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Drcd-1/Dmel      MSAQPSPHMNPQQQQQQQQQQQQTEQEKVYQWINELAHPDTRTALLELSKKRE--TDLA  58
Rcd-1/Hsap      MHSLATAAPVP-----TTLAQVDREKIYQWINESSPETRENALLELSKKRESVPDLA  53
Drcd-1r/Dmel    MSAEPPSPVMSP-----QQQAEREKVYQLI IELAYPATRETALLELSKNTY--ADLA  49
* : ..: *          * .:.*:* * *: * * * .*****: .***

Drcd-1/Dmel      PMLWNSFGTACALLQEIVNIYPSITPPTLTAHQSNRVCNALALLQCVASHPETRTAFLQA  118
Rcd-1/Hsap      PMLWHSFGTIAALLQEIVNIYPSINPPTLTAHQSNRVCNALALLQCVASHPETRSAFLAA  113
Drcd-1r/Dmel    PMLWKS VGTTC TLLQEIVNIYPIITPVLKANQSNRVCYAL TLLQCVASHPETRPAFLRD  109
*****:*.*. * .:***** * .*. * .:***** *:*****.***

Drcd-1/Dmel      QIPLYLYPFLSTTSKTRPF EYLRLTSLGVIGALVKTDEQEVITFLLTTEIVPLCLSIMDS  178
Rcd-1/Hsap      HIPLFLYLPFLHTVSKTRPF EYLRLTSLGVIGALVKTDEQEVINFLLTTEIIPLCRIMES  173
Drcd-1r/Dmel    QIPMYLYPFLSTTFKSRPF EQLRLTTLGVINALAETGDEVLIIFLIWSEVVP HCLTNMVR  169
*:*:***** * . *:***** *****:*****.*.:.: * *: * *: :*: * * *

Drcd-1/Dmel      GSELSKTVATFIIQKILLDEGLSYICQTYERFSHVAITLGMVIQLAKDPCARLLKHVV  238
Rcd-1/Hsap      GSELSKTVATFILQKILLDDTGLAYICQTYERFSHVAMILGKMVLQLSKEPSARLLKHVV  233
Drcd-1r/Dmel    GSKLTKIAATSILEKILLDEMGLTYICENHDRFSQVAITLGMVIHMLKFPCLRVLKHVV  229
*:*:* * .** *:*****: *:*:*:..:***:*: *****: * * . *:******

Drcd-1/Dmel      RCYLRLSDNTRARKALGQCLPDQLRDGTFALCLQEDKSTKQWLQMLLKNLELG--ATPQQ  296
Rcd-1/Hsap      RCYLRLSDNPRAREALRQCLPDQLKDTTFAQVLKDDTTTKRWLAQLVKNLQEGQVTDPRG  293
Drcd-1r/Dmel    RCYLLTENARARSALRVCLPDL LRDGTF TSLVQHDTCTKQWLQMLLKNLQTN-AVNPMG  288
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Drcd-1/Dmel      IGMSP LGS- 304
Rcd-1/Hsap      I---PLPPQ 299
Drcd-1r/Dmel    SS----- 290

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