

```
NTDB id 1193 PAKAF RS26665 WP 003161249.1
NTDB id 1009 ACIAD RS15175 WP 004923730.1
NTDB id 1052 ABD1 RS15850 WP 001017033.1
NTDB id 1039 HON27 RS01460 WP 031993779.1
consensus
```

[illegible]

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Sequence	Position
NTRSVTVVEAKDRTRLIIINLTTLSSYTTTRVEGNLNFVVVGNSPAGASVASTAPVKAS	169
EASSIDVSSDDKRARVVVNLKDAGAFTRVEGNVFILKINNIIQSTAT	151
EASSVDVTSDDQRSRLTVNLKDAGAFTRVEGNTFILKINS	150
EASSVDVTSDDQRSRLTVNLKDTGAFTTRVEGNTFILKINS	150



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RGSQEGELWYDLGSSNTPVDVQQQGSKWVIRFGTKIPTHLARRLNVNDFATPVSSIDAYNDKGVGITIQSSGSYEYMAVQAE AK N SDPTLSPIT E G IRLDFAKIQL DA RV DTK AFVNSSAQSDRTS S EPT L I D I L V I T D RGEKGEGNVVIDLSPTLSPDIQEQQGKIRLIDFAKTQLPDALRVRLDVKDFATPVQFVNSAQSDRTSITIEPSGLYDYLVYQTD AK N SDPTLSPIT E G IRLDFAKIQL DA RV DTK AFVNSSAQSDRTS S EPT L I D I L V I T D RGAQGEGLVVIDLQGTNTPVDVQQQGSKVVVRFPGIKIPTHLARRLNTTDFATPVASIDSYNDGSNGVISIQSTGSYEYMAVQAE AK N SDPTLSPIT E G IRLDFAKIQL DA RV DTK AFVNSSAQSDRTS S EPT L I D I L V I T D RGSQGEGLVVDLLGSNTPVDVQQQGSKVVIRTIGTKIPTHLARRLNVNDFATPVSSIDAYNDKGVGVITIQSSGSYEYMAVQAE AK N SDPTLSPIT E G IRLDFAKIQL DA RV DTK AFVNSSAQSDRTS S EPT L I D I L V I T D RGSQGEGLVVDLLGSNTPVDVQQQGSKVVIRTIGTKIPTHLARRLNVNDFATPVSSIDAYNDKGVGVITIQSSGSYEYMAVQAE AK N SDPTLSPIT E G IRLDFAKIQL DA RV DTK AFVNSSAQSDRTS S EPT L I D I L V I T D	254 236 235 235
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.....KEGGRGSSITVDDRNTNSIIAYQPQERLDELRRIVSQLDIPVRQVMTEARIVEANVGVDKSLGVRWCGAYHKGNWSG.
EPLGDSVGTLLSPRGTISLDPRNTNLIINDTSQKIDQIRKMIDLLDIPVKQVMTEARIVRATTSFSKEMGVKWGILSQTINQNSN
DSLGNNGVGSLLSPRGTITQDDRTNTLIINDTAQSIDQIRKMIDLLDVQVKQVMVEARIVRASTSFTELGVKWGILSQTITNNNN
DSLGNNGVGSLLSPRGTITQDDRTNTLIINDTAQSIDQIRKMIDLLDVQVKQVMVEARIVRASTSFTELGVKWGILSQTITNNNN

logo

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LLVGGSETTLWNLRPK

...YKGN.IGTKDEDMNCGPIA

LLVGGSETTLWNLRNP

LLVGGSETTLWNLRPK

LLVGGSETTLWNLRPK

*****!*****

KDETTGGYTYI

...SN.....GTYYI...

KDETTGGYKYYI

KDETTGGYKYYI

KDETTGGYKYYI

ERPDNLNVDLGV

...ERPDNLNVDLGVSNP

ERPDNLNVDLGV

ERPDNLNVDLGVSNP

ERPDNLNVDLGVSNP

*****!!!!*

ASS|AFGL|MSDFMLDLELSALQADGYGEVIST

...TSGLIGFTI.TDNIILDLQLSAMEKTNGEIVSQ

ASSIAFGLISLSDFMLDLELSALQADGYGEVIST

AGSIAFGLISMSDFMLDLELSALQADGYGEVIST

AGSIAFGLISMSDFMLDLELSALQADGYGEVIST

* *!***!*

561

555

567

567

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consensus

PKVMTADKQAKVATGQVPYQSTTNSAAGSTATTSEK

PKVVTSDKETA

PKVMTADKQAKVATGQVPYQSTTNSAAGSTATTSEK

PKVMTADKQAKVATGQVPYQSTTNSAAGSTATTSEK

!!!**!*!*!*!*!*!

ALLSLNVTPT

...TSTSEK

ALLSLNVTPT

DALLSLNVTPT

DALLSLNVTPT

*****!*

TPDGK|QVLRISKDSVAG

...TPDGKILMELN

TPDGKILMELN

TPDGKILMELN

TPDGKILMELN

! *!***!*

643

639

651

651

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TNVLVNNGETVYLGGVFEQTTMNSQTKVPFFGDPYVGRLEFRKDKSDKQELLIFVTPRIVNDTLARNH

AKILVNDGETIVLGGVFS

TNVLVNNGETVYLGGVFEQTTMNSQTKVPFFGDPYVGRLEFRKDKSDKQELLIFVTPRIVNDTLARNH

TNVLVDNGETVYLGGVFEQTTMNSQTKVPFFGDPYVGRLEFRKDKSDKQELLIFVTPRIVNDTLARNH

TNVLVDNGETVYLGGVFEQTTMNSQTKVPFFGDPYVGRLEFRKDKSDKQELLIFVTPRIVNDTLARNH

!! *!!!!**!*!!!!** *!!!!!!*! *!!!!*****!*****!*****

714

709

721

721

- ⓧ

 non conserved
- ⓧ

 similar
- ⓧ

 ≥ 50% conserved