Alignment of CMT2 sequences from different Accessions:

_ref = reference (Columbia genotype) _altA = CMT2A-nr, _altB= CMT2B-nr

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TAIR10      MLSPAKCESEEAQAPLDLHSSSRSEPECLSLVLWCPNPEEAAPSSTRELIKLPDNGEMSL 60
992_ref     MLSPAKCESEEAQAPLDLHSSSRSEPECLSLVLWCPNPEEAAPSSTRELIKLPDNGEMSL 60
6918_ref    MLSPAKCESEEAQAPLDLHSSSRSEPECLSLVLWCPNPEEAAPSSTRELIKLPDNGEMSL 60
6188_altA   MLSPAKCESEEAQAPLDLHSSSRSEPECLSLVLWCPNPEEAAPSSTRELIKLPDNGEMSL 60
1061_altA   MLSPAKCESEEAQAPLDLHSSSRSEPECLSLVLWCPNPEEAAPSSTRELIKLPDNGEMSL 60
6113_altB   MLSPAKCESEEAQAPLDLHSSSRSEPECLSLVLWCPNPEEAAPSSTRELIKLPDNGEMSL 60
6191_altB   MLSPAKCESEEAQAPLDLHSSSRSEPECLSLVLWCPNPEEAAPSSTRELIKLPDNGEMSL 60
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TAIR10      RRSTTLNCNSPEENGGEGRVSQRKSSRGKSQPLLMLTNGCQLRRSPRFRALHANFDNVCS 120
992_ref     RRSTTLNCNSPEENGGEGRVSQRKSSRGKSQPLLMLTNGCQLRRSPRFRAVHANFDNVCS 120
6918_ref    RRSTTLNCNSPEENGGEGRVSQRKSSRGKSQPLLMLTNGCQLRRSPRFRAVHANFDNVCS 120
6188_altA   RRSTTLNCNSPEENGGEGRVSQRKSSRGKSQPLLMLTNGCQLRRSPRFRALHANFDNVCS 120
1061_altA   RRSTTLNCNSPEENGGEGRVSQRKSSRGKSQPLLMLTNGCQLRRSPRFRAVHANFDNVCS 120
6113_altB   RRSTTLNCNSPEENGGEGRVSQRKSSRGKSQPLLMLTNGCQLRRSPRFRAVHANFDNVCS 120
6191_altB   RRSTTLNCNSPEENGGEGRVSQRKSSRGKSQPLLMLTNGCQLRRSPRFRAVHANFDNVCS 120
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TAIR10      VPVTKGGVSQRKFSRGKSQPLLTLTNGCQLRRSPRFRAVDGNFDSVCSVPVTGKFGSRKR 180
992_ref     VPVTEGGVSQRNSSRGKSQPLLTLTNGCQLRRSPRSRAVDGNFDSVCSVPVTGKFGSRKR 180
6918_ref    VPVTEGGVSQRNSSRGKSQPLLTLTNGCQLRRSPRFRAVDGNFDSVCSVPVTGKFGSRKR 180
6188_altA   VPVTKGGVSQRKFSRGKSQPLLTLTNGCQLRRSPRFRAVDGNFDSVCSVPVTGKFGSRKR 180
1061_altA   VPVTEGGVSQRNSSRGKSQPLLTLTNGCQLRRSPRFRAVDGNFDSVCSVPVTGKFGSRKR 180
6113_altB   VPVTEGGVSQRNSSRGKSQPLLTLTNGCQLRRSPRFKAVDGNFDSVCSVPVTGKFGSRKR 180
6191_altB   VPVTEGGVSQRNSSRGKSQPLLTLTNGCQLRRSPRFKAVDGNFDSVCSVPVTGKFGSRKR 180
            ****:******: ********************* :*******************

TAIR10      KSNSALDKKESSDSEGLTFKDIAVIAKSLEMEIISECQYKNNVAEGRSRLQDPAKRKVDS 240
992_ref     KSNSALDKKESSDSEGLTFKDIAVIAKSLEMEIISECQYKNNVAEGRSKLQDPAKRKVDS 240
6918_ref    KSNSALDKKESSDSEGLTFKDIAVIAKSLEMEIISECQYKNNVAEGRSRLQDPAKRKVDS 240
6188_altA   KSNSALDKKESSDSEGLTFKDIAVIAKSLEMEIISECQYKNNVAEGRSRLQDPAKRKVDS 240
1061_altA   KSNSALDKKESSDSEGLTFKDIAVIAKSLEMEIISECQYKNNVAEGRSRLQDPAKRKVDS 240
6113_altB   KSNSALDKKESSDSEGLTFKDIAVIAKSLEMEIISECQYKNNVAEGRSRLQDPAKRKVDS 240
6191_altB   KSNSALDKKESSDSEGLTFKDIAVIAKSLEMEIISECQYKNNVAEGRSRLQDPAKRKVDS 240
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TAIR10      DTLLYSSINSSKQSLGSNKRMRRSQRFMKGTENEGEENLGKSKGKGMSLASCSFRRSTRL 300
992_ref     DTLLYSSINSSKQSLGSNKRMRRSQRFMKGTENEGEENLGKSKGKGMSLASCSFRRSTRL 300
6918_ref    DTLLSSSINSSKQSLGSNKRMRRSQRFMKGTENEGEENLGKSKGKGMSLASCSFRRSTRL 300
6188_altA   DTLSSSSINSSKQNLGSNKRMRRSQRFMKGTENEGVENLGKSKGKGMSLASCSFRRSTRL 300
1061_altA   DTLSSSSINSSKQNLGSNKRMRRSQRFMKGTENEGVENLGKSKGKGMSLASCSFRRSTRL 300
6113_altB   DTLLYSSINSSKQSLGSNKRMRRSQRFMKGTENEGEENLGKSKGKGMSLASCSFRRSTRL 300
6191_altB   DTLLYSSINSSKQSLGSNKRMRRSQRFMKGTENEGEENLGKSKGKGMSLASCSFRRSTRL 300
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TAIR10      SGTVETGNTETLNRRKDCGPALCGAEQVRGTERLVQISKKDHCCEAMKKCEGDGLVSSKQ 360
992_ref     SGTVETGNTETLNRRKDCGPALCGAEQVRGTERLVQISKNDHCCEAMKKCEGDGLVSSKQ 360
6918_ref    SGTVETGNTETLNRRKDCGPALCGAEQVRGTERLVQISKNDHCCEAMKKCEGDGLVSSKQ 360
6188_altA   SGTVETGNTETLNRRKDCGPALCGAEQVRGTERLVQISKNDHCCEAMKKCEGDGLVSSKQ 360
1061_altA   SGTVETGNTETLNRRKDCGPALCGAEQVRGTERLVQISKNDHCCEAMKKCEGDGLVSSKQ 360
6113_altB   SGTVETGNTETLNRRKDCGPALCGAEQVRGTERLVQISKNDHCCEAMKKCEGDGLVSSKQ 360
6191_altB   SGTVETGNTETLNRRKDCGPALCGAEQVRGTERLVQISKNDHCCEAMKKCEGDGLVSSKQ 360
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TAIR10      ELLVFPSGCIKKTVNGCRDRTLGKPRSSGLNTDDIHTSSLKISKNDTSNGLTMTTALVEQ 420
992_ref     ELLVFPSGCIKKTVNGCRDRTLGKPRSSGLNTDDIHTSSLKISKNDTSNGLTMTTALVEQ 420
6918_ref    ELLVFPSGCIKKTVNVCRDRTLGKPRSSGLNTDDIHTSSLKISKNDTSNGLTMTTALVEQ 420
6188_altA   ELLVFPSGCIKKTVNVCRDRTLGKPRSSGLNTDDIHTSSLKISKNGTSNGLTMTTALVEQ 420
1061_altA   ELLVFPSGCIKKTVNVCRDRTLGKPRSSGLNTDDIHTSSLKISKNGTSNGLTMTTALVEQ 420
6113_altB   ELLVFPSGCIKKTVNGCRDRTLGKPRSSGLNTDDIHTSSLKISKNDTSNGLTMTTALVEQ 420
6191_altB   ELLVFPSGCIKKTVNGCRDRTLGKPRSSGLNTDDIHTSSLKISKNDTSNGLTMTTALVEQ 420
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TAIR10      DAMESLLQGKTSACGAADKGKTREMHVNSTVIYLSDSDEPSSIEYLNGDNLTQVESGSAL 480
992_ref     DAMESLLQGKTSACGAADKGKTREMHVNSTVIYLSDSDEPSSIEYLNGDNLTQVESGSAL 480
6918_ref    DAMESLLQGKTSACGAADKGKTREMHVNSTVIYLSDSDEPSSIEYLNGDNLTQVESGSAL 480
6188_altA   DAMESLLQGKTSACGAADKGKTREMHVNSTVIYLSDSDEPSSIEYLNGDNLTQVKSGSAL 480
1061_altA   DAMESLLQGKTSACGAADKGKTREMHVNSTVIYLSDSDEPSSIEYLNGDNLTQVKSGSAL 480
6113_altB   DAMESLLQGKTSACGAADKGKTREMHVNSTVIYLSDSDEPSSIEYLNGDNLTQVESGSAL 480
6191_altB   DAMESLLQGKTSACGAADKGKTREMHVNSTVIYLSDSDEPSSIEYLNGDNLTQVESGSAL 480
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TAIR10      SSGGNEGIVSLDLNNPTKSTKRKGKRVTRTAVQEQNKRSICFFIGEPLSCEEAQERWRWR 540
992_ref     SSGGNEGIVSLDLNNPTKSTNRKGKRVTRTAVQEQNKRSICFFIGEPLSCEEAQERWRWR 540
6918_ref    SSGGNEGIVSLDLNNPTKSTKRKGKRVTRTAVQEQNKRSICFFIGEPLSCEEAQERWRWR 540
6188_altA   SSGGNEGIVSLDLNNPTKSTKRKGKRVTRTAVQEQNKRSICFFIGEPLSCEEAQERWRWR 540
1061_altA   SSGGNEGIVSLDLNNPTKSTKRKGKRVTRTAVQEQNKRSICFFIGEPLSCEEAQERWRWR 540
6113_altB   SSGGNEGIVSLDLNNPTKSTKRKGKRVTRTAVQEQNKRSICFFIGEPLSCEEAQERWRWR 540
6191_altB   SSGGNEGIVSLDLNNPTKSTKRKGKRVTRTAVQEQNKRSICFFIGEPLSCEEAQERWRWR 540
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TAIR10      YELKERKSKSRGQQSEDDEDKIVANVECHYSQAKVDGHTFSLGDFAYIKGEEEETHVGQI 600
992_ref     YELKERKSKSRGQQSEDDEDKIVANVECHYSQAKVDGHTFSLGDFAYIKGEEEETHVGQI 600
6918_ref    YELKERKSKSRGQQSEDDEDKIVANVECHYSQAKVDGHTFSLGDFAYIKGEEEETHVGQI 600
6188_altA   YELKERKSKSRGQQSEDDEDKIVANVECHYSQAKVDGHTFSLGDFAYIKGEEEETHVGQI 600
1061_altA   YELKERKSKSRGQQSEDDEDKIVANVECHYSQAKVDGHTFSLGDFAYIKGEEEETHVGQI 600
6113_altB   YELKERKSKSRGQQSEDDEDKIVANVECHYSQAKVDGHTFSLGDFACIKGEEEETHVGQI 600
6191_altB   YELKERKSKSRGQQSEDDEDKIVANVECHYSQAKVDGHTFSLGDFACIKGEEEETHVGQI 600
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                                **BAH Domain**                   **Y586C**
TAIR10      VEFFKTTDGESYFRVQWFYRATDTIMERQATNHDKRRLFYSTVMNDNPVDCLISKVTVLQ 660
992_ref     VEFFKTTDGESYFRVQWFYRATDTIMERQATNHDKRRLFYSTVMNDNPVDCLISKVTVLQ 660
6918_ref    VEFFKTTDGESYFRVQWFYRATDTIMERQATNHDKRRLFYSTVMNDNPVDCLISKVTVLQ 660
6188_altA   VEFFKTTDGESYFRVQWFYRATDTIMERQATNHDKRRLFYSTVMNDNPVDCLISKVTVLQ 660
1061_altA   VEFFKTTDGESYFRVQWFYRATDTIMERQATNHDKRRLFYSTVMNDNPVDCLISKVTVLQ 660
6113_altB   VEFFKTTDGESYFRVQWFYRATDTIMERQATNHDKRRLFYSTVMNDNPVDCLISKVTVLQ 660
6191_altB   VEFFKTTDGESYFRVQWFYRATDTIMERQATNHDKRRLFYSTVMNDNPVDCLISKVTVLQ 660
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TAIR10      VSPRVGLKPNSIKSDYYFDMEYCVEYSTFQTLRNPKTSENKLECCADVVPTESTESILKK 720
992_ref     VSPRAGLKPNSIKSDYYFDMEYCVEYSTFQTLRNPKTSENKLECWADVVPTESTESILKK 720
6918_ref    VSPRAGLKPNSIKSDYYFDMEYCVEYSTFQTLRNPKTSENKLECCADVVPTKSTESILKK 720
6188_altA   VSPRAGLKPNSIKSDYYFDMEYCVEYSTFQTLRNPKTSENKLECCADVVPTESTESILKK 720
1061_altA   VSPRAGLKPNSIKSDYYFDMEYCVEYSTFQTLRNPKTSENKLECCADVVPTESTESILKK 720
6113_altB   VSPRAGLKPNSIKSDYYFDMEYCVEYSTFQTLRNPKTSENKLECCADVVPTKSTESILKK 720
6191_altB   VSPRAGLKPNSIKSDYYFDMEYCVEYSTFQTLRNPKTSENKLECCADVVPTKSTESILKK 720
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TAIR10      KSFSGELPVLDLYSGCGGMSTGLSLGAKISGVDVVTKWAVDQNTAACKSLKLNHPNTQVR 780
992_ref     KSFSGELPVLDLYSGCGGMSTGLSLGAKISGVDVVTKWAVDQNTAACKSLKLNHPNTQVR 780
6918_ref    KSFSGELPVLDLYSGCGGMSTGLSLGAKISGVDVVTKWAVDQNTAACKSLKLNHPNTQVR 780
6188_altA   KSFSGELPVLDLYSGCGGMSTGLSLGAKISGVDVVTKWAVDQNKAACKSLKLNHPNTQVR 780
1061_altA   KSFSGELPVLDLYSGCGGMSTGLSLGAKISGVDVVTKWAVDQNKAACKSLKLNHPNTQVR 780
6113_altB   KSFSGELPVLDLYSGCGGMSTGLSLGAKISGVDVVTKWAVDQNTAACKSLKLNHPNTQVR 780
6191_altB   KSFSGELPVLDLYSGCGGMSTGLSLGAKISGVDVVTKWAVDQNTAACKSLKLNHPNTQVR 780
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TAIR10      NDAAGDFLQLLKEWDKLCKRYVFNNDQRTDTLRSVNSTKETSGSSSSSSDDDSDSEEYEVE 840
992_ref     NDAAGDFLQLLKEWDKLCKRYVFNNDQRTDTLRSVNSTKETSESSSSSSDDDSDSEEYEVE 840
6918_ref    NDAAGDFLQLLKEWDKLCKRYVFNNDQRTDTLRSVNSTKETSESSSSSSDDDSDSEEYEVE 840
6188_altA   NDAAGDFLQLLKEWDKLCKRYVFNNDQRTDTLRSVNSTKETSESSSSSSDDDSDSEEYEVE 840
1061_altA   NDAAGDFLQLLKEWDKLCKRYVFNNDQRTDTLRSVNSTKETSESSSSSSDDDSDSEEYEVE 840
6113_altB   NDSAGDFLQLLKEWDKLCKRYVFNNDQRTDTLRSVNSTKETSESSSSSSDDDSDSEEYEVE 840
6191_altB   NDSAGDFLQLLKEWDKLCKRYVFNNDQRTDTLRSVNSTKETSESSSSSSDDDSDSEEYEVE 840
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                                    **CHROMO Domain**
TAIR10      KLVDICFGDHDKTGKNGLKFKVHWKGYRSDEDTWELAEELSNCQDAIREFVTSGFKSKIL 900
992_ref     KLVDICFGDPDKTGKNGLKFKVHWKGYRSDEDTWELAEELSNCQDAIREFVTSGFKSKIL 900
6918_ref    KLVDICFGDPDKTGKNGLKFKVHWKGYRSDEDTWELAEELSNCQDAIREFVTSGFKSKIL 900
6188_altA   KLVDICFGDPDKTGKNGLKFKVHWKGYRSDEDTWELAEELSNCQDAIREFVTSGFKSKIL 900
1061_altA   KLVDICFGDPDKTGKNGLKFKVHWKGYRSDEDTWELAEELSNCQDAIREFVTSGFKSKIL 900
6113_altB   KLVDICFGDPDKTGKNGLKFKVHWKGYRSDEDTWELAEELSNCQDAIREFVTSGFKSKIL 900
6191_altB   KLVDICFGDPDKTGKNGLKFKVHWKGYRSDEDTWELAEELSNCQDAIREFVTSGFKSKIL 900
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                            **C5 Methyltransferase Domain**
TAIR10      PLPGRVGVICGGPPCQGISGYNRHRNVDSPLNDERNQQIIVFMDIVEYLKPSYVLMENVV 960
992_ref     PLPGRVGVICGGPPCQGISGYNRHRNVDSPLNDERNQQIIVFMDIVEYLKPSYVLMENVV 960
6918_ref    PLPGRVGVICGGPPCQGISGYNRHRNVDSPLNDERNQQIIVFMDIVEYLKPSYVLMENVV 960
6188_altA   PLPGRVGVICGGPPCQGISGYNRHRNVDSPLNDERNQQIIVFMDIVEYLKPSYVLMENVV 960
1061_altA   PLPGRVGVICGGPPCQGISGYNRHRNVDSPLNDERNQQIIVFMDIVEYLKPSYVLMENVV 960
6113_altB   PLPGRVGVICGGPPCQGISGYNRHRNVDSPLNDEKNQQIIVFMDIVEYLKPSYVLMENVV 960
6191_altB   PLPGRVGVICGGPPCQGISGYNRHRNVDSPLNDEKNQQIIVFMDIVEYLKPSYVLMENVV 960
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                                    **R934K**
TAIR10      DILRMDKGSLGRYALSRLVNMRYQARLGIMTAGCYGLSQFRSRVFMWGAVPNKNLPPFPL 1020
992_ref     DILRMDKGSLGRYALSRLVNMRYQARLGIMTAGCYGLSQFRSRVFMWGAVPNKNLPPFPL 1020
6918_ref    DILRMDKGSLGRYALSRLVNMRYQARLGIMTAGCYGLSQFRSRVFMWGAVPNKNLPPFPL 1020
6188_altA   DILRMDKGSLGRYALSRLVNMRYQARLGIMTAGCYGLSQFRSRVFMWGAVPNKNLPPFPL 1020
1061_altA   DILRMDKGSLGRYALSRLVNMRYQARLGIMTAGCYGLSQFRSRVFMWGAVPNKNLPPFPL 1020
6113_altB   DILRMDKGSLGRYALSRLVNMRYQARLGIMTAGCYGLSQFRSRVFMWGAVPNKNLPPFPL 1020
6191_altB   DILRMDKGSLGRYALSRLVNMRYQARLGIMTAGCYGLSQFRSRVFMWGAVPNKNLPPFPL 1020
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TAIR10     PTHDVIVRYGLPLEFERNVVAYAEGQPRKLEKALVLKDAISDLPHVSNDEDREKLPYESL 1080
992_ref    PTHDVIVRYGLPLEFERNVVAYAEGQPRKLEKALVLKDAISDLPHVSNDEDREKLPYESL 1080
6918_ref   PTHDVIVRYGLPLEFERNVVAYAEGQPRKLEKALVLKDAISDLPHVSNDEDREKLPYESL 1080
6188_altA  PTHDVIVRYGLPLEFERNVVAYAEGQPRKLEKALVLKDAISDLPHVSNDEDREKLPYESL 1080
1061_altA  PTHDVIVRYGLPLEFERNVVAYAEGQPRKLEKALVLKDAISDLPHVSNDEDREKLPYESL 1080
6113_altB  PTHDVIVRYGLPLEFERNVVAYAEGQPRKLEKALVLKDAISDLPHVSNEEDREKLPYESL 1080
6191_altB  PTHDVIVRYGLPLEFERNVVAYAEGQPRKLEKALVLKDAISDLPHVSNEEDREKLPYESL 1080
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                                                          D1068E
TAIR10     PKTDFQRYIRSTKRDLTGSAIDNCNKRTMLLHDHRPFHINEDDYARVCQIPKRKGANFRD 1140
992_ref    PKTDFQRYIRSTKRDLTGSAIDNCNKRTMLLHDHRPFHINEDDYARVCQIPKRKGANFRD 1140
6918_ref   PKTDFQRYIRSTKRDLTGSAIDNCNKRTMLLHDHRPFHINEDDYARVCQIPKRKGANFRD 1140
6188_altA  PKTDFQRYIRSTKRDLTGSAIDNCNKRTMLLHDHRPFHINEDDYARVRQIPKRKGANFRD 1140
1061_altA  PKTDFQRYIRSTKRDLTGSAIDNCNKRTMLLHDHRPFHINEDDYARVRQIPKRKGANFRD 1140
6113_altB  PKTDFQRYIRSTKRDLTGSAIDNCNKRTMLLHDHRPFHINEDDYARVCQIPKRKGANFRD 1140
6191_altB  PKTDFQRYIRSTKRDLTGSAIDNCNKRTMLLHDHRPFHINEDDYARVCQIPKRKGANFRD 1140
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                                                  C1127R
TAIR10     LPGLIVRNNTVCRDPSMEPVILPSGKPLVPGYVFTFQQGKSKRPFARLWWDETVPTVLTV 1200
992_ref    LPGIIVRNNTVCRDPSMEPVILPSGKPLVPGYVFTFQQGKSKRPFARLWWDETVPTVLTV 1200
6918_ref   LPGLIVRNNTVCRDPSMEPVILPSGKPLVPGYVFTFQQGKSKRPFARLWWDETVPTVLTV 1200
6188_altA  LPGLIVRNNTVCRDPSMEPVILPSGKPLVPGYVFTFQQGKSKRPFARLWWDETVPTVLTV 1200
1061_altA  LPGLIVRNNTVCRDPSMEPVILPSGKPLVPGYVFTFQQGKSKRPFARLWWDETVPTVLTV 1200
6113_altB  LPGLIVRNNTVCRDPSMEPVILPSGKPLVPGYVFTFQQGKSKRPFARLWWDETVPTVLTV 1200
6191_altB  LPGLIVRNNTVCRDPSMEPVILPSGKPLVPGYVFTFQQGKSKRPFARLWWDETVPTVLTV 1200
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TAIR10     PTCHSQALLHPEQDRVLTIRESARLQGFPDYFQFCGTIKERYCQIGNAVAVSVSRALGYS 1260
992_ref    PTCHSQALLHPEQDRVLTIRESARLQGFPDYFQFCGTIKERYCQIGNAVAVSVSRALGYS 1260
6918_ref   PTCHSQALLHPEQDRVLTIRESARLQGFPDYFQFCGTIKERYCQIGNAVAVSVSRALGYS 1260
6188_altA  PTCHSQALLHPEQDRVLTIRESARLQGFPDYFQFCGTIKERYCQIGNAVAVSVSRALGYS 1260
1061_altA  PTCHSQALLHPEQDRVLTIRESARLQGFPDYFQFCGTIKERYCQIGNAVAVSVSRALGYS 1260
6113_altB  PTCHSQALLHPEQDRVLTIRESARLQGFPDYFQFCGTIKERYCQIGNAVAVSVSRALGYS 1260
6191_altB  PTCHSQALLHPEQDRVLTIRESARLQGFPDYFQFCGTIKERYCQIGNAVAVSVSRALGYS 1260
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TAIR10     LGMAFRGLARDEHLIKLPQNFSHSTYPQLQETIPH 1295
992_ref    LGMAFRGLARDEHLIKLPQNFSHSTYPQLQETIPH 1295
6918_ref   LGMAFRGLARDEHLIKLPQNFSHSTYPQLQETIPH 1295
6188_altA  LGMAFRGLARDEHLIKLPQNFSHSTYPQLQETIPH 1295
1061_altA  LGMAFRGLARDEHLIKLPQNFSHSTYPQLQETIPH 1295
6113_altB  LGMAFRGLARHEHLIKLPQNFSHSTYPQLQEAIPH 1295
6191_altB  LGMAFRGLARHEHLIKLPQNFSHSTYPQLQEAIPH 1295
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