

90 100 110 120 130 140 150 160 170

Medtru_MtrunA17_Chr2g0306641 P SKTKDIDGLLANVGYKVRSELHQVAQNLERLESAIVNSSSDISQFASDT-V-----HYDP-SDIGNWVDNLLSEFDH-
Musacu_GSMUA_Achr6P34550_001 GSSRGEIDSL LHGAGYRVRSTDLRHVAIGLEQLESTMV---GDQCVASSAEAI-----HYNP-SDLTAWVDSMLSELAPD
Zosmar_Zosma208g00370.1 ---AEIEVRLAEAGYLGRVADLQQVYRPDERRTVFSPPDPQIIQFSDSSTIIH-----GNNP-SDLSGWVDSMLSQISTP
Spipol_Spipo0G0167100 -----IDGLLAEAGYRVRSSDLRQVARRLERLESAMVGEAGPACLGSAAAAQVIDQQQQMFLAPDAVHYNP-SDLAAWVDSMLSEISP-
Bradis_Bradi1g32070.2 -----PSTGPAASSPLIETVPPPSTQAAATTNT-----NTNVRVNPSTYTSLSLQPAMS-
Bradis_Bradi1g47900.2 -----ANSSLLTGTVPSPSTQAVATTNTNVRVD-----PPSTHASHHLHPAMS-
Bradis_Bradi2g45117.1 -----LSSGVDGSLLP SFLPPPPAAAVPDDGTA-----YY--AASDMHSVPCLPELAA-
Horvul_HORVU3Hr1G058100.1 -----PTSSLDASLPPSLLPPPPAAV-PDDGAA-----YY--AAADMHA-SSMPDLAP-
Horvul_HORVU1Hr1G090800.1 PDAHPQPAVALAAFTQLALEEHMGHFAFGWQGMEPAPAASLSAAAAATNGADA-----AYC--VHPATYAPAALATVPP-
Orysat_LOC_Os05g49930.1 -----AAAAALGNVSGAV-----YH--ADPAAAVYASLVPGMA-
Orysat_LOC_Os01g45860.1 -----ASSGLDAGFLP-----PPAAVAPDDGVG-----YYDPPAGADVDA-AALPEFAA-
Setita_Seita.5G243400.1 -----GLDVSLPPLPTVVPDAAGVA-----YY--ADAAADMHAAMPVLP-
Setita_Seita.3G137200.1 -----AATFTGGIPPPF-----PAAADNGAA-----YC--IDPTTLLASLLPPGRQ-
Sorbic_Sobic.003G237201.1 -----
Sorbic_Sobic.008G168400.1 -----AAATLTADA AVPAAPIP IPTPTTTT DAAAMQH-----YY----LNSWLHASLMQPAV-
Zeamay_Zm00008a030834 -----TAMALSGTLSPSF-----STTSTNDT-----MYN--LNPALYA-SLVPPIRK-

DELLA§LxYxVxxxxMAxVaxxLExLEx§

TVHYNPxxLxxWxxxM