

logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 51141 SPAF RS07425 WP 014713656.1

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

consensus



Sequence logo for motif 1. The logo shows the conservation of amino acids at each position. The consensus sequence is MLDQLKQVFSSNFYFLLGFIIV. The logo is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

80

80

80

logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 51141 SPAF RS07425 WP 014713656.1

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

consensus



Sequence logo for motif 2. The logo shows the conservation of amino acids at each position. The consensus sequence is VRLTHENLEQETKRLTSILSYMTDGLVATNRRGQIIMNDMAKQLNLYRQVQVNTS. The logo is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

164

165

165

logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 51141 SPAF RS07425 WP 014713656.1

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

consensus



Sequence logo for motif 3. The logo shows the conservation of amino acids at each position. The consensus sequence is QDENG EYLSLRVRFALIRRESGFISGLVAVLHDTTEQKEERERRLFVSNVSHELRTPLTSVKSYLEALDDGALTESVAPDFIKV. The logo is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

249

250

250

logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 51141 SPAF RS07425 WP 014713656.1

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

consensus



Sequence logo for motif 4. The logo shows the conservation of amino acids at each position. The consensus sequence is SLDETNRMMRMVTDLLSLSRIDNQTSHLDVELTNFTAFITFILNRFDKIKSQ. The logo is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

333

335

333

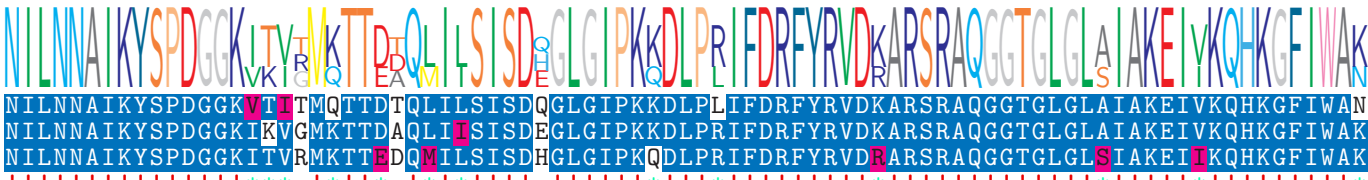
logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 51141 SPAF RS07425 WP 014713656.1

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

consensus



Sequence logo for motif 5. The logo shows the conservation of amino acids at each position. The consensus sequence is NILNNAIKYSPDGGKITVIMQTTDTQLILSISDQGLGIPKQDLPLIFDRFYRVDKARSRAQGGTGLGLAIAKEIVKQHKGFIWAK. The logo is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

418

420

418

<0

logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 51141 SPAF RS07425 WP 014713656.1

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

consensus



Sequence logo for motif 6. The logo shows the conservation of amino acids at each position. The consensus sequence is SEYKGSTFTIVLPYDKDAKDDWEDEDES. The logo is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

450

450

449

 non conserved
 similar
 $\geq 50\%$ conserved