR  LDYVAYGNEP  IFDNSDYLKY  FHA.......
K139 cI            MSDDKIMPFD  YLKGD..AFT  SKLKVITKCK  DFFELGALLN  IPKATFSTWN  THDRTSHELM  VRLHLALGIP  IEELALKPED  LKRFQPRVSE  PKKSYQFEIA

186 cI             .........I  EGFTLSE.EI  LKSDKQLSVD  AQFFT..KPL  TDGMAIRSEG  KIYFVDKQAS  .LSDGLWLVD  IEGAISIREL  TKLPGRKLHV  AGGKVPFECG
HP1 cI             .........I  KLESGKS.FI  VENKPFLLPY  LPNLDSRESY  DKVFRIDEDN  HTYFATSDYG  NLVDGEYFVI  VENSHLIRYI  TVLPAGKIRV  DGGKFSFECE
HP2 cI             .........I  KLESGKS.FI  MENKPFLLPY  LPNLDSRESY  DKVFRIDEDN  RTYFATSDYG  NLVDGEYFVI  VENSHLIRYI  TVLPAGKIRV  DGGKFSFECE
K139 cI            KNPQHETVIL  KSFCLTNGQL  LETGELPYPV  RRMNSFNLKS  GSTIEVETNE  ALYLVDNDSR  DAVSGNYLID  IDGRLSVNHI  QRLPGKKLAI  AFGESTIEVS

186 cI             IDDIKTLGRV  VGVYSEVN
HP1 cI             LSDIDVVGKV  ILKMEKM
HP2 cI             LSDIDVVGKV  ILKMEKM
K139 cI            EHDIKVLGRV  AVTLRKD
```

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