

logo

NTDB id 342171 ETT50 RS01405 WP 032464812.1

NTDB id 475 HSISS4 RS07005 WP 021143809.1

NTDB id 324 STU RS16140 WP 011226306.1

NTDB id 292 STER RS06940 WP 011681419.1

consensus



Sequence logo for position 1. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by exclamation marks (!) below the logo. The most conserved residues are M, K, K, S, K, W, L, A, L, A, G, V, A, L, L, S, V, G, V, L, A, A, C, S, S, K, S, N, T, S, G, T, T, Y, G, V, Y, S, S, D, P, E, T, L, D, Y, I, T, S, N, T, G, P, T, K, S, W, T, N, G, V, D, G, L, M, E, A, D, K, Y, G, N, L, V.

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consensus



Sequence logo for position 2. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by exclamation marks (!) below the logo. The most conserved residues are P, S, V, A, E, D, M, S, V, S, K, D, G, L, T, Y, T, Y, K, I, R, K, G, Y, K, M, Y, T, S, E, G, E, E, Y, A, V, T, A, K, D, F, V, T, G, L, K, H, A, A, D, K, A, G, G, L, Y, L, V, Q, D, S, I, A, G, L, S, D, Y, L, S, G, T, N, K, D, F, S, N.

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consensus



Sequence logo for position 3. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by exclamation marks (!) below the logo. The most conserved residues are V, G, V, K, A, I, D, P, Y, T, L, Q, Y, T, L, K, Q, P, E, P, Y, M, N, S, K, T, T, Y, S, L, L, F, P, V, N, E, D, F, L, K, N, K, G, K, D, F, G, K, S, T, D, P, T, S, I, L, Y, N, G, P, F, L, K, S, I, T, A, K, S, S, I, E, L, Y, K, N, E, N, Y.

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Sequence logo for position 4. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by exclamation marks (!) below the logo. The most conserved residues are W, D, K, K, N, V, H, F, D, A, I, K, L, S, Y, Y, D, G, S, D, Q, D, A, L, V, R, G, F, T, D, G, A, Y, S, F, A, R, V, Y, P, T, S, S, N, Y, S, V, E, K, K, Y, K, D, N, I, Y, T, A, P, G, A, S, T, S, A, I, G, N, L, D, R, Q, S, Y, K, Y, T.

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consensus



Sequence logo for position 5. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by exclamation marks (!) below the logo. The most conserved residues are A, K, K, T, D, S, E, K, S, T, K, K, A, L, L, N, K, D, F, R, Q, A, I, N, F, A, I, D, R, K, A, Y, Q, S, Q, I, N, G, K, D, G, A, T, L, A, Y, R, N, L, F, V, P, S, D, F, V, S, A, G, D, K, T, F, G, D, L, V, T, E, K, M, S, S, Y, G, D, E, W, S.

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logo

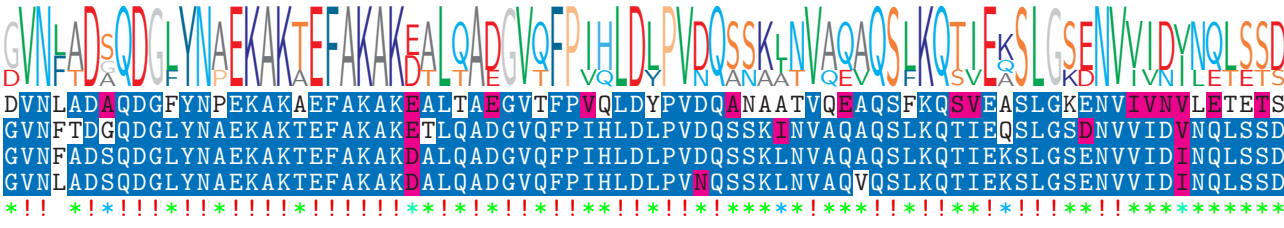
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NTDB id 324 STU RS16140 WP 011226306.1

NTDB id 292 STER RS06940 WP 011681419.1

consensus



Sequence logo for position 6. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by exclamation marks (!) below the logo. The most conserved residues are G, V, N, L, A, D, A, Q, D, G, L, Y, N, A, E, K, A, K, T, E, F, A, K, A, K, E, A, L, Q, A, D, G, V, Q, F, P, I, H, L, D, L, P, V, D, Q, S, S, K, L, N, V, A, Q, A, Q, S, L, K, Q, T, I, E, K, S, L, G, S, E, N, V, I, D, Y, N, Q, L, S, S, D.

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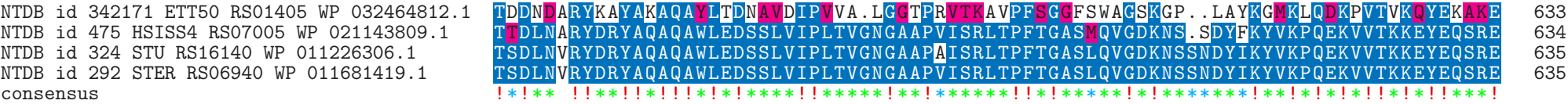
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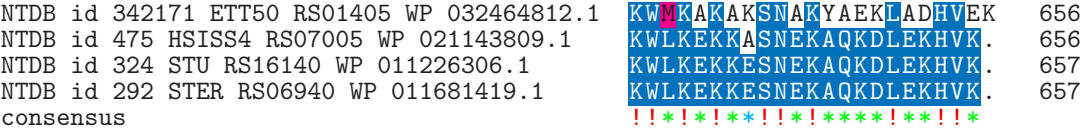
logo



logo



logo



X

 non conserved

X

 similar

X

 ≥ 50% conserved