

logo

NTDB id 1029	TT RS02230 WP 011228203.1	MAK	65
NTDB id 1402	DSB67 RS12670 WP 010643257.1	MPVYQYKARDRQGRLLVEATTEAEDLRTAARLLRDRGLFVAEIKKEPGKGLQAEVRIPALERGPGGLK	67
NTDB id 1169	A1552VC RS11075 WP 000648511.1	.MKT.....IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKKLKKGSISFITK.....ISHRVKGK	68
NTDB id 1113	AAA85695.1 219..1451()	MKAT.....QTLPLKNYRWKGINSSGKK.VSQQLAISIEIEVRDKLKDQHIQIKKKLKKGSVSLAR.....LTHR.VKSK	70
NTDB id 1112	NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252	GC085 RS07730 WP 011213805.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016	ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILTFFHYQGINKAGQK.MEGDIQARSLAIKADLRKQGIIVTNKVVKRKPFLFDR.....KNKKKITQA	69
NTDB id 1059	ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPVFAFEGVDRKGKIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVKPL	69
NTDB id 204611	BMR72 RS25385 WP 003094649.1	MAVK.....KAQMMPTFAYEGVDRKGKIK.LKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFFKKVTTTL	66
NTDB id 1198	PSJM300 03950 AFN76868.1	.MAD.....KALKTSVFFVWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....AGKKIKPM	66
consensus		.MAQ.....KAIKNSVFTWGLDRQGAK.TKGELSGVSPALVKAQLRKQGINPQKVRKKKSISLFS.....AGKKIKPM	66

logo

NTDB id 1029	TT RS02230 WP 011228203.1	DITIFTRQLATMAGYPLVQAFIVAEHNPMBRELLMEIKVEGSSSALRKHPQYFDLYCNLVAGFESGSL	144
NTDB id 1402	DSB67 RS12670 WP 010643257.1	DLAIFSRQLATMLGAGLTLLQALAILERQTEENR	

