

logo

NTDB id 368430 FIU05 RS02280 WP 010947130.1
NTDB id 1275 LPP RS06810 WP 025519545.1
NTDB id 1261 GCO85 RS07110 WP 025519545.1
consensus

MTEKPQLINCSFPNEASLYMAYMPFVKGGGLFIRTDHVSLSGSLSVKLLNENEPYLVTKIVWITPKGAQGNKPPGV
MTEKPQLINCSFPNEASLYMAYMPFVKGGGLFIRTDHVSLSGSLSVKLLNENEPYLVTKIVWITPKGAQGNKPPGV
MTEKPQLINCSFPNEASLYMAYMPFVKGGGLFIRTDHVSLSGSLSVKLLNENEPYLVTKIVWITPKGAQGNKPPGV

*!!!!!!!!!!!!!!

80
80
80

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A sequence logo visualization showing the conservation of amino acids at each position of a protein. The y-axis represents information content in bits, ranging from 0 to 1.6. The x-axis shows positions 1 through 20. The top row displays the most conserved residues: G, I, Q, F, T, G, E, N, S, R, Y, L, C, N, K, I, E, T, Y, L, A, G, M, L, K, S, C, Q, V, T, D, T. Below this, three rows show the specific amino acid distributions for different conditions or models, with red exclamation marks indicating positions of high conservation.

Position	Conserved Residues	Condition 1	Condition 2	Condition 3
1	G	G	G	G
2	I	I	I	I
3	Q	Q	Q	Q
4	F	F	F	F
5	T	T	T	T
6	G	G	G	G
7	E	E	E	E
8	N	N	N	N
9	S	S	S	S
10	R	R	R	R
11	Y	Y	Y	Y
12	L	L	L	L
13	C	C	C	C
14	N	N	N	N
15	K	K	K	K
16	I	I	I	I
17	E	E	E	E
18	T	T	T	T
19	Y	Y	Y	Y
20	L	L	L	L
21	A	A	A	A
22	G	G	G	G
23	M	M	M	M
24	L	L	L	L
25	K	K	K	K
26	S	S	S	S
27	C	C	C	C
28	Q	Q	Q	Q
29	V	V	V	V
30	T	T	T	T
31	D	D	D	D
32	T	T	T	T

113
113
113

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