

logo

NTDB id 44627 BANAU RS13350 WP 014418418.1
NTDB id 107 BSU 25570 NP 390435.1
consensus

85
85

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consensus

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170

logo

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255

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+TREKASILLLLFLPYVYMLTSGAAPSVLRASLMSGVYTAGISLVKWRVRSTATACTSYTLVLLLFPNPHLWQAGFQLSFAVSFSLIL
LTREKAGI L L L L FLPVYTLLSGAAPSVLRASLMLGFYITAGTLVKRGITHSSAAALSLSYL L L L L FNPYFLWQAGFQLSFAVSA SLIL
ITREKAS I L L L L FLPLVYMLTG AAPSVLRAALMSGVYLAGSLVKWRVRSTATACLSYIVL L L L FNPYH LFEAGFQLSFAVSFSLIL
* * * * *

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340

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424

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Sequence logo showing amino acid conservation across three rows. The top row shows residues T, Y, I, A, S, V, D, L, F, T, M, V, S, K, P, D, P, V, S, L, F, L, F, A, S, I, F, L, F, A, T, E, K, R, S, L, Q, R, V, T, V, L, F, L, F, C, T, V, M, F, Y, L, I, Y, P, Y, L, S, S, W, G, E, X, D, M, L, D, I, G, Q, G. The middle row shows residues M, K, P, V, H, D, F, I, T, Y, A, A, S, V, D, L, F, T, M, I, V, S, K, P, D, F, L, S, L, L, L, A, V, S, V, F, T, L, F, A, A, L, E, K, G, G, F, L, K, L, R, K, S, V, L, F, F, C, A, V, L, A, Y, L, I, C, R, P, Y, F, S, P, W, G, E, A, D, M, L, D, I, G, Q, G. The bottom row shows residues I, S, W, I, N, R, R, L, I, T, N, I, A, D, V, D, V, F, T, I, M, I, A, H, P, A, P, V, L, F, L, F, T, V, T, I, L, L, M, A, I, E, K, R, S, L, S, Q, L, M, V, T, G, G, I, C, T, V, M, F, L, F, L, I, Y, P, C, L, S, E, G, E, V, D, M, I, D, I, G, Q, G. Asterisks are placed below the bottom row at positions corresponding to conserved residues.

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764

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consensus



783
776

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