

logo

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NTDB id 275 KZH43 RS09240 WP 000250534.1
NTDB id 234 SPD RS09870 WP 000250534.1
NTDB id 200 SPR RS09405 WP 000250534.1
NTDB id 165 SP RS10355 WP 000250534.1
NTDB id 505 SM12261 RS00970 WP 000250509.1
NTDB id 533 SMSK321 RS09215 WP 000250512.1
NTDB id 591 KW2 RS10830 WP 014735174.1
NTDB id 978588 MGA37637 RS00685 WP 010921800.1
NTDB id 399 FSA28 RS09380 WP 002264245.1
NTDB id 390 SMU RS09010 WP 002263440.1
consensus

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Sequence	80
MVQNSCWQSKSHKVKAF ¹ TLL ² ESLL ³ ALIVISG ⁴ LLLFQAMSQ ⁵ LLISEVRYQQQSE ⁶ QKEWLLFVDQLE ⁷ VELDRSQFEKVEGN ⁸	80
MVQNSCWQSKSHKVKAF ¹ TLL ² ESLL ³ ALIVISG ⁴ LLLFQAMSQ ⁵ LLISEVRYQQQSE ⁶ QKEWLLFVDQLE ⁷ VELDRSQFEKVEGN ⁸	80
MVQNSCWQSKSHKVKAF ¹ TLL ² ESLL ³ ALIVISG ⁴ LLLFQAMSQ ⁵ LLISEVRYQQQSE ⁶ QKEWLLFVDQLE ⁷ VELDRSQFEKVEGN ⁸	80
MVQNSCWQSKSHKVKAF ¹ TLL ² ESLL ³ ALIVISG ⁴ LLLFQAMSQ ⁵ LLISEVRYQQQSE ⁶ QKEWLLFVDQLE ⁷ VELDRSQFEKVEGN ⁸	80
MVQNSCW ¹ L ² SKSHK ³ IKAF ⁴ TLL ⁵ ES ⁶ L ⁷ ALIVISG ⁸ LLLFQAMSQ ⁹ LLISEVRYQQQSE ¹⁰ QKEWLLFVDQLE ¹¹ AE ¹² LD ¹³ RSQFEKVEG ¹⁴ D ¹⁵	80
MVQNSCW ¹ L ² SKSHK ³ IKAF ⁴ TLL ⁵ ES ⁶ L ⁷ ALIVISG ⁸ LLLFQAMSQ ⁹ LLISEVRYQQQSE ¹⁰ QKEWLLFVDQLE ¹¹ AE ¹² LD ¹³ RSQFEK ¹⁴ TEG ¹⁵ N ¹⁶	80
.....MKL ¹ KIRAF ² TLL ³ EC ⁴ L ⁵ VAL ⁶ ISG ⁷ SV ⁸ ISGL ⁹ TRM ¹⁰ IEEQ ¹¹ MKIS ¹² QND ¹³ SRK ¹⁴ DW ¹⁵ QIF ¹⁶ CE ¹⁷ QMR ¹⁸ SEL ¹⁹ SGAK ²⁰ LND ²¹ VNQ ²² N ²³	71
.....MSK ¹ QLSN ² IKAF ³ TLL ⁴ E ⁵ AL ⁶ IAL ⁷ LVISG ⁸ LL ⁹ VYQ ¹⁰ GL ¹¹ TRT ¹² L ¹³ LKSH ¹⁴ YLARH ¹⁵ QDN ¹⁶ WLL ¹⁷ FSH ¹⁸ Q ¹⁹ REL ²⁰ SGAR ²¹ FYK ²² VAD ²³ N ²⁴	74
.....MLK ¹ SK ² LKAF ³ TLL ⁴ EC ⁵ L ⁶ LAL ⁷ VIAG ⁸ SV ⁹ SYNG ¹⁰ LT ¹¹ KA ¹² ISS ¹³ NI ¹⁴ HYLSKN ¹⁵ QED ¹⁶ AWLL ¹⁷ FCQ ¹⁸ QFR ¹⁹ SEL ²⁰ EG ²¹ TTL ²² QK ²³ LDS ²⁴ N ²⁵	72
.....MLK ¹ SK ² LKAF ³ TLL ⁴ EC ⁵ L ⁶ LAL ⁷ VIAG ⁸ SV ⁹ SYNG ¹⁰ LT ¹¹ KA ¹² ISS ¹³ NI ¹⁴ HYLSKN ¹⁵ QED ¹⁶ AWLL ¹⁷ FCQ ¹⁸ QFR ¹⁹ SEL ²⁰ EG ²¹ TTL ²² QK ²³ LDS ²⁴ N ²⁵	72

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RLVYKQDQDKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSVRITEDNQLVRFHFQFQKGLEREFYIRVEKEKS	153
RLYMKQDGKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSVRITEDNQLVRFHFQFQKGLEREFYIRVEKEKS	153
RLYMKQDGKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSVRITEDNQLVRFHFQFQKGLEREFYIRVEKEKS	153
RLYMKQDQDKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSVRITEDNQLVRFHFQFQKGLEREFYIRVEKEKS	153
RLYMKQDQDKDIAIGKSKSDDFRKTNARGRGYQPMVYGLKSAQITENQVVRFRFQFQKGLEREFYIRVEKA	153
RLYMKQDGKDIISIGKLSKSDDFRKTNARGRGYQPMVYGLKSAQITENQVVRFRFQFQKGLEREFYIRVEKA	153
FLYVTKDKKLRFLVGDDFRKSDKGGYQPMILYDLKGAKIQAENLIKITITIDFNDNGERVFIYRFTDTK	141
KLYVEKGKVLAFGQFKSHDFRKSASNGGYQPMILFGTISRSHIHIEQSQCITLKWKSGLERTFVYAFQD	144
KLYVQKNINQSLAFGKSKASDFRKTNSDGRGYQPMILTEIKAAANFSQSGKIILDLTLFKDGLERTFVYAFHEKN	144
KLYIQKNINQSLAFGKSKASDFRKTNSDGRGYQPMILTEIKAAANFSQSGKIILDLTLFKDGLERTFVYAFHEKN	144

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