



hsa-miR-192-3p

[illegible]

gccgagaccgagugcacagggcucugaccuaugaaugacagccagugcucgucuccccucuggcugccaauccauaggucacagguauguucgccucaaugccagc

.....cugaccGaugaaugacagcc.....	2	1	seq
.....cugaccuGugaaugacagcc.....	2	1	seq
.....cugaccuaugaaCugacagcc.....	4	1	seq
.....cugaccuGugaaugacagcc.....	6	1	seq
.....cugaccuUugaaugacagcc.....	2	1	seq
.....cugaccuaugaGuugacagcc.....	1	1	seq
.....cugaccuaugaaugacCgcc.....	2	1	seq
.....cugaccuauUaaugacagcc.....	3	1	seq
.....cugaccuaugCauugacagcc.....	1	1	seq
.....cugaccuaugaaugaGagcc.....	1	1	seq
.....cugaccuaugaaugaAagcc.....	2	1	seq
.....cugCccuaugaaugacagcc.....	54	1	seq
.....cCgaccuaugaaugacagcc.....	4	1	seq
.....cuCaccuaugaaugacagcc.....	3	1	seq
.....cugaccuaugaauCgacagcc.....	4	1	seq
.....cugaccuaugaaugacagUc.....	1	1	seq
.....cugaccuaugaUuugacagcc.....	3	1	seq
.....cugaccuaCgaauugacagcc.....	1	1	seq
.....cugaccuaugaaugCcagcc.....	1	1	seq
.....cugUccuaugaaugacagcc.....	1	1	seq
.....cugaccuaugaaugacaCcc.....	1	1	seq
.....cugaccAaugaaugacagcc.....	4	1	seq
.....cugaccuaugaaugacagcU.....	4	1	seq
.....cugaccuaugaaugacagcca.....	65	0	seq
.....cugaccuaugaaugacagccU.....	24	1	seq
.....Uugaccuaugaaugacagcca.....	1	1	seq
.....cugaccuaugaaUgacagcca.....	1	1	seq
.....cugaccuaugaaugacagccG.....	4	1	seq
.....cugaccuaugaaugacagccag.....	1	0	seq
.....cugaccuaugaaugacagccagu.....	6	0	seq
.....ugaccuaugaaugacag.....	1	0	seq
.....ugaccuaugaaugacagc.....	40	0	seq
.....ugaccuaugaaugacaUcc.....	1	1	seq
.....ugaccuaugaaCugacagcc.....	1	1	seq
.....ugaUcuugaaugacagcc.....	2	1	seq
.....ugaccuaugGauugacagcc.....	1	1	seq
.....ugaccuaugaaugaUagcc.....	1	1	seq
.....ugaccuaugaaugCcagcc.....	2	1	seq
.....ugGccuaugaaugacagcc.....	1	1	seq
.....ugaccuaugaauCgacagcc.....	2	1	seq
.....ugaccuaugaaugaAagcc.....	1	1	seq
.....ugaccuaugaGuugacagcc.....	2	1	seq
.....ugaccuGugaaugacagcc.....	1	1	seq
.....ugaccuaugaaUUacagcc.....	1	1	seq
.....ugaccuaugaaugacagcc.....	2183	0	seq
.....ugaccuaAgaauugacagcc.....	1	1	seq
.....ugacAuaugaaugacagcc.....	1	1	seq
.....ugaccuaugaaugacGgcc.....	1	1	seq
.....ugaccuaugaaugacagcG.....	1	1	seq
.....uCaccuaugaaugacagcc.....	1	1	seq
.....ugaccuaugaaugacaAcc.....	1	1	seq
.....ugaccuaCgaauugacagcc.....	1	1	seq
.....ugaccuauAaaugacagcc.....	3	1	seq
.....Agaccuaugaaugacagcc.....	1	1	seq
.....Cgaccuaugaaugacagcc.....	1	1	seq
.....ugaccuaugaaUgacagcc.....	1	1	seq
.....ugaccuaugaUuugacagcc.....	1	1	seq
.....ugaccuaugaaUugacagcc.....	1	1	seq
.....ugaccuaugaaUgacagcca.....	1	1	seq
.....uAaccuaugaaugacagcca.....	1	1	seq
.....Cgaccuaugaaugacagcca.....	1	1	seq
.....ugaccuaugaaugacagccG.....	3	1	seq
.....ugaccuaugaaugacagccU.....	1	1	seq
.....ugaccuaugaaugacagcca.....	348	0	seq
.....ugaccuaugaaugacagccaA.....	3	1	seq
.....ugaccuaugaaugacagccag.....	68	0	seq
.....uAaccuaugaaugacagccag.....	1	1	seq
.....ugaccuaugaaugacagccagG.....	1	1	seq
.....ugacUuaugaaugacagccagu.....	1	1	seq

hsa-miR-192-5p

hsa-miR-192-3p

gccgagaccgagugcacagggcucugaccuaugaauugacagccagugcucucgucuccccucuggcugccaauuccauaggucacagguauguucgccucaauggccagc

.....ugaccuaugaauugacagccagu.....	98	0	seq
.....ugaccuaugaauugacagccagA.....	53	1	seq
.....ugaccuaugaauugacagccagAg.....	1	1	seq
.....ugaccuaugaauugacagccaguU.....	1	1	seq
.....gaccuaugaauugacagccag.....	1	0	seq
.....cuggcugccaauuccUuaggu.....	1	1	seq