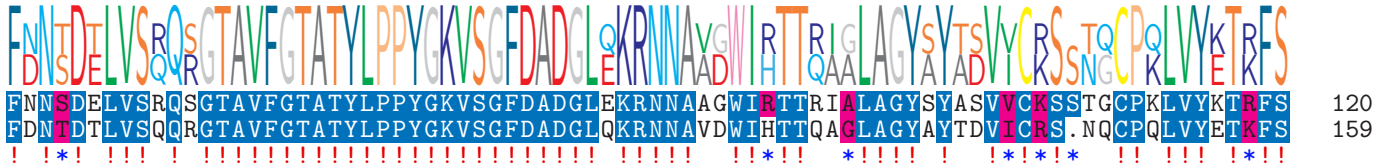
logo
NTDB id 231713 CCD83 RS00330 WP 149385320.1 .....MNEQNQPEVKQEGSYSTLREKDRERKFIYNKGRSGGGSVS 40
NTDB id 1090 CAA90909.1 1..3114( ) MNKTLKRQVFRHTALYAAILMFSHTGGGGAMAQTHKYAIIMNERNQLEVKGNGQYSTIKDKDRERKFIYNKDRGGGGSVF 80
consensus


logo
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NTDB id 1090 CAA90909.1 1..3114( ) FDNTDTLVSQQRGTAVFGTATYLPPYGKVSGFDADGLQKRNNAVDWIHTTQAGLAGYAYTDVICRS.NQCPQLVYETKFS 159
consensus

logo
NTDB id 231713 CCD83 RS00330 WP 149385320.1 FDNPDLEKIGGRLDRHTDPSRDNSPIYKLKDHPWLGVSFNLGSENTVKNGKSSSKLISSFNENNNNQTIVSTTEGDPISL 200
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consensus

logo
NTDB id 231713 CCD83 RS00330 WP 149385320.1 GDQQREHTAVVYYLNAKLHLLDKKGIKDITD.KTVQLGVLKPSIDVKTQKTGFSGILSFWANWDIKDTGQIPVKLGLQQV 279
NTDB id 1090 CAA90909.1 1..3114( ) SDWKREHTAMAYYLNAKLHLLDKKGIEDIAQGKTVDLGTLRPRVEATVRR...GELLNFWATWKIEDKGNITVRLGLPEV 316
consensus

logo
NTDB id 231713 CCD83 RS00330 WP 149385320.1 KADRCINKQNPNPKSQAPSPALTAPALWFGPVQNGKVQMYSASVSTYPDSSSSQIFLQNLSRKDDTSKPGRYSLKPLSTS 359
NTDB id 1090 CAA90909.1 1..3114( ) KAGRCVNKANPNPNAKAPSPALTAPALWFGPVKDGKAEMYSASVSTYPDSSSSRIYLQNLKRKTDPGKPGRHSLETLTEN 396
consensus

logo
NTDB id 231713 CCD83 RS00330 WP 149385320.1 EIKSKEPNFTGRQTIIRLDGGVRHIQLDRNNE.VTSFN...DDNGTFGIVKERSVVPESNEWKKVLLPWTVRGLDNDNQF 435
NTDB id 1090 CAA90909.1 1..3114( ) DIKSREPNFTGRQTIIRLNGGVREIKLDRNNTEVVNFNGNDGNNDTFGIVKDLGVEPDTSEWKKVLLPWTVRGFADDNKF 476
consensus

logo
NTDB id 231713 CCD83 RS00330 WP 149385320.1 KIFNQEA.KDGKPKYSQRYRIRENGNNGNNGKRDLGDIVNSPIVAVGGYLATSANDGMVHIFKKGNGGDERNYSLKLSYI 514
NTDB id 1090 CAA90909.1 1..3114( ) KAFNKEENNDNKPKYSQKYRSRDN....NKGERNLGDIVNSPIVAVGEYLATSANDGMVHIFKQ.SGGDKRSYNLKLSYI 551
consensus

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logo
```

```
NTDB id 231713 CCD83 RS00330 WP 149385320.1  PGTMPRKDIESQDSTLAKELRAFAEKGYVGDRYGVDGGFVLRQVE.RNGKDHVFMFGAMGFGGRGAYALDLTKIDSNNLT  593
NTDB id 1090 CAA90909.1 1..3114( )           PGTMPRKDIQNTESTLAKDVRTFAEKGYVGDRYGVDGGFVLRKVDNLNGQNRVFMFGAMGFGGRGAYALDLTKADGSDPT  631
consensus                                    !!!!!!!!!    *!!!!!**! !!!!!!!!!!!!!!!!!!!! !** !!  *!!!!!!!!!!!!!!!!!!!! !    *!
```

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logo
```

```
NTDB id 231713 CCD83 RS00330 WP 149385320.1  GVSMFDVPNDKNNNKNDNNRVELGYTVGTPQIGKTHDGKYAAFLASGYATKTI.DDQQNKTALYVYDLESSG..TLIKKI  670
NTDB id 1090 CAA90909.1 1..3114( )           AVSLFDVKDN...GNNGNNRVELGYTVGTPQIGKTHDGKYAAFLASGYATKEIITSGDNKTALYVYDLEGNGTNNLIKKI  708
consensus                                    *!!*!!!*   ***   ! !!!!!!!!!!!!!!!!!!!!
```

X non conserved
X similar
X $\geq$ 50% conserved