

# SARS-CoV-2 and T-cell escape

HLA		Epitope Mutant <sup>2</sup>
66	A*02:01	SIIVYTMRL
		SIAYTMLL
		PEAYTMRL
		SEIAYTMAL
		SFIAYTMRL
		SIIVAYTMRL
		SIAYAMRL
		SIAYTMRF
1236	A*24:02	QYIKWPWYT
		QIRKWPWYT
		QYIKWPWYS
408	A*02:01	RFQSLQTVV
77	A*02:01	RIQSLQTYA
		CLQRFITLL

Infection and immunisation against SARS-CoV-2 is capable of generating specific neutralising antibodies and T-cells. However, this immunity may begin to fade due to evolutionary mutations of the virus ([Read more here](#)).

Recent studies have reported that the specific T-cell response to SARS-CoV-2 is robust and are relatively unaffected by the mutations seen in the variants of concern (VOCs). It must be said that a loss of CD8+ T-cell responses has been observed in a small group of individuals who have either recovered from infection or who are vaccinated against the SARS-CoV-2 Omicron variant.

The evolution of CD8+ T-cell epitopes has left a weaker T-cell response in some individuals, therefore compromising the protection established through vaccinations and/or infection.

A recent paper by Ahmed, et al., aimed to identify and screen the mutations of SARS-CoV-2 involved in CD8+ T-cell escape. The researchers looked at 753 distinct HLA-specific CD8+ T-cell epitopes and SARS-CoV-2 genetic sequence data.

In this present study they found 83 SARS-CoV-2 mutations of CD8+ T-cell epitopes which may result in an escape of the T-cell response (Table 1). In future, these mutations may become of concern as they may affect the ability of SARS-CoV-2 to evade the immune response in previously-infected and vaccinated individuals.

Table 1: List of SARS-CoV-2 immunoprevalent HLA-specific CD8+ T cell epitope mutants recommended for experimental investigation (Ahmed, et al., 2022).

Epitope <sup>1</sup>	HLA	Epitope Mutant <sup>2</sup>	Count
S			
691SILAYTMSL699	A*02:01	SILVYTMSL	720
		SILAYTMLL	655
		PELAYTMSL	205
		SILAYTMAL	181
		SFIAYTMSL	38
		SIVAYTMSL	24
		SILAYAMSL	7
		SILAYTMSF	7
		THAYTMSL	5
		SILFYTMSL	5
128QYIKWPWY1216	A*24:02	QYIKWPWYT	314
		QRIKWPWYI	15
		QYIKWPWYS	13
308RLQSLQTYV1088	A*02:01	RFQSLQTYV	20
		RLQSLQTYA	10
268YLQPRITLL277	A*02:01	CLQPRITLL	6

Table 1. Cont.

Epitope <sup>1</sup>	HLA	Epitope Mutant <sup>2</sup>	Count
M			
		FLRLTWICF	1470
		FLRLFWCL	1384
		FLRLTCCL	154
		FLRLTWCL	85
20 <sub>1</sub> FLRLTWICL <sub>20</sub>	A*02:01	FLRLTWCL	33
		CLFLTWICL	17
		FWRLTWCL	14
		FLRLTWCI	13
		VLRLTWCL	8
		FLLLTWCL	7
N			
		KLDDKIDQNF	635
		KLNDKIDPNF	226
		KLNDKIDPNF	177
		KPDKKIDPNF	118
		KLDDKIDQNF	78
		KLDDKIDQNF	62
220 <sub>1</sub> KLDDKIDQNF <sub>220</sub>	A*02:01	KLDDKIDQNF	38
		KLDDKIDQNF	35
		KLDDKIDQNF	13
		KLDDKIDQNF	11
		KLDDKIDQNF	10
		KLDDKIDQNF	6
		KLDDKIDQNF	5
		KLDDKIDQNF	5
		KRFTTTEPK	303
		KTFPTTEPN	107
		KTFPTTEPN	57
301 <sub>1</sub> KRFTTTEPK <sub>301</sub>	A*03:01	KRFTTTEPK	30
		KTFPTTEPN	16
		KTFPTTEPN	14
		KTFPTTEPN	9
		KRFTTTEPK	303
		KTFPTTEPN	107
		KTFPTTEPN	57
301 <sub>1</sub> KRFTTTEPK <sub>301</sub>	A*11:01	KRFTTTEPK	30
		KTFPTTEPN	16
		KTFPTTEPN	14
		KTFPTTEPN	6

		AIEGALNTPK	9685
(156)AIEGALNTPK(143)	A*11:01	VIEGALNTPK	1162
		AEAGALNTPK	190
		ANEALNTPK	101
		APIEGALNTPK	36
		TIEGALNTPK	27
(36)KTFTPTIEPKK(20)	A*03:01	KKFTPTIEPKK	300
		KRFTPTIEPKK	30
		KTFTPTIEPKN	28
(30)SPRWYFYLL(23)	B*07:02	SKRWYFYLL	23

Epitope <sup>1</sup>	HLA	Epitope Mutant <sup>2</sup>	Count
ORF3a			
112 VYFLQSNF <sub>120</sub>	A*24:02	VHFLQSNF VYFLQSNAC VYFLQSNIS	339 112 56
138 LEYDANYFL <sub>147</sub>	A*02:01	LEFDANYFL LEYDANYFF	2562 1275
202 FTSDYYVQC <sub>213</sub>	A*01:01	FTSDYVQLC FTSDYYQLH	121 64

CRP1a			
		STDP1a.GLYM	2306
		TEP1a.GLYM	1360
100%TEP1a.GLYM <sub>max</sub>	A/0/0/0	TEP1a.GLYM	102
		TEP1a.GLYM	50
		TEP1a.GLYM	5
100%TEP1a.GLYM <sub>max</sub>	A/0/0/0	PER1a.GLYM	140
		PER1a.GLYM	13
		PER1a.GLYM	10
100%PER1a.GLYM <sub>max</sub>	A/0/0/0	HTP1a.GLYM	498
		HTP1a.GLYM	10
100%HTP1a.GLYM <sub>max</sub>	A/0/0/0	HTP1a.GLYM	5

**Journal article: Ahmed, S. F., et al., 2022. [Identification of Potential SARS-CoV-2 CD8+ T Cell Escape Mutants](#). *Vaccines*.**

*Summary by Stefan Botha*