Additional file 6: Protein sequence comparison of the Drosophila's DCC in the pea aphid. CLUSTAL multiple sequence alignment by MUSCLE (3.8) of *A. pisum*'s homologs of *D. melanogaster* DCC. Proteic domains of the Drosophila are represented in full color boxes above the alignments. *A. pisum* gene names found by BLASTp are indicated in parenthesis.

MSL1 (XM_003243415.1)

```
MSL1_DROME      MDKRFKWPPKKRANYLESPYPHIPSRGRQRNLHGHPNQTQHLHQHPGKIYERQQYGNGRG
MSL1_ACYPI      MARR-----------------------------------------------RNSRGVGRA
                * .*                                               *:. * **.

MSL1_DROME      GHGGGNNNYRKLLHSLPAEHGGGAMAPPSSGGTVCAGADMVKLISENNNLRRMVMLNLNL
MSL1_ACYPI      ------------------------------------------------------------


MSL1_DROME      MQEQTDSIAAKDKELDDQSAKMSVVKAQNEELKQAVAQLEAANQELCKQLRRKNQRRNDN
MSL1_ACYPI      --------SAMSKEKDEK------------------------------------------
                        :* .** *::

MSL1_DROME      DDDDDDPPLPPAAPQQKLIRCHAETQTVFREREQGTQTIDAQPQFANALPRGINMKESPA
MSL1_ACYPI      ------------------------------------------------------------


MSL1_DROME      LDHHAGAVTNQPASKRSESKGRGEFNGKKVSTFILQRMNQDFEHHIHEQTEVAEEHEMEA
MSL1_ACYPI      ---------------------------------IL-------------------------
                                                 **

MSL1_DROME      HKEQISQEEDQLVAEEDHLHMQEVHTEEVVGGDIFHDALESIEMEVVTEELVDMEEHGQS
MSL1_ACYPI      ---QLTNEVEYLKQKSDVLSFTQVSS----------------------------------
                   *:::* : *  :.* * : :* :

MSL1_DROME      VDANGHIEEDDDEDDEDDENSDKDDDSEEDDYPWMHSDADVNARTEEELWQNQNYLLELD
MSL1_ACYPI      ------------------------------------------------------------


MSL1_DROME      PTEEKTCAPSAHSTPNHQQKSSTQAEIRKEGNQNRITEKLLQLKPEPMVDALEAPILPKW
MSL1_ACYPI      -----TCSS---------------------------------------------------
                     **:.

MSL1_DROME      VAFKKKDKEHESVPESPEVPKQQPHQEDAIVDHNAIKNQLEVPKPDLKPKDQPKDEQRQD
MSL1_ACYPI      ----------------------------GIGDLSLAEKQYQQEHQHIKPK----------
                                            .* * .  ::* :  :  :***

MSL1_DROME      GQLDVRVEPQEDVRKVQKETLKRQPEDAPKHLPKAVAPKVTKTSSRESTLPKANTADIKD
MSL1_ACYPI      -------------KRTIRQAATKQPNPDP--------LESNQTKRRRTSIPQTKSAKLKN
                             ... .:: ..**:  *         : .:*. * :::*::::*.:*:

MSL1_DROME      APAQKVIANHQSTKT---QTDPVKTQRLQVKIRQYEMHPDMRTGSSAPSDIRKQKNVDPV
MSL1_ACYPI      TEELSLITADDAYYTCLGSYDPIKS--------------------------------NPV
                :   .:*:  ::  *   . **:*:                                :**

MSL1_DROME      STPETKTIKSKSMLVNDKKTTSETSQSPDQEIDVETVRRKLAEHLKKELLSQSHSSQVTL
MSL1_ACYPI      SKNTKRNI----------------------------------------------------
                *.  ...*

MSL1_DROME      KKIRERVATNLIYPPPSAPVSSTTITPAPTPSTTPTPGSTPQHAVTSSMDQEISAAKSKS
MSL1_ACYPI      ------------------------------------------------------------


MSL1_DROME      KAAEQIATPLTPQSNSSVSSTTSTIRKTLNNCSPHTYSKATARSGKLQSRFRTATFPYST
MSL1_ACYPI      ------------------------------------------------------------
```

```
                                             PEHE
MSL1_DROME      RTWEDQEFHCDNEFFLEEADELLADNPSLEIPKWRDVPVPPSSDKIDTELLSDATFERRH
MSL1_ACYPI      -----------------------------EIPNYRLKKYSCRNSAKGIELMSDAIFQKRH
                                             ***::*    .  ..  . **:*** *:.**

MSL1_DROME      QKYVKDEVDRKCRDARYMKEQIRLEQLRMRRNQDEVLVALDPLRA--STFYPLPEDIEAI
MSL1_ACYPI      FKHERSEQICKRRDLRQIRELIRVENLRKGRNKHHSQKSNDNNKEELTTLLPSPSNIKSI
                 *: ..*   * ** * :.* **:*:**  **:     : *  .   :*: * *.:*::*


MSL1_DROME      QFVNEVTVQAFGENVVNMEARDDFGVPWVDAIEAPTSIARSKALAEPVATLASKKIPTTA
MSL1_ACYPI      EITNKLPVSAFGINLYRLTC----------------------------------------
                ::.*::.*.*** *: .: .

MSL1_DROME      AEARHQENHSSYVFPKRRKRQKNR
MSL1_ACYPI      ------------------------
```

MSL2 (ACYPI49193)

```
MSL2_DROME      MAQTAYLKVTRIAMRSASNLSKRRVEELNSGLGELRQLLSCVVCCQLL--VDPYSPKGKR
MSL2_ACYPI      MALIEYYLSTSQIVLQAKSTDPLTWQKLHSLLPLLHEHLSCQVCHKLVDRLNPY------
                **   *   *   : .*.. .    ::*:* *  *.: *** ** :*:  ::**

                                   zf-RING10
MSL2_DROME      CQHNVCRLCLRGKKHLFPSCTQCEGCSDFKTYEENRMMAAQLLCYKTLCVHLLHSALFGE
MSL2_ACYPI      LDGYACTVCVNHQITENPS-------------------SAIIQCYKKLCAYIHSSPLYKV
                 :  .* :*:. :    **                   :* : ***.**.::  *.*:

MSL2_DROME      LAGMRPQVARELVPRIKLPPKTTQEFIREGSNISDTFDIFLPQPDLPFLKDMPTSLPAET
MSL2_ACYPI      MC-------------TRVEDKRLVELVTE-------------------------------
                :.              .:  *   *:: *

MSL2_DROME      PPTSAVTTPELPYDHHLNISDIEAEAAATAEQGHFSPLPLLPTGSRMGMLSHAGQIVIAT
MSL2_ACYPI      --------------------------------------------------------VISL
                                                                        **:

MSL2_DROME      ESSESGFMDQAWTDQVDLSGTVSVSKYTNSGNNFAVSYVMPTSATTKFDPQELQIGQVVQ
MSL2_ACYPI      PRSINGY-----------SGMVN--------------------------------GTVIK
                  * .*:           ** *.                                * *::

MSL2_DROME      MADSTQLAVLAAVEETVETSTQLTVLSTTVEETVETSTQLEVLTSAEEPNEISDQLANLQ
MSL2_ACYPI      QEKK---------EKDIEDDSTLMVNGTMNKQEIK-------------------------
                  ..         *: :* .: * * .*  :: ::

MSL2_DROME      VEESDEALVEETVEEAEGTSIPSEVVAEHMEEDQHLDVHTSQSPTQTEMEEAVEEHVATK
MSL2_ACYPI      ----EEDIEDDSTLMVNGTMNKQEIKEEDIEDDFTLMVNGIMNKQEIKEENSKDDI----
                    :* : :::.  .:**   .*:  * :*:*  * *:   .  : : *:: ::

MSL2_DROME      TQLGHVQTELQDAESLQKDFEDAKAAAEEAKEKEKDLHAISAELQKEDSDEPTLKRKRTR
MSL2_ACYPI      TLISSSDIQLPTVNETPEDYINYQIFDVQSQ-----------------------------
                * :.  : :*  .:.  :*: : :    :::

MSL2_DROME      TLKASQAAKIEPVPSEVKTKVQSGKGALRRIRGKDKEEKVKPPKPKCRCGISGSSNTLTT
MSL2_ACYPI      -----------------KHKIQN-QSVFNNIPKKKKNER----RWGCRCGNATTTPGKLT
                                 * *:*. :..:..*  *.*:*.    .  **** : ::    *

                           MSL2-CXC
MSL2_DROME      CRNSRCPCYKSYNSCAGCHCVCCKNPHKEDYVESDEDDDLEDFEMPKDVPEPMTQSEEPV
MSL2_ACYPI      CFGQRCPCYTEQKPCDQCKCRGCRNPRQK---RSNNDDNLE-------------------
                * ..*****.. :.*  *:*  *.**.::    *::**:**
```

```
MSL2_DROME      VAEPRQEENSMAPPDSSAPISLVPLNNLQQSQHPLVLVQNEKGEYQGFNIFQGSKPLDPV
MSL2_ACYPI      IDQIRRK-----------PVTLELVSSLKPSSH-----NNSNSLFSAYTMHD--------
                : : *.:           *::*  :..*: *.*     :*.:. :..:.:.:

MSL2_DROME      TVGFTIRVQLQHTDGFGSLPQYAYIMPTIDPPNPPAPSLSPPPPPAPDREVIEPPAKKFR
MSL2_ACYPI      MLQFS-----SHSQQFD-------------------------------------------
                 : *:     .*:: *.

MSL2_DROME      TSRTRRGRANFSALDTVDELVSGGSRSNSAAGDRSSATDNAHSLFEEIMSGSDDL
MSL2_ACYPI      ---------------------QGGTEDN---------LGHVNSIFHSP--------
                                     .**: .*          .:.:*:* .
```

MSL3 (ACYPI000966)

```
MSL3_DROME      MTELRDET-PLFHKGEIVLCYEPDKSKARVLYTSKVLNVFERRNEHGLRFYEYKIHFQGW
MSL3_ACYPI      MAAKKVLTKSKFEEGEKVLCYEPDPAKTKVLYDSKVLRVVPEKDEQGRKFCKFLIHFQGW
                *:  .  * . * :** ******* :*:.*** ****.*.  .:*:* .* :: ******

MSL3_DROME      RPSYDRCVRATVLLKDTEENRQLQRELAEAAKLQIRGDYSYKGTPDKPSAKKKRGGKAAH
MSL3_ACYPI      NSTWDRFVTDEFILKDTEENRKLQKELAEEAQLTPGGNL-YRKERKKRAVKLE---PKPL
                ..::** *   .:********:**.**** *:*   *:  *.   .* :.* :     .

MSL3_DROME      VEEPIVVPMDTGHLEAEHEMAPTPRAAGNRTRDNSGGKRKEKPPSGDGRLKGNRGRQTET
MSL3_ACYPI      VIEPAVVTIDDKSM-VENENVPVP------------------------------------
                * ** **.:*   : .*:* .*.*

MSL3_DROME      FYNNAINDVSVYNHVPQEDRIMMRVSERLRELIEYDRNMIKVLGKQHALPARVPIVTIME
MSL3_ACYPI      -----IDTI----LLPKRRLPDLEFPDNLKFHTGYNCYLVHEKNTLVQLPCQPNVVTLLE
                     *: :     :*:     : ..:.*.    *:  :::  ..   **..  :**::*

MSL3_DROME      NFVKQQAVELAISIKQDSSRARNTQSRNARMEREYDRVMSTVCMLKEVVDGLRIYFEFHV
MSL3_ACYPI      SYLRYLARNNFSDNKTTKKKRQPEVLDKKQLEKRY-----IICV--EVLDGLRICFNTFL
                .::.  * :   . *  ... .     : .:*. *      :*:  **:***** *: .:

                                            MRG
MSL3_DROME      DDHLLYTEEKE---YVHNYLTDDNMRNCSLILNKSYEYINPSGDTELIGLDGTPVVEGSG
MSL3_ACYPI      FRKLLVNEDEQAQYYEALKVTLQPPVNNIIPQNGEQDYDNVPNDEESESHDNKNNVKAKR
                  :** .*:::   *    :* :   *  :  * . :* * ..* *  . *..  *:..

MSL3_DROME      DTNGQIGVINIGGPEYEKQLQKCLLYIVTAS--GKNTAQAYERTSPYTAAYKLPVEMRGF
MSL3_ACYPI      DNTRS------STSQYASSQQTCSDCSLTKSQCSKIVKDTFEKARD------------EY
                *.. .      . .:* .. *.*    :* *  .* . :::*.:               :

MSL3_DROME      LNETFKWRLLS----AESPPEKSMVFGAPHLVRLMIKMPMFLNASPISNKKLEDLLPHLD
MSL3_ACYPI      VSKADSWKAVPDSAYDEEIKQPAVVYGVYHLLRLLENLPKILANTEVDGEKLSIVYLYSN
                :.:: .*. :.     *.  : ::*:*. **:**: ::* :*  : :..:**. :  : :

MSL3_DROME      AFINYLENHREWFDRENFVNSTALPQEDLQRELLDSLDGIAA
MSL3_ACYPI      GLLKYLSTQTYLFGMQYYVKNEMEDAVKSSAPIRNHRNHKNI
                .:::**..:   *. : :*:.      . .  : :  :
```

MOF (ACYPI002102)

```
MOF_DROME        MSEAELEQTPSAGHVQEQPIEEEHEPEQEPTDAYTIGGPPRTPVEDAAAELSASLDVSGS
MOF_ACYPI        -----------------------------------------MVVHHSATSVSMEVD----
                                                            *  :*:.:* .:*

MOF_DROME        DQSAEQSLDLSGVQAEAAAESEPPAKRQHRDISPISEDSTPASSTSTSSTRSSSSSRYDD
MOF_ACYPI        ------------------------------------------------------------


MOF_DROME        VSEAEEAPPEPEPEQPQQQQQEEKKEDGQDQVKSPGPVELEAQEPAQPQKQKEVVDQEIE
MOF_ACYPI        ------------------------------------------------------------


MOF_DROME        TEDEPSSDTVICVADINPYGSGSNIDDFVMDPDAPPNAIITEVVTIPAPLHLKGTQQLGL
MOF_ACYPI        ------------------------------------------------------------


MOF_DROME        PLAAPPPPPPPPAAEQVPETPASPTDDGEEPPAVYLSPYIRSRYMQESTPGLPTRLAPRD
MOF_ACYPI        ----------PPRNANSPDDPKT-------------------------------------
                           **   : *: * :

MOF_DROME        PRQRNMPPPAVVLPIQTVLSANVEAISDDSSETSSSDDDEEEEEDEDDALTMEHDNTSRE
MOF_ACYPI        --------------------------ANGSSENEKAEDSESSEDG---------------
                                           ::.***...::*.*..*:.

                                                  Tudor-knot
MOF_DROME        TVITTGDPLMQKIDISENPDKIYFIRREDGTVHRGQVLQSRTTENAAAPDEYYVHYVGLN
MOF_ACYPI        -----------PLDVGEH----YLVRRYDDSWHPAEVLHTRFNDTEHLF-EYYVHYEGYN
                             :*:.*:    *::** *.: * .:**::* .:.     ****** * *


MOF_DROME        RRLDGWVGRHRISDNADDLGGITVLPAPPLAPDQPSTSREMLAQQAAAAAAASSERQKRA
MOF_ACYPI        RRLDQWVPRDRIMNSRFDI--------------------------------SEKNWKQKD
                 **** ** * ** :.  *:                                :..:.::.

MOF_DROME        ANKDYYLSYCENSRYDYSDRKMTRYQKRRYDEINHVQKSHAELTATQAALEKEHESITKI
MOF_ACYPI        VNKNLDL-------LNQSDRKITRNQKRRHDEINHVPMSYAEMDPTTAALEKEHEAITKI
                 .**:  *        : ****:** ****:******  *:**: .* ********:****


MOF_DROME        KYIDKLQFGNYEIDTWYFSPFPEEYGKARTLYVCEYCLKYMRFRSSYAYHLHECDRRRPP
MOF_ACYPI        KYINKVQLGKYEIDTWYFSPFPAEYQKESKIWICEYCLKYSKLEKSFKYHMSQCTWRQPP
                 ***:*:*:*:************ ** *  .:::******* .: .*: **: :* .*.**


MOF_DROME        GREIYRKGNISIYEVNGKEESLYCQLLCLMAKLFLDHKVLYFDMDPFLFYILCETDKEGS
MOF_ACYPI        GVEVYHKGSLSIWEVNSSQHKMYCQNLCLLAKLFLDHKTLYFDVEPFLFYILCEVDKVGA
                 * *:*.**.:**:***..: .:*** ***:********.****::*********.** *:

                                           MOZ-SAS
MOF_DROME        HIVGYFSKEKKSLENYNVACILVLPPHQRKGFGKLLIAFSYELSRKEGVIGSPEKPLSDL
MOF_ACYPI        HLVGYFSKEKDSPDCNNVACILTMPPFQRQGYGKLLIAFSYELSKLEGLVASPEKPLSDL
                 *:********.* :  ******.:**.**:*:************. **::.*********


MOF_DROME        GRLSYRSYWAYTLLELMKTRCAPEQITIKELSEMSGITHDDIIYTLQSMKMIKYWKGQNV
MOF_ACYPI        GKLSYRSYWSWVLLEILKNACGS--LSIKDLSAMTSITQTDIISTLQSMNMVKYWKGQHV
                 *.*******::.***::*. *..  ::**:** *:.**: *** *****:*:******:*

MOF_DROME        ICVTSKTIQDHLQLPQFKQPKLTIDTDYLVWSPQT------AAAVVRAPGNSG
MOF_ACYPI        ICVTPKNVEQLVSSEQYKRPRFILEGSAIKWTPKKYNPRPGPSRHSRSQYLAG
                 ****.*.::: :.  *:*.*.: :: . : *:*:.      .:   *:   :*
```

MLE (ACYPI003650)

```
MLE_DROME       ------------------------------------------------------------
MLE_ACYPI       MANPKAYLHEWCAKNNLELQFETKQAGSNCKPRLFICEVTVTGHNYIGVGNSTNKKLAQA


MLE_DROME       ------------------------------------------------------------
MLE_ACYPI       NASKDYLLYLTKEGLISIDTYFLPSNCISGPASNGLMVNASQQLMNNVPPKSEYEEETSN


MLE_DROME       ------------------------------------------------------------
MLE_ACYPI       ILGEAYRPNEKTNFQLNDFLNDENNVEEAEGLNLHAAVCGDWTIDNAKSHLNQFIQSNKL

                                                  dsrm
MLE_DROME       --------MDIKSFLYQFCAKSQIEPKFDIRQTGPKNRQRFLCEVRVEPNTYIGVGNSTN
MLE_ACYPI       KNIDYKYSCNPKTFLHEWCEKNNLEPQFKTKQAGSNRKPRFICEVIITGHDYIGIGNSAN
                         : *:**:::* *.::**:*. .*:*.:.. **:*** :  : ***:***:*

MLE_DROME       KKDAEKNACRDFVNYLVRVGKLNTNDVPADAGASGGGPRTGLEGAGMAGGSGQQKRVFDG
MLE_ACYPI       IKYAQENASKDFLLYLTRKGLVSTDSLASNC-ISGPASNDLMVNASQKLMNVPPKSVYQD
                 * *::**..**: **.* * :.*:.:.::.  ** ...  : .*.    .   * *::.

MLE_DROME       QSGPQDLGEAYRPLNHDGGDGGNRYSVIDRIQEQRDMNEAEAFDVNAAIHGNWTIENAKE
MLE_ACYPI       HETPKMLGESYRPV------GKANFQFNDFLNDENNVEEAEHLDVNAAVHGGWTIDNAKS
                :. *: ***:***:      *  .:.. * ::::.:::*** :*****:**.***:***.

MLE_DROME       RLNIYKQTNNIRD-DYKYTPVGPEHARSFLAELSIYVPALNRTVTARESGSNKKSASKSC
MLE_ACYPI       RLNQFIQSNKLKNTDYKYSFIG----KSHVAELSIYIAKLGRNVTARESGLNKRSASTSC
                *** : *:*::.: ****: :*    .*.:******:. *.*.******* **.***.**

MLE_DROME       ALSLVRQLFHLNVIEPFSGTLKKKKDEQLKPYPVKLSPNLINKIDEVIKGLDLPVVNPRN
MLE_ACYPI       ALSFIRQLYHLGVIEPFSGSLKKSILNTVKPYEVNVDPLILNKVYNILQEFNIEPVIKND
                ***::***:**.*******:***.  : :*** *::.* ::**: :::: :::  *  .:

MLE_DROME       IKIELDGPPIPLIVNLSRIDSSQQDGEKRQESSVIPWAPPQANWNTWHACNIDEGELATT
MLE_ACYPI       TIIEPE-TTISLISNQKLAEFKELKPIKL--SRAILWSPPQPNWNPWLAINIDEGPLATA
                  ** : ..*.** * .  : .: .  *   * .* *:***.***.* * ***** ***:


MLE_DROME       SIDDLSMDYERSLRDRRQNDNEYRQFLEFREKLPIAAMRSEILTAINDNPVVIIRGNTGC
MLE_ACYPI       TLDQLSEELAKDYTKKLNSSKGFKESIEMRSQLPVFNKKNEILDIIRKNSIVIIQGSTGC
                ::*:** :  ..  .. :..: :.: :*:*.:**:   ..***  *..*.:***.*.***

                                              DEAD
MLE_DROME       GKTTQIAQYILDDYICSGQGGYANIYVTQPRRISAISVAERVARERCEQLGDTVGYSVRF
MLE_ACYPI       GKTTQVCQFILDEYLKNDQGAYCNIICTQPRKISAISIADRVAFERKEDIGLSVGYSVRF
                *****:.*:***:*: ..**.*.**  ****.*****:*:*** ** *::* :*******


MLE_DROME       ESVFPRPYGAILFCTVGVLLRKLEAGLRGVSHIIVDEIHERDVNSDFLLVILRDMVDTYP
MLE_ACYPI       DSIFPRSTGAILFCTVGVLLRKLENGMRGISHVIVDEIHERGVNSDFLMVVLKDMVYNYP
                :*:***. **************** *:**:**:********.******:*:*.*** .**


MLE_DROME       DLHVILMSATIDTTKFSKYFGICPVLEVPGRAFPVQQFFLEDIIQMTDFVPSAESRRKRK
MLE_ACYPI       DLRVIFMSATINTAMFSKYFNCCPVIDIKGRCYPVKEYFLEDIVQVLNYQPTPDIKKRMN
                **.**:*****:*: *****. ***::: **.:**:::*****:*: :: *:.: ... :


MLE_DROME       EVEDEEQLLSEDKDEAEINYNKVCEDKYSQKTRNAMAMLSESDVSFELLEALLMHIKSK-
MLE_ACYPI       KDYDDEYVI--DAQDHEENCNLLVSDDYPPEVKSKVALISEKYVDFEIIEALLTHIEIKM
                :  *:* ::  * :: * * * : .*.*. :... :*::**. *.**::**** **: *
```

```
                                        Helicase C
MLE_DROME       NIPGAILVFLPGWNLIFALMKFLQNTNIFGDTSQYQILPCHSQIPRDEQRKVFEPVPEGV
MLE_ACYPI       NIPGAVLIFLPGWTLISALQKYLTEKQFFA-SSKFCVLPLHSQLPCADQRRVFEPVPSGV
                *****:*:*****.** ** *:* :.::*. :*:: :** ***:*  :**.******.**

MLE_DROME       TKIILSTNIAETSITIDDIVFVIDICKARMKLFTSHNNLTSYATVWASKTNLEQRKGRAG
MLE_ACYPI       RKVILSTNIAETSITIDDVVFVINYGKAKIKFFTSHNNMTHYATVWASKTNMQQRKGRAG
                 *:***************:****:  **.:*:******:* **********::*******

MLE_DROME       RVRPGFCFTLCSRARFQALEDNLTPEMFRTPLHEMALTIKLLRLGSIHHFLSKALEPPPV
MLE_ACYPI       RVSDGFCFHLCTKARYDKMDDHVTPEMFRSPLHEIALSIKLLRLGDIGQFLSKAIEPPPI
                **  **** **:.**:: ::*::******:****:**:*******.* :*****:****:

MLE_DROME       DAVIEAEVLLREMRCLDANDELTPLGRLLARLPIEPRLGKMMVLGAVFGCADLMAIMASY
MLE_ACYPI       DAVNEALVMLKEMKCLGINEELTPLGRILAKLPVEPQIGRMMVLGNILMLGDAFAIIAAI
                *** ** *:*.**.**. *:*******:**.**:**.:*.***** ::  .* :**:*:

                                           HA2
MLE_DROME       SSTFSEVFSLDIGQRRLANHQKALSGTKCSDHVAMIVASQMWRREKQRGEHMEARFCDWK
MLE_ACYPI       CSNMTDIFVFD---HRMTPAQRAFSGNRCSDHLALLNAFQQW-QSLDYCNINPTEYCERK
                .*.::::* :*   .*::  *.*:**..****:*:: * * * .. :  :   : :*:.*

MLE_DROME       GLQMSTMNVIWDAKQQLLDLLQQAGFPEECMISHEVDERID-GDDPVLDVSLALLCLGLY
MLE_ACYPI       MLSEPSLTTTADAMEQLKDLFIKIGFPEICFEKQRFDFGVEMHDDPLLDVVSAILTMGFY
                 *. .::..  ** :** **: : **** *: .: .*  ::  ***:***  *:* :*:*

                                        OB NTP BIND
MLE_DROME       PNICVHKEKRKVLTTESKAALLHKTSVNCSN-LAVTFPYPFFVFGEKIRTRAVSCKQLSM
MLE_ACYPI       PNVCYHKVKRKVYTTEGKFALIHKTSVNCNNTMDGSFQSPFFVFAEKVRTTAVSCKQMTM
                **:* ** **** ***.* **:*******.* :  :*  *****.**:** ******::*

MLE_DROME       VSPLQVILFGSRKIDLAANNIVRVDNWLNFDIEPELAAKIGALKPALEDLITVACDNPSD
MLE_ACYPI       VTPIHLLLFGARKIEY-TKELVQLDNWINLKMDVTAASAIVALRPAIESLIVHASEEPGS
                *:*::::***:***:  ::::*.:***:*:.::   *: * **.**:*.**. *.::*..

MLE_DROME       ILRLEEPYAQLVKVVKDLCVKSAGDFGLQRESGILPHQSRQFSDGGGPPKRGRFETGRFT
MLE_ACYPI       IAMLSETDIKLINVLKELCNFNCGRYNLSPIT---------FVQGDRPNYRRPF------
                *  *.*.  :*::*:*:**  ..* :.*.  :         * :*. *  *  *

MLE_DROME       NSSFGRRGNGRTFGGGYGNNGGGYGNNGGGYGNIGGGYGNNAGGYGNNGGYGNNGGGYRN
MLE_ACYPI       NQTFNESGDAS------DNKVQHINHSHSSYNSFQRG---GRGRYNEGIGYRGNSSSLCD
                *.:*.  *:.       .*:    .:. ..*..:  *    . * *.:. ** .*...  :

MLE_DROME       NGGGYGNNGGGYGNKRGGFGDSFESNRGSGGGFRNGDQGGRWGNF
MLE_ACYPI       EYNQRTYHDGGRSVREQGF-----TGYRSENGFKRC--------F
                : .    :.** . .  **     :.  * .**..         *
```