

# SARS-CoV-2 and T-cell escape

HLA	Epitope Mutant <sup>2</sup>		
66	A*0201	SIIVYTMRL SIAYTMRL FIAYTMRL SIAYTMAL SFIAYTMRL SIVAYTMRL SIAYAMRL SIAYTMRF TIAYTMRL SIPTTMRL	
	123	A*2402	QVIRWFWYT QIRWFWYT QVIRWFWYS
		408	A*0201
	27		A*0201

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
<b>S</b>			
691SIAYTMSL <sub>699</sub>	A*02:01	SIIVYTM <sub>699</sub> SL	720
		SIAYTM <sub>699</sub> LL	655
		PIAYTMSL	205
		SIAYTM <sub>699</sub> AL	181
		SFIAYTMSL	38
		SIVAYTMSL	24
		SIAYAMSL	7
		SIAYTMSF	7
		TIAYTMSL	5
SIIFYTMSL	5		
1208QYIKWPWYI <sub>1216</sub>	A*24:02	QYIKWPWYI QH <sub>1216</sub> IKWPWYI QYIKWPWYS	314 15 13
1000RLQSLQTYV <sub>1008</sub>	A*02:01	RFQSLQTYV RLQSLQTYA	20 10
200YLQPRIFLL <sub>277</sub>	A*02:01	CLQPRIFLL	6

Table 1. Cont.

Epitope <sup>1</sup>	HLA	Epitope Mutant <sup>2</sup>	Count
<b>M</b>			
25FLRLTWK <sub>34</sub>	A*02:01	FLRLTWCF	1479
		FLRLW <sub>34</sub> KL	1384
		FLRLT <sub>34</sub> CL	134
		LLFLTW <sub>34</sub> CL	85
		FFL <sub>34</sub> TW <sub>34</sub> CL	33
		CLFLTW <sub>34</sub> CL	17
		IVRLTW <sub>34</sub> CL	14
		FLRLTW <sub>34</sub> CI	13
VLRLTW <sub>34</sub> CL	8		
FLLLTW <sub>34</sub> CL	7		
<b>N</b>			
128KLDKDPNF <sub>136</sub>	A*02:01	KLDKDPNF	633
		KLDNKDPNF	226
		KLNKDPNF	177
		KFDKDPNF	118
		KLDVDPNF	78
		KLDHKDPNF	62
		KLDGDPNF	38
		KLDKDKQNF	35
		KLDWKDPNF	13
		KLEKDPNF	11
		KLDGKDPNF	10
		KLADKDPNF	9
KLVKDPNF	6		
KLDAKDPNF	6		
KLDDKDPNS	5		
341KTFPTPEPK <sub>349</sub>	A*03:01	KKTFPTPEK	300
		KTFPTPELN	107
		KTFPTPEPI	57
		KRFTPTPEK	30
		KTFPTPEDE	16
		KTFPTPEPT	14
KTFPTPEPL	9		
341KTFPTPEPK <sub>349</sub>	A*11:01	KKTFPTPEK	300
		KTFPTPELN	107
		KTFPTPEPI	57
		KRFTPTPEK	30
		KTFPTPEDE	16
		KTFPTPEPT	14
KTFPTPEPL	9		

156ATEGALNTPK <sub>163</sub>	A*11:01	AIEGALNTPK	9685
		VIEGALNTPK	1162
		AAEGALNTPK	196
		ANEGALNTPK	101
		APEGALNTPK	36
TIEGALNTPK	27		
361KTFPTPEPK <sub>370</sub>	A*03:01	KKTFPTPEKK	300
		KRFTPTPEKK	30
		KTFPTPEPKN	28
305SPRWYFYLL <sub>323</sub>	F*07:02	SRWYFYLL	23

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Table 1. Cont.

Epitope <sup>1</sup>	HLA	Epitope Mutant <sup>2</sup>	Count
<b>O0F3a</b>			
102VYFLQSINF <sub>120</sub>	A*24:02	VHFLQSINF	339
		VYFLQSINC	112
		VYFLQSINS	50
138LLYDANYFL <sub>147</sub>	A*02:01	LIFDANYFL	2582
		LLYDANYFF	1276
207FTSDVYQLC <sub>215</sub>	A*01:01	FTSDVYQLC FTSDVYQLH	121 64

HLA	Epitope	Count
A*02:01	SIIVYTM <sub>699</sub> SL	720
	SIAYTM <sub>699</sub> LL	655
	PIAYTMSL	205
A*03:01	KKTFPTPEKK	300
	KRFTPTPEKK	30
	KTFPTPEPKN	28
A*11:01	KKTFPTPEK	300
	KTFPTPELN	107
	KTFPTPEPI	57
A*02:01	VHFLQSINF	339
	VYFLQSINC	112
	VYFLQSINS	50
A*02:01	LIFDANYFL	2582
	LLYDANYFF	1276
A*01:01	FTSDVYQLC	121
	FTSDVYQLH	64

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

*Summary by Stefan Botha*