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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 190736 A6L93 RS03840 WP 002216405.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus

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logo

NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVAMYLPIFNLMSV	LG.	408
NTDB id 1402	DSB67 RS12670 WP 010643257.1	VTAMYLPIFNLMSV	LG.	407
NTDB id 1113	AAA85695.1 219..1451()	LVAMYLPLFNLGN	VVA*	410
NTDB id 190736	AGL93 RS03840 WP 002216405.1	LVAMYLPLFNLGN	VVA.	410
NTDB id 1112	NGFG RS09215 WP 003689811.1	LVAMYLPLFNLGN	VVA.	410
NTDB id 1252	GC085 RS07730 WP 011213805.1	VVAMYLPIFKLGS	AV..	406
NTDB id 1198	PSJM300 03950 AFN76868.1	IIAMYLPIFQMG	SVV..	405
NTDB id 1059	ABD1 RS01610 WP 000279215.1	VIAMYLPIFQMG	SVV..	408
NTDB id 1016	ACIAD RS01680 WP 004920476.1	VIAMYLPIFQMG	SVV..	408
consensus		*****	*****	

Position	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
Sequence 1	E	I	R	D	V	A	G	S	M	T	S	A	M	R	T	E	L	F	P	N	M	L	Q	M	V	A	S	G	E	S	G	L	D	M	L	N	K	V	A	T	I	F	E	V	D	N	A	V	D	L	S	A	M	M	E	P	L	I	V	L	G	W	G	L																																				
Sequence 2	K	V	R	T	S	A	L	P	N	F	G	F	E	S	N	R	E	L	F	P	N	M	L	Q	M	V	A	S	G	E	S	G	L	D	M	L	N	K	V	A	T	I	F	E	V	D	N	A	V	D	L	S	A	M	M	E	P	L	I	V	L	G	W	G	L																																			
Sequence 3	E	V	Y	R	D	T	A	A	G	P	M	P	Y	I	A	M	R	N	T	E	A	F	F	M	L	Q	M	V	A	S	G	E	S	G	L	D	D	M	L	N	K	V	A	T	I	F	E	V	D	N	T	V	D	N	L	G	K	I	L	E	P	L	I	V	L	G	T	V	V	G	L																													
Sequence 4	E	Y	R	D	T	A	A	G	P	M	P	Y	I	A	M	R	H	C	H	V	F	P	E	L	V	L	Q	M	V	A	S	G	E	S	G	L	D	D	M	L	N	K	A	A	E	F	Y	E	F	E	V	D	N	T	V	D	N	L	S	K	I	L	E	P	L	I	V	L	G	V	V	G	L																											
Sequence 5	E	I	R	T	R	V	I	Q	G	L	S	M	T	S	G	M	R	A	T	E	L	F	P	N	M	L	Q	M	V	A	S	G	E	S	G	L	D	D	M	L	N	K	A	A	E	F	Y	E	D	E	V	D	N	A	V	G	R	L	S	A	M	M	E	P	I	I	I	L	G	V	I	G	T	L																										
Sequence 6	E	I	R	T	R	V	I	Q	G	L	S	M	T	S	G	M	R	A	T	E	L	F	P	N	M	L	Q	M	V	A	S	G	E	S	G	L	D	D	M	L	N	K	A	A	E	F	Y	E	D	E	V	D	N	A	V	G	R	L	S	A	M	M	E	P	I	I	I	L	G	V	I	G	T	L																										
Sequence 7	K	I	R	E	V	A	T	G	Q	Q	M	F	I	A	M	E	N	T	H	L	F	P	N	M	V	I	Q	M	V	A	S	G	E	S	G	A	L	D	M	L	S	K	V	A	T	I	F	E	E	V	E	N	A	V	D	A	L	S	S	L	E	P	T	I	M	S	I	L	G	I	L	V	G	L																										
Sequence 8	K	I	K	S	D	V	S	S	G	Q	L	N	F	S	M	R	T	T	G	T	F	P	S	M	A	V	Q	M	T	A	S	G	E	S	G	A	L	D	M	L	S	K	V	A	T	I	F	E	D	V	D	N	M	V	D	G	L	T	A	L	M	E	P	M	I	M	A	V	L	G	V	L	V	G	L																									
Sequence 9	K	I	R	E	D	V	A	T	G	Q	Q	L	F	A	M	R	I	S	N	R	F	P	S	M	A	I	Q	M	V	A	S	G	E	S	G	A	L	D</																																																														

V V A M Y L P I F N L G S W A
T L I S M N A L G

V V A M Y L P I F N L M S V L G .	408
V T A M Y L P I F N L M S V L G .	407
L V A M Y L P I F N L G N V V A *	410
L V A M Y L P I F N L G N V V A .	410
L V A M Y L P I F N L G N V V A .	410
V V A M Y L P I F K L G S A V . .	406
I I A M Y L P I F Q M G S V V . .	405
V I A M Y L P I F Q M G S V V . .	408
T I A M Y L P I F Q M G S V V . .	408
* * ! ! ! ! ! * ! * ! * ! * ! *	

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