

logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 61763 SAIN RS03480 WP 021001532.1

NTDB id 414 AAK55818.1 838..2187()

consensus



Sequence logo for position 1. The logo shows the conservation of amino acids across three sequences. The top sequence (SMU RS06880) has a high frequency of M, D, N, L, R, Q, T, F, S, R, D, F, Y, F, V, L, I, L, L, G, F, I, V, Y, T, L, S, L, E, N, R, R, D, N, V, R, I, R, Q, L, N, Q, K, V, K, D, L, I, A, G, N, Y, S, K, V, L, D, V, Q, G, G, S, E, I, T, N, I, T, N, Y, N, D, L, S, E, V, I, R, L. The middle sequence (SAIN RS03480) has a high frequency of M, T, N, V, F, E, S, S, P, L, F, R, I, L, A, V, L, I, L, L, F, F, Y, F, I, F, L, N, Y, R, E, Y, K, N, N, N, Q, V, K, Q, L, N, A, K, V, R, S, L, I, T, C, H, Y, T, D, K, L, K, V, E, D, N, S, D, L, S, E, I, V, N, N, V, N, D, L, S, E, V, F, R, L. The bottom sequence (AAK55818.1) has a high frequency of M, I, D, N, I, R, Q, F, I, V, S, K, D, F, V, F, V, L, I, L, G, F, I, L, V, T, L, L, S, L, E, N, R, R, D, N, V, R, I, R, Q, L, N, Q, K, V, K, D, L, I, A, G, N, Y, S, E, I, L, D, V, Q, G, G, P, E, I, T, D, I, T, N, S, I, N, D, L, S, E, V, I, R, L. The consensus sequence is M D N L R Q T F S R D F Y F V L I L L G F I V Y T L S L E N R R D N V R I R Q L N Q K V K D L I A G N Y S K V L D V Q G G S E I T N I T N Y N D L S E V I R L.

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consensus



Sequence logo for position 2. The logo shows the conservation of amino acids across three sequences. The top sequence (SMU RS06880) has a high frequency of T, H, E, N, L, E, Q, E, K, R, L, S, I, L, S, Y, M, T, D, G, V, L, A, T, N, R, R, G, Q, I, M, I, N, D, M, A, T, K, Q, L, G, V, Y, E, A, L, N, R, N, I, L, L, D, I, E, D, S, Y, T, Y, N, D, L, I, T, K, T, P, E, I, V, L, T, R, R, D, E, Y. The middle sequence (SAIN RS03480) has a high frequency of T, H, E, N, L, E, Q, E, K, R, L, S, I, L, S, Y, M, T, D, G, V, L, A, T, N, R, R, G, Q, I, M, I, N, D, M, A, T, K, Q, L, G, V, K, E, S, E, A, R, K, M, N, I, L, K, L, D, I, E, D, E, Y, D, L, R, D, L, I, T, K, V, P, E, L, T, I, D, S, Q, D, E, N. The bottom sequence (AAK55818.1) has a high frequency of T, Q, E, N, L, E, Q, E, S, K, R, L, N, S, I, L, F, Y, M, T, D, G, V, L, A, T, N, R, R, G, Q, I, M, I, N, D, T, A, K, K, Q, L, G, V, K, E, D, V, L, N, R, S, I, L, E, L, L, K, I, E, E, N, Y, E, L, R, D, L, I, T, Q, S, P, E, L, L, D, S, Q, D, I, N. The consensus sequence is T H E N L E Q E K R L S I L S Y M T D G V L A T N R R G Q I M I N D M A T K Q L G V Y E A L N R N I L L D I E D S Y T Y N D L I T K T P E I V L T R R D E Y.

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Sequence logo for position 3. The logo shows the conservation of amino acids across three sequences. The top sequence (SMU RS06880) has a high frequency of S, E, E, L, L, R, Y, R, F, A, L, N, R, R, E, S, G, F, I, S, G, L, V, A, V, L, H, D, T, T, E, Q, E, K, E, E, R, E, R, R, L, F, V, S, N, V, S, H, E, L, R, T, P, L, T, S, V, K, S, Y, L, E, A, L, D, E, G, A, L, E, V, A, P, D, F, I, K, V, S, L, D, E. The middle sequence (SAIN RS03480) has a high frequency of D, E, F, I, L, R, Y, R, F, A, L, N, R, R, E, S, G, F, I, S, G, L, V, A, V, L, H, D, T, T, E, Q, E, K, E, E, R, E, R, R, L, F, V, S, N, V, S, H, E, L, R, T, P, L, T, S, V, K, S, Y, L, E, A, L, D, E, G, A, L, E, S, V, A, P, S, F, I, K, V, S, L, D, E. The bottom sequence (AAK55818.1) has a high frequency of G, E, Y, L, N, L, R, V, R, F, A, L, I, R, R, E, S, G, F, I, S, G, L, V, A, V, L, H, D, T, T, E, Q, E, K, E, E, R, E, R, R, L, F, V, S, N, V, S, H, E, L, R, T, P, L, T, S, V, K, S, Y, L, E, A, L, D, E, G, A, L, C, E, T, V, A, P, D, F, I, K, V, S, L, D, E. The consensus sequence is S E E L L R Y R F A L N R R E S G F I S G L V A V L H D T T E Q E K E E R E R R L F V S N V S H E L R T P L T S V K S Y L E A L D E G A L E V A P D F I K V S L D E.

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Sequence logo for position 4. The logo shows the conservation of amino acids across three sequences. The top sequence (SMU RS06880) has a high frequency of T, N, R, M, R, M, V, T, D, L, L, S, L, S, R, I, D, N, A, T, S, H, L, D, V, E, L, T, N, F, T, A, F, I, T, F, I, L, N, R, F, D, K, I, R, S, Q, N, D, D, K, K, Y, E, I, I, R, D, Y, P, I, N, S, I, W, E, I, D, T, D, K, M, T, Q, V, I, D, N, I, L, N, N. The middle sequence (SAIN RS03480) has a high frequency of T, N, R, M, R, M, V, S, D, L, L, S, L, S, R, I, D, N, A, T, S, H, L, D, V, E, L, T, N, F, T, A, F, I, T, F, I, L, N, R, F, D, K, I, R, S, Q, N, D, D, K, K, Y, E, I, I, R, D, Y, P, I, N, S, I, W, E, I, D, T, D, K, M, T, Q, V, I, D, N, I, L, N, N. The bottom sequence (AAK55818.1) has a high frequency of T, N, R, M, R, M, V, T, D, L, L, S, L, S, R, I, D, N, A, T, S, H, L, D, V, E, L, T, N, F, T, A, F, I, T, F, I, L, N, R, F, D, K, I, R, S, Q, N, D, D, K, K, Y, E, I, I, R, D, Y, P, I, N, S, I, W, E, I, D, T, D, K, M, T, Q, V, I, D, N, I, L, N, N. The consensus sequence is T N R M R M V T D L L S L S R I D N A T S H L D V E L T N F T A F I T F I L N R F D K I R S Q N D D K K Y E I I R D Y P I N S I W E I D T D K M T Q V I D N I L N N.

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consensus



Sequence logo for position 5. The logo shows the conservation of amino acids across three sequences. The top sequence (SMU RS06880) has a high frequency of A, I, K, Y, S, P, D, G, G, K, I, T, V, M, K, T, T, D, T, Q, L, I, L, S, I, S, D, Q, G, L, G, I, P, K, K, D, L, P, I, F, D, R, F, Y, R, V, D, K, A, R, S, R, A, Q, G, G, T, G, L, G, L, A, I, A, K, E, I, I, K, Q, H, K, G, F, I, W, A, K, S, E, Y, G, K. The middle sequence (SAIN RS03480) has a high frequency of A, I, K, Y, S, P, D, G, G, K, I, T, V, M, K, T, T, D, T, Q, L, I, L, S, I, S, D, Q, G, L, G, I, P, K, K, D, L, P, I, F, D, R, F, Y, R, V, D, K, A, R, S, R, A, Q, G, G, T, G, L, G, L, A, I, A, K, E, I, I, K, Q, H, K, G, F, I, W, A, K, S, E, Y, G, K. The bottom sequence (AAK55818.1) has a high frequency of A, I, K, Y, S, P, D, G, G, K, I, T, V, M, K, T, T, D, T, Q, L, I, L, S, I, S, D, Q, G, L, G, I, P, K, K, D, L, P, I, F, D, R, F, Y, R, V, D, K, A, R, S, R, A, Q, G, G, T, G, L, G, L, A, I, A, K, E, I, I, K, Q, H, K, G, F, I, W, A, K, S, E, Y, G, K. The consensus sequence is A I K Y S P D G G K I T V M K T T D T Q L I L S I S D Q G L G I P K K D L P I F D R F Y R V D K A R S R A Q G G T G L G L A I A K E I I K Q H K G F I W A K S E Y G K.

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consensus



Sequence logo for position 6. The logo shows the conservation of amino acids across three sequences. The top sequence (SMU RS06880) has a high frequency of G, S, T, F, T, I, V, L, P, Y, D, K, D, A, V, K, D, Y, E, E, D, E, E, S. The middle sequence (SAIN RS03480) has a high frequency of G, S, T, F, T, I, V, L, P, Y, D, K, E, A, V, K, D, D, W, E, E, D, E, L, E, G. The bottom sequence (AAK55818.1) has a high frequency of G, S, T, F, T, I, V, L, P, Y, D, K, D, A, V, K, E, E, W, E, D, E, V, E, D, *. The consensus sequence is G S T F T I V L P Y D K D A V K D Y E E D E E S.

450
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 non conserved
 similar
 $\geq 50\%$ conserved