

CLUSTAL X (1.83) multiple sequence alignment

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drslr      CRSSEQVTFRCWWSSGTFQNLSEPGALRIFYQT-----KALSSDWYECPDYTQT
drghr      CFSRDMITFRCQWETGSSQNRTLEDLSFFYMLEKDP-----KKTYGKWIECPSYN-S
hsGHR      CRSPERETF SCHWTEVHHGTKNLGPIQLFYTRRNTQ-----EWTQEWKECPDYVSA
mmGhr      CRSPELETFSCYWTEGDNPDLPKTPGSIQLLYAKRESQRQAARIAHEWTQEWKECPDYVSA
drCRFA4    CRSPNMEVFCWWRPVEKQSNVS---YTLLYSTG-----ERAPQECPDYVSA
drprlr.a   CRSPEKETFTCWWEPEGDDGGLPTT--YALYYRLEN-----TETVKECPDYKTA
drprlr.b   CRSPEKETFTCWWEETGSSGGLPTR--YQLYYRKEN-----SLEVFECPDYHKA
hsPRLR     CRSPNKETFTCWWRPGTDGGLPTN--YSLTYHREG-----ETLMHECPDYITG
mmPrLr     CRSPDKETFTCWWNPGSDGGLPTN--YSLTYSKEG-----EKNTYECPDYKTS
hsTPOR_CHD2 CFTLDLKNVTCQWQQQDHASSQGFFYHSRARCPCPRDRYP---IWENCEEEKTNPGLQTP
mmTpor_CHD1 CFTLDLKMVTCQWQQQDRSTSSQGFFRHSRTRCCPTDRDP---TWEKCEEEEE-PRPGSQPA
hsEPOR     CFTERLEDLVCFWEEAASAGVGP-G-NYSFSYQLEDEPWK-----LCRLHQAPTARGA
mmEpor     CFTQRLLEDLVCFWEEAASSGMD-F-NYSFSYQLEGESRK-----SCSLHQAPTVRGS
hsTPOR_CHD1 CFSRTFEDLTCFWDEEEAAPSG---TYQLLYAYPREKPR-----ACPLSSQSMPHFG
mmTpor_CHD1 CFSQTFEDLTCFWDEEEAAPSG---TYQLLYAYRGEKPR-----ACPLYSQSVPTFG
hsCLF-3    CQKLIHGVNTAEDLVREGEIAMLG-----GVGEENEKLSWFTK
mmClf-3    CQKLIHGVNTADDLVREGEIAILG-----GIEEESDKLWFTK
drclf-3    CQKLIHGVSTADELLREGEAAIRC-----SINETEDKLNSFTK
drepor     CFVEGKDFTCFWEKEDGTNYSQD-NYTFYTYMNE-----NKMDCAVSSLFLL
drtpor_CHD1 CFTRNLEDFTCFWDAPVEKSYDFLYIIIEGLMEE-----KRCDVKQQTFEFK
drtpor_CHD2 CHTSDLIQIICKWRGDLYKDNTYSFYKQLNRSS-----WSSWKLCPNCNNS
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drslr      VKNECYFNKTFTRIWTSYCIQLRSVPQN--TTYDEACFTVENIVYPPVGLNWTLLNVS
drghr      QRNECYFDASHTFVWYTYVIQLRSVDN----VYEEMSFSIENIVFPDPPVGLNWTLLKMA
hsGHR      GENSICYFNSSFTSIWIPYCIKLTSSNGG----TVDEKCFVDEIVQDPPIALNWTLLNVS
mmGhr      GKNSCYFNSSYTSIWIPYCMNVTATHTRAGPVTSHRYCLDVADIVEPDPFNLTYYTLLNDS
drCRFA4    GPNSCFDAKHTQVWKVYCMNVTATHTRAGPVTSHRYCLDVADIVEPDPFNLTYYTLLNDS
drprlr.a   GENSCHFEKRHTAIWI IYNYITVVASNALGKAYSEPVEVDVVIYVQNPNTPENVKAVVIH--
drprlr.b   GINSCHFEGKRYTSMWRTYIMMVNATNMGSSFSDELYVDVTYIVQDPPELAVEVKQP-
hsPRLR     GPNSCHFGKQYTSIWKIYIITVNATNMGSSSTSDPLYVDVTYIVEPEPPRNLTLVVKQL-
mmPrLr     GPNSCFFSKQYTSIWKIYIITVNATNMGSSSTSDPLYVDVTYIVEPEPPRNLTLVVKQL-
hsTPOR_CHD2 QFSRCHFKSRNDSIIHILVEVTTAPGTVHSYLGSFPFIHQAVRL---PTPNLHWREIS--
mmTpor_CHD1 LVSRCHFKSRNDSVIHILVEVTTAQGAVHSYLGSPFIHQAVLL---PTPSLHWREVS--
hsEPOR     VRFWCSLP--TADTSSFVPLELRVTAASG-APRYHRVIHINEVLLDAPVGLVARLADE-
mmEpor     VRFWCSLP--TADTSSFVPLELRVTAASG-SPRYHRIHINEVLLDAPAGLLARRAEE-
hsTPOR_CHD1 TRYVCQFPD-QEEVRLFFPLHLWKNVFLNQTRTQRVLFVDSVGLPAPPSIIKAMGGSQ-
mmTpor_CHD1 TRYVCQFPA-QDEVRLFFPLHLWKNVSLNQTLIQRVLFVDSVGLPAPPRVIKARGGSQ-
hsCLF-3    KASHIQLDLSEVPLLDVDPCLSAQLDSDSILNIVKDHIFKHGTVASRPPVQIEELIEKP-
mmClf-3    KASHIQLDLSEVPLLDVDPCLSAQLDSDSILNIVKDHIFKHGTVASRPPVQIEELIEKP-
drclf-3    KALQIQLDLSEVPSLDVDPCLSAQLDSDSLLHMFRAHVARHGSVASHPPVQIEELVERP-
drepor     SSNRSVFFCKLPKALFFTSLDVQVLRDG--QMLYNRSLNVENILLTDPNRNVTWSSGK-
drtpor_CHD1 ILNICTFPP--SDVYLYVETHIRVIDKDTNTTIYSRAVSVEDQLLYPPSNISLHPTEE-
drtpor_CHD2 IHQCVLYGQKSNVFKFYLNLTGLQPFPSR-----TFYAETFYMNIQTRPPEGLKVQIGEE-
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drslr      RSGLHFDVLRWTPPPSADVKT--GWMSLVYQLQYR-----VKNNTY-----
drghr      SSSLHCDVLSWDPSPSAGVPLSDGWISLVYETQYR-----EKDSDQ-----
hsGHR      LTGIHADIQVRWEAPRNADIQK--GWMVLEYELQYK-----EVNETK-----
mmGhr      LTGIRGDIQVSWQPPNADV LK--GWIILEYELQYK-----EVNESK-----
drCRFA4    TCGSSCSVLLSWMYP IAAEVHQ--GWITLVYELRYRN----LLQPNT-----
drprlr.a   -EDRDPFVKVSWDKPRTADTRS--GWITLHYQLR-----VKQEEDKE-----
drprlr.b   -SQNSQYVLVKWLPHPHDVTRS--GWVTIKYEVR SKILNSRDEEDSS-----
hsPRLR     -EDRKPYLWIKWSPPTLIDLKT--GWFTLLYEIR-----LKPEKAAE-----
mmPrLr     -KDKKTYLWVKWLPPTITDVKT--GWFTMEYEIR-----LKSEEADE-----
hsTPOR_CHD2  ---SGHLELEWQHPSWAAQET-----CYQLRYT-----GEGHQD-----
mmTpor_CHD1  ---SGRLELEWQHSSWAAQET-----CYQLRYT-----GEGRED-----
hsEPOR     ---SGHVVLRLWLPPTPMTS-----HIRYEV DVSAGNGAGSVQR-----
mmEpor     ---GSHVVLRLWLPPTGAPMTT-----HIRYEV DVSAGNRAGGTQR-----
hsTPOR_CHD1  ---PGELQISWEEP-APEISD-----FLRYELRYGPRDPKNSTGPTVIQLIATETCCPA
mmTpor_CHD1  ---PGELQIHWEAP-APEISD-----FLRHELRYGPTDSSNATAPSVIQLLSTETCCPT
hsCLF-3     ---GGIIVRWCKVDDDFTAQ-----DYRLQFR-----KCTSNH-----
mmClf-3     ---GGIIVRWCKVDDDFTAQ-----DYRLQFR-----KCTANH-----
drclf-3     ---GGVLVRWCKVDDDFSPQ-----DYRLQFR-----RSNSSQ-----
drepor     ---EGQLNVSWLPPAVKYIDDS-----LIYEVRYA-----VEDSHMG-----
drtpor_CHD1  ---VGQMLVKWKR TSNEHEIR-----YSFKNT-----
drtpor_CHD2  ---RLCLTWDSPFLIISKH-----LMYQIRYQ-----HHEENQ-----
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drslr      -----WEMQELE-----SGTQQSIYGLHTDKEYEVRV
drghr      -----WNTLESD-----KNTQAYIYGLSNT EYELRV
hsGHR      -----WKMDPI-----LTTSPVYSLKV DKEYEVRV
mmGhr      -----WKVMGPI-----WLTYCPVYSLRMDKEHEVRV
drCRFA4    -----WKVKERL-----RERQVELFDLPVG-SYECVV
drprlr.a   -----WVEYDAE-----RQKNYNVFSLHSDREYMVQV
drprlr.b   -----WESYSAG-----KQLEFSIYSPHPGTNYVVDV
hsPRLR     -----WEIH FAG-----QQTEFKILSLHPGQKYL VQV
mmPrLr     -----WEIHFTG-----HQTQFKVFDLYPGQKYL VQT
hsTPOR_CHD2  -----WKVLEPP-----LGARGGTLELRPRSR YRLQL
mmTpor_CHD1  -----WKVLEPS-----LGARGGTLELRPRAR YSLQL
hsEPOR     -----VEILEG-----RTECVLSNLRGRTRYTF AV
mmEpor     -----VEVLEG-----RTECVLSNLRGGTRYTF AV
hsTPOR_CHD1  LQRPHSASALDQSPCAQPTMPWQDGP KQTSRSPREASALTAEGGSCLISGLQPGNSYWLQL
mmTpor_CHD1  LWMPNPVPVLDQPPCVHPTASQPHGP-----APFLT VKGGSCLVSGLQASKSYWLQL
hsCLF-3     -----FEDVYVG-----SETEFIVLHIDPNVDYQFRV
mmClf-3     -----FEDVYVG-----SETEFIVLHIDPNVDYQFRV
drclf-3     -----YEDAYIG-----KDTEFLVLHLDPHVDHLFRV
drepor     -----KVEETK-----ASTMLVLRGLQPDTRYKVWV
drtpor_CHD1  -----STVKSVS-----ENDYKLVSLVPGENCTVQM
drtpor_CHD2  -----WKGFKAS-----GSKTSTCLDVHRGGRYTIQV

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drslr	RCKMS---AFNNFGEFS
drghr	RAKMR---SFH-FGDFS
hsGHR	RSKQR---NSGNYGEFS
mmGhr	RSRQR---SFEKYSEFS
drCRFA4	RCRSA---NSRHWSEWS
drprlr.a	RCKP----DHGFWEWT
drprlr.b	RCKL----DQGLWSDWS
hsPRLR	RCKP----DHGYWSAWS
mmPrlr	RCKP----DHGYWSRWG
hsTPOR_CHD2	RARLNGPTYQGPWSSWS
mmTpor_CHD1	RARLNGPTYQGPWSAWS
hsEPOR	RARMAEPSFSGFWSAWS
mmEpor	RARMAEPSFSGFWSAWS
hsTPOR_CHD1	RSEPDGISLGGSWGWS
mmTpor_CHD1	RSQPDGVSLRGSWGPWS
hsCLF-3	CARGD---GRQEWSPWS
mmClf-3	CARGD---GRQEWSPWS
drclf-3	CARGE---GRTEWSPWS
drepor	RVKPDGVSYKGYWSSWT
drtpor_CHD1	RVKPSG-DFKRFWSDWS
drtpor_CHD2	RAQPNGSVYSGNWSWSDWS
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