

CLUSTAL

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gi311141403/1-440 GGTGGTGTGGATTTACCCAAATACGCATCTGCAGCTTATACTGACAATATTCTTGACGAT
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gi629633278/1-472 TTCGCTATTAGAAAC---GACGAAG---GT-----TTACCACTTGAAATGAGAG
gi145370874/1-445 TTCTCTATAAGAAAT---GACGAAG---GA-----TTACCACTTGAAATGAGAG
gi311141403/1-440 TTCTCTATAAGAAAT---GACGAAG---GA-----TTACCACTTGAAATGAGAG
gi629633284/1-466 TTATCAATTAGGAGT---GATGAAG---GT-----CTTATCCATGAATTAAGAG
gi629633280/1-466 TTATCTATTAGAAGT---GATGAAG---GA-----TTAATTCATGAATTAAGAG

gi309253887/1-472 GCGCAAACCTACCC-CAACTACGCCATGAA-CG
gi930068978/1-469 GACCAAACCTACCC-CAACTACGCCATGA----
gi930068946/1-466 GACCAAACCTACCC-CAACTATGCCA-----
gi954036668/1-468 GACCGAACTACCC-TAACTACGCAATG-----
gi930068996/1-469 GAGCCAACTATCC-CAACTATGCAATGA----
gi428274410/1-489 GACCGAACTACCC-CAACTATGCCATA-----
gi954036662/1-94 -----
gi954036666/1-486 GTCCAAACTATCC-CAACTACGCCATG-----
gi930068992/1-487 GTCCAAACTACCC-TAACTACGCCCTGA----
gi930068990/1-487 GTCCAAACTACCC-CAACTACGCCCTGA----
gi950655841/1-488 GTCCAAACTATCC-AAACTACGCCATGAA---
gi930068952/1-487 GTCCAAACTACCC-CAACTACGCCATGA----
gi58615486/1-470 GCGCAAACCTACCCCAACTACGCNATGA----
gi5616127/1-466 GCGCAAACCTACCC-TAACTACGCCATGA----
gi82492006/1-464 GTCCTAATATCC-TAACTACGC-----
gi262358095/1-470 GGCCAAACTACCC-AAACTACGCAATGAA---
gi629633272/1-472 GACCAAACCTATCC-TAACTACGCAATGAA-CG
gi629633282/1-472 GACCAAACCTATCC-TAACTACGCAATGAA-TG
gi334085683/1-468 GTCCTAATATCC-CAACTACGCCATA-----
gi217792440/1-467 GACCTAATATCC-TAACTACGCAATGAA---
gi498543114/1-395 GACCTAATATCC-TAACTACGCAATGAAA--
gi629633278/1-472 GACCTAATATCC-TAACTATGCAATGAA-TG
gi145370874/1-445 GACCAA-----
gi311141403/1-440 G-----
gi629633284/1-466 GTCCTAATTATCC-TAATTATGCAATGAA-TG
gi629633280/1-466 GGCCTAATATCC-TAACTATGCAATGAA-TG