

1 to 3 of 3 [view as excel spreadsheet](#) [download query output](#)

| miRNA ID | Target Gene                               | Grape contig with miRNA gene | mature miRNA GC content | Position Assembled Precursors | Similarity Assembled Precursors     | Target Ranking Group         | Selfcontain Score | Kegg pathway                                                    | Blast vs GO annotated proteins                                                                                       |
|----------|-------------------------------------------|------------------------------|-------------------------|-------------------------------|-------------------------------------|------------------------------|-------------------|-----------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|
| 155983   | <a href="#">twinscan VV78X131442.7_14</a> | REV_COM_VV78X231846.14       | 0.47                    | singlet                       | <a href="#">precursor Contig231</a> | <a href="#">target CL576</a> | 0.998154          | <a href="#">04130 SNARE interactions in vesicular transport</a> | <a href="#">Q9M229</a> (Bed-like SN1-1 OS=Arabidopsis thaliana GN=BET11 P SV=1, Arabidopsis thaliana), e value:5.605 |

ID: 155983

A1: [twinscan.VV78X131442.7\\_14](#) | [VV78X131442.7\\_33418\\_36951](#)

A2: [REV\\_COM\\_VV78X231846.14](#)

Kmer ranges:

Lower: 998 Upper: 1005

Lower: 19691 Upper: 19698

Normalized MIRNA Score: 1.94737

Current Window Size: 19

MIRNA Bounds: 988 1007:19689 19708

Precursor Score: 1.42105

MFE: -73

Precursor Length: 132

Transcript Length: 3534

Candidate Rank: 58

A1 Region (5' - 3'): CTCTCTACCTCTTCATGTA

Quality: |||||

A2 Region (3' - 5'): GAGAGATGGAGAAGTACGT

Precursor:

TGCAUGAAGAGGTAGAGAGGGTGGAAATTGAGCCAAGGATGACTTGCCGTCTTTGCATCAAGC

(UGCAUGAAGAGGUAGAGAGgguggaauugagccaagggaugacuugccguccuugcaucaagc

