

MGAS27556	SOF	1	MTNCKYKLRKLSVGLVSVGTMLIAPTVLQGQEVSTGASSTETSASTNTSTASAGTSTSETAASGTGSEAAVVSSEGSQSSSESGQASTQPQAQTLQESAATS	100
MGAS26786	SOF	1	MTNCKYKLRKLSVGLVSVGTMLIAPTVLQGQEVSTGASSTETSASTNTSTASAGTSTSETAASGTGSEAAVVSSEGSQSSSESGQASTQPQAQTLQESAATS	100
MGAS27027	SOF	1	MTNCKYKLRKLSVGLVSVGTMLIAPTVLQGQEVSTGASSTETSASTNTSTASAGTSTSETAASGTGSEAAVVSSEGSQSSSESGQASTQPQAQTLQESAATS	100
MGAS27556	SOF	101	PSSNSSTSSSEDKAPKAASKSSSATVASSSNGSNQGAGAEDAPQMMDVERYTVDRKTELNIKDGKTPKTRNSVDKDTKLIRNRDQKQRDIVDIKREVK	200
MGAS26786	SOF	101	PSSNSSTSSSEDKAPKAASKSSSATVASSSNGSNQGAGAEDAHR-----	145
MGAS27027	SOF	101	PSSNSSTSSSEDKAPKAASKSSSATVASSSNGSNQGAGAEDAPQMMDVERYTVDRKTELNIKDGKTPKTRNSVDKDTKLIRNRDQKQRDIVDIKREVK	200
MGAS27556	SOF	201	DNGDGLDVTLKVTPKEIDKGADVMALLDVSKKMTDADFKNADKIKKLVTTLTSKSASNSDNDHEHKHNSRNSVRLMTFYREISNPIDISGKTAELDKL	300
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	201	DNGDGLDVTLKVTPKEIDKGADVMALLDVSKKMTDADFKNADKIKKLVTTLTSKSASNSDNDHEHKHNSRNSVRLMTFYREISNPIDISGKTAELDKL	300
MGAS27556	SOF	301	LDDLRVKAKANYDWGVDLQGAHKAREIFNKEKESKKRQHIVLFSQGESTFSYDIQKSEKSSNLSRINEKITSNPLLPWPPIFDHTHQNDMINDVR	400
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	301	LDDLRVKAKANYDWGVDLQGAHKAREIFNKEKESKKRQHIVLFSQGESTFSYDIQKSEKSSNLSRINEKITS-----	376
MGAS27556	SOF	401	ALIAFASKLGIKNLSWIETLSALSVDGSLGVSFVGGGLGEYTLTKKEYDSQKLNEDQFDYTKRVGEGYHYHSFNSRESEDKMPLTEIKKALEAALPKF	500
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	377	-----	376
MGAS27556	SOF	501	EENNWFTKVLKYFLGKDKAEQAKLDVIMKVIKSVFYKRYHYHNLNSAIAEAKMAQKEGITYFYSVDVTALNTARRVKRQTAVLKNTKEEERNKKFDEYL	600
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	377	-----	376
MGAS27556	SOF	601	KKMSEGGNAFFNDVDKADKFKDTLTKLIKDEFDGGKSVDKTSYQSSSAINYSEASNSFWRTTKESLWTWISKEQLKAFEDGKPLTFTYKLVKVDNNKFK	700
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	377	-----	376
MGAS27556	SOF	701	TALEENKTKRSTPTENENSVTEKIIISNTTYEINEQKVEGNKLDVSLTYSKFKVPPQIDGHVIEPQAPLPLKPPVIEHGNPFYEEETGYQLP	800
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	377	-----	376
MGAS27556	SOF	801	LKHGSNAPDQVTIEEDTVPQRPDILVGGQSGPVDITDTPQMGSGSNDATVVEEDTAPKRPDVLVGGQSEPIDITDTPQSVSGSNDATVVEEDTVPQR	900
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	377	-----	376
MGAS27556	SOF	901	PDILVGGQSDPIDITDTPQMGSGSNDATVIEEDTKPKRFFHFDNEPQAEKPKQPSLSLPQAPVYKAAHHLPASGDKREASFTIVALTIIGAAGLLSK	1000
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	377	-----	376
MGAS27556	SOF	1001	KRRDTEEN	1008
MGAS26786	SOF	146	-----	145
MGAS27027	SOF	377	-----	376