

logo

NTDB id 1015 ACIAD RS12005 WP 004928865.1

NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 980550 AAFA16 RS14505 WP 000472707.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for position 1. The logo shows the relative frequency of amino acids at this position. The most prominent amino acids are M, F, K, I, L, L, G, W, I, G, G, I, A, L, M, G, I, D, F, P, L, I, M, Q, Y, E, K, V, G, E, A, L, L, L, A, F, I, F, Y, L, Y, K, R, P, M, F, V, D, R, P, F, L, K, A, V, F, C, L, L, C, T, T, S, L, F, M, V, G, Y, H, Y, A, E, K, A, L, I, E. The consensus sequence is MFKIILLGWIGGIALMGIDFPLIMQYEVGEALLLLAFIFYLYKRPMFVDRPFLKAVFCLLCTTSLFMVGHYHAEKALIE.

80
80
80
80

logo

NTDB id 1015 ACIAD RS12005 WP 004928865.1

NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 980550 AAFA16 RS14505 WP 000472707.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for position 2. The logo shows the relative frequency of amino acids at this position. The most prominent amino acids are R, L, E, Q, R, E, T, D, T, R, N, L, D, I, I, V, Y, I, N, R, L, S, E, E, K, D, N, K, V, Q, Q, T, A, Q, V, L, N, L, S, K, E, P, V, N, W, L, L, Y, L, K, S, N, N, Q, N, L, L, K, N, N, Q, N, L, E, L, G, H, Y, Y, R, I, S, G, K, T, R, P, A, H, S. The consensus sequence is RLEQRETDTRNLDIIIVYNRLSEEKDNKVQQTAAQVLNLSKEPVNWLLYLKSNQNLKNNQNLLELGHYYRISGKTRPAHS.

159
160
160
160

logo

NTDB id 1015 ACIAD RS12005 WP 004928865.1

NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 980550 AAFA16 RS14505 WP 000472707.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for position 3. The logo shows the relative frequency of amino acids at this position. The most prominent amino acids are Y, A, T, P, G, A, F, D, Q, E, K, W, F, I, Q, R, N, I, M, S, G, F, N, V, R, Y, I, E, P, L, S, D, E, I, Y, R, L, G, Y, Q, Q, H, L, K, E, Q, Q, S, F, S, S, F, R, L, N, I, E, K, L, R, L, T, F, R, Q, I, L, N, S, S, S, L, Q, Q, K, G, L, I. The consensus sequence is YATPGAFDQEKWFIQRNIMSGFNVRYPELSLDEIYRLGYQQHLKEQQSFSNSFRNLIEKLRLTFRQILNSSSLQQKGLI.

239
240
240
240

logo

NTDB id 1015 ACIAD RS12005 WP 004928865.1

NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 980550 AAFA16 RS14505 WP 000472707.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for position 4. The logo shows the relative frequency of amino acids at this position. The most prominent amino acids are L, A, L, L, T, G, D, E, S, L, L, S, D, E, T, Q, L, Q, F, K, Q, L, G, I, S, H, L, L, A, I, S, G, P, H, V, L, I, F, A, I, M, L, S, W, A, C, H, Q, F, I, S, R, Y, Y, P, Q, I, Y, L, W, K, P, K, Q, L, M, A, V, P, C, C, L, G, V, L, I, Y, T, A. The consensus sequence is LALLTGDRSLNPELEQQQFQRFGISHLLAISGPHVLIFAAMVSWIFTRLTHREKPEIYLSIPQKIVLPEFLMCVILYCA.

319
320
320
320

logo

NTDB id 1015 ACIAD RS12005 WP 004928865.1

NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 980550 AAFA16 RS14505 WP 000472707.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for position 5. The logo shows the relative frequency of amino acids at this position. The most prominent amino acids are F, V, G, F, E, I, P, A, L, R, T, L, L, S, Y, L, I, F, I, G, F, L, L, L, K, Q, I, K, P, F, T, L, L, V, S, A, S, L, L, L, L, M, D, P, F, S, V, L, S, A, G, F, I, L, S, Y, G, A, C, F, I, L, R, I, Y, Q, T, I, A, Q, L, P, E, Q, H, F, L. The consensus sequence is FVGFEIPALRTLFLSYLIFIGFLLLKQI KPFTLLVYSASLLLLMDPFSVLSAGFWLSYGACFILLRIYQTIAQLPEQHFL.

399
400
400
400

logo

NTDB id 1015 ACIAD RS12005 WP 004928865.1

NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 980550 AAFA16 RS14505 WP 000472707.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for position 6. The logo shows the relative frequency of amino acids at this position. The most prominent amino acids are S, L, S, S, K, M, I, F, M, S, K, V, L, I, E, S, Q, G, K, I, F, I, A, L, S, P, L, T, L, L, F, F, Q, Q, I, S, W, V, A, P, L, T, N, I, I, A, V, P, I, V, G, S, V, I, V, P, L, N, I, A, A, C, A, W, F, V, K, P, F, G, N, M, L, F, H, F, N, D. The consensus sequence is SLSSKMIFMSKVLIESQGKIFIALSPLTLLFFQQRISWVAPLTNIIAVPIVGSVIVPLNIIAACAWFVKPFGNMLFHFN.

478
480
480
480

