

logo

```
NTDB id 352784 E3983 RS11325 WP 135061045.1
NTDB id 1250 GC085 RS13065 WP 027219989.1
NTDB id 1399 DSB67 RS15600 WP 010645755.1
NTDB id 1152 A1552VC RS00200 WP 000654772.1
NTDB id 1388 A4U84 RS04945 WP 062924099.1
NTDB id 1361 HI 0985 AAC22646.1
consensus
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.....MRNLRRFFLALNRIPKLGPRSVMKLLQRWPDLKEMFSLSAHQLEKEGLPFSLAEEIAHFDFRLVDADFNWSG.QDD74
.....MNNLQPLLALNRMKRIGPRTVLKLQKRWPDLNLMFQLSSVDLEEAGLPSWLAQTIKNFDPDFIKTDLNLWLSSSEN75
MTPQNDDIDLAAWLKLSCLPGIGGVKMKNLLSKD.TPSNIVQYSTEQLQLLGLTAKQLQAW.SQVDKEVDACTLTWVAASSH78
...MKDQDLAAWLALCFTPKLGSKTISHLLATR.LPAQLQSFTPKWQLACGLKPEQLVFLTTQAARKAEQCLQWRSAANN76
.....MTHLTKLALLQVPQLGAQRIGRLSEV.DFGEFCQYDKTALKQMGNWERQIQRFWNPEHKWIDQALQWAEQD.Q73
....MNDITYTLRLRMQVPKLGGVGIDKILSNI.TLNEILLNYDDVAFRQMGWGAIQIRRWFKPEAKFIPEALVWSQKE.G74

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HHILTWEDKEYPQLLKEIHDPFVLYAIGQLPCLPQPALAMVGSRNPSITGSENAEYFARELAARDMTIVSGLALGIDAQ	154
HHILTWDSPPYPALLKEIADPPFIFYAKGELSAITQPSLAIVGSRNASVTGNENARAFSREISRHGVSIVSGLALGIDAH	155
HHILTLDALYPPLLKQTIVAPPPLLFVKGEASCLPQQPIAMVGSRNASVDGLQHTRTFASFSLVQHDLIVTSGLALGIDGH	158
RYIVTPHCPLYPRLLKEINSSPPVLFIIEGIWEAVHDPAAVAIVGSRNASVDGRQIARQFATELAQSGLVIVTSGLALGIDGY	156
QQILTLDFDEDYPFLFKQISTAPPPVLFRVGNVESLSLPQIAIVGSRDYSHYGEHWAGHFSAEVLKHQLAVTSGLAIGIDGF	153
NHLVNYFSPFPYFLLKQTASFPPPLFFVKGNLTALSQRQMAMVGSRYCTTYGEYWAKHFATELSLAGFTITSGLALGIDGH	154
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Sequence	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AHRGCLAE	A	H	R	G	C	L	A	E	G	K	T	I	A	V	M	G	T	G	I	D	H	I	T	Y	P	K	R	H	H	G	L	A	Q	D	I	R	K	.	N	G	L	L	S	E	F	P	L	K	S	P	P	T	A	G	H	F	P	P	R	R	N	R	I	S	G	L	S	L	A	T	L	V	V	E	A	A	V	K	S																					
AHLGCL	A	H	L	G	C	L	E	G	G	K	T	I	A	V	L	G	T	G	I	D	C	I	Y	P	R	R	H	L	K	L	A	E	Q	I	T	E	.	N	G	L	L	S	E	F	P	L	K	S	P	P	I	A	G	H	F	P	L	R	N	R	I	S	G	L	S	L	C	I	L	V	I	E	A	A	I	K	S																							
AHDGALL	A	H	D	G	A	L	L	A	G	G	K	T	I	A	V	L	G	S	G	L	E	Q	V	P	A	R	H	R	G	L	A	Q	R	V	A	E	.	N	G	A	L	V	S	E	F	R	P	D	A	K	P	R	A	E	N	F	P	P	R	R	N	R	I	S	G	L	S	L	G	V	L	V	E	A	A	E	K	S																						
AHDGALQA	A	H	D	G	A	L	Q	A	Q	Q	G	T	V	A	V	L	G	S	G	L	A	Q	V	Y	P	K	Q	H	Q	G	L	A	E	R	I	I	A	.	Q	G	A	L	V	S	E	F	A	P	H	T	P	P	K	A	D	H	F	P	P	R	R	N	R	I	S	G	L	S	L	G	V	V	V	E	A	A	E	K	S																					
CHQRAAN	C	H	Q	R	A	A	N	E	N	G	I	T	I	A	V	L	G	S	G	L	D	Q	V	P	A	R	H	K	K	L	A	E	Q	I	V	E	T	S	.	G	A	L	V	S	E	F	F	P	S	Q	P	P	I	A	E	N	F	P	P	R	R	N	R	I	S	G	L	S	L	G	T	L	V	I	E	A	T	V	N	S																				
CHQAVNI	C	H	Q	A	V	N	I	Q	Q	G	T	I	A	V	L	G	S	G	L	E	Q	I	Y	P	S	K	H	Q	R	L	S	A	Q	I	E	N	.	N	G	A	L	V	S	E	F	L	P	N	Q	A	P	I	A	E	N	F	P	P	R	R	N	R	I	S	G	L	S	V	G	T	L	V	E	A	T	E	K	S																						

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Row	Sequence	Position
1	..L....KLANSNEKLVKCI ^{1.87} G ^{1.90} FEMTTIDQII ^{1.90} VRSGL ^{1.90} EVEQVTCGLADLELEGIVKAVPGGYMRC....	356
2	..F.....SLASGKENLVKF ^{1.90} IGFETTTIDQIIDRSGYGM ^{1.90} EQVTSGLAEELELKGA ^{1.90} VI ^{1.90} AVPGGYIRCEYER	361
3	DLFSAPIDEDEELFPFQLLANVGNEATPVDILASRTINIPVQEVMMLLELELSGHVVAVSGGYIRKGGR.	369
4	TLFSAVQSDEELPFPELLANVGIEATPIDILASRTIQIPVQDIMMQLLELELLGHVVAVPGGYIRKGGR.	371
5	PKFAKNLPELTACQQQLFEQISLEPISSVDDLAKATDMAVETALIELLNLELLGVVKQVRGGYIT....	375
6	PR...RL.VEAPSHPKLYSRIGYTPVSIDDLAEEFNLSVDVLLVQLLDLELQDLIISENGLYKRIV....	373

* ! *

 non conserved
 similar
 $\geq 50\%$ conserved