

logo

NTDB id 1186 GTF74 RS01320 WP 000788426.1
NTDB id 1175 A1552VC RS12105 WP 000788426.1
NTDB id 1408 DSB67 RS13980 WP 010643500.1
NTDB id 1381 A4U84 RS02010 WP 021113424.1
NTDB id 39429 HIBPF RS09105 WP 013526477.1
NTDB id 1347 HI 0435 AAC22094.1
NTDB id 1373 NTHI RS02645 WP 011272046.1
consensus

Position	Sequence	Score
1	MKNGGLKT..YVAQTLTLWVGLALCASSMVFSAESATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSI	76
2	..MKNGGLKT..YVAQTLTLWVGLALCASSMVFSAESATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSI	76
3	MKMRHGLTLTPRKLTGLFSLWFSLLAP...FVAEEVQNSLKSIDFRTNKDKDAVIVVELVSPAAIVDIKRVQEGLSI	77
4		0
5		0
6		0
7		0
8		0
9		0
10		0

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ELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVVTVDGEFQHDYTLTKGKYLEVVISKLKADEKPKPKSVLEKEG 156
 ELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVVTVDGEFQHDYTLTKGKYLEVVISKLKADEKPKPKSVLEKEG 156
 DLLNTSVKDDQLYLLDVKDFSTVVESVEVFRDTSSTRLVAYIDEDYSHDYRLITGRYLEVVKVGLKANKEAIPDKSILDKEG 157
MRYLFLFFAT.....FPVLAN 17
MKKYFLKCGYFLVCFCLPLIVF.A...NPKTDN 29
MKKYFLKCGYFLVCFCLPLIVF.A...NPKTDN 29
MKKYFLKCGYFLVCFCLPLIVF.A...NPKTDN 29

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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
KLISIRLSQAPVAQVLCQQLFYQGVNLVVSDSVVGNLTRLRDGVPWQQVLDITILQVKGLDKRVDGNVILIPAKTELDLRE	K	L	I	S	I	R	L	S	Q	A	P	V	A	Q	V	L	C	Q	Q	L	F	Y	Q	G	V	N	L	V	S	D	S	V	V	G	N	L	T	R	L	R	D	G	V	P	W	Q	Q	V	L	D	I	T	I	L	Q	V	K	G	L	D	K	R	V	D	G	N	V	I	L	I	P	A	K	E	E	L	D	L	R	E	236																			
KLISINFDQIPVRNVLQLIADYNGFNLVVSDSVVGNLTRLRDGVPWQQVLDITILQVKGLDKRVDGNVILIPAKTELDLRE	K	L	I	S	I	N	F	D	Q	I	P	V	R	N	V	L	Q	L	I	A	D	Y	N	G	F	N	L	V	S	D	S	V	V	G	N	L	T	R	L	R	D	G	V	P	W	Q	Q	V	L	D	I	T	I	L	Q	V	K	G	L	D	K	R	V	D	G	N	V	I	L	I	P	A	K	E	E	L	D	L	R	E	236																			
KLISINFDQIPVRNVLQLIADYNGFNLVVSDSVVGNLTRLRDGVPWQQVLDITILQVKGLDKRVDGNVILIPAKTELDLRE	K	L	I	S	I	N	F	D	Q	I	P	V	R	N	V	L	Q	L	I	A	D	Y	N	G	F	N	L	V	S	D	S	V	V	G	N	L	T	R	L	R	D	G	V	P	W	Q	Q	V	L	D	I	T	I	L	Q	V	K	G	L	D	K	R	V	D	G	N	V	I	L	I	P	A	K	E	E	L	D	L	R	E	237																			
QQISLSIRNAPTAETIISYLAEEETGKNITISDEIKDGTKNFRVEKSHFDEILNSLIKTHQLNLKKENGITYYIHQAQE.....	Q	Q	I	S	L	S	I	R	N	A	P	T	A	E	T	I	I	S	Y	L	A	E	E	E	T	G	K	N	I	T	I	S	D	E	I	K	D	T	K	N	F	R	V	E	K	S	H	F	D	E	I	L	N	S	L	I	K	T	H	Q	L	N	L	K	K	E	N	G	I	T	Y	Y	I	H	Q	A	Q	E		92																				
ERFFIRLSQAPLAQTLEQLAFQQQDVNLVIGDTLENKISLKLNNIDMPRLQITIAKSKKLTLNKDEGIYYLNGGQS.....	E	R	F	F	I	R	L	S	Q	A	P	L	A	Q	T	L	E	Q	L	A	F	Q	Q	Q	D	V	N	L	V	I	G	D	T	L	E	N	K	I	S	L	K	L	N	N	I	D	M	P	R	L	Q	I	T	I	A	K	S	K	K	L	T	L	N	K	D	E	G	I	Y	Y	L	N	G	G	Q	S		104																						
ERFFIRLSQAPLAQTLEQLAFQQQDVNLVIGDILENKISLKLNNIDMPRLQITIAKSKHLLTNKDDGIYYLNGSQS.....	E	R	F	F	I	R	L	S	Q	A	P	L	A	Q	T	L	E	Q	L	A	F	Q	Q	Q	D	V	N	L	V																																																																							

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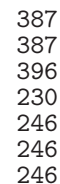
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[illegible]

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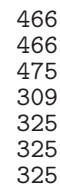
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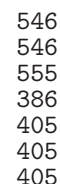
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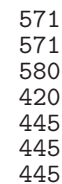
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- X non conserved
- X similar
- X >50% conserved