

miRBase precursor : dme-mir-31b_MI00000410

Total read count : 991

dme-miR-31b-3p_MIMAT0020825 read count

dme-miR-31b-5p_MIMAT00000389 read count

remaining reads : 0



dme-miR-31b-3p_MIMAT0020825

5' - sequence	-3'	exp	mm
.....	1	0
.....	1	1
.....	1	0
.....	3	0
.....	99	0
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	2	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	2	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	1	1
.....	390	0
.....	1	1

caaaauauggaauuuggcaagaugucggaaauagcugagagcacagcggaucgaacauuuuaucgcccggaaaaaaaugugauuuuuuugaaaagcggcuauugccucaucuagucaauugcauuacuuug

.....uggcaagaugucggaaauagcuCa.....	1	1
.....uggcaagaugucggaaauagAuga.....	1	1
.....uggcaagaugCggaaauagcuga.....	1	1
.....uggcaagaugugucgUaaauagcuga.....	1	1
.....Cggcaagaugucggaaauagcuga.....	1	1
.....uggcaagaugugucAgaaauagcuga.....	3	1
.....uggcaagaugugucgAaaauagcuga.....	5	1
.....uggcaagaugugucgaaAuugaCuga.....	1	1
.....uggcaagaugugucggaaauagcCga.....	1	1
.....uggcaagaugugucggaaGagcuga.....	1	1
.....uggcaagaugugucggaaCagcuga.....	3	1
.....Aggcgaagaugugcggaaauagcuga.....	6	1
.....uggcaagaugugcggaaauagcuAa.....	1	1
.....uggcaCgaugugcggaaauagcuga.....	1	1
.....uggcaagaugugcggaaauagcugU.....	4	1
.....Gggcaagaugugcggaaauagcuga.....	1	1
.....uggcaagaugugcggaaAagcuga.....	2	1
.....uggcaagaugAcgaaauagcuga.....	1	1
.....uggcaaaUaugugcggaaauagcuga.....	1	1
.....uggcaagaCgucggaaauagcuga.....	1	1
.....uggcaagaugugcggCauagcugag.....	3	1
.....uggcaagaugugcggaaauagcugaU.....	1	1
.....uggcaagaugugcggaaauagcugag.....	1	0
.....uggcaagaugugcggaaauagcugaA.....	42	1
.....uggcaagaugugcggaaauagcugaCa.....	1	1
.....uggcaagaugugcggaaauagcugaAa.....	47	1
.....uggcaagaugugcggaaauagcugaga.....	1	0
.....ggcaagaugugcggaaauagcug.....	1	0
.....ggcaagaugugcggaaauagcugU.....	1	1
.....Ucaagaugugcggaaauagcuga.....	1	1
.....ggcuauugccucaucuagu.....	1	0
.....ggcuauugccucaucuaguca.....	7	0
.....ggcuauugccucaucuGuca.....	1	1
.....ggcuauugccucaucuaguca.....	38	0
.....ggcuauugccucaucuAgcaa.....	1	1
.....ggcuacGccucaucuaguca.....	1	1
.....ggUuaugccucaucuagucaau.....	1	1
.....ggcuacGccucaucuagucaau.....	1	1
.....ggcuauugccucaucuagucaC.....	1	1
.....ggcuauugccucaCcuagucaau.....	1	1
.....ggcuauugccuUucuagucaau.....	1	1
.....ggcuauugccucaucuacuacuac.....	2	1
.....ggcuauugccucaucuagucaau.....	136	0
.....gAcuaugccucaucuagucaau.....	1	1
.....ggcuauugccucaucuacuac.....	1	1
.....gUcuauugccucaucuagucaau.....	1	1
.....ggcuauugccucaucuagucaA.....	10	1
.....ggcuauugccucaucuGucaau.....	1	1
.....ggcuacGccucaucuagucaau.....	1	1