

MMETSP0253-20130528/12949_1

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1 10 20 30 40 50 60

MMETSP0253-20130528|12949_1 PSKLMPPKGVVKGKCAAKVARGRGAKALVLNGRRERTAGGLKADMLMRNRSGKVSKRASA

DVNP2_sequencedMRNRSGKVSKRASA

MMETSP0253-20130528/12949_1

70 80 90 100 110 120

MMETSP0253-20130528|12949_1 AGRRNFAKIEPWLQAVMTARECLRVTGFVAINGRTLQ GKALYVKSRAIYGSGVKGTEADP

DVNP2_sequenced AGRRNFAKIEPWLQAVMTARECLRVTGFVAINGRTLQ GKALYVKSRAIYGSGFKGTEADP

MMETSP0253-20130528/12949_1

130 140 150 160

MMETSP0253-20130528|12949_1 VSSSAAASAGGDTMSSSLAKRGCSGGGLILNWRVVRGWSSGHICCC

DVNP2_sequenced VSSSAAASAGAHFVELGEAGL.....FWRPHELEAR.....