

```

EC_DHDPR      MH-----DANIRVAIAAGAGGRMGRQLIQAAALEGVQLG
MT_DHDPR      -----MRVGVLAGAKKVGATMVRAVAA-A-DDLT
TM_DHDPR      MGSDK---IH-----HHHHMKYGVIGYSGRMGQEIQKVFS-EKGHELV
SA_DHDPR      M-----ASMKILLIGY-GAMNQVRVARLAE-EKGHEIV
AT_DHDPR1     AMAD---SGEEAVKSVLPNGISIMVNGCSGKMGKAVIKAAD-SAGVNIV
AT_DHDPR2     LSMGKSETFEEAGNSVAPNGISIMVNGCSGKMGKAVIKAAD-SAGVNIV
                :   : * * :. : : :

```

```

EC_DHDPR      AAIER----EGSSLLGSDAGELAGAGKTGVTVQSSLDV--KDDFDVFD
MT_DHDPR      ISAE-----LDAGDPLSLLT-DGNTEVVID
TM_DHDPR      LKVD-----V-NGVEE--LDSPDVVID
SA_DHDPR      GVIEN-----TPKAT--TPY-QQYQHIADVKGADVAID
AT_DHDPR1     PISFGSAGEDGQ-RVEVCGKEITVHGP--TEREKVLSSVFEKHPPELIVVD
AT_DHDPR2     PTSFGSVEEAGQ-TVEVCGKEILVHGP--TEREKVLSSVFEKYPELIVVD
                . . : : *

```

```

EC_DHDPR      FTRPEGTLNHLAFCRQHGKGMVIGTTGFD EAGKQAIRDA---AADIAIVF
MT_DHDPR      FTHPDVVMGNLEFLIDNGIHAVVGTGFTAERFQQVESWLVAKPNTSVLI
TM_DHDPR      FSSPEALPKTVDLCKYRAGLVI GTTALKEEHLQMLREL---SKEVPVVQ
SA_DHDPR      FSNPNLLFPLI--DEDFHLP LVVA TTGEKEKLLNKLDEL---SQNM PVFF
AT_DHDPR1     YTI PSAVNDNAELYSKVGVPFVMGTTGGDRNKLYETVEE---AKIYA-VI
AT_DHDPR2     YTI PSAVNDNAELYGKVGVPFVMGTTGGDRTRLYKTVEE---SKIYA-VI
                :: * . . * : . ** . . .

```

```

EC_DHDPR      AANFSVGVNVM---LKLLEKAA-KVMGDYT DIEIIEAHRHKVDAPS GTA
MT_DHDPR      APNFAIGAVLS---MHFAKQAA-RFFD---SAEVIELHHPHKADAPS GTA
TM_DHDPR      AYNF SIGINVI---KRFLSELV-KVLEDW-DVEIVETHHRFKKDAPSGTA
SA_DHDPR      SANMSYGVHAL---TKILAAAV-PLIDDF-DIELTEAHHNKKVDAPSGTL
AT_DHDPR1     SPQMKGQVVAFLAAMEIMAEQFPGAFSGY-SLDVMESHQASKLDA-SGTA
AT_DHDPR2     SPQMKGQVVAFLAAMEIMSEQFPGAFAGY-SLEVMESHQASKLDA-SGTA
                : : : . : : : * * : * * * *

```

```

EC_DHDPR      LAMGEAIAHAL---DKDLKCAVYSREGHTGERVP-GTIGFATVRA GDIV
MT_DHDPR      ARTAKLIAEARKGLPPNP-DATSTSLPGARGADV--DGLPVHAVRLAGLV
TM_DHDPR      ILLESALGKS-----VPIHSLR VGGVP
SA_DHDPR      EKLYDVIVSLKENVTPVY-DRHELNE-----KRQP-QDIGIHSIRGGTIV
AT_DHDPR1     KAVISCFQ----ELGVSY-DMDQIQL-----IRDPKQQVEMVGVPEEHIS
AT_DHDPR2     KAVISCFQ----KLGVSY-DMDQIQL-----IRDPKQQIEVVGVPPEEHVS
                . : : . : :

```

```

EC_DHDPR      GE--HTAMFADIG--ERLEITHRASSRMTFANGAVRSALWLSGK-----E
MT_DHDPR      AH--QEVLFGE--ETLTIRHDSLDRTS FVPGVLLAVRRIAE R-----P
TM_DHDPR      GE--HVVVFCNIG--ETIEIKHRAISRTVFAIGALKAAEFLVGK-----D
SA_DHDPR      GE--HEVLFAGTD--ETIQITHRAQS KDIFANGAIQAAERLVNK-----P
AT_DHDPR1     GHAFHLYHLTSPDETVSFEFQHNVCGRSIYAEGTVDAVLFLAKKIRLKAD
AT_DHDPR2     GHAFHLYHLTSPDKTVSFEFQHNVCGRSIYAEGTVDAVLFLAKKIRSKAE
                .. : : . : : * . : : * : : : :

```

```

EC_DHDPR      SGLFDMRDVL-DLNNL
MT_DHDPR      -GLTVGLEPL--LDLH
TM_DHDPR      PCMYSFEEVI--FGGE
SA_DHDPR      NCFYT-----FDNL
AT_DHDPR1     QRIYNMIDVLREGNMR
AT_DHDPR2     KRIYNMIDVLREGNMR
                : .

```

Figure S5: Alignment of DHDPR sequences. Helical regions are shown in blue and β -sheet regions are shown in red.