

logo

NTDB id 126650 IY65 RS18680 WP 000016747.1
NTDB id 1435 BW25113 RS00535 WP 000360904.1
NTDB id 1365 NTHI RS01955 WP 011271973.1
consensus

MSGRLLDVPLNSLTGVGAAQSSKLAKIGLHTVQDLLLHPLRYEDRTHLYPIGELLPGIYATVEGEVLNCNITFGGRRM
MSGRLLDVPLNSLTGVGAAQSSKLAKIGLHTVQDLLLHPLRYEDRTHLYPIGELLPGIYATVEGEVLNCNITFGGRRM
.....

80
0
0

logo

NTDB id 126650 IY65 RS18680 WP 000016747.1
NTDB id 1435 BW25113 RS00535 WP 000360904.1
NTDB id 1365 NTHI RS01955 WP 011271973.1
consensus

MTCQISDGSGLTMRFFNFNAAMKNSLATGRRVLAYGEAKRGKYGAEMIHPEYRLQGDLSTPELQETLTPVYPTTEGVKQ
 MTCQISDGSGLTMRFFNFNAAMKNSLATGRRVLAYGEAKRGKYGAEMIHPEYRLQGDLSTPELQETLTPVYPTTEGVKQ

160
0
0

logo

```
NTDB id 126650 IY65 RS18680 WP 000016747.1
NTDB id 1435 BW25113 RS00535 WP 000360904.1
NTDB id 1365 NTHI RS01955 WP 011271973.1
consensus
```

ATLRLKTDQALELLDTCIAIPELLPELAQGMMSLPEALRTLHRPPPTLKLADLETGKHDPQRRLILELLAHNLSMLAIR
 ATLRLKTDQALELLDTCIAIPELLPELAQGMMSLPEALRTLHRPPPTLKLADLETGKHDPQRRLILELLAHNLSMLAIR
MDKQRGFTLIELMVVIGIIAIL
MK...LT.TQQTLLKGFTLIELMIVIAIIAIL
 * * * * *

240
22
28

logo

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consensus

[illegible]

320
91
99

logo

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NTDB id 1365 NTHI RS01955 WP 011271973.1
consensus

[illegible]

400
146
149

logo

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NTDB id 1365 NTHI RS01955 WP 011271973.1
consensus

RFGVHQRLALWEKGQQQGFFPHQLIMTATPIPRTLAMTAYADLDTSVIDELPPGRTPVTTVAIPDTRRHEIIDRVNACT
 RFGVHQRLALWEKGQQQGFFPHQLIMTATPIPRTLAMTAYADLDTSVIDELPPGRTPVTTVAIPDTRRHEIIDRVNACT

480
146
149

logo

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consensus

TEGRQAYWVCTLIEESDLLEAQAAEATWEELKLALPELNIGLVHGRMKPAEKQAVMQAFKQGEHLLVATTVIEVGVDVP	560
TEGRQAYWVCTLIEESDLLEAQAAEATWEELKLALPELNIGLVHGRMKPAEKQAVMQAFKQGEHLLVATTVIEVGVDVP	146
.....	149

logo

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NTDB id 1435 BW25113 RS00535 WP 000360904.1
NTDB id 1365 NTHI RS01955 WP 011271973.1
consensus

NASLMI IENPERLGLAQLHQLRGRVGRGAVASHCVLLYKSPLSKTAQKRLQVLRDSNDGFVIAQKDLEIRGPGELLGTRQ	640
NASLMI IENPERLGLAQLHQLRGRVGRGAVASHCVLLYKSPLSKTAQKRLQVLRDSNDGFVIAQKDLEIRGPGELLGTRQ	146
.....	149

logo

NTDB id 126650 IY65 RS18680 WP 000016747.1
NTDB id 1435 BW25113 RS00535 WP 000360904.1
NTDB id 1365 NTHI RS01955 WP 011271973.1
consensus

TGNAEFKVADLLRDQAI IPEVQRIARHIHERYPQQAQALIERWMPETERYSNA	693
TGNAEFKVADLLRDQAI IPEVQRIARHIHERYPQQAQALIERWMPETERYSNA	146
.....	149

 non conserved
 similar
 ≥ 50% conserved