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NTDB id 1177 A1552VC RS01165 WP 000422572.1
NTDB id 1203 PSJM300 01605 AFN76401.1
NTDB id 1019 ACIAD RS04205 WP 004922051.1
NTDB id 63006 CAETHG RS16735 WP 013237892.1
NTDB id 1307 DR RS10055 WP 01088593.1
NTDB id 1116 NGFG RS10615 WP 003690200.1
NTDB id 1086 NMV RS00245 WP 002218487.1
NTDB id 1185 GTF74 RS11940 WP 000350195.1
NTDB id 1176 A1552VC RS01160 WP 000350195.1
NTDB id 1283 ACE17W RS02630 WP 010947729.1
NTDB id 1259 GC085 RS10305 WP 010947729.1
NTDB id 1194 PAKAF RS01995 WP 003084552.1
NTDB id 1202 PSJM300 01600 AFN76400.1
NTDB id 1020 ACIAD RS04210 WP 011182164.1
NTDB id 1081 FDQ49 RS05335 WP 006581387.1
NTDB id 1060 ABD1 RS04380 WP 000355489.1
NTDB id 1040 HQN27 RS13360 WP 000355489.1
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[illegible]

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Sequence	Position 156
..SCRFRVSAFFQRELPCAVIRRIETIRIPTFEELKLPEVLQNLAIAKRGLVLVVGATGSGKSTTMAAMTGYRNQHRITGHI	153
G.IGRFRVSAFYQRNLACGMVLRRIETINIPTIEDLKLDPVLKKLALTKRGLVLFVGATGTGKSTSLAAMIGYRNKNSSGHI	155
EKNERFRVSAFQQRDMPGAMVIRRIETIKIPSPDDLHLPLILKELAMSKRGITIFSGATGTGKSTSLASMIQHRNQHSKGHI	156
G.LGRFRVNIQKQRGNSAIARVVGKLIPTLNELFKFPVIKNLISYKGLILVTGPTGCGKSTTLAAMINEINCTRAAHI	155
D.KARFRVNAFMQRGNVCGVMRLIPTITVRITIAEMGLPQTVIDIANAPRGLVLVTGPTGSGKSTTLASMDIHINTTKLKH	159
N.VARFRVNAFNTGRGPAAVFRTIPSTVLSLEELKAPSIQKIAESPGRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
N.VARFRVNAFNIGRGPAAVFRTIPSTVLSLEELKAPSIQKIAESPGRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
N.VGRFRVNAFHQARGCSAVFRTIPTVIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHHNKHI	155
N.VGRFRVNAFHQARGCSAVFRTIPTVIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHHNKHI	155
N.LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEHI	155
N.LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEHI	155
G.VARFRVNAFNQNRGAGAVFRTIPSKVLTMEELGGMGEVFRKIVSDVPRGLVLVTGPTGSGKSTTLAAMDYINNTKYHHI	155
G.VARFRVNAFNQNRGAGAVFRTIPSKVLTMEELGGMGEVFRKITDVPGRGLVLVTGPTGSGKSTTLAAMDYINNTKYHHI	155
N.LARFRVNVFNQNRGAGAVFRTIPSQVLTLEELGLGKIFRDI CDYPRGLVLVTGPTGSGKSTTLAAMDYINNHRYDHI	155
N.VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGIVLVTGPTGSGKSTTLAAMDYINENRYDHI	155
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N.VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGIVLVTGPTGSGKSTTLAAMDYINENRYDHI	155

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consensus

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