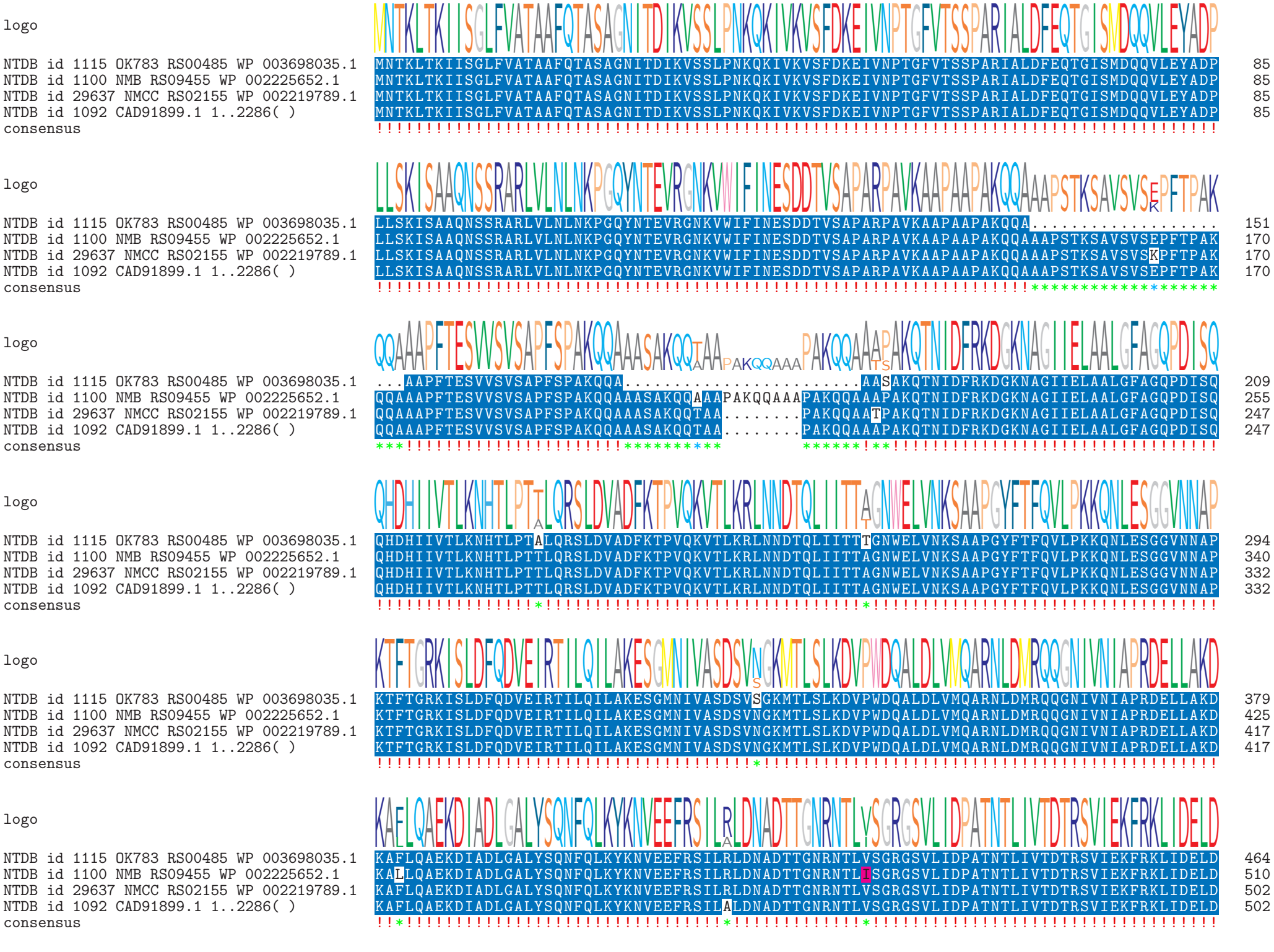
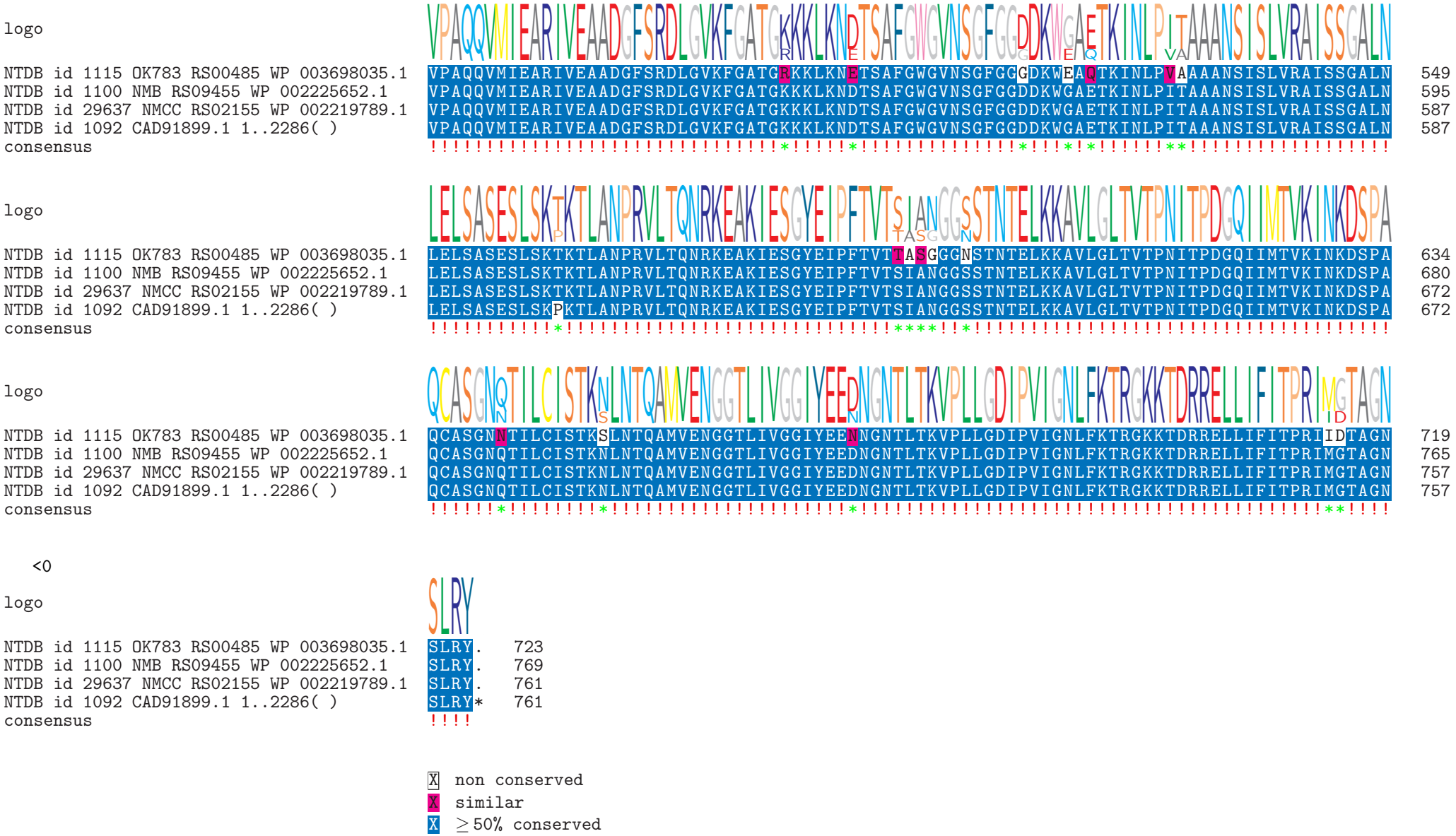

logo
NTDB id 1115 OK783 RS00485 WP 003698035.1
NTDB id 1100 NMB RS09455 WP 002225652.1
NTDB id 29637 NMCC RS02155 WP 002219789.1
NTDB id 1092 CAD91899.1 1..2286( )
consensus
MNTKLTKIISGLFVATAAFQTASAGNITDIKVSSLPNKQKIVKVSFDKEIVNPTGFVTSSPARIALDFEQTGISMDQQVLEYADP 85
MNTKLTKIISGLFVATAAFQTASAGNITDIKVSSLPNKQKIVKVSFDKEIVNPTGFVTSSPARIALDFEQTGISMDQQVLEYADP 85
MNTKLTKIISGLFVATAAFQTASAGNITDIKVSSLPNKQKIVKVSFDKEIVNPTGFVTSSPARIALDFEQTGISMDQQVLEYADP 85
MNTKLTKIISGLFVATAAFQTASAGNITDIKVSSLPNKQKIVKVSFDKEIVNPTGFVTSSPARIALDFEQTGISMDQQVLEYADP 85
LLSKISAAQNSSRARLVLNLNKPGQYNTEVRGNKVWIFINESDDTVSAPARPAVKAAPAAPAKQQAAAPSTKSAVSVSEPFTPAK 151
LLSKISAAQNSSRARLVLNLNKPGQYNTEVRGNKVWIFINESDDTVSAPARPAVKAAPAAPAKQQAAAPSTKSAVSVSEPFTPAK 170
LLSKISAAQNSSRARLVLNLNKPGQYNTEVRGNKVWIFINESDDTVSAPARPAVKAAPAAPAKQQAAAPSTKSAVSVSKPFTPAK 170
LLSKISAAQNSSRARLVLNLNKPGQYNTEVRGNKVWIFINESDDTVSAPARPAVKAAPAAPAKQQAAAPSTKSAVSVSEPFTPAK 170
QQAAAPFTESVVSVSAPFSPAKQQAAASAKQQTAAPAKQQAAAPAKQQAAAPAKQTNIDFRKDGKNAGIIELAALGFAGQPDISQ 209
QQAAAPFTESVVSVSAPFSPAKQQAAASAKQQAAAPAKQQAAAPAKQQAAAPAKQTNIDFRKDGKNAGIIELAALGFAGQPDISQ 255
QQAAAPFTESVVSVSAPFSPAKQQAAASAKQQTAAPAKQQAAATPAKQTNIDFRKDGKNAGIIELAALGFAGQPDISQ 247
QQAAAPFTESVVSVSAPFSPAKQQAAASAKQQTAAPAKQQAAAPAKQTNIDFRKDGKNAGIIELAALGFAGQPDISQ 247
QHDHIIVTLKNHTLPTALQRSLDVADFKTPVQKVTLKRLNNDTQLIITTTGNWELVNKSAAPGYFTFQVLPKKQNLESGGVNNAP 294
QHDHIIVTLKNHTLPTTLQRSLDVADFKTPVQKVTLKRLNNDTQLIITTAGNWELVNKSAAPGYFTFQVLPKKQNLESGGVNNAP 340
QHDHIIVTLKNHTLPTTLQRSLDVADFKTPVQKVTLKRLNNDTQLIITTAGNWELVNKSAAPGYFTFQVLPKKQNLESGGVNNAP 332
QHDHIIVTLKNHTLPTTLQRSLDVADFKTPVQKVTLKRLNNDTQLIITTAGNWELVNKSAAPGYFTFQVLPKKQNLESGGVNNAP 332
KTFTGRKISLDFQDVEIRTILQILAKESGMNIVASDSVSGKMTLSLKDVPWDQALDLVMQARNLDMRQQGNIVNIAPRDELLAKD 379
KTFTGRKISLDFQDVEIRTILQILAKESGMNIVASDSVNGKMTLSLKDVPWDQALDLVMQARNLDMRQQGNIVNIAPRDELLAKD 425
KTFTGRKISLDFQDVEIRTILQILAKESGMNIVASDSVNGKMTLSLKDVPWDQALDLVMQARNLDMRQQGNIVNIAPRDELLAKD 417
KTFTGRKISLDFQDVEIRTILQILAKESGMNIVASDSVNGKMTLSLKDVPWDQALDLVMQARNLDMRQQGNIVNIAPRDELLAKD 417
KAFLQAEKDIADLGALYSQNFQLKYKNVEEFRSILRLDNADTTGNRNTLVSGRGSVLIDPATNTLIVTDTRSVIEKFRKLIDELD 464
KALLQAEKDIADLGALYSQNFQLKYKNVEEFRSILRLDNADTTGNRNTLISGRGSVLIDPATNTLIVTDTRSVIEKFRKLIDELD 510
KAFLQAEKDIADLGALYSQNFQLKYKNVEEFRSILRLDNADTTGNRNTLVSGRGSVLIDPATNTLIVTDTRSVIEKFRKLIDELD 502
KAFLQAEKDIADLGALYSQNFQLKYKNVEEFRSILALDNADTTGNRNTLVSGRGSVLIDPATNTLIVTDTRSVIEKFRKLIDELD 502


logo
NTDB id 1115 OK783 RS00485 WP 003698035.1 VPAQQVMIEARIVEAADGFSRDLGVKFGATGRKKLKNETSAFGWGVNSGFGGGDKWEAQTKINLPVAAAANSISLVRAISSGALN 549
NTDB id 1100 NMB RS09455 WP 002225652.1 VPAQQVMIEARIVEAADGFSRDLGVKFGATGKKKLKNDTSAFGWGVNSGFGGDDKWGAETKINLPITAAANSISLVRAISSGALN 595
NTDB id 29637 NMCC RS02155 WP 002219789.1 VPAQQVMIEARIVEAADGFSRDLGVKFGATGKKKLKNDTSAFGWGVNSGFGGDDKWGAETKINLPITAAANSISLVRAISSGALN 587
NTDB id 1092 CAD91899.1 1..2286( ) VPAQQVMIEARIVEAADGFSRDLGVKFGATGKKKLKNDTSAFGWGVNSGFGGDDKWGAETKINLPITAAANSISLVRAISSGALN 587
consensus
logo
NTDB id 1115 OK783 RS00485 WP 003698035.1 LELSASESLSKTKTLANPRVLTQNRKEAKIESGYEIPFTVTTASGGGNSTNTELKKAVLGLTVTPNITPDGQIIMTVKINKDSPA 634
NTDB id 1100 NMB RS09455 WP 002225652.1 LELSASESLSKTKTLANPRVLTQNRKEAKIESGYEIPFTVTSIANGGSSTNTELKKAVLGLTVTPNITPDGQIIMTVKINKDSPA 680
NTDB id 29637 NMCC RS02155 WP 002219789.1 LELSASESLSKTKTLANPRVLTQNRKEAKIESGYEIPFTVTSIANGGSSTNTELKKAVLGLTVTPNITPDGQIIMTVKINKDSPA 672
NTDB id 1092 CAD91899.1 1..2286( ) LELSASESLSKPKTLANPRVLTQNRKEAKIESGYEIPFTVTSIANGGSSTNTELKKAVLGLTVTPNITPDGQIIMTVKINKDSPA 672
consensus
logo
NTDB id 1115 OK783 RS00485 WP 003698035.1 QCASGNNTILCISTKSLNTQAMVENGGTLIVGGIYEENNGNTLTKVPLLGDIPVIGNLFKTRGKKTDRRELLIFITPRIIDTAGN 719
NTDB id 1100 NMB RS09455 WP 002225652.1 QCASGNQTILCISTKNLNTQAMVENGGTLIVGGIYEEDNGNTLTKVPLLGDIPVIGNLFKTRGKKTDRRELLIFITPRIMGTAGN 765
NTDB id 29637 NMCC RS02155 WP 002219789.1 QCASGNQTILCISTKNLNTQAMVENGGTLIVGGIYEEDNGNTLTKVPLLGDIPVIGNLFKTRGKKTDRRELLIFITPRIMGTAGN 757
NTDB id 1092 CAD91899.1 1..2286( ) QCASGNQTILCISTKNLNTQAMVENGGTLIVGGIYEEDNGNTLTKVPLLGDIPVIGNLFKTRGKKTDRRELLIFITPRIMGTAGN 757
consensus
<0
logo
NTDB id 1115 OK783 RS00485 WP 003698035.1 SLRY. 723
NTDB id 1100 NMB RS09455 WP 002225652.1 SLRY. 769
NTDB id 29637 NMCC RS02155 WP 002219789.1 SLRY. 761
NTDB id 1092 CAD91899.1 1..2286( ) SLRY* 761
consensus
X non conserved
X similar
X ≥ 50% conserved