

logo

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NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 180805 A4201 RS08420 WP 016504529.1
NTDB id 1366 NTHI RS01950 WP 011271972.1
NTDB id 1355 HI 0298 AAC21962.1
NTDB id 1168 A1552VC RS11070 WP 000957200.1
NTDB id 1293 VP RS12240 WP 005479695.1
NTDB id 1401 DSB67 RS12665 WP 010643259.1
NTDB id 1251 GC085 RS07725 WP 011946523.1
NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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MSA: **TTTPKFGSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDITVPY** **MS**.....**QYTIC**.....**EQQTERIFDITSPSRW** 22
.....**MFHENPLCTV**.....**SAMTGEVFEIQQALW** 25
.....**MTSYALLHTQRV**.....**TAQNGEIFTISPDLW** 27
.....**MTSYALLHTQRV**.....**TAKNGEVFTISPDLW** 27
.....**MLTNLVAILRQAEILSATQEQAVVTQVSASGTSVPEALL****ELSIFHAQETEQLSHIFGLPETDLSRYDYANL** 72
.....**MHSNLSTILRKQGLTFSQEESLIEQVKASGISMP****ALLSGGFTSSSELAELHSSIFGLSQPELSQYEYASL** 72
.....**MLTNLSTVLRQAGILTFSQEESLIEQVKASGISMP****ALLSGGFFQSHEITELHSSVFGLSCTSLNQYEYASL** 72
MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKKNILSAEQIALTAQNFQVPMLDINCTDVGTI 80
MSALHTSPKFTIGFFRRLLVEEKHLSAATMQTALDAAKRAKQDITVAYLIEEVHLSPSLLAETISAEFAEPYFDLDVYDTSQI 80
MSAFTTPPKFISGFIRRLVEEGYVNAQNMQQALEKAKKFKQDITVPY**LIDNFSISPLTIAEILSLEFGPELLDLGVFDPAFL** 80
* * * * *

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QKNCEEKQLLLRYLAVPVQETEHKLWLAVDDNNLTACEIFAFTMTHKQIEPVVIASDELKYLLNALSPQQPIYESEE.. 100
QRNQQQQRFLRLRYFALPLQEDEKQLWLGVDNSLANLSACDAFSFLTINKHIEPVLSTNELKRALLQSLPPKIQVEENIP.. 103
ERNQQQSSLLLRYFALPLKEENNRLWLGVDLSNLNSACETIAFITGKPVEPILLESSQLKELLQQLTPHQMQVEEVK.. 105
ERNQQQSSLLLRYFALPLKEENNRLWLGVDLSNLNSACETIAFITGKPVEPILLESSQLKELLQQLTPNQMQVEEQVK.. 105
CQQLGLRELITRDALPTAKQGNNLLLVASDPITLLQAEEFFRFATGLQVELALADHRALQAATIRRLYGRSIIQGAANQGG.. 151
CQQLGLRELITRHNAALPLHRTPTSTLLAVADPTINQAEDDFRFATGLQVELVLADFRELSTAIRRLYGRSLSHKESGLK.. 151
CQTGLGLRDLITRHNAALPLNRSTSLLILAVADPTNLQAEDDFRFATGLQVELVLADFRELTAATIRRLYGRSLGHEKSGLK.. 151
PVNLVNEKLIKRRHAMVPPLFSRGNTLYLATDDPSKQASLKEIQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSEYVE.. 160
PKDLVDQKLLIKHRIPLIQRGGIILYVATSNPSNIEAIDAIRFNSKILLPEPVIIVEHHKLEKVLGHFAEESSFDNDDE.. 158
LKDIDEKLIQKYRIMPLVVRHGHLVYATSNPTNIEAMDIAIRFNSKLLKVEPTIIVEHDKLERLLSEHFVEETHFNFDTE.. 158

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Sequence	Residue 1	Residue 2	Residue 3	Residue 4	Residue 5	Residue 6	Residue 7	Residue 8	Residue 9	Residue 10	Residue 11	Residue 12	Residue 13	Residue 14	Residue 15	Residue 16	Residue 17	Residue 18	Residue 19	Residue 20	Residue 21	Residue 22	Residue 23	Residue 24	Residue 25	Residue 26	Residue 27	Residue 28	Residue 29	Residue 30	Residue 31	Residue 32	Residue 33	Residue 34	Residue 35	Residue 36	Residue 37	Residue 38	Residue 39	Residue 40	Residue 41	Residue 42	Residue 43	Residue 44	Residue 45	Residue 46	Residue 47	Residue 48	Residue 49	Residue 50	Residue 51	Residue 52	Residue 53	Residue 54	Residue 55	Residue 56	Residue 57	Residue 58	Residue 59	Residue 60	Residue 61	Residue 62	Residue 63	Residue 64	Residue 65	Residue 66	Residue 67	Residue 68	Residue 69	Residue 70	Residue 71	Residue 72	Residue 73	Residue 74	Residue 75	Residue 76	Residue 77	Residue 78	Residue 79	Residue 80	Residue 81	Residue 82	Residue 83	Residue 84	Residue 85	Residue 86	Residue 87	Residue 88	Residue 89	Residue 90	Residue 91	Residue 92	Residue 93	Residue 94	Residue 95	Residue 96	Residue 97	Residue 98	Residue 99	Residue 100
165	L	A	F	V	E	Q	E	Q	L	N	L	N	D	P	I	I	Q	L	L	D	N	I	F	K	F	C	L	A	Q	N	A	S	D	I	H	E	P	R	K	Q	K	L	I	I	R	L	R	I	D	G	V	L	H	L	Y	K	S	L	S	I	Q	L																																						
169	T	V	Y	Q	V	A	Q	L	L	D	S	D	S	A	T	E	P	L	I	Q	L	L	D	Q	V	F	E	R	A	L	Q	L	Q	A	S	D	I	H	F	E	P	Y	Q	H	S	L	Q	V	R	F	R	I	D	G	V	L	Q	V	Q	P	S	F	S	G	I																																			
170	F	Y	Q	H	Q	E	T	H	F	E	Q	E	D	D	E	P	V	I	R	L	L	N	Q	I	F	E	S	A	L	Q	K	N	A	S	D	I	H	L	E	T	L	A	D	Q	F	Q	V	R	F	R	I	D	G	V	L	Q	P	Q	P	L	S	K	I	F																																				
170	F	Y	Q	H	Q	E	T	H	F	E	Q	E	D	D	E	P	V	I	R	L	L	N	Q	I	F	E	S	A	L	Q	K	N	A	S	D	I	H	L	E	T	L	A	D	Q	F	Q	V	R	F	R	I	D	G	V	L	Q	P	Q	P	L	S	K	I	F																																				
230	E	I	S	Q	D	E	L	A	N	L	V	K	V	S	D	D	E	L	Q	S	I	E	D	L	S	Q	D	D	S	P	V	S	R	F	I	N	Q	I	L	L	D	A	V	R	K	G	A	S	D	I	H	F	E	P	Y	E	N	Q	Y	R	I	R	L	R	C	D	G	I	L	V	E	T	Q	Q	P	A	S	H																						
230	E	I	N	Q	E	E	L	A	S	L	V	D	G	A	D	E	I	D	N	E	L	S	Q	D	D	S	P	V	S	R	Y	I	N	Q	I	L	L	D	A	V	R	K	G	A	S	D	I	H	F	E	P	Y	E	K	M	Y	R	V	R	L	R	C	D	G	I	L	I	E	T	Q	Q	P	P	N	H																									
230	E	I	N	Q	E	L	A	G	L	V	D	I	G	A	D	E	I	N	E	L																																																																																

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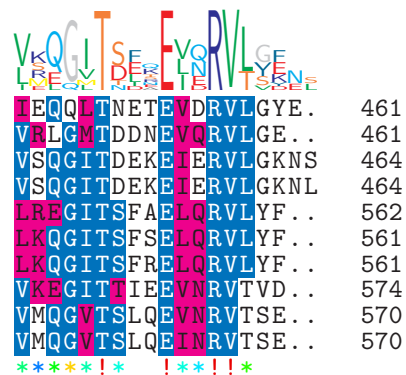
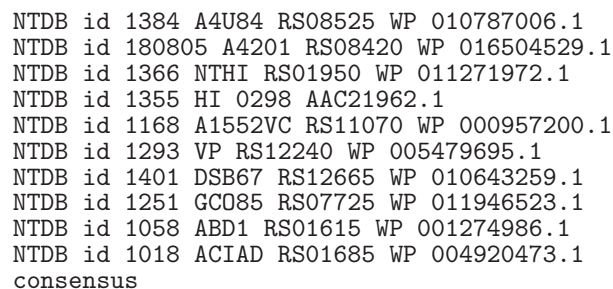
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consensus



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