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Sequence Alignment and Secondary Structure (DSSP)

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2A6:  secondary structure from 1Z10 (coumarin complex)
2A13: secondary structure from Scott lab structure
2B4:  secondary structure from 1SUO (4PI complex)
2E1:  secondary structure from ???
2A17: secondary structure from abiraterone structure for mol A/B, C/D, consensus

         1                                                  50
   2A6   MLASGMLLVA LLVCLTVMVL MSVWQQRKSK G.KLPPGPTP LPFIGNYLQL
  2A13   MLASGLLLVT LLACLTVMVL MSVWRQRKSR G.KLPPGPTP LPFIGNYLQL
   2B4   MEFSLLLLLA FLAGLLLLLF RG...HPKAH G.RLPPGPSP LPVLGNLLQM
   2E1   MSALGVT.VA LLVWAAFLLL VSMWRQVHSS W.NLPPGPFP LPIIGNLFQL
  17A1   M....WELVA LLLLTLAYLF ...WPKRRCP GAKYPKSLLS LPLVGSLPFL 43
17A1Δ19  M....~~~~~ ~~~~~~~~~~ ~~~~~~AKKT GAKYPKSLLS LPLVGSLPFL
                                                          A'

         51                                                 100
   2A6   NTE.QMYNSL MKISERYGPV FTIHLGPRRV VVLCGHDAVREA LVDQAEEF
  2A13   NTE.QMYNSL MKISERYGPV FTIHLGPRRV VVLCGHDAVKEA LVDQAEEF
   2B4   DRK.GLLRSF LRLREKYGDV FTVYLGSRPV VVLCGTDAIREA LVDQAEAF
   2E1   ELK.NIPKSF TRLAQRFGPV FTLYVGSQRM VVMHGYKAVKEA LLDYKDEF
AB17A1   PRHGHMHNNF FKLQKKYGPI YSVRMGTKTT VIVGHHQLA EV LIKKGKDF 93
CD17A1   PRHGHMHNNF FKLQKKYGPI YSVRMGTKTT VIVGHHQLA EV LIKKGKDF 93
  17A1   PRHGHMHNNF FKLQKKYGPI YSVRMGTKTT VIVGHHQLA EV LIKKGKDF 93
                A           β1-1      β1-2         B

         101                                                150
   2A6   SGRGEQATFD WVF.KGYGVV FS.NGERAKQ LRRFSIATLR DFGVGKRGIE
  2A13   SGRGEQATFD WLF.KGYGVA FS.NGERAKQ LRRFSIATLR GFGVGKRGIE
   2B4   SGRGKIAVVD PIF.QGYGVI FA.NGERWRA LRRFSLATMR DFGMGKRSVE
   2E1   SGRGDLPAFH .AH.RDRGII FN.NGPTWKD IRRFSLTTLR NYGMGKQGNE
AB17A1   SGRPQMATLD IASNNRKGIA FADSGAHWQL HRRLAMATFA LFKDGDQKLE 143
CD17A1   SGRPQMATLD IASNNRKGIA FADSGAHWQL HRRLAMATFA LFKDGDQKLE 143
  17A1   SGRPQMATLD IASNNRKGIA FADSGAHWQL HRRLAMATFA LFKDGDQKLE 143
          β1-5      B'                    C                   D

         151                                                200
   2A6   ERIQEEAGFL IDALRGTGGA NIDPTFFLSR TVSNVISSIV FGDRFDYKDK
  2A13   ERIQEEAGFL IDALRGTHGA NIDPTFFLSR TVSNVISSIV FGDRFDYEDK
   2B4   ERIQEEARCL VEELRKSKGA LLDNTLLFHS ITSNIICSIV FGKRFDYKDP
   2E1   SRIQREAHFL LEALRKTQGQ PFDPTFLIGC APCNVIADIL FRKHFDYNDE
AB17A1   KIICQEISTL CDMLATHNGQ SIDISFPVFV AVTNVISLIC FNTSYKNGDP 193
CD17A1   KIICQEISTL CDMLATHNGQ SIDISFPVFV AVTNVISLIC FNTSYKNGDP 193
  17A1   KIICQEISTL CDMLATHNGQ SIDISFPVFV AVTNVISLIC FNTSYKNGDP 193
               D                          E
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        201                                                  250
   2A6  EFLSLLRMML GIFQFTSTST GQLYEMFSSV MKHLPGPQQQ AFQLLQGLE
  2A13  EFLSLLRMML GSFQFTATST GQLYEMFSSV MKHLPGPQQQ AFKELQGLE
   2B4  VFLRLLDLFF QSFSLISSFS SQVFELFSGF LKHFPGTHRQ IYRNLQEIN
   2E1  KFLRLMYLFN ENFHLLSTPW LQLYNNFPSF LHYLPGSHRK VIKNVAEVK
AB17A1  ELNVIQNYNE GIIDNLSKDS LVDLVPWLKI FPN..KTLEK LKSHVKIRN 240
CD17A1  ELNVIQNYNE GIIDNLSKDS LVDLVPWLKI FPN..KTLEK LKSHVKIRN 240
  17A1  ELNVIQNYNE GIIDNLSKDS LVDLVPWLKI FPN..KTLEK LKSHVKIRN 240
                F               F'     G'                  G

251                                                 300
   2A6  DFIAKKVEHN QRTLDPNSPR DFIDSFLIRM QEEEKNP... ...NTEFYLK
  2A13  DFIAKKVEHN QRTLDPNSPR DFIDSFLIRM QEEEKNP... ...NTEFYLK
   2B4  TFIGQSVEKH RATLDPSNPR DFIDVYLLRM EKDKSDP... ...SSEFHHQ
   2E1  EYVSERVKEH HQSLDPNCPR DLTDCLLVEM EKEKHSA... ...ERLYTMD
AB17A1  DLLNKILENY KEKFRSDSIT NMLDTLMQAK MNSDNGNAGP DQDSELLSDN 290
CD17A1  DLLNKILENY KEKFRSDSIT NMLDTLMQAK MNSDNGNAGP DQDSELLSDN 290
  17A1  DLLNKILENY KEKFRSDSIT NMLDTLMQAK MNSDNGNAGP DQDSELLSDN 290
                                     H

        301                                                  350
   2A6  NLVMTTLNLF IGGTETVSTT LRYGFLLLMK HPEVEAKVHE EIDRVIGKNR
  2A13  NLVMTTLNLF FAGTETVSTT LRYGFLLLMK HPEVEAKVHE EIDRVIGKNR
   2B4  NLILTVLSLF FAGTETTSTT LRYGFLLMLK YPHVTERVQK EIEQVIGSHR
   2E1  GITVTVADLF FAGTETTSTT LRYGLLILMK YPEIEEKLHE EIDRVIGPSR
AB17A1  HILTTIGDIF GAGVETTTSV VKWTLAFLLH NPQVKKKLYE EIDQNVGFSR 340
CD17A1  HILTTIGDIF GAGVETTTSV VKWTLAFLLH NPQVKKKLYE EIDQNVGFSR 340
  17A1  HILTTIGDIF GAGVETTTSV VKWTLAFLLH NPQVKKKLYE EIDQNVGFSR 340
                I                                  J

        351                                                  400
   2A6  QPKFEDRAKM PYMEAVIHEI QRFGDVIPMS LARRVKKDTK FRDFFLPKGT
  2A13  QPKFEDRAKM PYTEAVIHEI QRFGDMLPMG LAHRVNKDTK FRDFFLPKGT
   2B4  PPALDDRAKM PYTDAVIHEI QRLGDLIPFG VPHTVTKDTQ FRGYVIPKNT
   2E1  IPAIKDRQEM PYMDAVVHEI QRFITLVPSN LPHEATRDTI FRGYLIPKGT
AB17A1  TPTISDRNRL LLLEATIREV LRLRPVAPML IPHKANVDSS IGEFAVDKGT 390
CD17A1  TPTISDRNRL LLLEATIREV LRLRPVAPML IPHKANVDSS IGEFAVDKGT 390
  17A1  TPTISDRNRL LLLEATIREV LRLRPVAPML IPHKANVDSS IGEFAVDKGT 390
          J'              K                  β1-4     β2-1    β2-2
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        401                                                  450
   2A6  EVYPMLGSVL RDPSFFSNPQ DFNPQHFLNE KGQ..FKKSD AFVPFSIGKR
  2A13  EVFPMLGSVL RDPRFFSNPR DFNPQHFLDK KGQ..FKKSD AFVPFSIGKR
   2B4  EVFPVLSSAL HDPRYFETPN TFNPGHFLDA NGA..LKRNE GFMPFSLGKR
   2E1  VVVPTLDSVL YDNQEFPDPE KFKPEHFLNE NGK..FKYSD YFKPFSTGKR
AB17A1  EVIINLWALH HNEKEWHQPD QFMPERFLNP AGTQLISPSV SYLPFGAGPR 440
CD17A1  EVIINLWALH HNEKEWHQPD QFMPERFLNP AGTQLISPSV SYLPFGAGPR 440
  17A1  EVIINLWALH HNEKEWHQPD QFMPERFLNP AGTQLISPSV SYLPFGAGPR 440
         β1-3    K'                  K″                      K'''

        451                                                  500
   2A6  NCFGEGLARM ELFLFFTTVM QNFRLKSSQS PKDIDVSPKH VGFATIPRNY
  2A13  YCFGEGLARM ELFLFFTTIM QNFRFKSPQS PKDIDVSPKH VGFATIPRNY
   2B4  ICLGEGIART ELFLFFTTIL QNFSIASPVP PEDIDLTPRE SGVGNVPPSY
   2E1  VCAGEGLARM ELFLLLCAIL QHFNLKPLVD PKDIDLSPIH IGFGCIPPRY
AB17A1  SCIGEILARQ ELFLIMAWLL QRFDLEVPDD GQLPSLEG.I PKVVFLIDSF 489
CD17A1  SCIGEILARQ ELFLIMAWLL QRFDLEVPDD GQLPSLEG.I PKVVFLIDSF 489
  17A1  SCIGEILARQ ELFLIMAWLL QRFDLEVPDD GQLPSLEG.I PKVVFLIDSF 489
                        L          β3-3       L'      β4-1   β4-2

   2A6  TMSFLPR 494
  2A13  TMSFLPR 494
   2B4  QIRFLAR
   2E1  KLCVIPRS
AB17A1  KVKIKVRQAW REAQAEGST 508
CD17A1  KVKIKVRQAW REAQAEGST 508
CD17A1  KVKIKVRQAW REAQAEGST 508
         β3-2
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