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NTDB id 1306 DR RS10060 WP 027479822.1	MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80
NTDB id 1384 A4U84 RS08525 WP 010787006.1	0
NTDB id 35489 D11S RS09940 WP 012821127.1	0
NTDB id 1366 NTHI RS01950 WP 011271972.1	0
NTDB id 1355 HI 0298 AAC21962.1	0
NTDB id 1168 A1552VC RS11070 WP 000957200.1	0
NTDB id 1401 DSB67 RS12665 WP 010643259.1	0
NTDB id 1293 VP RS12240 WP 005479695.1	0
NTDB id 1251 GC085 RS07725 WP 011946523.1	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	0
NTDB id 1058 ABD1 RS01615 WP 001274986.1	0
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NTDB id 1306 DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGDRRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGASDA	160
NTDB id 1384 A4U84 RS08525 WP 010787006.1	0
NTDB id 35489 D11S RS09940 WP 012821127.1	0
NTDB id 1366 NTHI RS01950 WP 011271972.1	0
NTDB id 1355 HI 0298 AAC21962.1	0
NTDB id 1168 A1552VC RS11070 WP 000957200.1	0
NTDB id 1401 DSB67 RS12665 WP 010643259.1	0
NTDB id 1293 VP RS12240 WP 005479695.1	0
NTDB id 1251 GC085 RS07725 WP 011946523.1	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	0
NTDB id 1058 ABD1 RS01615 WP 001274986.1	0
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NTDB id 1306 DR RS10060 WP 027479822.1	GRTGGKLGGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVLGSM	240
NTDB id 1384 A4U84 RS08525 WP 010787006.1	0
NTDB id 35489 D11S RS09940 WP 012821127.1	0
NTDB id 1366 NTHI RS01950 WP 011271972.1	0
NTDB id 1355 HI 0298 AAC21962.1	0
NTDB id 1168 A1552VC RS11070 WP 000957200.1	0
NTDB id 1401 DSB67 RS12665 WP 010643259.1	0
NTDB id 1293 VP RS12240 WP 005479695.1	0
NTDB id 1251 GC085 RS07725 WP 011946523.1	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	0
NTDB id 1058 ABD1 RS01615 WP 001274986.1	0
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NTDB id 1306 DR RS10060 WP 027479822.1	LRADALRLLAVPVDETEQGVTVLTS DPRKRPDI DAL I GRPVQLMLTRPRDI ER L I EQFYPPQRGR L GEQLVQEGT LSRDQL	320
NTDB id 1384 A4U84 RS08525 WP 010787006.1	0
NTDB id 35489 D11S RS09940 WP 012821127.1	0
NTDB id 1366 NTHI RS01950 WP 011271972.1	0
NTDB id 1355 HI 0298 AAC21962.1	0
NTDB id 1168 A1552VC RS11070 WP 000957200.1	0
NTDB id 1401 DSB67 RS12665 WP 010643259.1	0
NTDB id 1293 VP RS12240 WP 005479695.1	0
NTDB id 1251 GC085 RS07725 WP 011946523.1	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	0
NTDB id 1058 ABD1 RS01615 WP 001274986.1	0
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NTDB id 1306 DR RS10060 WP 027479822.1	REALQVQAREGKVKPLGEVITELGFASPDEVD SAI LQKQNVGGGRLED TLVQSGKLSPEMLARS LAAQLGYEFLDPIQNP	400
NTDB id 1384 A4U84 RS08525 WP 010787006.1	19
NTDB id 35489 D11S RS09940 WP 012821127.1	23
NTDB id 1366 NTHI RS01950 WP 011271972.1	24
NTDB id 1355 HI 0298 AAC21962.1	24
NTDB id 1168 A1552VC RS11070 WP 000957200.1	69
NTDB id 1401 DSB67 RS12665 WP 010643259.1	69
NTDB id 1293 VP RS12240 WP 005479695.1	69
NTDB id 1251 GC085 RS07725 WP 011946523.1	77
NTDB id 1018 ACIAD RS01685 WP 004920473.1	77
NTDB id 1058 ABD1 RS01615 WP 001274986.1	77
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NTDB id 1306 DR RS10060 WP 027479822.1	DPKVALMIPEATARRVYVVPVRLQGNLSLVVAMK DPRNVFALDD LKLITGKEILPAVMAEKDIIRLIERYFGEKGFELNK	480
NTDB id 1384 A4U84 RS08525 WP 010787006.1	SRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVD DENNLTA CEIFAFMTHKQIEPVV IASDELKYLLNAL SPEQQPIYEE S	99
NTDB id 35489 D11S RS09940 WP 012821127.1	ELWLKNQQQQT VILRLYLALPLAENGQTLWLGLDSFTNLSACEAFSFLTGKTIEPV LIESQTLKTA LQDLSPRVEKVEENQ	103
NTDB id 1366 NTHI RS01950 WP 011271972.1	DLWERNQQQQS LLLRYFALPLKEENNRLLWLGVDLSNLSACETIAFITGKPV EPILESSQLKELLQQLTPHQMVVEEQV	104
NTDB id 1355 HI 0298 AAC21962.1	DLWERNQQQQS LLLRYFALPLKEENNRLLWLGVDLSNLSACETIAFITGKPV EPILESSQLKELLQQLTPNQMVVEEQV	104
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ANLCQQLGLRELITRYDALPIAKQGNL LLLAVSDPTLLQAEEFRFATGLQVELALADHRALQAATIRRLYGRSIQGAANQ	149
NTDB id 1401 DSB67 RS12665 WP 010643259.1	ASLCQTLGLRDLITRHNALPLNRTSSTLILAVADPTNLQAEDDFRFATGLQVELV LADFRELTAATIRRLYGRSLGQEKSG	149
NTDB id 1293 VP RS12240 WP 005479695.1	ASLCQQLGLRELITRHNALPLHRTPTSTLLAVADPTNQAEDDFRFATGLQVELV LADFRELSTAIRRLYGRSLSHQEKSG	149
NTDB id 1251 GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFSRGTNLVYLATDPPSKQASLKEITQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSE	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDEKLIQKRYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSKLVKVEPIIVEHDKLERLLSEHFVEETHFNFD	157
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKLDVQKLLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSKLLVVEPVIVEHHKLEKVLGQHFAEESFDFND	157
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