

```
NTDB id 361 SMU RS01310 WP 002262737.1
NTDB id 95369 QMM10 RS08585 WP 000159554.1
NTDB id 478 HSISS4 RS06985 WP 021143811.1
NTDB id 327 STU RS16115 WP 011226304.1
NTDB id 295 STER RS06915 WP 011226304.1
consensus
```

[illegible]

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NTDB id 361 SMU RS01310 WP 002262737.1
NTDB id 95369 QMM10 RS08585 WP 000159554.1
NTDB id 478 HSISS4 RS06985 WP 021143811.1
NTDB id 327 STU RS16115 WP 011226304.1
NTDB id 295 STER RS06915 WP 011226304.1
consensus
```

EEDWVHIRGNDISMFQDPMTSLDPTMRIGLQIAEPITIKHEKVTKKEALKRALDMMEKVGIPNAGEHINDYPHQWSGGMRQRRAVI 166
HKDWEQIRGAKIATIFQDPMTSLDPIKTIGSQITEVIVKHQGKTAKEAKELADYMNKVGIPDAERFNEYFPQYSGGMRQRIVI 170
HQDWAHIRGAKIATIFQDPMTSLDPIKTIGSQIIEVIVKHQGKSAAKEAKKMAIDYMDKVGIPDAEKRFNEYFPQYSGGMRQRIVI 170
HQDWAIRGAKIATIFQDPMTSLNPIKTIGSQIIEVIVKHQGKTAKEAKKMAIDYMDKVGIPDAEKRFNEYFPQYSGGMRQRIVI 170
HQDWAIRGAKIATIFQDPMTSLNPIKTIGSQIIEVIVKHQGKTAKEAKKMAIDYMDKVGIPDAEKRFNEYFPQYSGGMRQRIVI 170

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consensus

AIALACRPDVLICDEPTTALDVTIQAQILDLKSLKEEYGFSVIFITHDLGVVASIADKVAVMYAGEII EYATVEEIFYEPCHPY
AIALACRPDVLICDEPTTALDVTIQAQILDLKSLKEEYGFSVIFITHDLGVVASIADKVAVMYAGEII EYATVEEIFYEPCHPY
AIALACRPDVLICDEPTTALDVTIQAQILDLKSLKEEYGFSVIFITHDLGVVASIADKVAVMYAGEII EYATVEEIFYEPCHPY
AIALACRPDVLICDEPTTALDVTIQAQILDLKSLKEEYGFSVIFITHDLGVVASIADKVAVMYAGEII EYATVEEIFYEPCHPY
AIALACRPDVLICDEPTTALDVTIQAQILDLKSLKEEYGFSVIFITHDLGVVASIADKVAVMYAGEII EYATVEEIFYEPCHPY


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consensus

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TWSLLSSLPQLADDNGKLFSPGTPPSLYTPVVGDAFALRSDYALQIDFEKAPQFQVSDTHWAKTWLLHEDAPKVEKPAVIQNL
 G N M T T N T A S S L H S I P G T P P D L L Q P P Q G D A F A P R N E F A L D I D L K E P P F F K V S D S H Y A A T W L L D D R A P K I T P P E R I L Q R
 TWSLLSSLPQLADDKGDLYSIPGTPPSLYTDLKGDFAFALRSDYAMQIDFEQKAPQFSVSETHWAKTWLLHEDAPKVEKPAVIANL 336
 TWSLLSSLPQLADDKGE LFSIPGTPPSLYTPVVGDAFALRSDYAMQIDFEKAPQFQVSDTHWAKTWLLHEDAPKVEKPAVIQNL 340
 TWSLLSSLPQLADDNGKLF SIPGTPPSLYTPVVGDAFALRSDYALQIDFEKAPQFQVSDTHWAKTWLLHEDAPKVDKPAVIQNL 340
 TWSLLSSLPQLADDNGKLF SIPGTPPSLYTPVVGDAFALRSDYALQIDFEKAPQFQVSDTHWAKTWLLHEDAPKVDKPAVIQNL 340
 TWSLLSSLPQLADDNGKLF SIPGTPPSLYTPVVGDAFALRSDYALQIDFEKAPQFQVSDTHWAKTWLLHEDAPKVDKPAVIQNL 340

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NTDB id 327 STU RS16115 WP 011226304.1
NTDB id 295 STER RS06915 WP 011226304.1
consensus

Sequence	Score (bits)
WEKWKSLQGEKHND.....	350
HDKIREKMGFAHLAD.....	355
HEKIRANMGFAHLGDEEEGNA	361
HEKILANMGFAHLGDEEEGNA	361
HEKILANMGFAHLGDEEEGNA	361

 non conserved
 similar
 $\geq 50\%$ conserved