

Figure S7

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CLUSTAL O(1.2.4) multiple sequence alignment

Dmau_TAM16      MAAGFLKSGDLGPHPHSYGGPHPHSVPHGPLPPGMPMPSLGPFGLPHGLEAVGFSQGVN 60
Dsim            MAAGFLKSGDLGPHPHSYGGPHPHSVPHGPLPPGMPMPSLGPFGLPHGLEAVGFSQGVN 60
Dmau            MAAGFLKSGDLGPHPHSYGGPHPHSVPHGPLPPGMPMPSLGPFGLPHGLEAVGFSQGVN 60
                *****
                Homeodomain
Dmau_TAM16      TRKQRRERTTFTRAQLDVLEALFGKTRYPDIFMREEVALKINLPESRVQVWFKNRRAKCR 120
Dsim            TRKQRRERTTFTRAQLDVLEALFGKTRYPDIFMREEVALKINLPESRVQVWFKNRRAKCR 120
Dmau            TRKQRRERTTFTRAQLDVLEALFGKTRYPDIFMREEVALKINLPESRVQVWFKNRRAKCR 120
                *****

Dmau_TAM16      QQLQQQQQSNLSSSKNASGGGSGGSCSSSSANSRNSNNNGSSSSNNNSQSSGGNNSNKS 180
Dsim            QQLQQQQQSNLSSSKNASGGGSGGSCSSSSANSRNSNNNGSSSSNNNSQSSGGNNSNKS 180
Dmau            QQLQQQQQSNLSSSKNASGGGSGGSCSSSSANSRNSNNNGSSSSNNNSQSSGGNNSNKS 180
                *****

Dmau_TAM16      SQKQGNSSQSQGGGSSGGNNSNNNSAAAAASAAAAVAAASQIKTHHSSFLSAAAAAASG 240
Dsim            SQKQGNSSQSQGGGSSGGNNSNNNSAAAAASAAAAVAAASQIKTHHSSFLSAAAAAASG 240
Dmau            SQKQGNSSQSQGGGSSGGNNSNNNSAAAAASAAAAVAAASQIKTHHSSFLSAAAAAASG 240
                *****

Dmau_TAM16      GTNQSANNNNSNNNQGNSTPNSSSSGGGGGQAGGHLAAAAAALNVTAAHQNSSPLL 300
Dsim            GTNQSANNNNSNNNQGNSTPNSSSSGGGGGQAGGHLAAAAAALNVTAAHQNSSPLL 300
Dmau            GTNQSANNNNSNNNQGNSTPNSSSSGGGGGQAGGHLAAAAAALNVTAAHQNSSPLL 300
                *****

Dmau_TAM16      TPATSVSPVSI VCKEHLSGGYGSSVGGGGGXXXXXXXXXXXXXXXXXXXXXVGVGVSQD 360
Dsim            TPATSVSPVSI VCKEHLSGGYGSSVGGGGGGGGGASSGGGLNLGVGVGVGVGVGVGVSQD 360
Dmau            TPATSVSPVSI VCKEHLSGGYGSSVGGGGGGGGGASSGGGLNLGVGVGVGVGVGVGVSQD 360
                *****

Dmau_TAM16      LLRSPYDQLKDAGGDIGAGVHHHSIYXXAAGSNPRLQPGGNITPMDSSSSITTPSPPI 420
Dsim            LLRSPYDQLKDAGGDIGAGVHHHSIYGAAGSNPRLQPGGNITPMDSSSSITTPSPPI 420
Dmau            LLRSPYDQLKDAGGDIGAGVHHHSIYGAAGSNPRLQPGGNITPMDSSSSITTPSPPI 420
                *****

Dmau_TAM16      TPMS PQSAAAAAHAAQSAQSAHHSAAHSAA YMSNHDSYNFVHNQYQQYPNNYAQAPS YYS 480
Dsim            TPMS PQSAAAAAHAAQSAQSAHHSAAHSAA YMSNHDSYNFVHNQYQQYPNNYAQAPS YYS 480
Dmau            TPMS PQSAAAAAHAAQSAQSAHHSAAHSAA YMSNHDSYNFVHNQYQQYPNNYAQAPS YYS 480
                *****

Dmau_TAM16      QMEYFSNQNVN YNMGHSGYTASNFGLSPPSPSFTGT VSAQAFSQNSLDYMS PQDKYANMV 540
Dsim            QMEYFSNQNVN YNMGHSGYTASNFGLSPPSPSFTGT VSAQAFSQNSLDYMS PQDKYANMV 540
Dmau            QMEYFSNQNVN YNMGHSGYTASNFGLSPPSPSFTGT VSAQAFSQNSLDYMS PQDKYANMV 540
                *****

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Figure S7. Alignment of *D. mauritiana* TAM16 and *D. simulans* y, v, f Otd protein sequences