

logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 58450 I872 RS05705 WP 015605197.1

NTDB id 414 AAK55818.1 838..2187()

consensus



Sequence logo for position 1. The logo shows the conservation of amino acids across three sequences. The most conserved residues are Lysine (K), Aspartate (D), and Glutamate (E) at the beginning, followed by a highly conserved Lysine (K) and Glutamate (E) at the end. The consensus sequence is K...D...E...K...E....

82

82

82

logo

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NTDB id 414 AAK55818.1 838..2187()

consensus



Sequence logo for position 2. The logo shows the conservation of amino acids across three sequences. The most conserved residues are Lysine (K), Aspartate (D), and Glutamate (E) at the beginning, followed by a highly conserved Lysine (K) and Glutamate (E) at the end. The consensus sequence is K...D...E...K...E....

166

167

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logo

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NTDB id 414 AAK55818.1 838..2187()

consensus



Sequence logo for position 3. The logo shows the conservation of amino acids across three sequences. The most conserved residues are Lysine (K), Aspartate (D), and Glutamate (E) at the beginning, followed by a highly conserved Lysine (K) and Glutamate (E) at the end. The consensus sequence is K...D...E...K...E....

251

252

252

logo

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NTDB id 414 AAK55818.1 838..2187()

consensus



Sequence logo for position 4. The logo shows the conservation of amino acids across three sequences. The most conserved residues are Lysine (K), Aspartate (D), and Glutamate (E) at the beginning, followed by a highly conserved Lysine (K) and Glutamate (E) at the end. The consensus sequence is K...D...E...K...E....

336

336

336

logo

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NTDB id 58450 I872 RS05705 WP 015605197.1

NTDB id 414 AAK55818.1 838..2187()

consensus



Sequence logo for position 5. The logo shows the conservation of amino acids across three sequences. The most conserved residues are Lysine (K), Aspartate (D), and Glutamate (E) at the beginning, followed by a highly conserved Lysine (K) and Glutamate (E) at the end. The consensus sequence is K...D...E...K...E....

421

421

421

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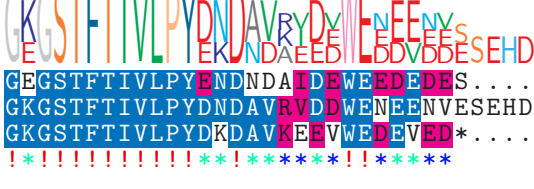
logo

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NTDB id 414 AAK55818.1 838..2187()

consensus



Sequence logo for position 6. The logo shows the conservation of amino acids across three sequences. The most conserved residues are Lysine (K), Aspartate (D), and Glutamate (E) at the beginning, followed by a highly conserved Lysine (K) and Glutamate (E) at the end. The consensus sequence is K...D...E...K...E....

450

454

449

 non conserved
 similar
 $\geq 50\%$ conserved