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gi | 17534013 | ref | NP_495099.1 | 59 | ---- | 58-AARNPENVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 114NPEEHS|SAMVLOKMRST
gi | 17507981 | ref | NP_492485.1 | 59 | ---- | 58-AARNPENVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 114NPEEHS|SAMVLOKMRST
gi | 66800327 | ref | XP_629089.1 | 56 | ---- | 55-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 113SPPEHS|SAMVLOKMRST
gi | 66826525 | ref | XP_646177.1 | 56 | ---- | 55-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 113SPPEHS|SAMVLOKMRST
gi | 66922147 | ref | XP_643428.1 | 57 | ---- | 56-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 112TPEEHS|SAMVLOKMRST
gi | 85110248 | ref | XP_643386.1 | 57 | ---- | 56-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 112TPEEHS|SAMVLOKMRST
Phpat.004G083500 | Phpat.004G083500.1 | 62 | ---- | 61-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 118AAEES|SAMVLOKMRST
GRMZM2G366532 | GRMZM2G366532.T01 | 63 | ---- | 62-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1198AAEES|SAMVLOKMRST
LOC_Os03g16920 | LOC_Os03g16920.1 | 63 | ---- | 62-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1198AAEES|SAMVLOKMRST
PGSC0003DMG400027750 | PGSC0003DMG40007133 | 62 | ---- | 61-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1188AAEES|SAMVLOKMRST
Carubv10008420m.g | Carubv10008420m.g | 62 | ---- | 61-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1188AAEES|SAMVLOKMRST
LOC_Os05g38530 | LOC_Os05g38530.1 | 61 | ---- | 60-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1178AAEES|SAMVLOKMRST
GRMZM5G802801 | GRMZM5G802801.T01 | 61 | ---- | 60-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1178AAEES|SAMVLOKMRST
AC209784.3.FG007 | AC209784.3.FG007 | 61 | ---- | 60-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1178AAEES|SAMVLOKMRST
GRMZM2G310431 | GRMZM2G310431.T01 | 61 | ---- | 60-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1178AAEES|SAMVLOKMRST
gi | 34419635 | ref | NP_023146.2 | 61 | ---- | 60-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 116YPEEHS|SAMVLOKMRST
gi | 167466173 | ref | NP_025337.2 | 59 | ---- | 58-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 114NPEEHS|SAMVLOKMRST
gi | 124256496 | ref | NP_005518.3 | 61 | ---- | 61-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1188AAEES|SAMVLOKMRST
gi | 530381921 | ref | XP_005249127.1 | 125 | ---- | 124-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 116YPEEHS|SAMVLOKMRST
gi | 530428004 | ref | XP_005272871.1 | 61 | ---- | 60-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1178AAEES|SAMVLOKMRST
gi | 530428002 | ref | XP_005272870.1 | 125 | ---- | 124-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 116YPEEHS|SAMVLOKMRST
gi | 530427781 | ref | XP_005274915.1 | 61 | ---- | 60-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1178AAEES|SAMVLOKMRST
gi | 530427783 | ref | XP_005274916.1 | 125 | ---- | 124-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 116YPEEHS|SAMVLOKMRST
gi | 136768578 | ref | NP_068944.0 | 60 | ---- | 59-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 115TPEEHS|SAMVLOKMRST
gi | 5729877 | ref | NP_065888.1 | 59 | ---- | 58-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 114NPEEHS|SAMVLOKMRST
gi | 530398061 | ref | XP_005271593.1 | 59 | ---- | 58-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 114NPEEHS|SAMVLOKMRST
gi | 85080590 | ref | XP_955667.1 | 94 | ---- | 93-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 149TPEEHS|SAMVLOKMRST
gi | 66818991 | ref | XP_643155.1 | 87 | ---- | 86-ATNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 142SPEEHS|SAMVLOKMRST
gi | 165072371 | ref | NP_000345.1 | 84 | ---- | 83-ATNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 142SPEEHS|SAMVLOKMRST
Cre02.g080600 | Cre02.g080600.t.2 | 112 | ---- | 111-VAMNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 116YPEEHS|SAMVLOKMRST
PGSC0003DMG400024707 | PGSC0003DMG40006354 | 97 | ---- | 96-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 153SPEEHS|SAMVLOKMRST
Bra031657 | Bra031657 | 106 | ---- | 105-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
Carubv10008520m.g | Carubv10008520m.g | 95 | ---- | 94-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 150SPEEHS|SAMVLOKMRST
Potri.013G018000 | Potri.013G018000.1 | 86 | ---- | 85-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 145SPEEHS|SAMVLOKMRST
Phpat.010G061700 | Phpat.010G061700.1 | 86 | ---- | 85-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 145SPEEHS|SAMVLOKMRST
Phpat.010G067200 | Phpat.010G067200.1 | 86 | ---- | 85-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 145SPEEHS|SAMVLOKMRST
440900 | 440900 | 83 | ---- | 82-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 139SPEEHS|SAMVLOKMRST
Bra028521 | Bra028521 | 89 | ---- | 88-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 145SPEEHS|SAMVLOKMRST
Bra015047 | Bra015047 | 90 | ---- | 89-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 146SPEEHS|SAMVLOKMRST
Bra022819 | Bra022819 | 92 | ---- | 91-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 148SPEEHS|SAMVLOKMRST
Potri.012G017600 | Potri.012G017600.1 | 92 | ---- | 91-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 148SPEEHS|SAMVLOKMRST
GRMZM2G114793 | GRMZM2G114793.T01 | 88 | ---- | 87-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 145SPEEHS|SAMVLOKMRST
GRMZM2G415007 | GRMZM2G415007.T01 | 88 | ---- | 87-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 145SPEEHS|SAMVLOKMRST
LOC_Os02g02410 | LOC_Os02g02410.1 | 81 | ---- | 80-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 144SPEEHS|SAMVLOKMRST
PGSC0003DMG400018544 | PGSC0003DMG40004771 | 91 | ---- | 90-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 147SPEEHS|SAMVLOKMRST
Glyma08g02960 | Glyma08g02960.1 | 131 | ---- | 130-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 187SPEEHS|SAMVLOKMRST
Glyma08g03620 | Glyma08g03620.1 | 131 | ---- | 130-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 187SPEEHS|SAMVLOKMRST
Glyma05g36620 | Glyma05g36620.1 | 40 | ---- | 39-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 145SPEEHS|SAMVLOKMRST
Glyma08g02940 | Glyma08g02940.1 | 91 | ---- | 90-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 146SPEEHS|SAMVLOKMRST
PGSC0003DMG400012254 | PGSC0003DMG40003193 | 91 | ---- | 90-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 147SPEEHS|SAMVLOKMRST
GSVIVG01019607001 | GSVIVT01019607001 | 143 | ---- | 142-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 199SPEEHS|SAMVLOKMRST
Eucgr.E01024 | Eucgr.E01024.1 | 90 | ---- | 89-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 147SPEEHS|SAMVLOKMRST
Cucsa.303949 | Cucsa.303949.1 | 91 | ---- | 90-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 147SPEEHS|SAMVLOKMRST
30068.t000021 | 30068.t000021.1 | 90 | ---- | 89-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 146SPEEHS|SAMVLOKMRST
Potri.001G087500 | Potri.001G087500.1 | 91 | ---- | 90-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 146SPEEHS|SAMVLOKMRST
Potri.003G143600 | Potri.003G143600.1 | 58 | ---- | 57-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 110APEEHS|SAMVLOKMRST
CMV163C | 58 | ---- | 57-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 110APEEHS|SAMVLOKMRST
Cre06.g250100 | Cre06.g250100.t.1 | 97 | ---- | 96-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 148APEEHS|SAMVLOKMRST
Vocar20003521m.g | Vocar20003521m.g | 96 | ---- | 95-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 147SPEEHS|SAMVLOKMRST
230659 | 230659 | 84 | ---- | 83-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 138APEEHS|SAMVLOKMRST
Phpat.004G105700 | Phpat.004G105700.1 | 131 | ---- | 130-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 183AAEES|SAMVLOKMRST
Phpat.007G061700 | Phpat.007G061700.1 | 135 | ---- | 134-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 187AAEES|SAMVLOKMRST
Phpat.007G061800 | Phpat.007G061800.1 | 135 | ---- | 134-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 187AAEES|SAMVLOKMRST
Phpat.007G061900 | Phpat.007G061900.1 | 135 | ---- | 134-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 187AAEES|SAMVLOKMRST
Phpat.026G031600 | Phpat.026G031600.1 | 133 | ---- | 132-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 185AAEES|SAMVLOKMRST
Carubv10008629m.g | Carubv10008629m.g | 134 | ---- | 133-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 186AAEES|SAMVLOKMRST
Carubv10004245m.g | Carubv10004245m.g | 133 | ---- | 132-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 185AAEES|SAMVLOKMRST
Bra013786 | Bra013786 | 131 | ---- | 130-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 183AAEES|SAMVLOKMRST
Bra019231 | Bra019231 | 128 | ---- | 127-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 180AAEES|SAMVLOKMRST
Bra002461 | Bra002461 | 1 | ---- | 0 - MGPCFTRRLVDDASRF | 0
Bra010498 | Bra010498 | 132 | ---- | 131-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 184AAEES|SAMVLOKMRST
267815 | 267815 | 86 | ---- | 85-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 142SPEEHS|SAMVLOKMRST
LOC_Os05g23740 | LOC_Os05g23740.1 | 106 | ---- | 105-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 158AAEES|SAMVLOKMRST
GRMZM2G079668 | GRMZM2G079668.T01 | 101 | ---- | 100-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 153AAEES|SAMVLOKMRST
GRMZM2G111475 | GRMZM2G111475.T01 | 109 | ---- | 108-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
Cucsa.079370 | Cucsa.079370.1 | 40 | ---- | 39-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 145SPEEHS|SAMVLOKMRST
LOC_Os12g14070 | LOC_Os12g14070.1 | 116 | ---- | 115-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 169AAEES|SAMVLOKMRST
GSVIVG01026014001 | GSVIVT01026014001 | 126 | ---- | 125-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 178AAEES|SAMVLOKMRST
Eucgr.G00235 | Eucgr.G00235.1 | 126 | ---- | 125-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 178AAEES|SAMVLOKMRST
PGSC0003DMG400024887 | PGSC0003DMG40006403 | 108 | ---- | 107-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 160AAEES|SAMVLOKMRST
Glyma16g00410 | Glyma16g00410.1 | 124 | ---- | 123-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 176AAEES|SAMVLOKMRST
Cucsa.266110 | Cucsa.266110.1 | 127 | ---- | 126-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 179AAEES|SAMVLOKMRST
Medtr2g005690 | Medtr2g005690.1 | 128 | ---- | 127-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 177AAEES|SAMVLOKMRST
Eucgr.I02771 | Eucgr.I02771.1 | 128 | ---- | 127-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 177AAEES|SAMVLOKMRST
Potri.003G006300 | Potri.003G006300.1 | 126 | ---- | 125-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 178AAEES|SAMVLOKMRST
Potri.004G224400 | Potri.004G224400.1 | 125 | ---- | 124-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 177AAEES|SAMVLOKMRST
29765.t000021 | 29765.t000021.1 | 123 | ---- | 122-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 175AAEES|SAMVLOKMRST
GSVIVG01008331001 | GSVIVT01008331001 | 86 | ---- | 85-MVNPAENVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 115APEEHS|SAMVLOKMRST
gi | 6680557 | ref | XP_629204.1 | 86 | ---- | 85-MVNPAENVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 115APEEHS|SAMVLOKMRST
XIR045C | 86 | ---- | 85-MVNPAENVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 115APEEHS|SAMVLOKMRST
gi | 164426355 | ref | XP_961753.2 | 101 | ---- | 100-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 1389APEEHS|SAMVLOKMRST
gi | 24234688 | ref | NP_004125.3 | 103 | ---- | 102-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 151SPEEHS|SAMVLOKMRST
gi | 299469993 | emb | CBN79170.1 | 109 | ---- | 108-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
CML205C | 109 | ---- | 108-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
Cre09.g393200 | Cre09.g393200.t.1 | 156 | ---- | 155-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 198SPEEHS|SAMVLOKMRST
Vocar20005243m.g | Vocar20005243m.g | 159 | ---- | 158-GRDORRVDMLRFGIRCLRHRHETGPPVYR1 | 198SPEEHS|SAMVLOKMRST
168287 | 168287 | 69 | ---- | 68-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 121SPEEHS|SAMVLOKMRST
Phpat.001G091000 | Phpat.001G091000.1 | 107 | ---- | 106-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 159SPEEHS|SAMVLOKMRST
Phpat.001G091100 | Phpat.001G091100.1 | 107 | ---- | 106-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 159SPEEHS|SAMVLOKMRST
Phpat.002G052800 | Phpat.002G052800.1 | 111 | ---- | 110-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 163SPEEHS|SAMVLOKMRST
Phpat.002G053100 | Phpat.002G053100.1 | 109 | ---- | 108-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
GRMZM2G365374 | GRMZM2G365374.T01 | 109 | ---- | 108-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
LOC_Os09g31486 | LOC_Os09g31486.1 | 111 | ---- | 110-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 163SPEEHS|SAMVLOKMRST
LOC_Os09g31486 | LOC_Os09g31486.2 | 1 | ---- | 0 - MKMVPYKIVRG-PNGDAWEM---GGQKY 25SPSQIGAFVLTMRK
Bra010620 | Bra010620 | 103 | ---- | 102-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 155SPEEHS|SAMVLOKMRST
Bra011794 | Bra011794 | 108 | ---- | 107-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 160SPEEHS|SAMVLOKMRST
AT4037911 | 108 | ---- | 107-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 160SPEEHS|SAMVLOKMRST
Carubv10006443m.g | Carubv10006443m.g | 108 | ---- | 107-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 160SPEEHS|SAMVLOKMRST
Eucgr.G01045 | Eucgr.G01045.1 | 116 | ---- | 115-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 168SPEEHS|SAMVLOKMRST
PGSC0003DMG400003122 | PGSC0003DMG40000809 | 40 | ---- | 39-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 159SPEEHS|SAMVLOKMRST
PGSC0003DMG400010677 | PGSC0003DMG40002770 | 113 | ---- | 112-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Carubv10013121m.g | Carubv10013121m.g | 113 | ---- | 112-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Bra006027 | Bra006027 | 109 | ---- | 108-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
Bra028628 | Bra028628 | 113 | ---- | 112-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 163SPEEHS|SAMVLOKMRST
GRMZM2G153815 | GRMZM2G153815.T01 | 108 | ---- | 107-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
LOC_Os02g53420 | LOC_Os02g53420.1 | 108 | ---- | 107-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
LOC_Os03g02260 | LOC_Os03g02260.1 | 108 | ---- | 107-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 161SPEEHS|SAMVLOKMRST
GSVIVG01006769001 | GSVIVT01006769001 | 113 | ---- | 112-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
29804.t000060 | 29804.t000060.1 | 113 | ---- | 112-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Potri.001G285500 | Potri.001G285500.1 | 113 | ---- | 112-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Potri.009G079700 | Potri.009G079700.1 | 113 | ---- | 112-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Eucgr.I02583 | Eucgr.I02583.1 | 113 | ---- | 112-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Medtr2g010020 | Medtr2g010020.1 | 110 | ---- | 109-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
GSVIVG0103571001 | GSVIVT0103571001 | 111 | ---- | 110-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Cucsa.331940 | Cucsa.331940.1 | 110 | ---- | 109-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Medtr4g092920 | Medtr4g092920.1 | 107 | ---- | 106-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 159SPEEHS|SAMVLOKMRST
Glyma07g30290 | Glyma07g30290.1 | 110 | ---- | 109-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Glyma08g06950 | Glyma08g06950.1 | 110 | ---- | 109-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 162SPEEHS|SAMVLOKMRST
Glyma13g32790 | Glyma13g32790.1 | 107 | ---- | 106-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 159SPEEHS|SAMVLOKMRST
Glyma15g06530 | Glyma15g06530.1 | 107 | ---- | 106-AALNPNVVDKARLLIGRRFSDPSVSDMLWFFKVVGG--KQKGFVIEVEVK-GEKRRQ | 159SPEEHS|SAMVLOKMRST

gi | 17534013 | ref | NP_495099.1 | 131 | ABTVLGHVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 174EPTAAALAYGDKGI--QDEKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 17507981 | ref | XP_492485.1 | 131 | ABVVLGHVSRDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 174EPTAAALAYGDKGI--TDEKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 68800327 | ref | XP_629089.1 | 130 | ABSYLGKPVNNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 173EPTAAALAYGDKKSGSGGKIKVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 66826525 | ref | XP_646617.1 | 129 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 172EPTAAALAYGDKKSG--GKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 66922147 | ref | XP_644428.1 | 130 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 173EPTAAALAYGDKKSG--GKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 85110248 | ref | XP_653338.1 | 134 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 172EPTAAALAYGDKKSG--GKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.004G083500 | Phpat.004G083500.1 | 135 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 178EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G366532 | GRMZM2G366532.T01 | 136 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 178EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_080316920 | LOC_080316920.1 | 136 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 179EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
PGSC0003DM40027750 | PGSC0003DM40027750.1 | 135 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 178EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Carubv10004240m.g | Carubv10004240m.g | 135 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 177EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_080593850 | LOC_080593850.1 | 134 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 178EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G580280 | GRMZM2G580280.T01 | 134 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 177EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
AC209784.3.FG007 | AC209784.3.FG007 | 134 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 177EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G310431 | GRMZM2G310431.T01 | 134 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 177EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 34419635 | ref | NP_022146.2 | 133 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 176EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 174466173 | ref | NP_025337.2 | 131 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 176EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
124256496 | ref | NP_005518.3 | 132 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 176EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 53038187 | ref | XP_005249127.1 | 194 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--QGRHVLLFDLGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 530428004 | ref | XP_005272870.1 | 133 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 176EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 530428002 | ref | XP_005272870.1 | 194 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--QGRHVLLFDLGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 530427781 | ref | XP_005274915.1 | 133 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 176EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 530427783 | ref | XP_005274915.1 | 132 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 176EPTAAALAYGDKKSSSTGKKNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
136765785 | ref | NP_068844.2 | 181 | KCVNLYLGHVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--QGRHVLLFDLGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 5298777 | ref | NP_065888.1 | 131 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 174EPTAAALAYGDKK--VGAERNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 53039861 | ref | XP_005271593.1 | 107 | EAYLGKTVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 149EPTAAALAYGLDKK--VGAERNVIFDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 20
gi | 85080590 | ref | XP_955667.1 | 165 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 209EPTAAALAYGLDKGTG--G--EROIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 66818991 | ref | XP_643155.1 | 158 | TABSGLGKTVTHAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 202EPTAAALAYGLDKGTG--DREKNIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 16507273 | ref | NP_063318.1 | 156 | KCVNLYLGHVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--QGRHVLLFDLGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--QGRHVLLFDLGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
PGSC0003DM40024707 | PGSC0003DM40024707.1 | 169 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 212EPTAAALAYGLDKGTG--K--EONIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra031657 | Bra031657 | 175 | KEVYEAFLGKIKIDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 221EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Carubv10008520m.g | Carubv10008520m.g | 166 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 210EPTAAALAYGLDKGG--G--HSNIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Potri.013G018000 | Potri.013G018000.1 | 161 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 205EPTAAALAYGLDKGG--G--DNIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.001G067100 | Phpat.001G067100.1 | 158 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 202EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_010G067200 | Phpat.010G067200.1 | 155 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 202EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
440900 | 440900 | 161 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 205EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra028521 | Bra028521 | 162 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 206EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra015047 | Bra015047 | 162 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 206EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra022819 | Bra022819 | 162 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 206EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Potri.012G017600 | Potri.012G017600.1 | 164 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 204EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G114793 | GRMZM2G114793.T01 | 160 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 204EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G415007 | GRMZM2G415007.T01 | 160 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 204EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_080292410 | LOC_080292410.1 | 163 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 204EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
PGSC0003DM400018544 | PGSC0003DM400018544.1 | 160 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 202EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Glyma08g02960 | Glyma08g02960.1 | 200 | MKETAEFLGKIKIDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 247EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Glyma08g03660 | Glyma08g03660.1 | 194 | MKETAEFLGKIKIDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 247EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Glyma08g036620 | Glyma08g036620.1 | 194 | MKETAEFLGKIKIDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 247EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Glyma08g02940 | Glyma08g02940.1 | 162 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 206EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
PGSC0003DM400012254 | PGSC0003DM400012254.1 | 163 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 207EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GSVTVG0101960700 | GSVTVG0101960700.1 | 163 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 207EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Eucgr.E01024 | Eucgr.E01024.1 | 212 | MKETAEFLGKIKIDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 259EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Cucsa.301024 | Cucsa.301024.1 | 163 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 206EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
30068.t.000021 | Cucsa.t.00021.1 | 162 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 206EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Potri.001G087500 | Potri.001G087500.1 | 162 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 206EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Potri.003G143600 | Potri.003G143600.1 | 162 | HAYGLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 206EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
CMV163c | 127 | ASQVYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 170EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Cre06.g250120 | Cre06.g250120.t.1 | 162 | DAKKFNPLGKIKIDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 208EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Vocar20003252m.g | Vocar20003252m.g | 163 | DAKKFNPLGKIKIDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 208EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
230659 | 230659 | 163 | DAKKFNPLGKIKIDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 19EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.004G105700 | Phpat.004G105700.1 | 196 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 243EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.007G061700 | Phpat.007G061700.1 | 200 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 247EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.007G061800 | Phpat.007G061800.1 | 200 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 247EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.007G061900 | Phpat.007G061900.1 | 200 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 247EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.026G03100 | Phpat.026G03100.1 | 198 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 245EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Carubv100042425m.g | Carubv100042425m.g | 198 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 245EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Carubv100042425m.g | Carubv100042425m.g | 198 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 245EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra013786 | Bra013786 | 198 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 245EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra019231 | Bra019231 | 193 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra020461 | Bra020461 | 193 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra014998 | Bra014998 | 193 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
26781K | 26781K | 193 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_080593740 | LOC_080593740.1 | 193 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 240EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G079668 | GRMZM2G079668.T01 | 178 | DMSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 213EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G111475 | GRMZM2G111475.T01 | 168 | DMSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 213EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Cucsa.079370 | Cucsa.079370.1 | 110 | SKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 152EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 20
LOC_08124970 | LOC_08124970.1 | 182 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 229EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GSVTVG01026014001 | GSVTVG01026014001.1 | 198 | FLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 94EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 1490
Eucgr.G00235 | Eucgr.G00235.1 | 191 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 238EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
PGSC0003DM400024887 | PGSC0003DM400024887.1 | 189 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 238EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Glyma16g00410 | Glyma16g00410.1 | 174 | VDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 220EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Cucsa.266110 | Cucsa.266110.1 | 192 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 239EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Medtr2g005690 | Medtr2g005690.1 | 190 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 237EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Eucgr.I02771 | Eucgr.I02771.1 | 191 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 237EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Potri.003G063000 | Potri.003G063000.1 | 191 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 237EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Potri.004G224400 | Potri.004G224400.1 | 190 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 238EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
29765.t.000021 | 29765.t.000021.1 | 188 | LVDDSKFLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 235EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GSVTVG01008331001 | GSVTVG01008331001.1 | 31 | FLNDKTKAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 71EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 126DF
gi | 6680557 | ref | XP_629204.1 | 154 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 198EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
XK045c | 246 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 208EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 164426355 | ref | XP_961753.2 | 168 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 213EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 24234688 | ref | NP_004125.3 | 176 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 213EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
gi | 299469993 | emb | CNB9179.1 | 170 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 215EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
CML205C | 173 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 218EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Cre09.g393200 | Cre09.g393200.t.1 | 164 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 208EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Vocar20005243m.g | Vocar20005243m.g | 168 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 218EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
168287 | 168287 | 138 | ABVYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 181EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.001G091000 | Phpat.001G091000.1 | 174 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 219EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.001G091100 | Phpat.001G091100.1 | 174 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 219EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.002G052800 | Phpat.002G052800.1 | 177 | KDTNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 223EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Phpat.002G053100 | Phpat.002G053100.1 | 176 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 223EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G365374 | GRMZM2G365374.T01 | 176 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 221EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_080931486 | LOC_080931486.1 | 177 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 223EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_080931486 | LOC_080931486.2 | 45 | FLKTVSNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 85EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 139F
Bra010620 | Bra010620 | 170 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 215EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra011794 | Bra011794 | 175 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 220EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
AT403791 | 175 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 220EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Carubv10006443m.g | Carubv10006443m.g | 175 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 220EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Eucgr.G01045 | Eucgr.G01045.1 | 182 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 228EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
PGSC0003DM40003122 | PGSC0003DM40003122.1 | 110 | EAYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 152EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 20
PGSC0003DM400010677 | PGSC0003DM400010677.1 | 110 | EAYLGKTIINNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 152EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 20
AT5009590 | 179 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 225EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Carubv10013121m.g | Carubv10013121m.g | 179 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 225EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra006027 | Bra006027 | 176 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 221EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Bra028628 | Bra028628 | 179 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 225EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GRMZM2G153815 | GRMZM2G153815.T01 | 176 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 221EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_0802953420 | LOC_0802953420.1 | 176 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 221EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
LOC_080392260 | LOC_080392260.1 | 176 | ETNENYLGKVVTVDAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 221EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
GSVTVG01006769001 | GSVTVG01006769001.1 | 156 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 202EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
29804.t.0000129 | 29804.t.0000129.1 | 179 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 225EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Potri.001G285500 | Potri.001G285500.1 | 179 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 225EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Potri.009G079700 | Potri.009G079700.1 | 179 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 225EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Eucgr.I02583 | Eucgr.I02583.1 | 179 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 225EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG 2
Medtr2g010020 | Medtr2g010020.1 | 176 | KEVYEAFLGHPVNAVTVPAAYFNSQROATKADAGIAGLVLRVIRIN 222EPTAAALAYGLDKGG--G--EINIIVYDGGGTFDVSILSIBG--VFEVKSTAGDTHLGG

gi | 17534013 | ref | NP_495089.1 | 333 | DEVLVVGSTRIPKQ | 348KLLKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKVDET- | IKDVLVDDVAPLSG | GETA | 407 | GGVTMLNDRNTRIPAKSFTFYA
gi | 17507981 | ref | NP_492485.1 | 332 | DEVLVVGSTRIPKQ | 348KLLKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKVDET- | IKDVLVDDVAPLSG | GETA | 407 | GGVTMLNDRNTRIPAKSFTFYA
gi | 66800327 | ref | XP_626089.1 | 333 | DEVLVVGSTRIPKQ | 348QLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 407 | GGVTMLNDRNTRIPAKSFTFYA
gi | 66802625 | ref | XP_644917.1 | 330 | HEIVLVGSTRIPKQ | 3450LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 404 | GGVTMLNDRNTRIPAKSFTFYA
gi | 66922147 | ref | XP_644428.1 | 331 | HEIVLVGSTRIPKQ | 3460LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 404 | GGVTMLNDRNTRIPAKSFTFYA
gi | 85112048 | ref | XP_663336.1 | 330 | HEIVLVGSTRIPKQ | 3460LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 404 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.004G083500 | Phpat.004G083500.1 | 338 | QEVVLVGGSTRIPKQ | 3535LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G366532 | GRMZM2G366532.T01 | 339 | HDVVLVGGSTRIPKQ | 3540LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 413 | GGVTMLNDRNTRIPAKSFTFYA
LOC_0s03g16920 | LOC_0s03g16920.1 | 339 | HDVVLVGGSTRIPKQ | 3540LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 413 | GGVTMLNDRNTRIPAKSFTFYA
PGSC0003DM40027750 | PGSC0003DM40027750.1 | 338 | HDVVLVGGSTRIPKQ | 3530LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
Carubv10004240m | Carubv10004240m.1 | 337 | HDVVLVGGSTRIPKQ | 3520LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 411 | GGVTMLNDRNTRIPAKSFTFYA
LOC_0s05g38530 | LOC_0s05g38530.1 | 338 | HDVVLVGGSTRIPKQ | 3530LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G580280 | GRMZM2G580280.T01 | 337 | HDVVLVGGSTRIPKQ | 3520LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 411 | GGVTMLNDRNTRIPAKSFTFYA
AC209784.3 | FG007 | AC209784.3 | FG007 | 337 | HDVVLVGGSTRIPKQ | 3520LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 411 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G310431 | GRMZM2G310431.T01 | 337 | HDVVLVGGSTRIPKQ | 3520LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 411 | GGVTMLNDRNTRIPAKSFTFYA
gi | 34419635 | ref | NP_022146.2 | 334 | HDVVLVGGSTRIPKQ | 349KLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 408 | GGVTMLNDRNTRIPAKSFTFYA
gi | 16746613 | ref | NP_025337.2 | 334 | HDVVLVGGSTRIPKQ | 349KLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 408 | GGVTMLNDRNTRIPAKSFTFYA
gi | 124256496 | ref | NP_005518.3 | 334 | HDVVLVGGSTRIPKQ | 349KLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 408 | GGVTMLNDRNTRIPAKSFTFYA
gi | 53081881 | ref | XP_005249127.1 | 335 | ARHIDVVLGGSTRIPKQ | 411RLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
gi | 530428004 | ref | XP_005272871.1 | 334 | HDVVLVGGSTRIPKQ | 349RLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 408 | GGVTMLNDRNTRIPAKSFTFYA
gi | 530428002 | ref | XP_005272870.1 | 335 | ARHIDVVLGGSTRIPKQ | 411RLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
gi | 530427781 | ref | XP_005274915.1 | 334 | HDVVLVGGSTRIPKQ | 349RLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 408 | GGVTMLNDRNTRIPAKSFTFYA
gi | 530427783 | ref | XP_005274916.1 | 335 | ARHIDVVLGGSTRIPKQ | 411RLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
gi | 13674578 | ref | NP_068442.1 | 335 | DEVLVVGSTRIPKQ | 350KLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
gi | 5729877 | ref | NP_065888.1 | 332 | HDVVLVGGSTRIPKQ | 347KLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 406 | GGVTMLNDRNTRIPAKSFTFYA
gi | 530398061 | ref | XP_005271593.1 | 338 | DVLVGGSTRIPKQ | 322KLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 381 | GGVTMLNDRNTRIPAKSFTFYA
gi | 85080590 | ref | XP_956657.1 | 365 | LDDVVLVGGSTRIPKQ | 381AILEEFDFFGKPKKSC | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 438 | GGVTMLNDRNTRIPAKSFTFYA
gi | 66818991 | ref | XP_643155.1 | 359 | HEIVLVGSTRIPKQ | 3750LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 432 | GGVTMLNDRNTRIPAKSFTFYA
gi | 16507237 | ref | NP_005336.1 | 330 | HEIVLVGSTRIPKQ | 3460LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 404 | GGVTMLNDRNTRIPAKSFTFYA
381 | HEIVLVGSTRIPKQ | 349KLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 408 | GGVTMLNDRNTRIPAKSFTFYA
2 | PGSC0003DM40027750 | PGSC0003DM40027750.1 | 338 | HDVVLVGGSTRIPKQ | 3530LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
3 | PGSC0003DM40027750 | PGSC0003DM40027750.1 | 338 | HDVVLVGGSTRIPKQ | 3530LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 412 | GGVTMLNDRNTRIPAKSFTFYA
34 | Bra031657 | Bra031657 | 375 | SEIDVVLVGGSTRIPKQ | 393EMLLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 454 | GGVTMLNDRNTRIPAKSFTFYA
Carubv10008520m | Carubv10008520m.1 | 366 | LDEIVLVGGSTRIPKQ | 3820LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 441 | GGVTMLNDRNTRIPAKSFTFYA
Petri.013G018000 | Petri.013G018000.1 | 361 | LKEIVLVGGSTRIPKQ | 3778LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 436 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.010G067200 | Phpat.010G067200.1 | 358 | HEIVLVGSTRIPKQ | 3740LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 433 | GGVTMLNDRNTRIPAKSFTFYA
449090 | 449090 | 355 | HEIVLVGSTRIPKQ | 3710LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 430 | GGVTMLNDRNTRIPAKSFTFYA
Bra028521 | Bra028521 | 361 | LDEIVLVGGSTRIPKQ | 3770LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 436 | GGVTMLNDRNTRIPAKSFTFYA
Bra015047 | Bra015047 | 362 | LDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
Bra022819 | Bra022819 | 362 | LDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
Petri.012G017600 | Petri.012G017600.1 | 364 | LDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G114793 | GRMZM2G114793.T01 | 360 | HEIVLVGSTRIPKQ | 3740LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 433 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G415007 | GRMZM2G415007.T01 | 360 | HEIVLVGSTRIPKQ | 3760LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 435 | GGVTMLNDRNTRIPAKSFTFYA
LOC_0s02g02410 | LOC_0s02g02410.1 | 363 | HEIVLVGSTRIPKQ | 3790LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 438 | GGVTMLNDRNTRIPAKSFTFYA
PGSC0003DM40018544 | PGSC0003DM40018544.1 | 360 | LDEIVLVGGSTRIPKQ | 3790LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 438 | GGVTMLNDRNTRIPAKSFTFYA
Glyma08g02960 | Glyma08g02960.1 | 400 | KNCDEIVLVGGSTRIPKQ | 4190LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 478 | GGVTMLNDRNTRIPAKSFTFYA
Glyma09g36620 | Glyma09g36620.1 | 394 | KSCDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
Glyma09g36620 | Glyma09g36620.1 | 394 | KSCDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
Glyma08g02940 | Glyma08g02940.1 | 362 | LDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
PGSC0003DM40012254 | PGSC0003DM40012254.1 | 363 | LDEIVLVGGSTRIPKQ | 3790LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 438 | GGVTMLNDRNTRIPAKSFTFYA
GSVLVG01019607001 | GSVLVG01019607001 | 412 | KNCDEIVLVGGSTRIPKQ | 4190LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 478 | GGVTMLNDRNTRIPAKSFTFYA
Eucgr.E01024 | Eucgr.E01024.1 | 363 | LDEIVLVGGSTRIPKQ | 3790LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 438 | GGVTMLNDRNTRIPAKSFTFYA
Cucsa.319490 | Cucsa.319490.1 | 363 | LDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
30068 | t000021 | 30 | Petri.001G087500 | Petri.001G087500.1 | 362 | LDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
Petri.001G087500 | Petri.001G087500.1 | 362 | LDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
Petri.003G143600 | Petri.003G143600.1 | 362 | LDEIVLVGGSTRIPKQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
CMV163c | 330 | DEVLVVGSTRIPAVQ | 3450LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 399 | GGVTMLNDRNTRIPAKSFTFYA
Cre06.g2501200 | Cre06.g2501200.t.1.2 | 367 | MDEVVLVGGSTRIPAVQ | 3831EVRLKLTGKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 438 | GGVTMLNDRNTRIPAKSFTFYA
Vocar20003521m | Vocar20003521m.1 | 366 | HEIVLVGSTRIPAVQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
230659 | 230659 | 361 | HEIVLVGSTRIPAVQ | 3780LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 437 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.004G105700 | Phpat.004G105700.1 | 403 | YKDLNEVLLVGGSTRIPAVQ | 4228LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 476 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.007G061700 | Phpat.007G061700.1 | 403 | YKDLNEVLLVGGSTRIPAVQ | 4228LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 476 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.007G061800 | Phpat.007G061800.1 | 403 | YKDLNEVLLVGGSTRIPAVQ | 4228LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 476 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.007G061900 | Phpat.007G061900.1 | 403 | YKDLNEVLLVGGSTRIPAVQ | 4228LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 476 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.026G031400 | Phpat.026G031400.1 | 402 | YKDLNEVLLVGGSTRIPAVQ | 4228LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 475 | GGVTMLNDRNTRIPAKSFTFYA
Carubv10002829m | Carubv10002829m.1 | 401 | FKDDEVLLVGGSTRIPAVQ | 4208LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 474 | GGVTMLNDRNTRIPAKSFTFYA
Carubv10004245m | Carubv10004245m.1 | 399 | FKDDEVLLVGGSTRIPAVQ | 4188LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 472 | GGVTMLNDRNTRIPAKSFTFYA
Bra013786 | Bra013786 | 396 | FKDDEVLLVGGSTRIPAVQ | 4158LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 469 | GGVTMLNDRNTRIPAKSFTFYA
Bra019231 | Bra019231 | 396 | FKDDEVLLVGGSTRIPAVQ | 4158LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 469 | GGVTMLNDRNTRIPAKSFTFYA
Bra020461 | Bra020461 | 223 | VGGSTRIPAVQ | 233EVRLKLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 287 | GGVTMLNDRNTRIPAKSFTFYA
Bra010498 | Bra010498 | 448 | FKDDEVLLVGGSTRIPAVQ | 4208LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 474 | GGVTMLNDRNTRIPAKSFTFYA
267815 | 267815 | 377 | DIEVVLVGGSTRIPAVQ | 3888LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 442 | GGVTMLNDRNTRIPAKSFTFYA
LOC_0s05g23740 | LOC_0s05g23740.1 | 376 | DIEVVLVGGSTRIPAVQ | 393DLVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 441 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G079668 | GRMZM2G079668.T01 | 371 | DIEVVLVGGSTRIPAVQ | 3888LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 442 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G111475 | GRMZM2G111475.T01 | 371 | DIEVVLVGGSTRIPAVQ | 3888LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 442 | GGVTMLNDRNTRIPAKSFTFYA
Cucsa.079370 | Cucsa.079370.1 | 313 | EVLVGGSTRIPAVQ | 3278LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 381 | GGVTMLNDRNTRIPAKSFTFYA
LOC_0s12g14070 | LOC_0s12g14070.1 | 385 | EVLVGGSTRIPAVQ | 4048LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 458 | GGVTMLNDRNTRIPAKSFTFYA
GSVLVG026014001 | GSVLVG026014001 | 258 | VLVGGSTRIPAVQ | 69DILVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 323 | GGVTMLNDRNTRIPAKSFTFYA
Eucgr.G00235 | Eucgr.G00235.1 | 394 | FKDDEVLLVGGSTRIPAVQ | 4138LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 467 | GGVTMLNDRNTRIPAKSFTFYA
PGSC0003DM40042487 | PGSC0003DM40042487.1 | 392 | FKDDEVLLVGGSTRIPAVQ | 4118LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 465 | GGVTMLNDRNTRIPAKSFTFYA
Glyma16g0410 | Glyma16g0410.1 | 377 | LDEIVLVGGSTRIPAVQ | 3958LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 449 | GGVTMLNDRNTRIPAKSFTFYA
Cucsa.266110 | Cucsa.266110.1 | 395 | FKDDEVLLVGGSTRIPAVQ | 4148LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 468 | GGVTMLNDRNTRIPAKSFTFYA
Medr2g005690 | Medr2g005690.1 | 392 | FKDDEVLLVGGSTRIPAVQ | 4128LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 466 | GGVTMLNDRNTRIPAKSFTFYA
Eucgr.I2771 | Eucgr.I2771.1 | 394 | FKDDEVLLVGGSTRIPAVQ | 4158LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 469 | GGVTMLNDRNTRIPAKSFTFYA
Petri.003G063000 | Petri.003G063000.1 | 394 | FKDDEVLLVGGSTRIPAVQ | 4138LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 467 | GGVTMLNDRNTRIPAKSFTFYA
Petri.004G224400 | Petri.004G224400.1 | 393 | FKDDEVLLVGGSTRIPAVQ | 4128LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 466 | GGVTMLNDRNTRIPAKSFTFYA
29765 | t000021 | 29 | Eucgr.I2583 | Eucgr.I2583.1 | 391 | FKDDEVLLVGGSTRIPAVQ | 4108LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 464 | GGVTMLNDRNTRIPAKSFTFYA
GSVLVG01008331001 | GSVLVG01008331001 | 235 | LVGGSTRIPAVQ | 2468LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 300 | GGVTMLNDRNTRIPAKSFTFYA
66800557 | ref | XP_629204.1 | 357 | HEIVLVGSTRIPAVQ | 3730LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 427 | GGVTMLNDRNTRIPAKSFTFYA
XRO45c | 373 | HEIVLVGSTRIPAVQ | 3730LLQDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 427 | GGVTMLNDRNTRIPAKSFTFYA
gi | 164426355 | ref | XP_961753.2 | 371 | EIVLVGGSTRIPKQ | 3888LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 442 | GGVTMLNDRNTRIPAKSFTFYA
gi | 24234688 | ref | NP_004125.3 | 379 | DIGEVVLVGGSTRIPKQ | 3960LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 450 | GGVTMLNDRNTRIPAKSFTFYA
gi | 299469993 | emb | CNB71970.1 | 373 | EVHEVVLVGGSTRIPKQ | 3908LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 444 | GGVTMLNDRNTRIPAKSFTFYA
CM1205c | 377 | DISVVLVGGSTRIPKQ | 3948LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 448 | GGVTMLNDRNTRIPAKSFTFYA
Cre09.g393200 | Cre09.g393200.t.1.2 | 366 | KNDDEVLLVGGSTRIPKQ | 3828LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 436 | GGVTMLNDRNTRIPAKSFTFYA
Vocar20005243m | Vocar20005243m.1 | 448 | KNDDEVLLVGGSTRIPKQ | 4678LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 474 | GGVTMLNDRNTRIPAKSFTFYA
168287 | 168287 | 340 | DEVLVVGSTRIPKQ | 3558LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 409 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.001G091000 | Phpat.001G091000.1 | 376 | DVEVVLVGGSTRIPKQ | 3938LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 447 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.001G091100 | Phpat.001G091100.1 | 377 | DVEVVLVGGSTRIPKQ | 3938LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 447 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.002G052800 | Phpat.002G052800.1 | 379 | KDDEVLLVGGSTRIPKQ | 3978LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 451 | GGVTMLNDRNTRIPAKSFTFYA
Phpat.002G053100 | Phpat.002G053100.1 | 378 | KDDEVLLVGGSTRIPKQ | 3958LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 449 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G365374 | GRMZM2G365374.T01 | 379 | KDDEVLLVGGSTRIPKQ | 3958LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 449 | GGVTMLNDRNTRIPAKSFTFYA
LOC_0s09g31486 | LOC_0s09g31486.1 | 379 | KDDEVLLVGGSTRIPKQ | 3978LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 451 | GGVTMLNDRNTRIPAKSFTFYA
LOC_0s09g31486 | LOC_0s09g31486.2 | 248 | LVGMTRIPKQ | 299DILVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 313 | GGVTMLNDRNTRIPAKSFTFYA
Bra010620 | Bra010620 | 377 | EVHEVVLVGGSTRIPKQ | 3898LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 443 | GGVTMLNDRNTRIPAKSFTFYA
Bra011794 | Bra011794 | 377 | EIVLVGGSTRIPKQ | 3948LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 448 | GGVTMLNDRNTRIPAKSFTFYA
AT40391 | 377 | EIVLVGGSTRIPKQ | 3948LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 448 | GGVTMLNDRNTRIPAKSFTFYA
Carubv10006443m | Carubv10006443m.1 | 377 | EIVLVGGSTRIPKQ | 3948LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 448 | GGVTMLNDRNTRIPAKSFTFYA
Eucgr.G01045 | Eucgr.G01045.1 | 384 | KDDEVLLVGGSTRIPKQ | 4028LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 450 | GGVTMLNDRNTRIPAKSFTFYA
PGSC0003DM40003122 | PGSC0003DM40003122.1 | 312 | EVLVGGSTRIPKQ | 3268LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 380 | GGVTMLNDRNTRIPAKSFTFYA
PGSC0003DM40010677 | PGSC0003DM40010677.1 | 312 | EVLVGGSTRIPKQ | 3268LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 380 | GGVTMLNDRNTRIPAKSFTFYA
AT5009590 | 381 | KEVDEVLLVGGSTRIPKQ | 3998LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 453 | GGVTMLNDRNTRIPAKSFTFYA
Carubv10013121m | Carubv10013121m.1 | 378 | KEVDEVLLVGGSTRIPKQ | 3958LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 449 | GGVTMLNDRNTRIPAKSFTFYA
Bra006027 | Bra006027 | 381 | KEVDEVLLVGGSTRIPKQ | 3958LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 449 | GGVTMLNDRNTRIPAKSFTFYA
Bra028628 | Bra028628 | 381 | KEVDEVLLVGGSTRIPKQ | 3998LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 453 | GGVTMLNDRNTRIPAKSFTFYA
GRMZM2G153815 | GRMZM2G153815.T01 | 378 | EVHEVVLVGGSTRIPKQ | 3958LVKRLT-GKDFEENKELNLS | INPDEAVYGAARVAOALVLSGKSSR- | ISELFLDVAFLS | GETV | 449 | GGVTMLNDRNTRIPAKSFTFYA
LOC_0s02g53420 | LOC_0s02g53420.1 | 378 | DVEVVL

gi | 17534013 | ref | NP_496509.1 | 646 45
gi | 17507981 | ref | NP_492485.1 | 644 43
gi | 66800327 | ref | XP_629089.1 | 631 30
gi | 66826525 | ref | XP_646617.1 | 641 40
gi | 66922147 | ref | XP_644428.1 | 633 32
gi | 85110248 | ref | XP_963366.1 | 647 46
Phpat.004G083500 | Phpat.004G083500.1 | 650 49
GRMZM2G366532 | GRMZM2G366532.T01 | 653 52
LOC_Os03g16920 | LOC_Os03g16920.1 | 654 53
PGSC0003DMG400027750 | PGSC0003DMT40007133 | 650 49
Carubv10000420m.g | Carubv10000420m | 652 51
LOC_Os05g38530 | LOC_Os05g38530.1 | 647 46
GRMZM5G082801 | GRMZM5G082801.T01 | 650 49
AC209784.3.FG007 | AC209784.3.FGT007 | 649 48
GRMZM2G310431 | GRMZM2G310431.T01 | 649 48
gi | 34419635 | ref | NP_002146.2 | 644 43
gi | 167466173 | ref | NP_005337.2 | 642 41
gi | 124256496 | ref | NP_005518.3 | 642 41
gi | 530381921 | ref | XP_005249127.1 | 706 - 705
gi | 530428004 | ref | XP_005272871.1 | 642 41
gi | 530428002 | ref | XP_005272870.1 | 706 - 705
gi | 530427781 | ref | XP_005274915.1 | 642 41
gi | 530427783 | ref | XP_005274916.1 | 706 - 705
gi | 13676857 | ref | NP_068814.2 | 640 39
gi | 5729877 | ref | NP_006588.1 | 647 46
gi | 530398061 | ref | XP_005271593.1 | 622 1
gi | 85080590 | ref | XP_956567.1 | 662 661
gi | 66818991 | ref | XP_643155.1 | 659 658
gi | 16507237 | ref | NP_005338.1 | 635 654
Cre02.g080600 | Cre02.g080600.t1.2 | 687 - 686
PGSC0003DMG400024707 | PGSC0003DMT40006354 | 670 669
Bra031657 | Bra031657 | 674 - 673
Carubv10008520m.g | Carubv10008520m | 666 665
Potri.013G018000 | Potri.013G018000.1 | 661 660
Phpat.003G016000 | Phpat.003G016000.1 | 663 662
Phpat.010G067200 | Phpat.010G067200.1 | 663 662
440900 | 440900 | 661 660
Bra028521 | Bra028521 | 666 665
Bra015047 | Bra015047 | 667 666
Bra022819 | Bra022819 | 670 669
Potri.012G017600 | Potri.012G017600.1 | 669 668
GRMZM2G114793 | GRMZM2G114793.T01 | 664 663
GRMZM2G415007 | GRMZM2G415007.T01 | 664 663
LOC_Os02g02410 | LOC_Os02g02410.1 | 666 665
PGSC0003DMG400018544 | PGSC0003DMT40004771 | 669 668
Glyma08g02960 | Glyma08g02960.1 | 709 -- 708
Glyma05g36620 | Glyma05g36620.1 | 702 -- 701
Glyma05g36620 | Glyma05g36620.1 | 669 668
Glyma08g02940 | Glyma08g02940.1 | 668 667
PGSC0003DMG400012254 | PGSC0003DMT40003193 | 668 667
GSVIVG01019607001 | GSVIVT01019607001 | 607 606
Eucgr.E01024 | Eucgr.E01024.1 | 720 -- 719
Cucsa.303940 | Cucsa.303940.1 | 666 665
30068.t000021 | 30068.m002531 | 665 664
Potri.001G087500 | Potri.001G087500.1 | 667 666
Potri.003G143600 | Potri.003G143600.1 | 667 666
CMV163C | 608 07
Cre06.g250100 | Cre06.g250100.t1.2 | 680 679
Vocar20003521m.g | Vocar20003521m | 667 666
230659 | 230659 | 658 657
Phpat.004G105700 | Phpat.004G105700.1 | 708 -- 707
Phpat.007G061700 | Phpat.007G061700.1 | 715 -- 714
Phpat.007G061800 | Phpat.007G061800.1 | 715 -- 714
Phpat.007G061900 | Phpat.007G061900.1 | 715 -- 714
Phpat.026G035400 | Phpat.026G035400.1 | 711 -- 710
Carubv100028629m.g | Carubv100028629m | 720 -- 719
Carubv10004245m.g | Carubv10004245m | 718 -- 717
Bra013786 | Bra013786 | 712 -- 711
Bra019231 | Bra019231 | 711 -- 710
Bra002461 | Bra002461 | 718 -- 717
Bra010498 | Bra010498 | 661 660
267815 | 267815 | 690 689
LOC_Os05g23740 | LOC_Os05g23740.1 | 684 683
GRMZM2G079668 | GRMZM2G079668.T01 | 684 683
GRMZM2G114755 | GRMZM2G114755.T01 | 619 8
Cucsa.079370 | Cucsa.079370.1 | 699 -- 698
LOC_Os12g14070 | LOC_Os12g14070.1 | 707 -- 706
GSVIVG01026014001 | GSVIVT01026014001 | 707 -- 706
Eucgr.G00235 | Eucgr.G00235.1 | 690 - 689
PGSC0003DMG400024887 | PGSC0003DMT40006403 | 708 -- 707
Glyma16g00410 | Glyma16g00410.1 | 708 -- 707
Cucsa.266110 | Cucsa.266110.1 | 708 -- 707
Medtr2g005690 | Medtr2g005690.1 | 719 -- 718
Eucgr.I02771 | Eucgr.I02771.1 | 707 -- 706
Potri.003G006300 | Potri.003G006300.1 | 706 -- 705
Potri.004G224400 | Potri.004G224400.1 | 704 -- 703
29765.t000021 | 29765.m000739 | 659 658
GSVIVG01008331001 | GSVIVT01008331001 | 655 654
gi | 6800557 | ref | XP_629204.1 | 669 668
YJRO45C | 680 679
gi | 164426355 | ref | XP_961753.2 | 689 688
gi | 24234688 | ref | NP_004125.3 | 692 691
gi | 299469993 | emb | CBN79170.1 | 664 663
CML205C | 808 -- 807
Cre09.g393200 | Cre09.g393200.t1.2 | 637 36
Vocar20005243m.g | Vocar20005243m | 677 676
168287 | 168287 | 677 676
Phpat.001G091000 | Phpat.001G091000.1 | 681 - 680
Phpat.001G091100 | Phpat.001G091100.1 | 679 678
Phpat.002G052800 | Phpat.002G052800.1 | 682 681
Phpat.002G053100 | Phpat.002G053100.1 | 685 - 684
GRMZM2G365374 | GRMZM2G365374.T01 | 677 676
LOC_Os09g31486 | LOC_Os09g31486.1 | 683 682
LOC_Os09g31486 | LOC_Os09g31486.2 | 680 679
Bra010620 | Bra010620 | 677 676
Bra011794 | Bra011794 | 683 682
AT4G37910 | 683 682
Carubv10006443m.g | Carubv10006443m | 684 683
Eucgr.G01045 | Eucgr.G01045.1 | 685 - 684
PGSC0003DMG400003122 | PGSC0003DMT40000809 | 609 8
PGSC0003DMG400010677 | PGSC0003DMT40002770 | 605 4
AT5G09590 | 683 - 682
Carubv10013121m.g | Carubv10013121m | 684 - 683
Bra006027 | Bra006027 | 682 681
Bra028628 | Bra028628 | 681 - 680
GRMZM2G153815 | GRMZM2G153815.T01 | 679 678
LOC_Os02g53420 | LOC_Os02g53420.1 | 680 679
LOC_Os03g02260 | LOC_Os03g02260.1 | 677 676
GSVIVG01006769001 | GSVIVT01006769001 | 572 - 571
29804.t000060 | 29804.m001529 | 658 657
Potri.001G285500 | Potri.001G285500.1 | 684 - 683
Potri.009G079700 | Potri.009G079700.1 | 683 - 682
Eucgr.I02583 | Eucgr.I02583.1 | 683 - 682
Medtr2g010020 | Medtr2g010020.1 | 677 - 676
GSVIVG0103517001 | GSVIVT0103517001 | 614 613
Cucsa.331940 | Cucsa.331940.1 | 681 - 680
Medtr4g092920 | Medtr4g092920.1 | 676 675
Glyma07g30290 | Glyma07g30290.1 | 678 - 677
Glyma08g06950 | Glyma08g06950.1 | 678 - 677
Glyma13g32790 | Glyma13g32790.1 | 675 674
Glyma15g06530 | Glyma15g06530.1 | 675 674

