

logo

NTDB id 31674 HPG27 RS00105 WP 000890552.1
NTDB id 1219 C694 RS00105 WP 000890508.1
consensus

[illegible]85
85

logo

NTDB id 31674 HPG27 RS00105 WP 000890552.1
NTDB id 1219 C694 RS00105 WP 000890508.1
consensus

VARLVKRRKYDHQQNIQSDSYLQAILNQFENKEVEYENQYFLVLES^AHSLQGVL EHKKKSLMHANRENFKDILSYKAHFLQETL

170
170

logo

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consensus

KSLEIQLKNYAPKLLSSKEVLNFYAEYINGFDLPKPLVGGYLSDSYIASSITFEKDYFIQESFNQKTYNRLIGIKAYESERITS
KSLEIQLKNYAPKLLSSKEVLNFYAEYINGFDLPKPLVGGYLSDSYIASSITFEKDYFIQESFNQKTYNRLIGIKAYESERITS
KSLEIQLKNYAPKLLSSKEVLNFYAEYINGFDLPKPLVGGYLSDSYIASSITFEKDYFIQESFNQKTYNRLIGIKAYESERITS

255
255

logo

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consensus

I A I G A L L Y Q E T P L D I I F S I E P M S **I** N K T L ^G F L K E R A K F S M S N L V K N E L L E Y Q E L V K T K R L S M Q K F A L N I L I K A P S L E ^N L D A Q T S L Y
 I A I G A L L Y Q E T P L D I I F S I E P M S **I** N K T L S F L K E R A K F S M S N L V K N E L L E Y Q E L V K T K R L S M Q K F A L N I L I K A P S L E ^N L D A Q T S L Y
 * * * * *

340
340

logo

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consensus

LGLLFKENLVGV¹ETFGLKGGYFSFFPERIHLN²HLR³FLTSKALACLM⁴VF⁵ERQNLGFKANS⁶WGNS⁷PLSV⁸FKNL⁹DYSP¹⁰FL¹¹FN¹²FHN¹³Q

425
425

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EVSHNAKEIARVNGHTLIIGATGSGKSTLISFLMMSALKYQNMHLLAFDRMQGLYSFTKFFKGHYHDGQSFSINPFCLPNLQNM
EVSHNAKEIARVNGHTLIIGATGSGKSTLISFLMMSALKYQNMHLLAFDRMQGLYSFTKFFKGHYHDGQSFSINPFCLPNLQNM
EVSHNAKEIARVNGHTLIIGATGSGKSTLISFLMMSALKYQNMHLLAFDRMQGLYSFTKFFKGHYHDGQSFSINPFCLPNLQNM

510
510

logo

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LEFLQSFFLSMFDLAPSRDKEALEDMNAISSAIKSLEYETLYPKAFSLDDFKETLKRTSSNQLGLSLEPYLNNPLFNALNDAFNSS

595
595

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680
680

logo

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consensus



765
765

logo

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consensus



787
787

☐ non conserved
☒ similar
☒ ≥ 50% conserved