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                                   .   *** *** *::*** *** ****:****:*   ::*:**:*:.:*::**:***:.**:*:    :     .
CanF_MEF2A     MGRKKIQIQRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
MacM_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
PanT_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
SusS_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESGTNSDIVEALNKKEHRGCDSPD   100
EquC_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKEHRGCDSPD   100
PonA_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
HomS_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
CalJ_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
AilM_MEF2A     VNTVKIPETRVTEAQAHRVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
MusM_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
DanR_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEKLRNKGHNDCPSPD   100
GalG_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
RatN_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKEHRGCDSPD   100
BosT_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKEHRGCDSPD   100
MonD_MEF2A     MERSDKLVSRKMGER-REVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD    99
XenL_MEF2A     MGRRKIQITRIMDDRNKQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKENRGCDSPD   100
OrnA_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
TaeG_MEF2A     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD   100
OryC_MEF2A     -----------MDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPD    89
CanF_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
MacM_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
PanT_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKENKGCESPD   100
SusS_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
EquC_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
PonA_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
HomS_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLNKKENKGCESPD   100
CalJ_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
AilM_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
MusM_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
GalG_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
RatN_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
BosT_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
XenT_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
MonD_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
XenL_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
OrnA_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
TaeG_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
OviA_MEF2C     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
OryC_MEF2C     FGYTKVEEHRKVNTNSLMVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
DanR_MEF2Ca    MGRKKIQIARIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
DanR_MEF2Cb    MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCDSPD   100
CanF_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
MacM_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
PanT_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
SusS_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
EquC_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
PonA_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
HomS_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
CalJ_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
AilM_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKK-----DSPE    95
MusM_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
DanR_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIEALNKKEHRDSESPD   100
GalG_MEF2D     WGAKLLSMLGSGDIQAAAVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
RatN_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
BosT_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
XenT_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
MonD_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
TaeG_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
OryC_MEF2D     MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
XenL_MEF2Db    MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
XenL_MEF2Da    MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
CanF_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRRGVGLDGPE-    99
MacM_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRRGIGLDGPE-    99
PanT_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRRGIGLDGPE-    99
EquC_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRRGVGLDGPE-    99
PonA_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRRGIGLDGPE-    99
HomS_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRRGIGLDGPE-    99
CalJ_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRRGIGLDGPE-    99
AilM_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRRGVGLDGPE-    99
MusM_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCDIALIIFNSAQRLFQYASSDMDRVLLKYTEYSEPHESRTNADILQTLKRRGVGLDGPE-    99
RatN_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCDIALIIFNSAQRLFQYASSDMDRVLLKYTEYSEPHESRTNADILQTLKRRGVGLDGPE-    99
BosT_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNRLFQYASTDMDRVLLKYTEYSEPHESRTITDILETLKRRGVGLDGPE-    99
MonD_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRKGLGLESQE-    99
OrnA_MEF2B     MGRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTEYSEPHESRTNTDILETLKRKGLGLESQE-    99
DroMel_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroSim_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroAna_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroEre_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroGri_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroMoj_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroPer_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroSec_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroVir_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroWil_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroYak_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
DroPse_MEF2    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPE   100
AnoG_MEF2      MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDKVLLKYTEYNEPHESLTNKNIIEKENKNGTMSPDSPE   100
CulQ_MEF2d     MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDKVLLKYTEYNEPHESLTNKNIIEKENKNGTMSPDSPE   100
AedA_MEF2d     MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSTNKLYQYASTDMDKVLLKYTEYNEPHESLTNKNIIEKENKNGTMSPDSPE   100
TriC_MEF2      MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDKVLLKYTEYNEPHESLTNKNIIEKEHKNGVMSPDSPE   100
ApiM_MEF2      MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDKVLLKYTEYNEPHESLTNKNIIEKEHKGAMSPESPEP   100
BomM_MEF2      MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSNNKLYQYASTDMDKVLLKYTEYNEPHESLTNRNIIEALTKKEHKNGVMSP   100
CioI_MEF2      MGRKKIQISRIGDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIEMLNKKDNKNCDSPD   100
BraF_MEF2      MGRKKIQIARIDDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKEHKGGESPD   100
CaeB_MEF2      MGRKKIQITRIQDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIVFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNNDIMDALNRKEGNNGGGGS   100
CaeE_MEF2      MGRKKIQITRIQDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIVFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNNDIMEALNRKEGNQGGGNS   100
CaeR_MEF2      MGRKKIQITRIQDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIVFNSTNKLFQYASTDMDKVLLKYTEYNEPHESRTNNDIMEALNRKEGNQGGGGS   100
NasV_MEF2d     MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDKVLLKYTEYNEPHESLTNKNIIEALNKKEHKGAMSPE   100
SacK_MEF2      MGRKKIQISRINDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNHDIIEALNKKENKGCESPE   100
GalG_MEF2      MGRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTEYNEPHESRTNADIIETLRKKGFNGCDSPE   100
PhyI_MEF2      MGRKKIQIKRIEDDRNRQVTFAKRKNGIFKKAMELSKLCDCEIALIVFDSNEKLYQYSSTSVDQILLKYTEYGEPYETKDNNDYEIMFGE----------    90
SchM_MEF2a     MGRKKILIKKITDERNRQVTFTKRKLGLMKKAYELSILCDCEIALIVFTSSQKLFQYASSDMDKILLRYTEFNEPHESKTNRDIAELINRKEGKFSYLSD   100
               1.......10........20........30........40........50........60........70........80........90.......100
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CanF_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLADSSMLSPPQATLHRN-   188
MacM_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLTDSSMLSPPQTTLHRN-   188
PanT_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLTDSSMLSPPQTTLHRN-   188
SusS_MEF2A   P--DTYVL-TPHTEEKYKKINEEFDNMM---------RNHKPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLADSSMLSPPQATLHRN-   187
EquC_MEF2A   P--DTYVL-TPHTEEKYKKINEEFDNMM---------RNHKPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLADSSMLSPPQATLHRN-   187
PonA_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLTDSSMLSPPQTTLHRN-   188
HomS_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLTDSSMLSPPQTTLHRN-   188
CalJ_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLTDSSMLSPPQSTLHRN-   188
AilM_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLADSSMLSPPQATLHRN-   188
MusM_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLADSSMLSPPPATLHRN-   188
DanR_MEF2A   P--DDCFGHSPLMDDRFGKLNEESDLMY---------KRGPTALPPQNFSMHVAVPVTNPNAMSY-NPGASLSSQSLAAAASLSDGAMLSPPQGSMHRS-   187
GalG_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPAQNFSMSVTVPVSNPNTLTYSNPGSSLVSPSLAASSSLTSTTMLSPPQTTLHRN-   188
RatN_MEF2A   P--DTYVL-TPHTEEKYKKINEEFDNMM---------RNHKPGLPPQNFSMSVTVPVTSPNALSYTNPGSSLVSPSLAASSTLAESSMLSPPPATLHRN-   187
BosT_MEF2A   P--DTYVL-TPHTEEKYKKINEEFDNMM---------RNHKPGLPPQNFSMSVTVPVTSPSALSYTNPGSSLVSPSLAASSALADTSMLSPPQATLHRN-   187
MonD_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTNHNALTYTNPGSSLVSPSLAASSSLTDTSMLSPPQATMLRN-   187
XenL_MEF2A   P--DGYVL-TPHTEEKYKKINEEFDNMM---------RSHKPGLPQQTFPMSVTVPVSNPNTLPYSSPGNTMVTASLAASASLTDARMLSPPPTTLHRN-   187
OrnA_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTNPNALSYSNPGSSLVSPSLAASSSLADTSMLSPPQATLHRN-   188
TaeG_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPAQNFSMSVTVPVSNPNTLTYSNPGSSLVSPSLAASSSLTDTTMLSPPQSSLHRN-   188
OryC_MEF2A   --ADDYFEHSPLSEDRFSKLNEDSDFIF---------KRGPPGLPPQNFSMSVTVPVTSPSALPYSNPGNSLVSPSLAASSTLADSSMLSPPQATLHRN-   177
CanF_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
MacM_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
PanT_MEF2C   PD-SSYAL-TPRTEEKYKKINEEFDNMI--------KSHKIPAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   179
SusS_MEF2C   PDADDSVGHSPESEDKYRKINEDLDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
EquC_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
PonA_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
HomS_MEF2C   PD-SSYAL-TPRTEEKYKKINEEFDNMI--------KSHKIPAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   179
CalJ_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
AilM_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
MusM_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPSFEMPVTIPVSSHNSLVYSNPVSTLGNPNLL---PLAH--------PSLQRNS   181
GalG_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSNHSSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
RatN_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVTIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
BosT_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
XenT_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSNPNSLAYSNPAVSLGNHNLL---PLSH--------PSLHRNS   181
MonD_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSNHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
XenL_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSNPNSLIYSNPAGSLGNHNLL---PLSH--------PSLHRNS   181
OrnA_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSNHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
TaeG_MEF2C   PDADDSVGHSPESEDKYRKLNEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSNHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
OviA_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
OryC_MEF2C   PDADDSVGHSPESEDKYRKINEDIDLMI--------SRQRLCAVPPPNFEMPVSIPVSSHNSLVYSNPVSSLGNPNLL---PLAH--------PSLQRNS   181
DanR_MEF2Ca  IDAEDS-GHSPESEDKYRKINEDIDLMI--------SRQRLCAIPQSNYDMPVSIPVSNPNSLIYGHPGASLGNPNLL---PLTH--------PSLQRNS   180
DanR_MEF2Cb  PDADDSVGHSPESKDKYREINDDIDLMI--------SRQRICAVPSSTYDM--TIPVNNQ---IY--PG----NHNLL---PLAH--------HGLQRNS   170
CanF_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
MacM_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
PanT_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
SusS_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
EquC_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
PonA_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
HomS_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSTVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
CalJ_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
AilM_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSSQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   185
MusM_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSSVPAPNFAMPVTVPVSNQSSMQFSNPSSSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
DanR_MEF2D   PEE--PFSLTPRTEEKYKKIDEEFDKMM---------QSYRSTVPAPTFSMPVTVPVSNQSPLPFSNPS-SLVTTSFVTSTLTDPRLLSPQQ-PQLQRNT   187
GalG_MEF2D   PDGDDSIDQSPLMEDKYRKGSEDLDILF---------KRYGSAVPTPNFAMPVTVPVTNQNTLQFSSPGSSLVTQSLVTSSLTDPRLLSPQQ-PTLQRNT   190
RatN_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSSVPAPNFAMPVTVPVSNQSSMQFSNPSSSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
BosT_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSSQSSLQFSNPSGSLATPSLVTSSLTDPRLLSPQQ-PALQRSS   190
XenT_MEF2D   PDGDDSIDQSPLMEDKYRKASEDLDILF---------KRYGSAVPAPNFAMPVTVPVTNQNALQFSNPGGSLVTQSLMTSSLTDPRLLSPPQ-PALQRNT   190
MonD_MEF2D   PDGEDSLEQSPLLEDKYRPASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQNSLQFSNPGGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
TaeG_MEF2D   PDGDDSIDQSPLMEDKYRKGSEDLDILF---------KRYGSTVPAPNFAMPVTVPVTNQNTLQFSNPGSSLVTQSLVTSSLTDPRLLSPQQ-PALQRNT   190
OryC_MEF2D   PDGEDSLEQSPLLEDKYRRASEELDGLF---------RRYGSAVPAPNFAMPVTVPVSNQSSLQFSNPSGSLVTPSLVTSSLTDPRLLSPQQ-PALQRNS   190
XenL_MEF2Db  PDGDDSIDQSPLMEDKYRKTSEDLDILF---------KRYGSAVPAPNFAMPVTVPVTNQNSLHFSNPGGSLVTQSLMTSSLTDPRLLSPPQ-SALQRNT   190
XenL_MEF2Da  PDGDDSIDQSPLMEDKYRKSSEDLDILF---------KRYGSAVPAPNFAMPVTVPVTNQNALHFSNPGGSLITQSLMTSSLTDPRLLSPPQ-PSLQRNT   190
CanF_MEF2B   ----------LEPDEGPEGPGEKLRRLA--------GDGGDPALPR-----------------------------------------PRL--YPAAPTMPSPD   141
MacM_MEF2B   ----------MEPDEGPEEPGEKFRRLA--------GEGGDPALPR-----------------------------------------PRL--YPAAPAMPSPD   141
PanT_MEF2B   ----------LEPDEGPEEPGEKFRRLA--------GEGGDPALPR-----------------------------------------PRL--YPAAPAMPSPD   141
EquC_MEF2B   ----------LDPDEGPEGPGEKLRRLA--------GDGGDPALPR-----------------------------------------PRL--YPAAPTMPSPD   141
PonA_MEF2B   ----------LEPDEGPEEPGEKFRRLA--------GEGGDPALPR-----------------------------------------PRL--YPAAPAMPSPD   141
HomS_MEF2B   ----------LEPDEGPEEPGEKFRRLA--------GEGGDPALPR-----------------------------------------PRL--YPAAPAMPSPD   141
CalJ_MEF2B   ----------LEPDEGPEEPGEKFRRLA--------GEGGDPALPR-----------------------------------------PRL--YPAAPAMPSPD   141
AilM_MEF2B   ----------LEPDEGPEGPGEKLRRLA--------GDGGDPTLPR-----------------------------------------PRL--YPAAPTMPSPD   141
MusM_MEF2B   ----------LDMEEGPEGPGEKLLRTL--------GGDRGSASPP-----------------------------------------PRI--YPVAPAMSVSE   141
RatN_MEF2B   ----------LDMEEGPEGPGEKLLRTL--------GGDRGLVSPP-----------------------------------------PRI--YPVAPAMSVSE   141
BosT_MEF2B   ----------LEPDEGLEGPGEKLRRLA--------GDGGDPALPR-----------------------------------------PRL--YPAAPTMPSPD   141
MonD_MEF2B   ----------LELEEGLVEPGEKLRRLG--------GDGADLALVR-----------------------------------------PRF--YSATPALPSPD   141
OrnA_MEF2B   ----------LELDEGPAEPAEKLRRL----------SDGVDLSLTR-----------------------------------------QRL--YSAAPPLPSHN   140
DroMel_MEF2  AET--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGGAGAPRQLPNSSYTLPVSVPVPGSYGDNLLQASPQMSHTNISPRPSSSETDSIYPSGSMLEM-S   197
DroSim_MEF2  AET--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGGAGAPRQLPNSSYTLPVSVPVPGSYGDNLLQASPQMSHTNISPRPSSSETDSVYPSGSMLEM-S   197
DroAna_MEF2  AET--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGGAGAPRQLPNSSYTLPVSVPVPGSYGENLLQASPQMSHTNISPRPSSSETDSVYPSGSMLEM-S   197
DroEre_MEF2  AET--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGGAGATRQLPNSSYTLPVSVPVPGSYGDNLLQASPQMSHTNISPRPSSSETDSVYPSGSMLEM-S   197
DroGri_MEF2  AEA--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAI-GA-PNRPMPNTSYTLPVSVPVPGSYGENLLQASPQMSHTNISPRPSSSETDSVYPSGTMLEM-S   195
DroMoj_MEF2  AEA--DYTLTPRTEAKYNKIDEEFQNMMQRSQMNIGGA-PNRPMPNASYTLPVSVPVPGSYGENLLQASPQMSHTNISPRPSSSETDSVYPSGTMLEM-S   196
DroPer_MEF2  AET--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGVTGAPRQLPNSSYTLPVSVPVPGSYGENLLQASPQMSHTNISPRPSSSETDSVYPSGSMLEM-S   197
DroSec_MEF2  AET--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGGAGAPRQLPNSSYTLPVSVPVPGSYGDNLLQASPQMSHTNISPRPSSSETDSVYPSGSMLEM-S   197
DroVir_MEF2  AEA--DYTLTPRTEAKYNKIDEEFQNMMQRNQMALSGGAPNRAMPNTSYTMPVSVPVPGSYGENLLQASPQMSHTNISPRPSSSETDSVYPSGTMLEM-S   197
DroWil_MEF2  AEA--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGGPGAPRQLPNTSYTLPVSVPVPGSYGENMLQASPQMSHTNISPRPSSSETDSVYPSGSMLEM-S   197
DroYak_MEF2  AET--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGGAGGPRQLPNSSYTLPVSVPVPGSYGDNLLQASPQMSHTNISPRPSSSETDSVYPSGSMLEM-S   197
DroPse_MEF2  AET--DYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGVTGAPRQLPNSSYTLPVSVPVPGSYGENLLQASPQMSHTNISPRPSSSETDSVYPSGSMLEM-S   197
AnoG_MEF2    PED--SYTLTPRTEAKYNKIDEDFQIMMQRNQQLT-AGGARPNMATNSYSLPVSVPVIGTYNDSMLQSSPQMAHNSISPRPSSSETDSVYPSGGILEM-S   196
CulQ_MEF2d   PED--SYTLTPRTEAKYNKIDEDFQIMMQRNQQLS-AAGGGVGMSGNSYSLPVSVPVIGTYNDSMLQSSPQMAHNSISPRPSSSETDSVYPSGGLLEM-S   196
AedA_MEF2d   PED--SYTLTPRTEAKYNKIDEDFQIMMQRNQQLS-ASG-RVNMAGNSYSLPVSVPVIGTYNDSMMQSSPQMAHNSISPRPSSSETDSVYPSGGILEM-S   195
TriC_MEF2    PET--EYQLTPRTEAKYSKIDEEFQMMLQRNQ----INGQRVSMSSSNYTQPVSVPVNISYGDSLLQSSPQMAHTSISPRPSSSETDSVYPSGGMPEM-S   193
ApiM_MEF2    DAI--EYNLTPRTEAKYTKIDEEFQLMMQRHQ-----HNGTRAMGQSNYSLPVSVPV-NSYGESLLGSSPQIAHTSISPRPSSSETDSVYPPGGMLEM-S   191
BomM_MEF2    DSPEAEYNLTPRTEAKYSKIDEEFQMMMQRNQ----LNGSRVGVGVTGSNYNLPVSVPVGNYDQSLLQASPQMHTSISPRPSSSETDSVYPSGGMLEM-S   195
CioI_MEF2    VDHQ-AQLPTPGTLQRYETINKQFDDMIN--------SMRPPP---QQSSMPVTVPVTGIHPLHGYPSPIGMHQIQHE----------QPHHPPNRRS-P   177
BraF_MEF2    DQDVEYNLLTPRTEAKYQKINEEFDRMMQ--------MNMRVTNMPPQMPVAVPVTQQQQNNILGYGAG------------------LLQPQQIPAR-N   172
CaeB_MEF2    DDDSPGPSISPAIQIPIPAVN-------------------------------------------------------------------GHNSNQNNSV-A   132
CaeE_MEF2    DDESPGPSTSPVIQITMPAV--------------------------------------------------------------------VNGHSSNNSV-A   131
CaeR_MEF2    DDESPGPSTSPAIQIPIPTINGH-----------------------------------------------------------------TSNQSNSV-A   132
NasV_MEF2d   PEPDQYNSLTPRTEAKYAKIDEDFQMLI-------------------------------------------------RNQHNGSRVVYPPGGMLEM-S   148
SacK_MEF2    PGDE-PYQLTPRTEAKYSKINEEFELMMHSN-----TVMPRGSIRNYPQNMPVSIPVSQANNMTGYSSNASSSM-------------LQPQHTLGRN-S   179
GalG_MEF2    PDGDDSIDQSPLMEDKYRKGSEDLDILF----------KRYGSAVPTFAMPVTVPVTNQNTLQFSSPGSSLVTQSLVTSSLL-----SPQQPTLQRN-T   183
PhyI_MEF2    ----------------------------KKKQLQQAAKEAAAAAAAGANAEAANFNMGHGSTSNG------------AAVQSYQTMHGGMNGASLGLTN   149
SchM_MEF2a   GDAVSNNNDPFFSNTTDQLSEADVSIRTGTKTPITSSVSMALEFPGSISDIPKHIPGITHSVTPESITDQHMNATYAPSSSMHFTTSAEREKKAENLMYH   200
             .......110.......120.......130.......140.......150.......160.......170.......180.......190.......200
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CanF_MEF2A     VSPGVPQRPPSTGSAGGMLSTSDLTVPNGAGSSPVGNGFVNSRASPNLIGTT--GANS--LGKVMPTKSPPPP-GGGNLGMNSRK-PDLRVVIPPTSKGM   282
MacM_MEF2A     VSPGAPQRPPSTGNAGGMLSTTDLSVPNGAGSSPVGNGFVNSRASPNLIGTT--GANS--LGKVMPTKSPPPP-GGGNLGMNSRK-PDLRVVIPPSSKGM   282
PanT_MEF2A     VSPGAPQRPPSTGNAGGMLSTTDLTVPNGAGSSPVGNGFVNSRASPNLIGAT--GANS--LGKVMPTKSPPPP-GGGNLGMNSRK-PDLRVVIPPSSKGM   282
SusS_MEF2A     VSPGAPQRPPSTGSAGGMLSTSDLTVPNGAGSSPVGNGFVNSRASPNLVGTT--GANS--LGKVMPTESPPPP-GGGNLGMNSRK-PDLRVVIPPSSKGM   281
EquC_MEF2A     VSPAAPQRPPSTGSAGGMLSTSDLTVPNGAGSSPVGNGFVNSRASPNLIGTT--GANS--LGKVMPTKSPPPP-GGGNLGMNNRK-PDLRVVIPPSSKGM   281
PonA_MEF2A     VSPGAPQRPPSTGNAGGMLSTTDLIVPNGAGSSPVGNGFVNSRASPNLIGAT--GANS--LGKVMPTKSPPPP-GGGNLGMNSRK-PDLRVVIPPSSKGM   282
HomS_MEF2A     VSPGAPQRPPSTGNAGGMLSTTDLTVPNGAGSSPVGNGFVNSRASPNLIGAT--GANS--LGKVMPTKSPPPP-GGGNLGMNSRK-PDLRVVIPPSSKGM   282
CalJ_MEF2A     VSPGAPQRPPSTGNAGGMLSTTDLTVPNGAGSSPVGNGFVNSRASPNLIGAT--GANS--LGKVMPTKSPPPP-GGGNLGMNSRK-PDLRVVIPPSSKGM   282
AilM_MEF2A     VSPGVPQRPPSTGSAGGMLSTSDLTVPNGAGSSPVGNGFVNSRASPNLIGTT--GANS--LGKVMPTKSPPPP-GGGSLGMNSRK-PDLRVVIPPSSKGM   282
MusM_MEF2A     VSPGAPQRPPSTGSASGMLSTTDLTVPNGAGNSPVGNGFVNSRASPNLIGNT--GANS--LGKVMPTKSPPPP-GGGSLGMNSRK-PDLRVVIPPSSKGM   282
DanR_MEF2A     VVP--PQRPPSTGST--------------------GNGFVNPRGSPGLLGTP--SGNG--LGKVMPAKSPPPP--GGNMGIGSRK-PDLRVVIPPSSKGM   258
GalG_MEF2A     VSPGAPQRPPSTGNAGGILGTTDLTVPNGAGTSPVGNGVWNSRASPSLLGTA--GGNG--LGKVMPTKSPPPP-GGGGLGMNNRK-PDLRVVIPPSSKGM   282
RatN_MEF2A     VSPGAPQRPPSTGSAGGMLSTTDLTVPNGAGNSPVGNGFVNSRASPNLIGNT--GANS--VGKVMPTKSPPPP-GGGSVGMNSRK-PDLRVVIPPSSKGM   281
BosT_MEF2A     VSPGAPQRPPSTGSAGGMLSTSDLTVPNGAGSSPVGNGFVNSRASPNLIGTT--GANS--LGKVMPTKSPPPP-GGGSLGMNSRK-PDLRVVIPPSSKGM   281
MonD_MEF2A     VSPGAPQRPPSTGNTGGMLSTADLTVPNGSGNSPVGNGFVNSRASPNLLVST--GGSN--LGKVMPTKSPPPP-GNGNLGMNNRK-PDLRVVIPPSSKGM   281
XenL_MEF2A     VFPGYPSEPPSTGNAGVMLCSSDLSVPNGAGTSPVGNGFVNPRASPSHLGPT--GGNV--LGKVMPTKSPPPP--GGNLVMNSRK-PDLRVVIPPSSKGM   280
OrnA_MEF2A     VSPGAPQRPPSTGNAGGMLSTADLTVPNGAGNSPVGNGFVNSRASPNLLGTS--GGNS--LGKVMPTKSPPPP-GGGNLGMNNRK-PDLRVVIPPSSKGM   282
TaeG_MEF2A     VSPGAPQRPPSAGSSGGMLGTADLSVPNGAGTSPVGNGFVNSRASPSLLGTS--GGNG--LGKVMPTKSPPPP-GGGNLGMNNRK-PDLRVVIPPSSKGM   282
OryC_MEF2A     VSPGAPQRPPSTGNAGGMLSTTDLTMPNGAGGSPVGNGFVNSRASPNLIGTT--GANS--LGKVMPTKSPPPP-GGGNLGMNSRK-PDLRVVIPPSSKGM   271
CanF_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
MacM_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
PanT_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   264
SusS_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
EquC_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
PonA_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
HomS_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   264
CalJ_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
AilM_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
MusM_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNIQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
GalG_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--TGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
RatN_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNIQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
BosT_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
XenT_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--TGAGTS-AGNGYGNHRNSPGLLVSP--GN----LNKNMQTKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
MonD_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--TGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNA   266
XenL_MEF2C     MSPG-VTHRPPSA---GGLMGGDLT--TGAGTS-AGNGYGNHRNSPGLLVSP--GN----LNKNMQTKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   263
OrnA_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--TGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
TaeG_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--TGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKST   266
OviA_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLA--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKNT   266
OryC_MEF2C     MSPG-VTHRPPSAGNTGGLMGGDLT--SGAGTS-AGNGYGNPRNSPGLLVSP--GN----LNKNMQAKSPPP----MNLGMNNRK-PDLRVLIPPGSKSA   266
DanR_MEF2Ca    MSPG-VTHRPPSAGNTGGLMAADLG--SGAGTS-TGNGYGNHRNSPGLLVSP--GN----MSKNLQAKSPPS----MNMSL-SRK-PDLRVLIPPGAKNT   264
DanR_MEF2Cb    MSPG-VTHRPPSA---GGLMGTDLS--TGAGTS-AGNGYGNHRNSPGLLVSS--GG----MNKSMQAKSPPP----VNLGMNSRK-PDLRVLIPPGAKNN   252
CanF_MEF2D     VSPG-LPQRPASA---GAMLGGELNSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKGIPAKSPPPPTHSAQLGAPSRK-PDLRVITSQGGKGL   281
MacM_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPGAN-GNS---LNKSFPAKSPPPPTHGTQLGAPSRK-PDLRVITSQAGKGL   281
PanT_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPTHSTQLGAPSRK-PDLRVITSQAGKGL   281
SusS_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPTHSAQLGAPSRK-PDLRVITSQGGKGL   281
EquC_MEF2D     VSPG-LPQRPASA---GAMLGGDLTSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPTHSAQLGAPSRK-PDLRVITSQGGKGL   281
PonA_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPTHSTQLGAPSRK-PDLRVITSQAGKGL   281
HomS_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPTHSTQLGAPSRK-PDLRVITSQAGKGL   281
CalJ_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPTHSTQLGAPSRK-PDLRVITSQAGKGL   281
AilM_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYGSARASPGLLPVAN-GNS---LNKGIPAKSPPPPTHSAQLGAPSRK-PDLRVITSQGGKGL   276
MusM_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPTHNTQLGAPSRK-PDLRVITSQGGKGL   281
DanR_MEF2D     VSPG-LPQRPASA---GALLGGDLNNSNGACPSPVANGYVSARASPGLLSVSN-GNS---MGKVVQAKSPPPP--STQMA-NSRK-PDLRVITSQSSKGL   275
GalG_MEF2D     VSPG-LPQRPASA---GAMLGGDLNNTNGACPSPVGNGYVSARASPGLLPVSN-GST---LGKIIPAKSPPPPPHSTQLASNSRK-PDLRVITSQSGKGL   281
RatN_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPVAN-GNG---LNKVIPAKSPPPPTHNTQLGAPSRK-PDLRVITSQGGKGL   281
BosT_MEF2D     VSPG-LPQRPASA---GAMLGGDLSSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPAHSAQLGAPSRK-PDLRVITSQGGKGL   281
XenT_MEF2D     VSPG-LPQRPASA---GAMLGGELNNSNGTCPSPVGNGYISARASPGLIPVSN-GNS---LGKVIPAKSPPPPNQNSQLGANSRK-PDLRVITSQGGKGL   281
MonD_MEF2D     VSPG-LPQRPASA---GAMLGGDLNSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LSKVIPAKSPPPPTHSAQLGAPSRK-PDLRVITSQGGKGL   281
TaeG_MEF2D     VSPG-LPQRPASA---GAMLGGDLNNTNGACPSPVGNGYVSARASPGLLPVSN-GSS---LGKIIPAKSPPPPAHGAQLAANSRK-PDLRVITSQSGKGL   281
OryC_MEF2D     VSPG-LPQRPASA---GAMLGGDLTSANGACPSPVGNGYVSARASPGLLPVAN-GNS---LNKVIPAKSPPPPHGAQLGAPSRK-PDLRVITSQGGKGL   281
XenL_MEF2Db    VSPG-LPQRPASA---GAMLGGELN-SNGTCPSPVGNGYISARASPGLLPVSN-GNS---MGKVIPAKSPTPPNQNNQLGVNSRK-PDLRVITSQGGKGL   280
XenL_MEF2Da    VSPG-LPQRPASA---GAMLGGELNNSNGTCPSPVGNGYISARASPGLLPVSN-GNS---LGKVIQAKSPPSPNQNSQLGANSRK-PDLRVITSQGGKGL   281
CanF_MEF2B     MVYG-ALPPPGCD------------PSGLGEALPAQSRPSPFRPAAPKAGPP-GLA---HPLFSPSHLASKTPPPLYLAADGRR-PDLPGSLAGARGGLS   223
MacM_MEF2B     MVYG-ALPPPGCD------------PSGLGEALPAQSRPSPFRPAAPKAGPP-GLV---HPLFSPSHLTSKTPPPLYLPTEGRR-PDLPGGLAGPRGALN   223
PanT_MEF2B     VVYG-ALPPPGCD------------PSGLGEALPAQSRPSPFRPAAPKAGPP-GLV---HPLFSPSHLTSKTPPPLYLPTEGRR-SDLPGGLAGPRGGLS   223
EquC_MEF2B     MVYG-ALPPPGCE------------PSGLGEALSAQSRPSPFRPAAPKAGPP-GLA---HPLFSPSHLASKTPPPLYLAADGRR-PDLPGGLAGARGGLS   223
PonA_MEF2B     VVYG-ALPPPGCD------------PSGLGEALPAQSRPSPFRPAAPKAGPP-GLV---HPLFSPSHLTSKTPPPLYLPTEGRR-SDLPGGLAGPRGGLN   223
HomS_MEF2B     VVYG-ALPPPGCD------------PSGLGEALPAQSRPSPFRPAAPKAGPP-GLV---HPLFSPSHLTSKTPPPLYLPTEGRR-SDLPGGLAGPRGGLN   223
CalJ_MEF2B     MVYG-ALPPPGCD------------PSGLGEALPAQSRPSPFRPAAPKAGPP-GLA---HPLFSPSHLTSKTPPPLYLPADGRR-ADLPGGLAGPRGGLN   223
AilM_MEF2B     MVYG-ALPPPGCD------------PSGLGEALPAQSRPSPFRPAAPKAGPP-GLA---HPLFSPSHLASKTPPPLYLAADGRR-PDLPGSLAGARGGLS   223
MusM_MEF2B     LSYR-VPPAPGCD------------PGGLGEAPSVHSRPPHFRP-------P-GLG---HPIFSPSHLASKTPPPLYLATDGRR-PDLPPGLVGARGGLG   216
RatN_MEF2B     LSYR-VPPASGCD------------PGGLGEAPSVHSRSPHFRP-------P-GLG---HPIFSPSHLAGKTPPPLYLATDGRR-PDLPPGLVGARGGLG   216
BosT_MEF2B     MVYG-ALPPPACE------------PTGLGEALPAQSRPSPFRPAAPKAGPP-GLA---HPLFSPSHLASKTPPPLYLAADGRR-PDLPGGLAGTRGGLS   223
MonD_MEF2B     LAYG-AVPPPGSG------------PEPCGEATPGQGRPSPFRPAASKAGPP-GLG---HPLFSPRALANKTPPPLYLTADGRR-SDLPGNLAAPRAGLG   223
OrnA_MEF2B     VAYG-AVPPPRTD------------PAGLGEPSPSQSHPPPFKPAGPKPGPP-GLS---YPLFSTRALASKTPPPLYLGADARR-PDLTSSLGGARGTLS   222
DroMel_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLSIKQQSPGSQNGRASNLRVVIPPTIA---PIPPNMSAPDDVGYADQRQSQTSLNT-PVVTLQTPIPALT   288
DroSim_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLSIKQQSPGSQNGRASNLRVVIPPTIA---PIPPNMSAPDDGGYADQRQSQTSLNT-PVVTLQTPIPALT   288
DroAna_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLSIKQQSPGSQNGRASNLRVVIPPTIA---PLPPNMSAPDDVGYGDQRQSQTSLNT-PVVTLQTPIPALT   288
DroEre_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLSIKQQSPGSQNGRASNLRVVIPPTIA---PIPPNMSAPDDGGYADQRQSQTSLNT-PVVTLQTPIPALT   288
DroGri_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLPIKQQSPGSQNGRASNLRVVIPPTIA---P-NMSATA-DDVAYADPRQSQTSLNT-PVVTLQTPMPPLT   284
DroMoj_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLPIKQQSPGSQNGRASNLRVVIPPTIA---P-NMSATA-DDVAYADQRQSHTSLNT-PVVTLQTPMPPLA   285
DroPer_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLPIKQQSPGSQNGRAANLRVVIPPTIA---TIPPNMSAPEDVAYTDQRQSQTSLNT-PVVTLQTPIPALT   288
DroSec_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLSIKQQSPGSQNGRASNLRVVIPPTIA---PIPPNMSAPDDGGYADQRQSQTSLNT-PVVTLQTPIPALT   288
DroVir_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLPIKQQSPGSQNGRASNLRVVIPSTIA---P-NMSATA-DDVAYADQRQSQTSLNT-PVVTLQTPMPPLA   286
DroWil_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHMPIKQQSPGSQNGRASNLRVVIPPSIG---P-NMS-TA-DDVAYGDHRQSQTSLNT-PVVTLQTPIPALT   285
DroYak_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLSIKQQSPGSQNGRASNLRVVIPPTIA---PIPPNMSAPDDGGYADQRQSQTSLNT-PVVTLQTPIPALT   288
DroPse_MEF2    NGYP-HSHSPLVGSPSPGPSPGI----AHHLPIKQQSPGSQNGRAANLRVVIPPTIA---TIPPNMSAPEDVAYTDQRQSQTSLNT-PVVTLQTPIPALT   288
AnoG_MEF2      NGYP-HSASPLGGSPSPGPSPGIGSHQAHTIKQSPSGGSGSSGSRS-LRVVIPAPMN---P---TITA-DDISYVEHTRQQTNLNT-PVVALQTPIPGLT   286
CulQ_MEF2d     NGYP-HSASPLGGSPSPGPSPGI----VQHQSLKQNSPGSSSTRSSNLRVVIPTPMN---P---SMG-NDDMSYVEHSRQQTNLNT-PVVALQTPIPGLS   283
AedA_MEF2d     NGYP-HSASPLGGSPSPGPSP------VQHQTIKQGSPGSSNGRSSNLRVVIPTPMN---P---TIN-TDDLSYVEHSRQQSSNLNTPVVALQTPIPGLS   281
TriC_MEF2      NGYP-NSASPMDGSPSPGPSPG-----PGLSSSKQHPKQHSPGPRSNLRVVIPTALG---P---SIT-PEEVSYGEHNRTQSTLNT-PVVALQTP--GLS   277
ApiM_MEF2      NGYP-PSASPLGGSPSPGPSPALGVG-SRHSPQPPPPPPPPHPHRTNLRVVIPTPLTQ--P-----L-SEDTSY-DNGHTQSALNT-PVVALQTPSVPAG   279
BomM_MEF2      NGYP-GSASPLG-APSPSPGPAPSPHRHPHKSHAHAPPPHHSPRHNNLRVVIPSSMP---P----------------------PQDD--ISYAETPLSYS   266
CioI_MEF2      LPKS-PLARGHSPSRSPSGQMYSPEVNMISDTPSPGGNGYSGGNQPPPPQQRGPSPH----MDRTSPMPHKPMQQSPT-SPARGHR-PGLHVVIPPS---   267
BraF_MEF2      VSPG-VQPQRPPSNGVPGAMLGADLTGTSAGAGTAGNGYVNQNRASPGVMVSSAAQS-------------------------KQPS-PSLPRSGGHPTLR   245
CaeB_MEF2      SASS-ASAAAVAAAAAAVAAVEGTSSGAAAAAAALQASNAQRHHNLNLYQNLIFNPN----YTRHLPQRNDPLTSSSSAAPSSSSS-SSKHLDFPPSTSF   226
CaeE_MEF2      SAAS-ASAAAVAAAAAAVAAVEGTSSGAAAAAAALQASNAQRHHNLNLYQNLIFNPN----YTRHLNQRNDPLSSTS-VAPSSSSS---KHLDFPPSTSF   222
CaeR_MEF2      SAAS-ASAAAVAAAAAAVAAVEGTSSGAAAAAAALQASNAQRHHNLNLYQNLIFNPN----YARHLPPRNEPLPSSS-AAPSSSSS-SSKHLDFPPSTSF   225
NasV_MEF2d     NGYP-PSASPLGGSPSPGPSPSLGVSKGNPSRHSPQPPPPPHPHRGALRVVIPTPLGQ--SLAEEPSYDSGHAQSSLNTPVVALQT-PSVPPSYTSFGPT   244
SacK_MEF2      VSPV-SNMTQPQRPSSSGPPSTVLSNDSSSATSTSTGTGTTDHHLNYRKIGYSSNQE----------------YISSSVGSNYGNP-SRTSPGGTSPGGL   261
GalG_MEF2      VSPG-LPQRPASAGAMLGGDLNN----TNGACPSPVGTGYVSARASAGLLPVSNGST----LKIILAKSLPRSPHSTQLASNSRKQ-NMRVITSQSGKGL   273
PhyI_MEF2      DPDQ-----------------YMLNSRSRPPTQKKRVHRGFQQLLKKEHGG-------------------------------------------------   183
SchM_MEF2a     EQDTTSGVVIGESRVNELCREIILDDETNQPFNSDLRSSSRNHIPQIHFGSQEFSTHNRGSSLIDPNMKSIVSSDHLSSFRPENIQNFRSEVQDCFNNNL   300
               .......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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CanF_MEF2A   MPPLSEEEELELNTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   368
MacM_MEF2A   MPPL--------NTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   360
PanT_MEF2A   MPPLSEEEELELNTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   368
SusS_MEF2A   MPPLSEEEELELNTQRISSSQAPQPLATPVVSVTTPSLPQQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   367
EquC_MEF2A   MPPLSEEEELELNTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   367
PonA_MEF2A   MPPL--------NTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   360
HomS_MEF2A   MPPL--------NTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   360
CalJ_MEF2A   MPPL--------NTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   360
AilM_MEF2A   MPPL--------NTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   360
MusM_MEF2A   MPPLSEEEELELNAQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFTSPGMLSLGQASAWQQH-----------   368
DanR_MEF2A   MPPL--------NTQRISSSQSTQPLATPVVSVTTPSLAPQGL-VY-SGMPTAYNSEYSLSSAELSSLQGFGSPG-LSIGSVSAWQQH-----------   335
GalG_MEF2A   MPPLTEEDELELNTQRISSSQSTQPLATPVVSVTTPSFPPAGL-VY-SAMPTAYNTDYSLTSADLSAFEGFNSPGMLSLGQVSPWQQH-----------   368
RatN_MEF2A   MPPL--------NAQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFTSPGMLSLGQASAWQQH-----------   359
BosT_MEF2A   MPPL--------NTQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   359
MonD_MEF2A   MPPLSEEDELELNSQRISSSQSTQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   367
XenL_MEF2A   MPPL--------NTQRVTSSQGTQPLATPIVSVATPSLAPQGL-IY-SAMPTAYNTDYPLTSADLSMLQGFNSPGILPLGQVSAWQQH-----------   358
OrnA_MEF2A   MPPLSEEDELELNTQRISSSQSTQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   368
TaeG_MEF2A   MPPLSEEDELELNPQRISSSQSTQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   368
OryC_MEF2A   MPPLSEEEELELNPQRISSSQATQPLATPVVSVTTPSLPPQGL-VY-SAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQH-----------   357
CanF_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
MacM_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
PanT_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   351
SusS_MEF2C   MPSV--------N-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   345
EquC_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
PonA_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
HomS_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   351
CalJ_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
AilM_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
MusM_MEF2C   MPSV--------N-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   345
GalG_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADISSLSGFNTASALHLGSVTGWQQQ-----------   353
RatN_MEF2C   MPSV--------N-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   345
BosT_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
XenT_MEF2C   MPSV--------N-QRINNSQSAQSLATPVVPVATPTLPGQGMGGYPTAISTTYGTEYSLSSADLSSLSGFNT-SALHLGSVTGWQQH-----------   344
MonD_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
XenL_MEF2C   MPSV--------N-QRINNSQSAQSLATPVVPVATPTLPGQGMGGYPTAISTTYGTEYALSSADLSSLSGFNT-SALHLGSVTGWQQH-----------   341
OrnA_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   353
TaeG_MEF2C   MPSVSEDVDLLLN-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADISSLSGFNTASALHLGSVTGWQQQ-----------   353
OviA_MEF2C   MPSV--------N-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNTASALHLGSVTGWQQQ-----------   345
OryC_MEF2C   MPSV--------N-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTTYGTEYSLSSADLSSLSGFNAASALHLGSVTGWQQQ-----------   345
DanR_MEF2Ca  MPSI--------N-QRISSSQSAQSLSTPVVSVATPTLPGEVMGGYPSAINTSYGTEYSLSSGDLSSLSAFNSSASLHLGSMTGWPQN-----------   343
DanR_MEF2Cb  MPSI--------N-QRINNSQSAQSLATPVVSVATPTLPGQGMGGYPSAISTSYGTEYSLSSADLSSISGFNSANTLHLGSMSGWQQH-----------   331
CanF_MEF2D   MHHL-------NNAQRLGASQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLSSAELSSLPTFSSPGGLSLGGVT----------------   355
MacM_MEF2D   MHHLTEDHLDLNNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPAFSSPGGLSLGNVTAWQQPQQPQQPQQPQPP   379
PanT_MEF2D   MHHLTEDHLDLNNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPAFSSPGGLSLGNVTAWQQPQQPQQPQQPQPP   379
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EquC_MEF2D   MHHLTEDHLDLNNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPSFSSPGGL----------------------   356
PonA_MEF2D   MHHLTEDHLDLNNVQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPAFSSPGGLSLGNVTAWQQPQQPQQPQQPQPP   379
HomS_MEF2D   MHHLTEDHLDLNNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPAFSSPGGLSLGNVTAWQQPQQPQQPQQPQPP   379
CalJ_MEF2D   MHHLTEDHLDLNNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPAFSSPGGLSLGNVTAWQQPQQPQ--------   371
AilM_MEF2D   MHHLTEDHLDLNNAQRLGASQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLSSAELSSLPTFSSPGGLQPQPQ------------------   356
MusM_MEF2D   MHHL-------NNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLPSAELSSLPAFSSPAGLALGNVTAWQQPQPPQQPQPPQPP   372
DanR_MEF2D   MQLTDEEELVSENAQRLGTSQVTQPLTTPVVSVATPSLLT-----PF-SMPTAYNTEYQLTSADLTALQAFTPSGALLPGNMTTWQQQQQPSVSQQPQQQ   369
GalG_MEF2D   MHHLTEDHLALQNTQRLGVSQATHSLTTPVVSVATPSLLTQGL--PFSAMPTAYNTARSLGGIRTHSEAERQR-------------------------   352
RatN_MEF2D   MHHL-------NNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLPSAELSSLPAFSSPAGLALGNVTAWQQPQQPQQPQPPQPP   372
BosT_MEF2D   MHHLTEDHLDLNNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPAFSSPGGLSLSNVTAWQQPQQPPQPQPPQQP   379
XenT_MEF2D   MHHLTEEQLEMSAQRLGGVSQAAHSLTTPVVSVATPSLLSHGL--PFSAMPTAYNTDYQLTSADLSSLSTFSSPSSLSLGNVTAWQQQQQQQH-------   372
MonD_MEF2D   MHHLTEDHLDLNNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPAFSSTGGLSLGNVTAWQQQQPQPPQQQPQP   379
TaeG_MEF2D   MHHLVSAHSSQN-TQRLGVSQATHSLTTPVVSVATPSLLTQGL--PFSAMPTAYNT--VHTSA-GSHLSHTTTLTVNTNPN------------------   356
OryC_MEF2D   MHHL-------NNAQRLGVSQSTHSLTTPVVSVATPSLLSQGL--PFSSMPTAYNTDYQLTSAELSSLPAFSSPGGLSLGNVTAWQQPQQPQQPQPPQPQ   372
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CanF_MEF2B   TS----------RGLYGSLQSPCSATAPGPPLGSFPFLPAGPPAA-----------------------------------------------------   258
MacM_MEF2B   TS----------RSLYSGLQSPCSTATPGPPLGSFPFLPAGPAEYGLGDPPPPPGLLQPPTLAPWQPSRGDGPPAV-----------------------   289
PanT_MEF2B   TS----------RSLYSGLQNPCSTATPGPPLGSFPFLPGGPPEYGLGDPPPPPGLLQPPTLAPWQPSRGDGPPAV-----------------------   289
EquC_MEF2B   TS----------RGLYGSLQSPGSAAAPGPPLGSFPFLPAGPPEYGLGDPPPPPGLLQPPTLAPWQPSRGDGPPAG-----------------------   289
PonA_MEF2B   TS----------RSLYSGLQNPCSTATPGPPLGSFPFLPGGPPEYGLGDPPPPPGLLQPPTLAPWQPSRGDGPPAV-----------------------   289
HomS_MEF2B   TS----------RSLYSGLQNPCSTATPGPPLGSFPFLPGGPPEYGLGDPPPPPGLLQPPTLAPWQPSRGDGPPAV-----------------------   289
CalJ_MEF2B   TS----------RSLYSGLQSPCSAAPGPPLGSFPFLPAGPPEYGLGDPPPPPGLLQPPTLASWQPSRGEGPPAV-----------------------   289
AilM_MEF2B   TS----------RGLYGSLQSPCSATAPGPPLGSFPFLPAGPP--GM-HHPHVSFCGRHPYTCLLGHSRGDGPPAA-----------------------   286
MusM_MEF2B   TS----------RSLYSGLQSP---GAPGPALGSFAFLPSGSTDCSPGDAAQGP--LQPSPWPPTRDAV-----------------------------   270
RatN_MEF2B   TS----------RSLYSGLQSP---GAPGPALGSFAFLPPGSADCSPGDAAQVP--LQPSPWPPTRDAV-----------------------------   270
BosT_MEF2B   SS----------RGLYGGLQSPCSTAAPGPPLGSFPFLPAGPPEYGLGDPPPPPGLLQPPTLAPWQPSRADGPPAT-----------------------   289
MonD_MEF2B   AT----------RTLYGSLQSPSPISAPGNGLGAFPFISSSQAEYGHGDPSPHPGLLQPTALVPWQPPRGDRSPSS-----------------------   289
OrnA_MEF2B   ST----------RTLYSSLQNSSPMVATGNGLGAFPFLPSGPTEYGPGEASPHPGFLQPNAMASWQPPRDNPTSL-----------------------   287
DroMel_MEF2  SYSFGAQDFSSSGVMNSADIMSLNTWHQGLVPHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQNSNGSTGSGGSSSSTSSNASGGAGG   388
DroSim_MEF2  SYSFGAQDFSSSGVMNSADIMSLNTWHQGLVPHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQNSNGSTGSGGSSSSTSSNASGGAGG   388
DroAna_MEF2  SYSFGAQDFSSSGVMGSADIMSLNTWHQSLVPHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQNSNGSTGSGGSSSTTSSNTSGNGGG   388
DroEre_MEF2  SYSFGAQDFSSSGVMNSADIMSLNTWHQGLVPHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQNSNGSTGSGGSSSSTSSNASGGGGG   388
DroGri_MEF2  SYSFGAQDFSQSGAM-SADIMSLPQWHQGLVQHTSLSHLAVSNSTPPPASSPVSIKVKAEPQSPPRDLSASGHQHNSNGSTGSGSSSSSTSSNVSTAGGV   383
DroMoj_MEF2  SYTFGAQDFSQSGAM-SADIMSLPQWHQGLVQHTSLSHLAVSNSTPPPASSPVSIKVKAEPQSPPRDLSASGHQHNSNGSTGSGSSSSSTSSNVSTAGVL   384
DroPer_MEF2  SYSFGAQDFSSSGVIGSADIMSLPTWHQGLVQHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQNSNGSTGSGGSSSSTSSNASAGGGG   388
DroSec_MEF2  SYSFGAQDFSSSGVMNSADIMSLNTWHQGLVPHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQNSNGSTGSGGSSSSTSSNASGGAGG   388
DroVir_MEF2  SYSFGAQDFSQSGAM-SADIMGLPQWHQGLVQHTSLSHLAVSNSTPPPATSPGSVKVKSEPQSPPRDLSASGHQHNSNGSTGSGSSSSSNSSNVSTTGGV   385
DroWil_MEF2  SYTFGAQDFSSSGAMSSADIMSLPQWHPGLTQHTSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQHSNGSTGSGGSSSSTSSNASASGLV   385
DroYak_MEF2  SYSFGAQDFSSSGVMNSADIMSLNTWHQGLVPHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQNSNGSTGSGGSSSSTSSNASGGGGA   388
DroPse_MEF2  SYSFGAQDFSSSGVIGSADIMSLPTWHQGLVQHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQNSNGSTGSGGSSSSTSSNASAGGGG   388
AnoG_MEF2    NYSFGAQDFS----LNPDIMIGPWSAASSHSLFSGLPHLAVSNSTPPPSTSPLSVKIKAEPISPPRDHHNTSHHHGGAPGGGSSSGASGSA---------   373
CulQ_MEF2d   NYSFGAQDFSINSDLSMIASWGAAAANNAHHSSSGLPHLAVSNSTPPPSTSPLSVKIKAEPISPPREHSSSSHHQHQHQQQQQQ---------------   368
AedA_MEF2d   NYSFGAQDFSINSDLSMIASWGAAA-SNAHHSSSGLPHLAVPNSTPPPSTSPLTVKIKAEPISPPREHQSS-----------------------------   351
TriC_MEF2    NYSFGAQDFSMGADMGLSSISWSGHQIS-HTSN-CLPHLAVSSSTPPPSSSSPIVKIKSEPISPPREHHP-------------------------------   345
ApiM_MEF2    YSSFGPTDYSSDLGSLAWSHQRYVDDLSYSSSISGLPHLAVSSSTPPPATSPLPVKIKSEPISPPRDPHGGNSGSNSSGPSNTSNL--------------   365
BomM_MEF2    LTNFGPQDFSMTSDMGIGLTWGAHQLQTQHNRYIGSLPVLGGGGTPPPAASPSNVKIKAEPVSPPR---------------------------------   332
CioI_MEF2    ---------------RNMPGMDGGNDQLSTPVVSLATPNIIQ-----QYQHAPQTSYNPVDYQVLAGGEVTGFASPGS-----------------------   325
BraF_MEF2    VAIPSSRGVLPSMPQQNMRTNNQSLSTPVVSVATPSMNPGLPN-YPSAMPTAYNNDFALNSADLVGLGNFSSPISS-------------------------   320
CaeB_MEF2    AYDTS------RLHPLAAADADCDLVPSSRAA-DQNIWSTNLQQRPVSQPAPSTSNLSANGISNGSSGLLSPNIS-------------------------   294
CaeE_MEF2    AYDTS------RLHPIAAADADCDLVPSSRAAADQNIWSSALQQRPVSQPAPSISNSSTNGISNGTSGLLSPNVS-------------------------   291
CaeR_MEF2    AYDTS------RLHPIAAADADCDLVPSSRAA-E-NIWSTALQQRPVSQPAPSISNSSSNGLSNGTSGLLSPNIS-------------------------   292
NasV_MEF2d   DYSTDLSSLAWSHQRYVDDLSMYSAATMSSISSL--PHLAVSSSTPPPSTSPIPVKIKSEPISPPRDPHAGSGGSNGSISGPSNSSSLH-----------   331
SacK_MEF2    VTKAMTKQSPTATRPQLRANPNQSLATPTVSLATPSNPPGIPNYPSAMPTAFQSGDFALNTADLSQLSNFNSPGTSAVSA-------------------   341
GalG_MEF2    MHHL--------NTQRLGSQATHSLTTPVVSVATPSLLTQGL-PFSAMPTA-YNTDYQLTSAELSSLPAFSSPGGG-------------------------   339
PhyI_MEF2    ------------------------------------------------------------------YVPPSLPLYQHGMGMMGGLSGHHMLGPLPSPPNLSGILPSP   224
SchM_MEF2a   LSALSIGNQNTDNFGNRPATSAHLSPGSFSEPSSYATQRSSLTSSRRIKRPVFEPYDEYFYPKTSPNIESRSRSPILPLKQTTVSPPTSYCDSNRVTHLP   400
             .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400
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CanF_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQPQQQQ---------PP   428
MacM_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQQQPP-----PPPQPQ   424
PanT_MEF2A   -----------------------HLGQAALSSLVCKS-----NLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQQQPP-------PPPQ   430
SusS_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQPPPPS---QAPQPQPP   433
EquC_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQQQQQ--------QSQ   428
PonA_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQQQQQ------PPPPP   423
HomS_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-ISIKSEPISPPRDRMT-PSGFQQQQQQQQQ---QQPPPPPQ   426
CalJ_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQQQPP--------PPQ   421
AilM_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQPQP-------------   416
MusM_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQQPQQ----------Q   427
DanR_MEF2A   -----------------------QLGQAALSSLVGGG-----HLPQGSNLSINTSQN-VNIKSEPISPPREVT-PSGFPPQQQQPPS----------   393
GalG_MEF2A   -----------------------HLGPATLSSLVSGS-----QLSQGSNLSINTNQN-INIKSEPISPPRDRVN-SSGFPQQQPPQQP----------Q   427
RatN_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQQQPQ-------QQPP   421
BosT_MEF2A   -----------------------HLGQAALNSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQPQPP----------P   418
MonD_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFPQQQQQQQQ-----QQQQQQ   431
XenL_MEF2A   -----------------------HVGQAALSSFVATG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRIT-PSGFQSHQHHQHQ-----------   416
OrnA_MEF2A   -----------------------HLGQAALGSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFPQQQQQQQQ---QQQQQQQQQ   434
TaeG_MEF2A   -----------------------HLGPAALSSLVTGS-----QLSQGSNLSINTNQN-INIKSEPISPPRDRVT-PSGFPPQQPQQPQP----------   427
OryC_MEF2A   -----------------------HLGQAALSSLVAGG-----QLSQGSNLSINTNQN-INIKSEPISPPRDRMT-PSGFQQQQQQQQQTQPPQPQPPPPP   426
CanF_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   407
MacM_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   407
PanT_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   405
SusS_MEF2C   -----------------------HLHNMPPSALSQLG-------------------------------------DRTTTPSR---------------------   367
EquC_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   407
PonA_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   407
HomS_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   405
CalJ_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   407
AilM_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   407
MusM_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LSIKSEPVSPPRDRTTTPSR---------------------   399
GalG_MEF2C   -----------------------HLHNMPPSALSQLG-------------------------------------------------------------   367
RatN_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   399
BosT_MEF2C   -----------------------HLHSMPPSALSQLGDRTTTPSR-----------------------------------------------------   375
XenT_MEF2C   -----------------------HLHNMPHSALSQLGDRTTTPSG-----------------------------------------------------   366
MonD_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSTNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   407
XenL_MEF2C   -----------------------HLHNMPHSALSQLGDRTTTPSG-----------------------------------------------------   363
OrnA_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHVSQSTNLSLPSTQS-LHIKSEPVSPPRDRTTTPSR---------------------   407
TaeG_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSTNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   407
OviA_MEF2C   -----------------------HLHNMPPSALSQLGDRTTTPSR-----------------------------------------------------   367
OryC_MEF2C   -----------------------HLHNMPPSALSQLGACTSTHLSQSSNLSLPSTQS-LNIKSEPVSPPRDRTTTPSR---------------------   399
DanR_MEF2Ca  --------------------------MQHSGLGHLGNCSSAQLCQSSALSLPSNQN-LHIKSEPVSPPRDRSGTPGL---------------------   393
DanR_MEF2Cb  -----------------------QIQNMQHSALSQLGNCSSSHLCQGSNLSLPSTQS-LHIKSEPVSPPRDRSTTPGG---------------------   385
CanF_MEF2D   ------------------------------------------------------------ACIKFEPVSPSRERSPAP----------------------   373
MacM_MEF2D   QQQPPQPQQPQPQQPQQPQQP---PQQQSHLVPVSLSNLIPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   453
PanT_MEF2D   QQQPPQPQQPQPQQPQQPQQP---PQQQSHLVPVSLSNLIPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   453
SusS_MEF2D   QPQP----QP--QPQPPQQPQQPPQQQPHLVPVSLSSLIPGAPVQLGGAPLAPSGEPE-PRIAAEPSTPARERTDGH----------------------   449
EquC_MEF2D   ------------------------------------SSPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   395
PonA_MEF2D   QQQPPQPQQPQPQQPQQPQQP---PQQQSHLVPVSLSNLIPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   453
HomS_MEF2D   QQQPPQPQQPQPQQPQQPQQP---PQQQSHLVPVSLSNLIPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   453
CalJ_MEF2D   ------------------------------------------------------------------------------------------------------   371
AilM_MEF2D   -----------------------PQPQPHLVPVSLSSLIPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   409
MusM_MEF2D   QSQPQPPQPQPQQP----------PQQQPHLVPVSLSNLIPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   439
DanR_MEF2D   PSVSQQQTQQQQQQ----------QQQPQQLTLASLSNLVPVGTIPHGATLTVNTNPS-ISIKSEPVSPNRDRSSS----------------------   434
GalG_MEF2D   ------------------------------------------------------------------------------------------------------   352
RatN_MEF2D   QSQPQPPQPQPQQP----------PQQQPHLVPVSLSNLIPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   439
BosT_MEF2D   QPQPPQPPQQPQQP----------PQQQPHLVPVSLSNLIPGSPLPHVGAALTITTHPHISIKSEPVSPSRERSPAP----------------------   446
XenT_MEF2D   -----------------------HHQAQQLIPVSLSNLVSSGQLPHTATLTVNTNPN-ISIKKEPPSPNRERST----------------------   422
MonD_MEF2D   PQQPPPQPQPQQQQQPPPPPPPP-PQQQSHLVPVSLSNLIPGSPLPHVAAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   455
TaeG_MEF2D   ------------------------------------------------------------ISIKSEPVSPNRERNTA----------------------   373
OryC_MEF2D   PQPQPPQPQPPQQPPQP-------PQQQSHLVPVSLSSLIPGSPLPHVGAALTVTTHPHISIKSEPVSPSRERSPAP----------------------   442
XenL_MEF2Db  -----------------------HNQQQQLIPVSLSNLVSSSHLPHTATLTVNTNPN-ISIKREPASPNRERST----------------------   422
XenL_MEF2Da  -----------------------HNQPQQLIPVSLSNLVSSSHLPHTATLTVNTNPN-ISIKREPASPNRERST----------------------   423
CanF_MEF2B   ----------------------PPQPSGAQTLIKKGPPPRGASPRTPQLRINSKPF-------------------------------------------   292
MacM_MEF2B   ----------------------PSQPSGGRSLGEEGPPTRGASPPTPPVSIKSERL-------------------------------------------   323
PanT_MEF2B   ----------------------PSQPSGGRSLGEEGPPTRGASPPTPPVSIKSERL-------------------------------------------   323
EquC_MEF2B   ----------------------PAQPSGGRSHGREGPY-----------------------------------------------------------   305
PonA_MEF2B   ----------------------PSQPSGGRSLGEEGPPTRGASPPTPPVSIKSERL-------------------------------------------   323
HomS_MEF2B   ----------------------SSQPSGGRSLGEEGPPTRGASPPTPPVSIKSERL-------------------------------------------   323
CalJ_MEF2B   ----------------------PSQPSGGRSLGEEGPPTHSASPPTPPVSIKSERL-------------------------------------------   323
AilM_MEF2B   ----------------------PPQPSGSRSLSEEGPAARGASPPTPPVSIKSERL-------------------------------------------   320
MusM_MEF2B   ----------------------DPARPVARSLCKEGPPSRGASPPTPPVSIKSERL-------------------------------------------   304
RatN_MEF2B   ----------------------DPAGPAARSLCEEGPPSREASPPTPPVSIKSERL-------------------------------------------   304
BosT_MEF2B   ----------------------PTQPSGGRSLGEDGPPARGASSPTPPVSIKSERL-------------------------------------------   323
MonD_MEF2B   ----------------------QSHLSVGPGPGEEAPVAPGGSPPAPALSIKSERV-------------------------------------------   323
OrnA_MEF2B   ----------------------HSQLGSRIPPGDEGPPAPGVSPHPQPISIKSERV-------------------------------------------   321
DroMel_MEF2  GGAVSAANVITHLNNVSVLA-----GGPSGQGGGGGGGGSNGNVEQATNLSVLSHAQQHHLGMPNSRPSSTGHITPTPGH--------------------   463
DroSim_MEF2  GGAVSAANVITHLNNVSVLA-----GGPSGQGGGGGGGGSNGNVEQATNLSVLSHAQQHHLVMSNSRPSSTGHITPTPGH--------------------   463
DroAna_MEF2  GGGGLAAASTANVITHLNNVSVLA-GGPSGGGGSGSGGGGSNGSVEQATNLSVLSHSQQQHLGMPSSRPSSTGHITPTTGH--------------------   467
DroEre_MEF2  AVGGGAVSAANVITHLNNVSVLA--GGPSGQGGGGGGGGSNGNVEQATNLSVLSHAQQHHLVMPNSRPSSTGHITPTPGH--------------------   466
DroGri_MEF2  ANVLTAINAQ---------------LGSASVLTGTPGGGGTNGSAEQATNLSVLSHSQQHLVMPNSRPSSTGHITPTPGH--------------------   448
DroMoj_MEF2  TAINAITQLGGA-------------GVLTSGGGGGGGGGGTNGSAEQATNLSVLSHSQQHLVMPNSRPSSTGHITPTPGH--------------------   451
DroPer_MEF2  AGSSAANAGNVITHLNNA-------SILGGGGPPGGGGGGGSNGNAEQATNLSVLGHSQQHLVMPNSRPSSTGHLITPTPGH--------------------   461
DroSec_MEF2  GGAVSAANVITHLNNVSVLA-----GGPSGQGGGGGGGGSNGNVEQATNLSVLSHAQQHHLVMSNSRPSSTGHITPTPGH--------------------   463
DroVir_MEF2  LTAINA-------------------ITQLGGAGVGGGGGGSNGSADQATNLSVLSHSQQHLVMSNSRPSSTGHITPTPGH--------------------   446
DroWil_MEF2  TSASSVSVAANVISHLNQASV----LAGASGGGGGGGGGGSNGNAEQATNLSVLSHSQQHLVMPNSRPSSTGHITPTPGH--------------------   461
DroYak_MEF2  GGGGAVSAANVITHLNNVSVLA---GGPSGQGGGGGGGGSNGNVEQATNLSVLSHAQQHHLVMPNSRPSSTGHITPTPGH--------------------   465
DroPse_MEF2  AGSSAANAGNVITHLNNA-------SILGGGGPPGGGGGGSNGNAEQATNLSVLGHSQQHLVMPNSRPSSTGHLITPTPGH--------------------   461
AnoG_MEF2    -----------------------PGANGVQSASGGGASSTATGLTAMGNVVVTGGGGGGSGGGAGTSSLGANLNHSHLI----------------------   429
CulQ_MEF2d   -----------------------QQQQHHHHSNLSGGGGSNGQQQHNNQLTVTSMASVIGGGGHSSNSSMGNSL-------------------------   419
AedA_MEF2d   -----------------------SHHHHHHSNLSGSGGGGGGGGGPGGSGGANGQQNNNQLIVTSMAQVGGHSNSQSV--------------------   406
TriC_MEF2    -----------------------HLSVGVHHSHVQSLNLTHSHHPRP-----------------------------------------------------   369
ApiM_MEF2    -----------------------HHTALNVGPSSSTGAPPPHHVPHPGPQSLNLVSN-----------------------------------------   399
BomM_MEF2    ------------------------------APDHLHRGPPPASVPQPAHQMPG-----------------------------------------------   355
CioI_MEF2    -----------------------LLQNWPHQSPFPQPLTTPQHLLPHPSLMTQQVPM-IRIKREPETEASPD-------------------------   373
BraF_MEF2    -----------------------WQQQHPLSAAVQAAGITGSTPSSSTPGLLITDRGMGGIKSEPISPPRDKNQLNPTAGRC-----------------   374
CaeB_MEF2    ------------------------------------------------------------------------------------------------------   294
CaeE_MEF2    ------------------------------------------------------------------------------------------------------   291
CaeR_MEF2    ------------------------------------------------------------------------------------------------------   292
NasV_MEF2d   -----------------------HPGHTSLNVGGPSSSSGGPQPPPPHHVSQQQQHGGQTLNLVSVSRPG-------------------------------   378
SacK_MEF2    -----------------------WQHQHPLSAAVQAAGITGSTPSSSTPGLLITDRGMGGIKSEPISPPRDKNQLNPTAGRC-----------------   400
GalG_MEF2    ------------------------------------------------------------------------------------------------------   339
PhyI_MEF2    -------------TTGMLIHDFSPQNAGLFGHHPMLSGGMTGDFHDNKSSVLGLNLVPSDFNHGGAGSVHPQQLQQSKEQYYAHSKQTDSPEKSLGDRPG   311
SchM_MEF2a   LSKHLNITSWEGNQTPAIADSSRPNQSELYNNSFNLSSTSPSNRQLLSGSYDRNLSSCSNLKCKDDPYVTLIRDIQNSSHNLQTSSSTPSMQERFSHFPV   500
             .......410.......420.......430.......440.......450.......460.......470.......480.......490.......500
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CanF_MEF2A   PPQPSQPPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNTEDRESPSVKRMRM-DAWVT   499
MacM_MEF2A   PQPQPPQPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNTEDRESPSVKRMRM-DAWVT   495
PanT_MEF2A   PQPQPPQPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNTEDRESPSVKRMRM-DAWVT   501
SusS_MEF2A   QPQPQPQPQARQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPVVLGRPPNTEDRESPSVKRMRM-DAWVT   504
EquC_MEF2A   PPQPQPQPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNTEDRESPSVKRMRM-DAWVT   499
PonA_MEF2A   PQPQPPQPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNTEDRESPSVKRMRM-DAWVT   494
HomS_MEF2A   PQPQPPQPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNTEDRESPSVKRMRM-DAWVT   497
CalJ_MEF2A   PQPQPQQPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNAEDRESPSVKRMRM-DAWVT   492
AilM_MEF2A   ------------------------------------------------------------------------   416
MusM_MEF2A   PPPQPPQPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNTEDRESPSVKRMRM-DTWVT   498
DanR_MEF2A   ---------GRPDMGRSPVDSLSSSCS-SYDGSDREDHRPDFHSPLGLGRPPAADERESPSVKRMRM-DTWVT   455
GalG_MEF2A   PPQPPQQPPQRQEMGRSPVDSLSSSSS-SYDGSDREDPRSDFHSPVVLGRPPNSEDRESPSVKRMRM-DTWVT   498
RatN_MEF2A   PQPPQPQPQPRQEMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNAEDRESPSVKRMRM-DTWVT   492
BosT_MEF2A   PPPQAPQPQPRQEVGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPVVLGRPPNSEDRESPSVKRMRM-DAWVT   489
MonD_MEF2A   QQQQQQQQQARQEMGRSPVDSLSSSSS-SYDGSDREDPRSDFHSPIGLGRPPNTEDRESPSVKRMRM-DTWVT   502
XenL_MEF2A   ---------PRPEM-----DSLSSSSS-SYDGSDREDVRNDFHSPIGLGRPANNEDRDSPSVKRMRM-DAWVT   473
OrnA_MEF2A   QQQPQQQQSSRQEIGRSPVDSLSSSSS-SYDGSDREDPRSDFHSPIGLGRPPNTEDRESPSVKRMRM-DTWVT   505
TaeG_MEF2A   -----PPPPSRQELGRSPVDSLSSSSS-SYDGSDREDPRSDFHSPVVLGRPPNAEDRESPSVKRMRM-DTWVT   493
OryC_MEF2A   PQPPQPQPQPRQDMGRSPVDSLSSSSS-SYDGSDREDPRGDFHSPIVLGRPPNPEDRESPSVKRMRM-DAWVT   497
CanF_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
MacM_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
PanT_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   471
SusS_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   433
EquC_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
PonA_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
HomS_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   471
CalJ_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
AilM_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
MusM_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   465
GalG_MEF2C   ------------------------------------------------------------------------   367
RatN_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   465
BosT_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   441
XenT_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNDFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   432
MonD_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
XenL_MEF2C   -----YPHHTRHDAGRSPVDSLSSCSS-SYDGSDREDHRNDFHSPIGLTRP-LQDERESPSVKRMRLSEGWAT   429
OrnA_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
TaeG_MEF2C   -----YQQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   473
OviA_MEF2C   -----YPQHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   433
OryC_MEF2C   -----YPPHTRHEAGRSPVDSLSSCSS-SYDGSDREDHRNEFHSPIGLTRP-SPDERESPSVKRMRLSEGWAT   465
DanR_MEF2Ca  -----YPQQTRQDSGRSPVDSLSSCGS-SYDGSDREDEHRANFHSPVGLMRAAEN-ERQSPSVKRMRLSEGWAS   459
DanR_MEF2Cb  -----YPSHQRQDSGRSPADSLSSCGS-SHEGSDRDEHRPDFHSPLGLGRPGLD-DQDSPSIKRVRLSEGWAT   451
CanF_MEF2D   -----PPPAVFPATRPEPGDGLSSPASSSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGPAVKRM-RLDTWDA   440
MacM_MEF2D   -----PPPAVFPAARPEPGDGLSSPAGGSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGSAVKRM-RLDTWVL   520
PanT_MEF2D   -----PPPAVFPAARPEPGDGLSSPAGGSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGSAVKRM-RLDTWTL   520
SusS_MEF2D   -----PTRSLFQAARIQPGAGLSTPAQASAAAAERLHGRGKAGRTLGLQGPEEDPAAVGPQDRTV-GATFHFL   516
EquC_MEF2D   -----PPPAVFPATRPEPGDGLSSPAGGSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGSAVKRM-RLDTWGL   462
PonA_MEF2D   -----PPPAVFPAARPEPGDGLSSPAGGSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGSAVKRM-RLDTWVL   520
HomS_MEF2D   -----PPPAVFPAARPEPGDGLSSPAGGSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGSAVKRM-RLDTWTL   520
CalJ_MEF2D   ----------------------------QPQQPQPPQQQPPQPQQPQPQQPQQPQQPPQPQSHLVPVSLSNLM   416
AilM_MEF2D   -----PPPAVFPAARPEPGDGLSSPASGSYETGDRDDGRGDFGPTLGLLRPAQEPEAEGPAVKRMRCSNGAG-   476
MusM_MEF2D   -----PPPAVFPAARPEPGEGLSSPAGGSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGSAVKRM-RLDTWTL   506
DanR_MEF2D   -----TPTVSQYPTLRLEPGRSISSNGSSYEGSDRDDSGQPDFSSLGLLRATGDQQQESANVKRM-RLDTWVT   501
GalG_MEF2D   ------------------------------------------------------------------------   352
RatN_MEF2D   -----PPPAVFPAARPEPGEGLSSPAGGSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGSAVKRM-RLDTWTL   506
BosT_MEF2D   -----PPPAVFPATRPEPGDALSSPAGPSYETGDRDDGRGDFGPTLGLLRPAPEPEAEGSAVKRM-RLDTWTL   513
XenT_MEF2D   -----GTPLSSFPQSRHEVGRSLSSNASSFEGNDREDVRGDYTSSLGLLRPSGDTESESQSVKRM-RLDAWVT   489
MonD_MEF2D   -----PAPAPFPPARPEPGDGLSSPASASYEAGERDDGRGDFGPTLGLLRPAPEPDTESSAVKRM-RLDTWVT   522
TaeG_MEF2D   -----TPLSTFPHQPRHEPGRSLSSNTSSYEGSERDDPARDFGSSLGLLRPTSEPEGESPSVKRM-RLDTWVT   440
OryC_MEF2D   -----PPPAVFPAARPEPDDSLSSPAGGAYETGDRDDGRGDFGPTLGLLRPAPEPDAEGSAVKRM-RLDTWVL   509
XenL_MEF2Db  -----GTPLSCFPQSRHEVGRSLSSNASSFEGNDREDPRGDYTSSLGLLRPSGDTESESQSVKRM-RLDAWVT   489
XenL_MEF2Da  -----GTPLSCFSQSRHEAGRSLSSNASSFEGNDREDPRGDYTSSLGLLRPSGDTESESQSVKRM-RLDAWVT   490
CanF_MEF2B   --------------------------SPPPGAPENFPKIFPYPLFFSRPLGKPLRPGPPLPEFPIGNAWPR-   337
MacM_MEF2B   --------------------------SPAPGGPGDFPKTFPYPLLLARSLAEPLRPGPALRRLPLADGWPR-   368
PanT_MEF2B   --------------------------SPAPGGPGDFPKTFPYPLLLARSLAEPLRPGPALRRLPLADGWPR-   368
EquC_MEF2B   ------------------------------------------------------------------------   305
PonA_MEF2B   --------------------------SPAPGGPGDFPKTFPYPLLLARSLAEPLRPGPVLRRLPLADGWPR-   368
HomS_MEF2B   --------------------------SPAPGGPGDFPKTFPYPLLLARSLAEPLRPGPALRRLPLADGWPR-   368
CalJ_MEF2B   --------------------------SPAPGGPGDFPKTFPYPLLLARSLAEPLRPGPALRRLPLADGWPR-   368
AilM_MEF2B   --------------------------SPAPGGPGDFPKTFPYPLLLSRPLAEPLRPGPPLRRLPTADGWAR-   365
MusM_MEF2B   --------------------------SPVTGTSGDFPRSFPYPLLLARPLAEPLRPSASLHRL-TPDSWPR-   348
RatN_MEF2B   --------------------------SPVTGTSGDFPRSFPYPLLLARPLAEPLRP-ASLRRL-TPDSWPR-   347
BosT_MEF2B   --------------------------SPAPGGPGDFPKTFPYPLLLARPLAEPLRPGPPLRRLPTADGWPR-   368
MonD_MEF2B   --------------------------SPGAVPRDDFTKSYQYPVGLARP-------GQPLRRLHVADSWPR-   361
OrnA_MEF2B   --------------------------SPGATCREDFTKGYPYPLVLARPLNEEPRTGLPTRRLQVAEMVVV-   366
DroMel_MEF2  ------DKYEGYPYRALMGHNPRWNFAGAPSSDQDVRLAAVAQQQQQQQPHQQQQLGDYDAPNHKRPRISGGWG   530
DroSim_MEF2  ------DKYEGYPYRALMGHNPRWNFAGAPSSDQDVRLAAVAQQQQQQQPHQQQQLGDYDAPNHKRPRISGGWG   530
DroAna_MEF2  ------DKYDGYPYRALMGHNPRWNFAGAPSSDQDVRMAAAAHQQQQQQQQQQQQLGDYDAPNHKRPRISGGFG   534
DroEre_MEF2  ------DKYEGYPYRALMGHNPRWNFAGAPSSDQDVRLAAVAQQQQQQQPHQQQQLGDYDAPNHKRPRISGGWG   533
DroGri_MEF2  ------DKYEGYPYRALMGHNSRWNFAGAPGSEQDVRLAAVAQQQHQQQQQQQQLSDYDAPNHKRPRISGGWG   515
DroMoj_MEF2  ------DKYEGYPYRALMGHNPRWNFAGAPNGEQDVRLQAVAQQQQQQPHQQQQLSDYDAPNHKRPRISGGWG   518
DroPer_MEF2  ------DKYEGYQYRLLMGHNPRWNSAGAPSSEQDVRLAAVAQQHQQHQQQQQQLGDYDAPNHKRPRISGGWG   528
DroSec_MEF2  ------DKYEGYPYRALMGHNPRWNFAGAPSSDQDVRLAAVAQQQQQQQPHQQQQLGDYDAPNHKRPRISGGWG   530
DroVir_MEF2  ------DKYEGYQYRALMGHNPRWNFAGAPSSEQDVRLAAVAQQQQQHQQQQQQLSDYDAPNHKRPRISGGWG   513
DroWil_MEF2  ------DKYEGYPYRALMGHNPRWNFAGTPTSEQDVRLQQQQHQQQQQHQQQQQLNDYDAPHQKRPRISGGWA   528
DroYak_MEF2  ------DKYEGYPYRALMGHNPRWNFAGAPSSDQDVRLAAVAQQQQQQQPHQQQQLGDYDAPNHKRPRISGGWG   532
DroPse_MEF2  ------DKYEGYQYRLLMGHNPRWNSAGAPSSEQDVRLAAVA-QHQQHQQQQQQQLGDYDAPNHKRPRISGGWG   527
AnoG_MEF2    ------HSRPSSTGHLTPTPDSYMPIGGHLAGSVTPTNAPSPVDIRHLSTGGSHLPEYDAPTHKRPRISEGWA   496
CulQ_MEF2d   ------NHSHLIHSRPSSTGHLTPTPGSVTPTNAPSPVDIRHINVGGGGGNSSHLPDYDSPVHKRPRISEGWA   486
AedA_MEF2d   ------ALGSSLNHSHLIHSRPSSTGHLTPTPGSVTPTNAPSPVDIRHLGGGGPLPDYDSPVHKRPRISEGWA   473
TriC_MEF2    ----------------------------SSAGHITPTPGSVTPTNLPSPTGPPSGGDYENIQHKRARLSDWP   413
ApiM_MEF2    -----------RPSSNPPPSHSGSITPTNLPSPGSATVADIRTSHSNTGGNGGNNSDYENGPMKRSRITEGWA   461
BomM_MEF2    ----------------------------VIDGSVSSSNMGSPAGQDMRHSNAVALDYEQPHTKRP-RIEGWA   398
CioI_MEF2    ------KDPDQRPAAGRSPMEVMSPYEMRMDDRSMMVENGGNLPVKRQRVESGPN------------ASPTWT   428
BraF_MEF2    ----NNQGGLHANNTSPVNSLCSSSSSPFPADGEDRGDGSFHSPGGSRMRKAMEDEGRGMRLSL--------   435
CaeB_MEF2    --------------------------SLNGHSVLDLGGPIPPYKMDPNAYIKVEPHSPPQKRPRITTEWRQQ   340
CaeE_MEF2    --------------------------SLNGHSVLDLGGPNLPYKLDPNTYVKMEPHSPPEKRPRITTEWRPQ   337
CaeR_MEF2    --------------------------SLNGHSVLDLGGPIPPYKLDPNAYVKLEPHSPPQKRPRITTEWRPQ   338
NasV_MEF2d   ------SNPPPSHSGSITPTNLPSPGPQGGGGGGNGGVVVGDRTSHGPGASGGSGSDYENGPHKRSRITEGWA   445
SacK_MEF2    ----TPHDTAMSPGRHSHCSSASASPFAGSDREDGRGGGDSNYQSSGNRGSIMGDKDGPPTKRQRIENAWST-   468
GalG_MEF2    --------------------------NISAWQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ---------   376
PhyI_MEF2    SPEASGDKPSDEVVCKVEKPTEKEQSRQDDESNNEDSQSAKENETTDKAKSLSPKRE----------------   368
SchM_MEF2a   IHESIASLNSCKIQQQPPQQLQNPPNILDDEIGVGSIPSNQRSFKPDQFIESVPSPELLLFLSSNNNNSNNLK   573
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