```
logo
NTDB id 275 KZH43 RS09240 WP 000250534.1     MVQNSCWQSKSHKVKAFTLLESLLALIVISGGLLLFQAMSQLLISEVRYQQQSEQKEWLLFVDQLEVELDRSQFEKVEGNRLYMK   85
NTDB id 234 SPD RS09870 WP 000250534.1       MVQNSCWQSKSHKVKAFTLLESLLALIVISGGLLLFQAMSQLLISEVRYQQQSEQKEWLLFVDQLEVELDRSQFEKVEGNRLYMK   85
NTDB id 200 SPR RS09405 WP 000250534.1       MVQNSCWQSKSHKVKAFTLLESLLALIVISGGLLLFQAMSQLLISEVRYQQQSEQKEWLLFVDQLEVELDRSQFEKVEGNRLYMK   85
NTDB id 165 SP RS10355 WP 000250534.1        MVQNSCWQSKSHKVKAFTLLESLLALIVISGGLLLFQAMSQLLISEVRYQQQSEQKEWLLFVDQLEVELDRSQFEKVEGNRLYMK   85
NTDB id 505 SM12261 RS00970 WP 000250509.1  MVQNSCWLSKSHKIKAFTLLESLIALIVISGSLLLFQAMSQLLISEVRYQQQSEQKEWLLFVDQLEAELDRSQFEKVEGDRIYMK   85
NTDB id 533 SMSK321 RS09215 WP 000250512.1  MVQNSCWLSKSHKVKAFTLLESLIALIVISGSLLLFQAMSQLLISEVRYQQQSEQKEWLLFVDQLEAELDRSQFEKIEGNRIYMK   85
NTDB id 591 KW2 RS10830 WP 014735174.1      .........MKLKIRAFTLLECLVALLAISGSVLVISGLIRMIEEQMKISQNDSRKDWQIFCEQMRSELSGAKLDNVNQNFLYVT   76
NTDB id 66156 SRT RS01100 WP 128832753.1    ........MLKSKLKAFTLLECLLALLVIAGSVSVYNGLIKAISSNIHYLSENQEDAWLLFCQQFRSELEGTTLQKLDSNKLYIQ   77
NTDB id 390 SMU RS09010 WP 002263440.1      ........MLKSKLKAFTLLECLLALLVIAGSVSVYNGLIKAISSNIHYLSKNQEDAWLLFCQQFRSELEGTTLQKLDSNKLYIQ   77
NTDB id 399 FSA28 RS09380 WP 002264245.1    ........MLKSKLKAFTLLECLLALLVIAGSVSVYNGLIKAISSNIHYLSKNQEDAWLLFCQQFRSELEGTTLQKLDSNKLYVQ   77
consensus                                   ******* ****!**!!!!!!*!*!!**!*!*****************************!**!**!** !!**************!**
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logo
NTDB id 275 KZH43 RS09240 WP 000250534.1     QDGKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSVRITEDNQLVRFHFQFQKGLEREFIYRVEKEKS   153
NTDB id 234 SPD RS09870 WP 000250534.1       QDGKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSVRITEDNQLVRFHFQFQKGLEREFIYRVEKEKS   153
NTDB id 200 SPR RS09405 WP 000250534.1       QDGKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSVRITEDNQLVRFHFQFQKGLEREFIYRVEKEKS   153
NTDB id 165 SP RS10355 WP 000250534.1        QDGKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSVRITEDNQLVRFHFQFQKGLEREFIYRVEKEKS   153
NTDB id 505 SM12261 RS00970 WP 000250509.1  QDGKEIAIGKSKSDDFRKTDASGRGYQPMVYGLKSAQITEENQVVRFRFQFQKGLEREFIYRVEKAKS   153
NTDB id 533 SMSK321 RS09215 WP 000250512.1  QDGKDISIGKLKSDDFRKTDASGRGYQPMVYGLKSAQITEDNQLVRFRFQFQKGLEREFIYRVEKAKS   153
NTDB id 591 KW2 RS10830 WP 014735174.1      KDK.KLRFGL.VGDDFRKSDDKGQGYQPMLYDLKGAKIQAEENLIKITIDFDNGGERVFIYRFTDTK.   141
NTDB id 66156 SRT RS01100 WP 128832753.1    KNNQSLAFGKSKVSDFRKTNSDGRGYQPMLMGIKAANFSQSGKIIKLDVTFKDGLERTFVYAFHEKN.   144
NTDB id 390 SMU RS09010 WP 002263440.1      KNNQSLAFGKSKASDFRKTNSDGRGYQPMLTEIKAANFSQSGKIIKLDLTFKDGLERTFVYAFHEKN.   144
NTDB id 399 FSA28 RS09380 WP 002264245.1    KNNQSLAFGKSKASDFRKTNSDGRGYQPMLTEIKAANFSQSGKIIKLDLTFKDGLERTFVYAFHEKN.   144
consensus                                   ********!*****!!!!****!*!!!!!****!** ********** **!**!*!!*!*!**** **
```

X non conserved

X similar

X $\geq$ 50% conserved