

|                    |                                                                                                                                                          |     |
|--------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| MEL03C019337.2     | -----                                                                                                                                                    | 0   |
| Cla97C02G036020    | -----                                                                                                                                                    | 0   |
| At4G18020.1        | -----MVITANDLSKWENFPKGLKVLNNGC-----                                                                                                                      | 27  |
| Cla97C09G175170    | -----MVCTVDDLQEWKDFPKGLRVLLL-----                                                                                                                        | 23  |
| MEL03C003375.2.1   | -----MVCTADDLQEWKDFPKGLRVLLL-----                                                                                                                        | 23  |
| CsAMJ39435.1       | -----MVCTADDLQEWKDFPKGLRVLLL-----                                                                                                                        | 23  |
| MEL03C013874.2.1   | -----MVCTANDLHGWKDFPKGLRVLLL-----                                                                                                                        | 23  |
| Cla97C10G186530    | -----MVCTANDLHGWKDFPKGLRVLLL-----                                                                                                                        | 23  |
| CA06g13040         | -----MVCTENDLLGWKDFPKGLRVLLL-----                                                                                                                        | 23  |
| SMEL_006g257080.1  | -----MVCTENELLEWKDFPKGLKVLNLL-----                                                                                                                       | 23  |
| Solyc06g061030.3.1 | -----MVCTENELLEWKDFPKGLKVLNLL-----                                                                                                                       | 23  |
| SMEL_008g315370.1  | -----MICIEDELLGWKDFPKGLKVLNLL-----                                                                                                                       | 23  |
| Solyc08g077230.3.1 | -----MICIENELLGWKDFPKGLKVLNLL-----                                                                                                                       | 23  |
| CA00g25180         | MFAGR <sup>D</sup> G <sup>F</sup> VAVVLMIGISGVVNGPGAGCNG <sup>R</sup> EMICIEDELLGWKDFPKGLKVLNLL-----                                                     | 56  |
|                    |                                                                                                                                                          |     |
| MEL03C019337.2     | -----                                                                                                                                                    | 0   |
| Cla97C02G036020    | -----                                                                                                                                                    | 0   |
| At4G18020.1        | DSDGDGSSAAET <sup>R</sup> SELESMDYIVTTFTDETEALS <sup>V</sup> AVVKN <sup>P</sup> ESFHIAIVEV-NMSAESES <sup>F</sup>                                         | 86  |
| Cla97C09G175170    | --DRDS <sup>R</sup> SASEIR <sup>S</sup> KLEEM <sup>E</sup> YVVYSCSDEKEALSAILNTPGNFHV <sup>A</sup> ILEV-CAKNHDES <sup>F</sup>                             | 80  |
| MEL03C003375.2.1   | --DRDSCSATEIR <sup>S</sup> KLEEM <sup>E</sup> YVVYSC <sup>T</sup> DEKEALSAILNTPGNFHV <sup>A</sup> ILE-----                                               | 70  |
| CsAMJ39435.1       | --DRDS <sup>F</sup> SATEIR <sup>S</sup> KLEEM <sup>E</sup> YVVYSC <sup>T</sup> DEKEASSAILNTPGNFHV <sup>A</sup> ILEV-CARNYDES <sup>F</sup>                | 80  |
| MEL03C013874.2.1   | --DGD <sup>T</sup> SSAAEIK <sup>T</sup> KLEEM <sup>E</sup> YVVVSYCNENDALS <sup>I</sup> SSK <sup>P</sup> ETFHVAIVEV-TTSNHG <sup>N</sup> F                 | 80  |
| Cla97C10G186530    | --DGDSSSAAEIK <sup>T</sup> KLEEM <sup>E</sup> YVVVTYCNENDALS <sup>I</sup> SSK <sup>P</sup> ETFHVAIVEV-TTSNHNG <sup>N</sup> F                             | 80  |
| CA06g13040         | --DKDSNSASDMRS <sup>R</sup> LEEM <sup>E</sup> YIVYAF <sup>C</sup> NETEALS <sup>I</sup> SSK <sup>S</sup> EVFHV <sup>A</sup> IVEV-SAGNSD <sup>G</sup> GL   | 80  |
| SMEL_006g257080.1  | --DKDCSSASQMRS <sup>R</sup> LQEMDYIVHTFCNENEALS <sup>I</sup> SSK <sup>S</sup> EVFHV <sup>A</sup> IVEV-SDGNSD <sup>G</sup> EL                             | 80  |
| Solyc06g061030.3.1 | --D <sup>T</sup> DSNFASQMRS <sup>R</sup> LQMDYIVY <sup>T</sup> FCNENEALS <sup>I</sup> SSK <sup>S</sup> EVFHV <sup>A</sup> IVEV-SAGNSD <sup>G</sup> GF    | 80  |
| SMEL_008g315370.1  | --DED <sup>S</sup> NSAAEMRS <sup>R</sup> LKMDYIVY <sup>S</sup> FCNESEAL <sup>T</sup> AISSK <sup>S</sup> SEG <sup>F</sup> HVAIVEV-SEGNSD <sup>G</sup> VL  | 80  |
| Solyc08g077230.3.1 | --DED <sup>S</sup> NSAAEMK <sup>S</sup> RLEKMDYIVY <sup>S</sup> FCNESEAL <sup>T</sup> AISSK <sup>S</sup> SEG <sup>F</sup> HVAIVEV-SAGNSD <sup>G</sup> VL | 80  |
| CA00g25180         | --DED <sup>S</sup> NSAAEMK <sup>S</sup> RLEKMDYIVY <sup>T</sup> FCNESEAL <sup>T</sup> AISSK <sup>S</sup> SEG <sup>F</sup> HVAIVEVVSAGND <sup>G</sup> VL  | 114 |
|                    |                                                                                                                                                          |     |
| MEL03C019337.2     | -----                                                                                                                                                    | 0   |
| Cla97C02G036020    | -----                                                                                                                                                    | 0   |
| At4G18020.1        | KFLEAAKDVLPTI-----                                                                                                                                       | 99  |
| Cla97C09G175170    | KLLGTSKD-LPII-----                                                                                                                                       | 92  |
| MEL03C003375.2.1   | -----                                                                                                                                                    | 70  |
| CsAMJ39435.1       | KLLGASKD-LPII-----                                                                                                                                       | 92  |
| MEL03C013874.2.1   | KFLEAAKD-LPTI-----                                                                                                                                       | 92  |
| Cla97C10G186530    | KFLEAAKD-LPTI-----                                                                                                                                       | 92  |
| CA06g13040         | KFLEGAKD-LPTI-----                                                                                                                                       | 92  |
| SMEL_006g257080.1  | KFLESAKD-LPTI-----                                                                                                                                       | 92  |
| Solyc06g061030.3.1 | KFLESAKD-LPTI-----                                                                                                                                       | 92  |
| SMEL_008g315370.1  | RFLESAKD-LPTIKQFGGHYRMESLCGRYIMTE <sup>P</sup> ELGIVCSSSNVINAKTYLRELHLLCA                                                                                | 139 |
| Solyc08g077230.3.1 | RFLESAKD-LPTI-----                                                                                                                                       | 92  |
| CA00g25180         | QFLESAKN-LPTI-----                                                                                                                                       | 126 |
|                    |                                                                                                                                                          |     |
| MEL03C019337.2     | -----                                                                                                                                                    | 0   |
| Cla97C02G036020    | -----                                                                                                                                                    | 0   |
| At4G18020.1        | MISTDHCITTTMKCIALGAVEFLQKPLSPE <sup>L</sup> KLNIWQHVVHKA <sup>F</sup> NDGGSNV <sup>S</sup> ISLKP <sup>V</sup> KE                                         | 159 |
| Cla97C09G175170    | MTSDVHCLSTMMKCIALGAVEFLLKPLSE <sup>D</sup> KL <sup>R</sup> NIWQHVIHKAFSNT-----SKP <sup>D</sup> ED                                                        | 145 |
| MEL03C003375.2.1   | -----LGAVEFLLKPLSE <sup>D</sup> KL <sup>R</sup> NIWQHVIHKAYSNT-----SKP <sup>G</sup> EE                                                                   | 107 |
| CsAMJ39435.1       | MTSDVHCLSTMMKCIALGAVEFLLKPLSE <sup>D</sup> KL <sup>R</sup> NIWQHVIHKAYSNS-----SKP <sup>D</sup> ED                                                        | 145 |
| MEL03C013874.2.1   | MISNIHCLSTMMKCIALGAVEFLQKPLSD <sup>D</sup> KL <sup>R</sup> NIWQHVVHKA <sup>F</sup> NAGGS <sup>A</sup> VPNSL <sup>K</sup> PIKE                            | 152 |
| Cla97C10G186530    | MISNIHCLSTMMKCIALGAVEFLQKPLSE <sup>D</sup> KL <sup>R</sup> NIWQHVVHKA <sup>F</sup> NAGGS <sup>P</sup> VPNSL <sup>K</sup> PIKE                            | 152 |
| CA06g13040         | MVSN <sup>I</sup> HSISTMMKCIALGAVEFLQKPLSD <sup>D</sup> KL <sup>R</sup> NIWQHVVHKA <sup>F</sup> HSGGK <sup>N</sup> VAESL <sup>K</sup> PVKE               | 152 |
| SMEL_006g257080.1  | MVSN <sup>I</sup> HSISTMMKCIALGAVEFLQKPLSD <sup>D</sup> KL <sup>R</sup> NIWQHVVHKA <sup>F</sup> HSGGK <sup>N</sup> VESL <sup>K</sup> PVKE                | 152 |
| Solyc06g061030.3.1 | MVSD <sup>I</sup> HSINIMMKCIALGAVEFLQKPLSD <sup>D</sup> KL <sup>R</sup> NIWQHVVHKA <sup>F</sup> HSGGK <sup>S</sup> VESL <sup>K</sup> PVKE                | 152 |
| SMEL_008g315370.1  | VTSNIHSLSTMMKCIALGAVEFLQKPLSD <sup>D</sup> KL <sup>R</sup> NIWQHVVHKA <sup>F</sup> NS-RKDVSRSLDP <sup>V</sup> KE                                         | 198 |

|                    |                                                                    |     |
|--------------------|--------------------------------------------------------------------|-----|
| Solyc08g077230.3.1 | MTSNIHSLSTMKCIALGAVEFLQKPLSDDKLKNIQHVHKAFNTRKDVSKSLEPVKD           | 151 |
| CA00g25180         | MTSNIHSLSTMKCIALGAVEFLQKPLSDDKLKNIQHVHKAFNTRKDVSGPLEPVKE           | 185 |
| MEL03C019337.2     | ---MLALSPIRSGNKDEKQGEMERFSI-----GGDDFP-----DFDDDTNLLDS             | 41  |
| Cl97C02G036020     | ---MLALSPIRSGNKDEKQGEMERFSI-----GGDDFP-----DFDDDTNLLDS             | 41  |
| At4G18020.1        | SVVSMHLHLETDMTI-----EEKDPAPSTPQLKQDSRLLD                           | 193 |
| Cl97C09G175170     | SIASLMQLQLENEDKNGVPEDMEILSWIQDIVWEQPEGSNGS-----Q                   | 188 |
| MEL03C003375.2.1   | SVASLMQLQLENEDKNGVPEDMEILSWIQDIVWEQPEGSDDKS-----QLNLGASRQGS        | 161 |
| CsAMJ39435.1       | SVASLMQFQLQNEDKNGVPEDMEILSWIQDIVWEQPEGSDDRS-----QLNLGASRQAS        | 199 |
| MEL03C013874.2.1   | SVVSMHLHLELESENENQVEKKLEILSGDDNNHLELGS DKYPAPSTPQQKHGMRLVDD        | 212 |
| Cl97C10G186530     | SVASMLHLELESENENQIQKELEISSRNDNDHLELGS DKYPAPSTPQQKHGMRLVDD         | 212 |
| CA06g13040         | SLLSMLELQPVKREADSENENAEPLTSVLENKQKSPNCCDKYPAPSTPQHKQGVRSVDD        | 212 |
| SMEL_006g257080.1  | SLLSLELQVVKRE-----DTNEAEPLTSVLENKQKSPNCCDKYPAPSTPQHKQGVRSVDD       | 208 |
| Solyc06g061030.3.1 | SLLSLELQVVKREADSENENAEPLTSVLENKQKASSSCDKYPAPSTPQHKQGVRSVDD         | 212 |
| SMEL_008g315370.1  | SLLSMQLQKPAKDEADDKNSNRIEPLTAIAESNTEQLSGCDKYPAPSTPQLKQGVRSVDD       | 258 |
| Solyc08g077230.3.1 | SVLSMLQLQLEMGAEADKSSNGTEPPTAVAESNTEQSSGCDKYPAPSTPQLKQGVRSVDD       | 211 |
| CA00g25180         | SLLSMQLQPEKGEPPDKSSNGTEPLIAVADNNTQSSGCDKYPAPSTPQLKQGVRSVDD         | 245 |
|                    | :: :: . . .                                                        |     |
| MEL03C019337.2     | INFDDLFGVINDGVDLPDLEMPPELLAEFSVSGGEESEVNASVSLEKFFDNTLKIIGNKD       | 101 |
| Cl97C02G036020     | INFDDLFGVINDGVDLPDLEMPPELLAEFSVSGGEESEVNASVLEKFFDNTLKAID----       | 97  |
| At4G18020.1        | GDCQENINFSMENVNS-----STEKDNMEDHQD-IGESKVD-TTNRLKDDD-----           | 238 |
| Cl97C09G175170     | LNLDGMNCSMETDCR-----DKD-----VQSKFLE-TTSHDLVCEGPLPE-----            | 228 |
| MEL03C003375.2.1   | WESGDQMNCMETDCK-----DKD-----VQSKFVE-TTSHDLVCEGPIQE-----            | 201 |
| CsAMJ39435.1       | WESGDQMNCMETDCK-----DKD-----VQSKFVE-TTSHDLICEGPIQE-----            | 239 |
| MEL03C013874.2.1   | GDCQDQLNSSLKECKG-----EQD-----GESKVE-TTCINSLVEGTSVQ-----            | 252 |
| Cl97C10G186530     | GDCHDQLNSSLKECKG-----EQD-----GESKVE-TTCINSLVEGTSVQ-----            | 252 |
| CA06g13040         | GDFQDHTILSNEQDSG-----VHE-----GDTKSVE-TTCCDSVAETSILA-----           | 252 |
| SMEL_006g257080.1  | NDLQDHTILSNEQDSG-----VHE-----GDTKSVE-TTCCGSI AETAVLA-----          | 248 |
| Solyc06g061030.3.1 | VDYQDHTILSNEQDSG-----MHE-----GDTKSVE-TTSCDSVAETT VLA-----          | 252 |
| SMEL_008g315370.1  | GDCHDHTIFSTDQDSG-----EHD-----GDTKSVE-TTYNNSLAENTVQT-----           | 298 |
| Solyc08g077230.3.1 | GDCHDHTIFSTDQDSG-----EHD-----ADTKSVE-TTYNNSLAENNVQT-----           | 251 |
| CA00g25180         | SDCHDHTIFSTDQDNG-----EHD-----GDTKSVE-TTYNNSLAENTVQI-----           | 285 |
|                    | : : : : : . . :: :: :                                              |     |
| MEL03C019337.2     | NDDDEDQKDLDSRSSSQ-----VVDQEILSKRDDELATPTN-----                     | 137 |
| Cl97C02G036020     | NKDEDEQKELDRSSCGQVESIDKEIVSKP-DELATPTN-----                        | 135 |
| At4G18020.1        | -----KVVVKKEERGDESEKEEGET-----                                     | 257 |
| Cl97C09G175170     | -----GQPQLSDK-----NKSQV-----                                       | 241 |
| MEL03C003375.2.1   | -----GQPQLSDKRVTFIIPQLKFGV-----                                    | 223 |
| CsAMJ39435.1       | -----GQPQLSDK-----KKIGV-----                                       | 252 |
| MEL03C013874.2.1   | -----ENSQLPDREAIKEEENSADGGCAASNIDH-----                            | 281 |
| Cl97C10G186530     | -----ENSQLPDQEGIKEEENSADGGCAASNIDH-----                            | 281 |
| CA06g13040         | -----DSAGRLEVAITKDERDSADATQNMEDIAT-----                            | 281 |
| SMEL_006g257080.1  | -----DSA-----RAITKEEHDSAVDQNMEDIAT-----                            | 273 |
| Solyc06g061030.3.1 | -----DSSERLGEAITKEEHYSAADQHMEIDIAT-----                            | 281 |
| SMEL_008g315370.1  | -----SPPGQGERILKEENVSPDKMEANIAT-----                               | 327 |
| Solyc08g077230.3.1 | -----SPTVQQGDIIILKEDNVSSPDLKTETIDIAT-----                          | 280 |
| CA00g25180         | -----SPPGQQQDIIILKEENGSSPHQTMEADIATFSQINDCADNSDGSSPHQKT            | 334 |
| MEL03C019337.2     | -----IIE-----ANPLVKDSGDKSIKPQKAS-----SSQSKNSQGRKRVKVDWTPELHRRFVQAV | 188 |
| Cl97C02G036020     | -----INIE-----GNSLVKDGDKIKPKCKS-----SQSKNSQGRKRVKVDWTPELHRRFVQAV   | 186 |
| At4G18020.1        | -GDLISEKTDSDVI-HKKEDETKPKINKSSGINKVSGNKTS-RKKKVDWTPELHKKFVQAV      | 313 |
| Cl97C09G175170     | -----KSSPLAAEHSIQGSDVNHSAGTK-AKKTVDWTSSELHGKFVQAI                  | 284 |
| MEL03C003375.2.1   | -----ESDPLAAENSIQGTGVNQSAGSK-AKKTVDWTPELHRRKFVQAV                  | 266 |
| CsAMJ39435.1       | -----KSDPLAAENSIQGTGVNQSAGSK-AKKTVDWTPELHRRNFVQAV                  | 295 |
| MEL03C013874.2.1   | -----DTHDQYNISSSEKKNKPKCGLSNPKGIVKRSKKLKVVDWTPELHRRKFVQAV          | 331 |
| Cl97C10G186530     | -----DTHDRDNISSSEKKNKPKCGVNNPCGTVKSRKKLKVVDWTPELHRRKFVQAV          | 331 |
| CA06g13040         | -----CSRSNDYPADGSTRSAESNKASGLHSSSGTKANKKKMKVDWTPELHKKFVKAV         | 334 |
| SMEL_006g257080.1  | -----CNDCP-----INSSIGSAHRNKASGVHSSSGTKANKMKKVVDWTPELHKKFVKAV       | 323 |
| Solyc06g061030.3.1 | -----CSPSN-----DNGSTCSADPNKASGLHSSSGTKANKKKMKVDWTPELHKKFVKAV       | 331 |
| SMEL_008g315370.1  | -----SSQSNDCPDSSISHSAEPSKASGPHSSSGTKSNKKLKVVRKKWCLV-FIKK-          | 378 |
| Solyc08g077230.3.1 | -----TSRSNDPCDNSIMHSAEPSKASGPHSSSGTKSNRKKIKVDWTPELHKKFVQAV         | 333 |
| CA00g25180         | EADIATTSQSKDCPDNSISHSAEPSKASGPHSSSGTKSNKKKVKVDWTPELHKKFVQAV        | 394 |
|                    | . : . ** *. *: :                                                   |     |

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|--------------------|----------------------------------------------------------------|-----|
| MEL03C019337.2     | EQLGVDKAVPSRIEELMGIECLTRHNVASHLQ-KYRSHRKHLAREAEASWSQRRQMYG     | 247 |
| ClA97C02G036020    | EQLGVDKAVPSRIEELMGIECLTRHNVASHLQ-KYRSHRKHLAREAEASWSQRRQMYG     | 245 |
| At4G18020.1        | EQLGVDAQIPSRIEELMKVGLTRHNVASHLQ-KFRQHRKNILPKDDHNRHWISQRENHR    | 372 |
| ClA97C09G175170    | EQIGIDHAIPSKIEELMKVEGLTRHNVASHLQ-KYRMQKKHMQREEN-P-----R-C      | 334 |
| MEL03C003375.2.1   | EQLGIDHAIPSKIEELMKVEGLTRHNIASHLQ-KYRMQKKHVMQREEN-TRWSHPY-R-S   | 322 |
| CsAMJ39435.1       | EQLGIDHAIPSKIEELMKVEGLTRHNIASHLQ-KYRMQKKHVMQREEN-TRWSHPYTR-S   | 352 |
| MEL03C013874.2.1   | EQLGVNQAIPSRILEELMKVEGLTRHNVASHLQ-KYRMHKKRHILPKEED-GSWSHSK---D | 386 |
| ClA97C10G186530    | EQLGVNQAIPSRILEELMKVEGLTRHNVASHLQ-KYRMHKKRHILPKEED-GSWSHSK---D | 386 |
| CA06g13040         | EKLGRIDQAIPSRILEELMKVEGLTRHNIASHLQ-KFRMQRQILPKEDE-KRWPRPQLR-D  | 391 |
| SMEL_006g257080.1  | EKLGRIDQAIPSRILEELMKVEGLTRHNIASHLQ-KFRMQRQILPKEDE-KRWPRPQPR-D  | 380 |
| Solyc06g061030.3.1 | EKIGIDQAIPSRILEELMKVEGLTRHNIASHLQ-KFRMQRQILPKEDE-KRWPRPQPR-D   | 388 |
| SMEL_008g315370.1  | -----                                                          | 378 |
| Solyc08g077230.3.1 | EQLGIDQAIPSRILDLMKVEGLTRHNVASHLQ-KYRMHRKQILPKEVE-KRWPNPQPI-D   | 390 |
| CA00g25180         | EQLGIDQAIPSRILDVMKVEGLTRHNIASHLQKQYRMHRRQILPREVE-KRWPHPQPR-D   | 452 |
|                    |                                                                |     |
| MEL03C019337.2     | GG-GGGGGKREVSSWGAPPTMGFPMPMP-MH---PHFRPLHVWGHPAMPDQSL-L-HVWPKH | 302 |
| ClA97C02G036020    | GAAGGGGGKREVSSWGA-PTMGFPMPMT-MH---PHFRPLHVWGHP-TMDQSLM-HVWPKH  | 299 |
| At4G18020.1        | PN---QRNYNVFQQHRPVMAYP-----VWGLPGVYPPGAIPPLWPP                 | 411 |
| ClA97C09G175170    | TM---QTNH-----LKPIMAYP-SYHPNCGISVSAVYPTWRQTNGHPANFN-----HP     | 378 |
| MEL03C003375.2.1   | TL---QTNH-----LKPIMAYP-SYHPNCGISVSAVYPTWRQTNDPPNIH---VCGP      | 368 |
| CsAMJ39435.1       | TL---QTNH-----LKPIMAYP-SYHPNCGISVSAVYPTWRQTNDHPPNVH---VWGP     | 398 |
| MEL03C013874.2.1   | PM---RKN---YYPQRPVMAFPYPYHSNHIMPVAPIYPPWGHMACPSPGV-R-MWVP      | 435 |
| ClA97C10G186530    | PM---KKN---YYPQRPVMAFPYPYHSNHIMPVAPIYPPWGHMACPSPGVQ-MWVP       | 435 |
| CA06g13040         | SV---QRTY---YPHKPVMAFP-TYHPNNAQTAGQFYPPWIPPGGYPNGAH---MWGS     | 440 |
| SMEL_006g257080.1  | LV---QRTY---YPHKPVMAFP-TYHSNHASTAGQFYPAWIPPGGHPNGAH---MWGS     | 428 |
| Solyc06g061030.3.1 | PV---QRTY---YPHKPVMAFP-THSNHATTAGQFYPAWIPPGGYPNGAH---MWN       | 436 |
| SMEL_008g315370.1  | -----                                                          | 378 |
| Solyc08g077230.3.1 | SV---QRSY---YPHKPIMTFP-QYHSNHVAPGGQFYPAWVTPASYPNGLQ---VWGS     | 438 |
| CA00g25180         | SV---QRNY---YPHKPVMTFP-PYHSNHVAPAGGCYPAWVPPASYPNGLQ---VWGS     | 500 |
|                    |                                                                |     |
| MEL03C019337.2     | LPHSPSPPPPPPTPPSSWPHAAAPPPPPDPSYWHHHHQRPVNGLTSGTPCFPQPIPTTR    | 362 |
| ClA97C02G036020    | LPHSPSPPP-PPTPPSSWPHAAAPPPPPDPSYWHHHHQRPVNGLTSGTPCFPQPIPTTR    | 358 |
| At4G18020.1        | -----PL-QSIGQPPPHWKPPY-PTVSGNAW-----GCPVGGPVTGSYITPSNT---      | 454 |
| ClA97C09G175170    | -----PGYRHWPPQGIQPN-SY-AGVRADAW-----GCPVMLPSHTPYFSYPQH---      | 421 |
| MEL03C003375.2.1   | -----FGYRHWPPQGIQPN-SY-ARVQADTW-----GCPVMPPSHAPYFSYPQL---      | 411 |
| CsAMJ39435.1       | -----LGYRHWPPQGIQPN-SY-AGVQADTW-----GCPVMPPSHAPYFSYPQL---      | 441 |
| MEL03C013874.2.1   | -----PGYPPWRPPEIWPWK-SY-PGMHADTW-----GCPVTPLPHSPLSSHQP---      | 477 |
| ClA97C10G186530    | -----PGYPPWRPPEIWPWK-SY-PGMHADTW-----GCPVTTPPHSLSSHQP---       | 478 |
| CA06g13040         | -----PYYPGWQPPENWHWN-PH-SGLYADVW-----GCPVTPPSLGSTPYLQ---       | 482 |
| SMEL_006g257080.1  | -----PYYPGWPPPETWHWN-PQ-PGLYADVW-----GCPVTPPSLGSTPYYPQ---      | 470 |
| Solyc06g061030.3.1 | -----PYYHGWQPPETWHWN-PQ-PGLYADVW-----GCPVTPPSLGSTPYYPQ---      | 478 |
| SMEL_008g315370.1  | -----                                                          | 378 |
| Solyc08g077230.3.1 | -----PYYPGWKPAETWHWT-PR-PELHADTW-----GSPIMSPSLGSYPYPQ---       | 480 |
| CA00g25180         | -----PYYPGWKPAETWHWK-PH-PGLLADTW-----GSPVMPPSFGSYPYPQ---       | 542 |
|                    |                                                                |     |
| MEL03C019337.2     | FGGASFSVIPPPHPMYKAAEPTTSVGRSPTHPLDYSYPSKESIDSAIGDVLAKPWLPLPL   | 422 |
| ClA97C02G036020    | FGGAGFSVPPPPHPMYKAA-EPTATVGRSPTHPLDYSYPSKESIDSAIGDVLAKPWLPLPL  | 417 |
| At4G18020.1        | -TAGGFQYPN-----GAETGFKIMP-----ASQDDEMLDQVVKEAISKPWLPLPL        | 499 |
| ClA97C09G175170    | -VSA-SHNMH-----TVNKSYGMPQGLFDLQPDKEKVDKIVKEAMRPWSPPLPL         | 468 |
| MEL03C003375.2.1   | -VSAQHNMH-----TVNKSYGMPQGLFDLQPDDEEVDKIVKEAMREPWSPPLPL         | 459 |
| CsAMJ39435.1       | -VSAQHNMH-----TVNKSYGMPQGLFDLQDDEEVDKIVKEAMKPPWSPPLPL          | 489 |
| MEL03C013874.2.1   | -HISGFENAD-----PYDKSYSIAFSPIDLQLADEEIDKVVEKAISKPWLPPLPL        | 525 |
| ClA97C10G186530    | -HISRFESTD-----PYDKSYGIAFSPIDLQLADEEIDKVVEKAISKPWLPPLPL        | 526 |
| CA06g13040         | -NAS-----GIHNRYSIIQSVDLHPAAEEVIDKVVEKAISKPWLPPLPL              | 524 |
| SMEL_006g257080.1  | -NASRFHRAE-----GIHNRYSIEKSVDLHPAAEEVIDKVVEKAISKPWLPPLPL        | 518 |
| Solyc06g061030.3.1 | -NASGFHRAE-----GMLNGYSIIQSVDLHPAAEEVIDKVVEKAISKPWLPPLPL        | 526 |
| SMEL_008g315370.1  | -----                                                          | 378 |
| Solyc08g077230.3.1 | -NAGV-YRPH-----GTHNRYSMLEKSFDLHPAAEVIDKVVEKAITKPWLPLPL         | 527 |
| CA00g25180         | -NAGM-YQSH-----GMHNRYSMLEKSFVHPAAEVIDKVVEKAITKPWLPLPL          | 589 |
|                    |                                                                |     |
| MEL03C019337.2     | GLKPPSLDSVKVELQRQGIKPPTCAA-----                                | 450 |
| ClA97C02G036020    | GLKPPSLDSVKVELQRQGIKPPTCAA-----                                | 446 |

|                    |                                       |     |
|--------------------|---------------------------------------|-----|
| At4G18020.1        | GLKPPSAESVLAELTRQGISAVPSSSCLINGSHRLR  | 535 |
| Cla97C09G175170    | GLKPP-TESVLTELSKQGISTVPPR---INGSKPP-  | 499 |
| MEL03C003375.2.1   | GLKPPSTESVLTLSKQGISTVPPQ---IDGSRSP-   | 491 |
| CsAMJ39435.1       | GLKPPSTESVLTLSKKGISTVPPQ---IDGSRSP-   | 521 |
| MEL03C013874.2.1   | GLKPPSTESVLSSELSKQGISTVPSH---INGSKVIQ | 558 |
| Cla97C10G186530    | GLKPPSTESVLSSELSRQGISTVPSH---INGSKLLQ | 559 |
| CA06g13040         | GLKSPSTESVLDALSKQGISAVPSR---INGSRRPH  | 557 |
| SMEL_006g257080.1  | GLKPPSTESVLDALSKQGVSTVPPR---INGSHRPH  | 551 |
| Solyc06g061030.3.1 | GLKPPSTESVLDALSKQGIPAVPPR---HHRSHRPH  | 559 |
| SMEL_008g315370.1  | -----                                 | 378 |
| Solyc08g077230.3.1 | GLKAPSTESVLDELSRQGISTIPSQ---INDSRCRR  | 560 |
| CA00g25180         | GLKPPSMEGVLDDELSRQGISTVPPR---INGSRCWR | 622 |