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AT10182 WP 005547298.1 NC 013416:1648241-1648495  .....................................MILAWTETAWEDYLYWQQVDKKTLLRINKLTQNITR  36
AT728 15903628 NC 003098:c1566962-1566708         MEAVLYSTFRNHLKDYMKKVNDEFEPLTVVNKNPDEDIVVLSKSEWDSIQETLRIAQNKE.LSDKVLRGMAQVRA  74
AT10021 WP 005687754.1 NZ JMSI01000003:c191403-191134 MEATNYSDFRRNLKHYMSQVNEDAEPLLVTAKDDDDNVVVMSKHDFDAIEETLYLLSNPK.LMAKIKRGDAQIAA  74
AT10020 WP 005687754.1 NZ JPZB01000034:15154-15423 MEATNYSDFRRNLKHYMSQVNEDAEPLLVTAKDDDDNVVVMSKHDFDAIEETLYLLSNPK.LMAKIKRGDAQIAA  74
AT6237 WP 005687754.1 NC 013199:2763807-2764076   MEATNYSDFRRNLKHYMSQVNEDAEPLLVTAKDDDDNVVVMSKHDFDAIEETLYLLSNPK.LMAKIKRGDAQIAA  74
AT6143 WP 005687754.1 NC 017491:2755711-2755980   MEATNYSDFRRNLKHYMSQVNEDAEPLLVTAKDDDDNVVVMSKHDFDAIEETLYLLSNPK.LMAKIKRGDAQIAA  74
AT6138 WP 005687754.1 NC 013199:2763807-2764076   MEATNYSDFRRNLKHYMSQVNEDAEPLLVTAKDDDDNVVVMSKHDFDAIEETLYLLSNPK.LMAKIKRGDAQIAA  74
AT6115 WP 000388479.1 NC 014959:c5482-5213        MEAVAYSNFRQNLRSYMKQVNEDAETLIVTSKDVEDTVVVLSKRDYDSMQETLRTLSNNY.VMEKIRRGDEQFSK  74
AT6022 WP 000388479.1 NC 005000:c5482-5213        MEAVAYSNFRQNLRSYMKQVNEDAETLIVTSKDVEDTVVVLSKRDYDSMQETLRTLSNNY.VMEKIRRGDEQFSK  74
AT10072 WP 012848468.1 NC 013508:1725106-1725351  MHTVTFSDARKHFADTMNRVTNNAEPVRVMRRD.APDIVMVDAGEYEAMLETIYLFSNPA.NAAHLNESLAQLER  73
AT10077 WP 010972003.1 NC 003062:c1979853-1979599 MANVRFTEFRQNFATHFDRVLETRAPLLVTRQG.KEAVVVLAEGEYESMQETLHLLSNPA.NASRLRASMGELER  73
AT2427 88196332 NC 007795:c2477698-2477447       MIIKNYSYARQNLKALMTKVNDDSDMVTVTSTD.DKNVVIMSESDYNSMMETLYLQQNPN.NAEHLAQSIADLER  73
AT613 21284059 NC 003923:c2479924-2479673         MIIKNYSYARQNLKALMTKVNDDSDMVTVTSTD.DKNVVIMSESDYNSMMETLYLQQNPN.NAEHLAQSIADLER  73
AT1074 WP 000584499.1 NC 002745:c2466518-2466267  MIIKNYSYARQNLKALMTKVNDDSDMVTVTSTD.DKNVVIMSESDYNSMMETLYLQQNPN.NAEHLAQSIADLER  73
AT130 NP 217874.1 NC 000962:3770773-3771048       .MSISASEARQRLFPLIEQVNTDHQPVRITSRA.G.DAVLMSADDYDAWQETVYLLRSPE.NARRLMEAVARDKA  71
AT6122 NP 626485.1 NC 003888:2405942-2406205      .MSITASEARQNLFPLIEQVNEDHAPVHITSRK.G.NAVLMSEEDFTAWTETVHLLRSPR.NARRLLDSIAEAEA  71
AT310 26989659 NC 002947:c3343006-3342722         MHVLTFSQARAELKQTMDDVCRDHEPAVITRQR.GEPVVMMSLEDYNGMNETIHLLGSSK.NASRLRSSIAQLRD  73
AT1043 NP 416521.2 NC 000913:c2089713-2089462     MRTISYSEARQNLSATMMKAVEDHAPILITRQN.GEACVLMSLEEYNSLEETAYLLRSPA.NARRLMDSIDSLKS  73
AT4918 WP 005598318.1 NC 010278:1417602-1417853   MQAITYTEARQNLAGTMSKVAEDFEPILITRSK.GGNCVLMSYEQYCSLEETAYLMRSPT.NAKRLLDSVAELRQ  73
consensus                                         *  * *** *****  *  ****  ****** ** *********  ***** ****** **  ** **   ****
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AT10182 WP 005547298.1 NC 013416:1648241-1648495  APFEGLGNPEPLKHQLSGFWSRRIDKEHRLVYQVSDSHLTIIQCRYHY  84
AT728 15903628 NC 003098:c1566962-1566708         GST........QVHVIEE.................................  84
AT10021 WP 005687754.1 NZ JMSI01000003:c191403-191134 GKA........KQHELLTDFDHD.........................  89
AT10020 WP 005687754.1 NZ JPZB01000034:15154-15423 GKA........KQHELLTDFDHD.........................  89
AT6237 WP 005687754.1 NC 013199:2763807-2764076   GKA........KQHELLTDFDHD.........................  89
AT6143 WP 005687754.1 NC 017491:2755711-2755980   GKA........KQHELLTDFDHD.........................  89
AT6138 WP 005687754.1 NC 013199:2763807-2764076   GKA........KQHELLTDFDHD.........................  89
AT6115 WP 000388479.1 NC 014959:c5482-5213        GAF........KTHDLIEVESDD.........................  89
AT6022 WP 000388479.1 NC 005000:c5482-5213        GAF........KTHDLIEVESDD.........................  89
AT10072 WP 012848468.1 NC 013508:1725106-1725351  GEV........VTVDY................................  81
AT10077 WP 010972003.1 NC 003062:c1979853-1979599 GDT........IERDPTEE.............................  84
AT2427 88196332 NC 007795:c2477698-2477447        GKT........ITKDIDV..............................  83
AT613 21284059 NC 003923:c2479924-2479673         GKT........ITKDIDV..............................  83
AT1074 WP 000584499.1 NC 002745:c2466518-2466267  GKT........ITKDIDV..............................  83
AT130 NP 217874.1 NC 000962:3770773-3771048       GHS........AFTKSVDELREMAGGEE....................  91
AT6122 NP 626485.1 NC 003888:2405942-2406205      GDA........TEHDLIDPDAERA........................  87
AT310 26989659 NC 002947:c3343006-3342722         GQA........LTKELDLNEQEPEAAEQE...................  94
AT1043 NP 416521.2 NC 000913:c2089713-2089462     GKG........TEKDIIE..............................  83
AT4918 WP 005598318.1 NC 010278:1417602-1417853   GQG........IERELIE..............................  83
consensus                                         *             ****
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X non conserved
X similar
X ≥50% conserved