

	(1)	10	20	30	40	50	63
Ara h 1.01 (wt)	(1)	MRGRVSP	LMLLLGI	LVLASVS	ATHAKS	SPYQK	KTENPCAQRCLQSCQQEPDDLKQKACESRCT
Ara h 1.01 (53-3)	(1)	MRGRVSP	LMLLLGI	LVLASVS	ATHAKS	SPYQK	KTENPCAQRCLQSCQQEPDDLKQKACESRCT
Ara h 1.01 (56-3)	(1)	MRGRVSP	LMLLLGI	LVLASVS	ATHAKS	SPYQK	KTENPCAQRCLQSCQQEPDDLKQKACESRCT
Ara h 1.01 (95-1)	(1)	MRGRVSP	LMLLLGI	LVLASVS	ATHAKS	SPYQK	KTENPCAQRCLQSCQQEPDDLKQKACESRCT
Ara h 1.02 (wt)	(1)	MRGRVSP	LMLLLGI	LVLASVS	ATQAK-	SPY-	RKTENPCAQRCLQSCQQEPDDLKQKACESRCT
Ara h 1.02 (133)	(1)	MRGRVSP	LMLLLGI	LVLASVS	ATQAK-	SPY-	RKTENPCAQRCLQSCQQEPDDLKQKACESRCT

	(64)	64	70	80	90	100	110	126
Ara h 1.01 (wt)	(64)	KLEYDPRCVYD	PRGHTGT	TNQR	SPPGERTRGRQPGDYDDRRQP	RREEGGRWGPA	GRERERE	
Ara h 1.01 (53-3)	(64)	KLEYDPRCVYD	PRGHTGT	TNQR	SPPGERTRGRQPGDYDDRRQP	RREEGGRWGPA	GRERERE	
Ara h 1.01 (56-3)	(64)	KLEYDPRCVYD	PRGHTGT	TNQR	SPPGERTRGRQPGDYDDRRQP	RREEGGRWGPA	GRERERE	
Ara h 1.01 (95-1)	(64)	KLEYDPRCVYD	PRGHTGT	TNQR	SPPGERTRGRQPGDYDDRRQP	RREEGGRWGPA	GRERERE	
Ara h 1.02 (wt)	(62)	KLEYDPRCVYD	- - - -	TGATNQR	HPPGERTRGRQPGDYDDRRQP	RREEGGRWGPA	EPRERERE	
Ara h 1.02 (133)	(62)	KLEYDPRCVYD	- - - -	TGATNQR	HPPGERTRGRQPGDYDDRRQP	- - - - -	- - - - -	

	(127)	127	140	150	160	170	189	
Ara h 1.01 (wt)	(127)	EDWRQPR ED WRRP SH QQPRKIRPEGREG EQ EWGTPGSHVREETS SR NNPFYF PS R RF STRYGNQ						
Ara h 1.01 (53-3)	(127)	EDWRQPR ED WRRP SH QQPRKIRPEGREG EQ EWGTPGSHVREETS SR NNPFYF PS R RF STRYGNQ						
Ara h 1.01 (56-3)	(127)	EDWRQPR ED WRRP SH QQPRKIRPEGREG EQ EWGTPGSHVREETS SR NNPFYF PS R RF STRYGNQ						
Ara h 1.01 (95-1)	(127)	EDWRQPR ED WRRP SH QQPRKIRPEGREG EQ EWGTPGSHVREETS SR NNPFYF PS R RF STRYGNQ						
Ara h 1.02 (wt)	(121)	EDWRQPR ED WRRP SH QQPRKIRPEGREG EQ EWGTPGS E VREETS SR NNPFYF PS R RF STRYGNQ						
Ara h 1.02 (133)	(102)	-----						

	(190)	190	200	210	220	230	240	252	
Ara h 1.01 (wt)	(190)	NGRIRVLQRFDDQSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQGQATVTVANGNN							
Ara h 1.01 (53-3)	(190)	NGRIRVLQRFDDQSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQGQATVTVANGNN							
Ara h 1.01 (56-3)	(190)	NGRIRVLQRFDDQSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQGQATVTVANGNN							
Ara h 1.01 (95-1)	(190)	NGRIRVLQRFDDQSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQGQATVTVANGNN							
Ara h 1.02 (wt)	(184)	NGRIRVLQRFDDQRSKQFQNLQNHRIVQIEARPNTLVLPKHADADNILVIQQGQATVTVANGNN							
Ara h 1.02 (133)	(102)	-----							

[illegible]

Section 6

	(316)	316	330	340	350	360	378
Ara h 1.01 (wt) (316)		FSRNTLEAAFNAEFNEIRRVLLLEENAGGEQEERGQRRWSTRSSENNEGVIIVKVSKEHVEELTK					
Ara h 1.01 (53-3) (316)		FSRNTLEAAFNAEFNEIRRVLLLEENAGGEQEERGQRRWSTRSSENNEGVIIVKVSKEHVEELTK					
Ara h 1.01 (56-3) (316)		FSRNTLEAAFNAEFNEIRRVLLLEENAGGEQEERGQRRWSTRSSENNEGVIIVKVSKEHVEELTK					
Ara h 1.01 (95-1) (316)		FSRNTLEAAFNAEFNEIRRVLLLEENAGGEQEERGQRRWSTRSSENNEGVIIVKVSKEHVEELTK					
Ara h 1.02 (wt) (310)		FSRNTLEAAFNAEFNEIRRVLLLEENAGGEQEERGQRRRSTRSSDN-EGVIIVKVSKEHVQELTK					
Ara h 1.02 (133) (102)		-----					

Section 7

	(379)	379	390	400	410	420	430	441
Ara h 1.01 (wt) (379)		HAKSVSKKGSEEEGDITNPINLREGEPDLSNNFGKLFVVKPDKKNPQLQDLDMMLTCVEIKEG						
Ara h 1.01 (53-3) (379)		HAKSVSKKGSEEEGDITNPINLREGELDLSNNFGKLFVVKPDKKNPQLQDLDMMLTCVEIKEG						
Ara h 1.01 (56-3) (379)		HAKSVSKKGSEEEGDITNPINLREGEPDLSNNFGKLFVVKPDKKNPQLQDLDMMLTCVKIKEG						
Ara h 1.01 (95-1) (379)		HAKSVSKKGSEEEGDITNPINLREGEPDLSNNFGKLFVVKPDKKNPQLQDLDMMLTCVEIKEG						
Ara h 1.02 (wt) (372)		HAKSVSKKGSEEE-DITNPINLRDGEPLDLSNNFGRLFEVVKPDKKNPQLQDLDMMLTCVEIKEG						
Ara h 1.02 (133) (102)		-----						

Section 8

	(442)	442	450	460	470	480	490	504
Ara h 1.01 (wt) (442)		ALMLPHFNSKAMVIIVVNKGTGNLELVAVRKEQQQGRRE--EEEDEDEEEEGSNREVRRT						
Ara h 1.01 (53-3) (442)		ALMLPHFNSKAMVIIVVNKGTGNLELVAVRKEQQQGRRE--EEEDEDEEEEGSNREVRRT						
Ara h 1.01 (56-3) (442)		ALMLPHFNSKAMVIIVVNKGTGNLELVAVRKEQQQGRRE--EEEDEDEEEEGSNREVRRT						
Ara h 1.01 (95-1) (442)		ALMLPHFNSKAMVIIVVNKGTGNLELVAVRKEQQQGRRE--EEEDEDEEEEGSNREVRRT						
Ara h 1.02 (wt) (434)		ALMLPHFNSKAMVIIVVNKGTGNLELVAVRKEQQQGRREQEWEEEEEDEDEEEEGSNREVRRT						
Ara h 1.02 (133) (102)		-----						

Section 9

	(505)	505	510	520	530	540	550	567
Ara h 1.01 (wt) (502)		ARLKEGDVFIMPAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQAKDLAFP						
Ara h 1.01 (53-3) (502)		ARLKEGDVFIMPAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQAKDLAFP						
Ara h 1.01 (56-3) (502)		ARLKEGDVFIMPAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQAKDLAFP						
Ara h 1.01 (95-1) (502)		ARLKEGDVFIMPAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQAKDLAFP						
Ara h 1.02 (wt) (497)		ARLKEGDVFIMPAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQAKDLAFP						
Ara h 1.02 (133) (102)		-----						

Section 10

	(568)	568	580	590	600	610	629
Ara h 1.01 (wt) (565)		GSGEQVEKLIKQKESHFVSARPQSQSQSPSSPEKESPEKEDQEEENQGGKGPLLSSILKAFN					
Ara h 1.01 (53-3) (565)		GSGEQVEKLIKQKESHFVSARPQSQSQSPSSPEKESPEKEDQEEENQGGKGPLLSSILKAFN					
Ara h 1.01 (56-3) (565)		GSGEQVEKLIKQKESHFVSARPQSQSQSPSSPEKESPEKEDQEEENQGGKGPLLSSILKAFN					
Ara h 1.01 (95-1) (565)		GSGEQVEKLIKQKESHFVSARPQSQSQSPSSPEKESPEKEDQEEENQGGKGPLLSSILKAFN					
Ara h 1.02 (wt) (560)		GSGEQVEKLIKQRESHFVSARPQSQS--PSS-----PEKEDQEEENQGGKGPLLSSILKAFN					
Ara h 1.02 (133) (102)		-----					