

Read Sequence:CPT2 (1537 nt)
 =====
 Performing Scan: gga-miR-214 vs CPT2
 =====

Forward: Score: 154.000000 Q:2 to 19 R:758 to 778 Align Len (17) (70.59%) (76.47%)

Query: 3' gacGGACAGACACGGACGACa 5'
 ||:| || | |||||
 Ref: 5' ataCTTTTCAAAGCCTGCTGc 3'

Energy: -18.370001 kCal/Mol

Scores for this hit:
 >gga-miR-214 CPT2 154.00 -18.37 2 19 758 778 17 70.59% 76.47%

Forward: Score: 140.000000 Q:2 to 9 R:899 to 919 Align Len (7) (100.00%) (100.00%)

Query: 3' gacggacagacacGGACGACa 5'
 |||||
 Ref: 5' ttccaatattcctCCTGCTGt 3'

Energy: -15.780000 kCal/Mol

Scores for this hit:
 >gga-miR-214 CPT2 140.00 -15.78 2 9 899 919 7 100.00% 100.00%

Score for this Scan:
 Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions
 >>gga-miR-214 CPT2 294.00 -34.15 154.00 -18.37 871745 21 1537 758 899
 Complete

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 13 **Supplementary Figure S1.** The target relationship of miR-214 and CPT2 analyzed by miRanda.