

logo

NTDB id 49518 SPYALAB49 RS01375 WP 002992227.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for position 1. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The most conserved residues are M, K, K, Y, I, L, R, T, L, R, S, L, S, I, F, V, V, T, A, L, Y, T, I, I, Y, T, M, V, P, R, R, L, I, F, R, Q, D, P, N, Y, N, K, I, A, K, T, A, D, S, K, A, N, Y, E, N, T, I, Y, E, R, M, G, Y, I, D, Y, Y, D, T, K, E, L, Q, E, K, A, S.

80

80

80

80

logo

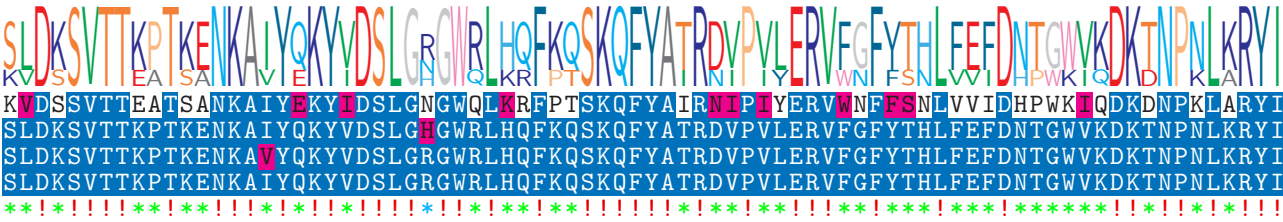
NTDB id 49518 SPYALAB49 RS01375 WP 002992227.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



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

160

160

160

160

logo

NTDB id 49518 SPYALAB49 RS01375 WP 002992227.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for position 3. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The most conserved residues are R, I, E, N, D, P, A, I, G, W, S, V, V, G, S, G, T, K, H, K, Y, L, L, Y, F, N, S, Q, F, P, F, V, H, Q, N, F, V, K, M, N, L, G, T, S, Y, P, T, Y, A, E, Q, G, V, L, D, V, I, T, Q, G, Q, G, Q, T, Q, S, S, E, V, N, F, P, T, G, K, K, I, S, S.

240

239

239

239

logo

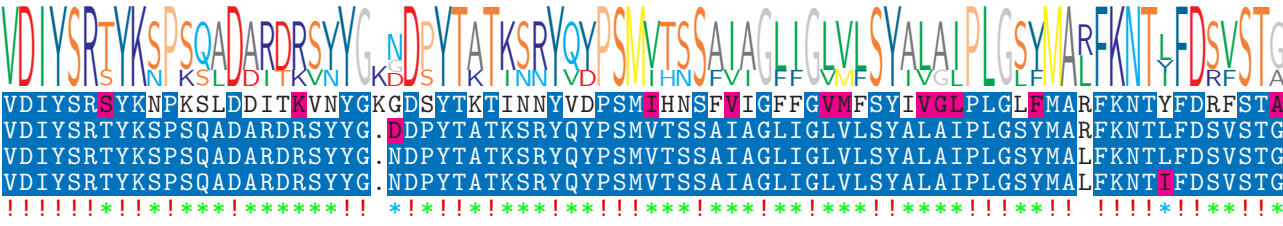
NTDB id 49518 SPYALAB49 RS01375 WP 002992227.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for position 4. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The most conserved residues are V, D, I, Y, S, R, T, Y, K, S, P, S, Q, A, D, A, R, D, R, S, Y, Y, G, D, D, P, Y, T, A, T, K, S, R, Y, Q, Y, P, S, M, V, T, S, S, A, I, A, G, L, I, G, L, V, L, S, Y, A, L, A, I, P, L, G, S, Y, M, A, R, F, K, N, T, L, F, D, S, V, S, T, G.

320

318

318

318

logo

NTDB id 49518 SPYALAB49 RS01375 WP 002992227.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



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

400

398

398

398

logo

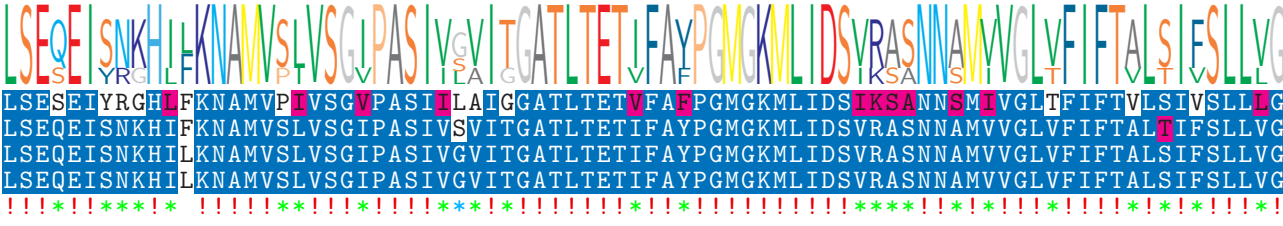
NTDB id 49518 SPYALAB49 RS01375 WP 002992227.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



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

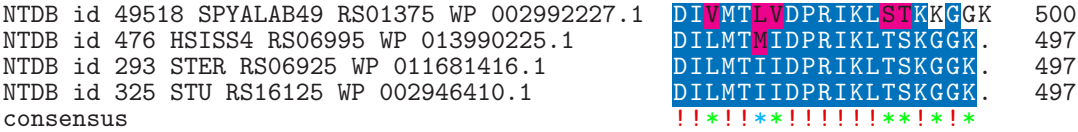
480

478

478

478

logo



- X

 non conserved
- X

 similar
- X

 ≥ 50% conserved