

logo

NTDB id 375 SMU RS06880 WP 002262929.1

NTDB id 41999 SPPN RS05865 WP 000886221.1

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, L, D, L, L, K, Q, T, I, F, T, R, D, F, I, F, I, L, L, G, F, I, L. The middle sequence (SPPN RS05865) has a high frequency of M, L, D, L, L, K, Q, T, I, F, T, R, D, F, I, F, I, L, L, G, F, I, L. The bottom sequence (AAK55818) has a high frequency of M, L, D, L, L, K, Q, T, I, F, T, R, D, F, I, F, I, L, L, G, F, I, L. The consensus sequence is MLDLLKQTI FTRDFIFILLLGFIL.

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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 V, I, R, L, 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, I, M, I, N, D, T, A, K, K, Q, L, G, L, V, Q, E, D, V, L, N, R, S, I, L, E, V, L, K, I, E, E, S, Y, E, L, R, D, L, I, T, Q, S, P, E, L, L, D, S. The middle sequence (SPPN RS05865) has a high frequency of V, I, R, L, 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, I, M, I, N, D, T, A, K, K, Q, L, G, L, V, Q, E, D, V, L, N, R, S, I, L, E, V, L, K, I, E, E, S, Y, E, L, R, D, L, I, T, Q, S, P, E, L, L, D, S. The bottom sequence (AAK55818) has a high frequency of V, I, R, L, 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, I, M, I, N, D, T, A, K, K, Q, L, G, L, V, Q, E, D, V, L, N, R, S, I, L, E, V, L, K, I, E, E, S, Y, E, L, R, D, L, I, T, Q, S, P, E, L, L, D, S. The consensus sequence is V I R L 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 I M I N D T A K K Q L G L V Q E D V L N R S I L E V L K I E E S Y E L R D L I T Q S P E L L D S.

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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 Q, D, I, N, 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. The middle sequence (SPPN RS05865) has a high frequency of Q, D, I, N, 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. The bottom sequence (AAK55818) has a high frequency of Q, D, I, N, 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. The consensus sequence is Q D I N 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.

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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 S, L, D, E, T, N, R, M, R, M, V, T, D, L, L, H, L, S, R, I, D, N, A, T, S, H, L, D, V, E, L, I, N, F, T, A, F, I, T, F, I, L, N, R, F, D, K, M, K, G, Q, E, K, E, K, Y, E, L, V, R, D, Y, P, I, N, S, I, W, E, I, D, T, D, K, M, T, Q, V, V, D, N. The middle sequence (SPPN RS05865) has a high frequency of S, L, D, E, T, N, R, M, R, M, V, T, D, L, L, H, L, S, R, I, D, N, A, T, S, H, L, D, V, E, L, I, N, F, T, A, F, I, T, F, I, L, N, R, F, D, K, M, K, G, Q, E, K, E, K, Y, E, L, V, R, D, Y, P, I, N, S, I, W, E, I, D, T, D, K, M, T, Q, V, V, D, N. The bottom sequence (AAK55818) has a high frequency of S, L, D, E, T, N, R, M, R, M, V, T, D, L, L, H, L, S, R, I, D, N, A, T, S, H, L, D, V, E, L, I, N, F, T, A, F, I, T, F, I, L, N, R, F, D, K, M, K, G, Q, E, K, E, K, Y, E, L, V, R, D, Y, P, I, N, S, I, W, E, I, D, T, D, K, M, T, Q, V, V, D, N. The consensus sequence is S L D E T N R M R M V T D L L H L S R I D N A T S H L D V E L I N F T A F I T F I L N R F D K M K G Q E K E K Y E L V R D Y P I N S I W E I D T D K M T Q V V D N.

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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 I, L, N, N, A, I, K, Y, S, P, D, G, G, K, I, T, V, R, M, K, T, T, E, D, Q, M, I, L, S, I, S, D, Q, G, L, G, I, P, K, Q, D, L, P, R, I, F, D, R, F, Y, R, V, D, R, A, R, S, R, A, Q, G, G, T, G, L, G, L, S, I, A, K, E, I, I, K, Q, H, K, G, F, I, W, A, K, S. The middle sequence (SPPN RS05865) has a high frequency of I, L, N, N, A, I, K, Y, S, P, D, G, G, K, I, T, V, R, M, K, T, T, E, D, Q, M, I, L, S, I, S, D, Q, G, L, G, I, P, K, Q, D, L, P, R, I, F, D, R, F, Y, R, V, D, R, A, R, S, R, A, Q, G, G, T, G, L, G, L, S, I, A, K, E, I, I, K, Q, H, K, G, F, I, W, A, K, S. The bottom sequence (AAK55818) has a high frequency of I, L, N, N, A, I, K, Y, S, P, D, G, G, K, I, T, V, R, M, K, T, T, E, D, Q, M, I, L, S, I, S, D, Q, G, L, G, I, P, K, Q, D, L, P, R, I, F, D, R, F, Y, R, V, D, R, A, R, S, R, A, Q, G, G, T, G, L, G, L, S, I, A, K, E, I, I, K, Q, H, K, G, F, I, W, A, K, S. The consensus sequence is I L N N A I K Y S P D G G K I T V R M K T T E D Q M I L S I S D Q G L G I P K Q D L P R I F D R F Y R V D R A R S R A Q G G T G L G L S I A K E I I K Q H K G F I W A K S.

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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 E, Y, K, G, S, T, F, T, I, V, L, P, Y, D, K, D, A, V, K, E, E, V, W, E, D, E, V, E, D. The middle sequence (SPPN RS05865) has a high frequency of E, Y, K, G, S, T, F, T, I, V, L, P, Y, D, K, D, A, V, K, E, E, V, W, E, D, E, V, E, D. The bottom sequence (AAK55818) has a high frequency of E, Y, K, G, S, T, F, T, I, V, L, P, Y, D, K, D, A, V, K, E, E, V, W, E, D, E, V, E, D. The consensus sequence is E Y K G S T F T I V L P Y D K D A V K E E V W E D E V E D.

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 non conserved
 similar
 $\geq 50\%$ conserved