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Characterization of the class I Major Histocompatibility Complex of the *Macaca fascicularis*

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Appendix A

table 1.

Query results

<i>Parameters</i>	
Length of peptide sequence	
Calculated subsequence scores	
Max. number of results	20
Min. score	0.5
Matrices to get values	BIMAS

<i>HLA B 2702 - 9 mers</i>				
Max. score that could've been reached using this molecule type				3000
<i>Rank</i>	<i>Start position</i>	<i>Sequence</i>	<i>% of max. score</i>	<i>Score</i>
1	381	ARFQCRGEF	33.33 %	1000
2	197	MRYCNQSTI	10 %	300
3	501	RRYEGPESA	10 %	300
4	37	WRNSAAPLF	6.66 %	200
5	219	IRMCAPAGF	6.66 %	200
6	395	TRMFNSSQY	6.66 %	200
7	584	ARLTAIEKY	6.66 %	200
8	4	RRTLKVLLL	6 %	180
9	515	RRREVSLLV	6 %	180
10	852	RRIRQGLEI	6 %	180
11	483	ARWKLVELT	3.33 %	100
12	3	VRRTLKVLL	2 %	60
13	171	KRVMYEAHC	2 %	60
14	187	DRETNQTY Y	2 %	60
15	293	FRKSSVIKL	2 %	60
16	329	RRAIRRAAC	2 %	60
17	462	NRTHITLTL	2 %	60
18	474	VRQVWRAEL	2 %	60
19	513	SRRRREVSL	2 %	60
20	514	RRRREVSLV	2 %	60

<i>HLA B 2702 - 10 mers</i>				
Max. score that could've been reached using this molecule type				3000
<i>Rank</i>	<i>Start position</i>	<i>Sequence</i>	<i>% of max. score</i>	<i>Score</i>
1	381	ARFQCRGEFF	33.33 %	1000
2	797	HRHSLILLY	6.66 %	200
3	4	RRTLKVLLLI	6 %	180
4	514	RRRREVSLVL	6 %	180
5	516	RREVSLVLGL	6 %	180
6	197	MRYCNQSTIT	3.33 %	100
7	25	KQYVTVFYGI	3 %	90
8	3	VRRTLKVLLL	2 %	60
9	187	DRETNQTYYY	2 %	60
10	385	CRGEFFYCNL	2 %	60
11	478	WRAELARWKL	2 %	60
12	562	LRAVEGHSAL	2 %	60
13	714	SRLCRGYSPL	2 %	60
14	717	CRGYSPLLQI	2 %	60
15	841	TRAAREVVAI	2 %	60
16	852	RRIRQGLEIV	2 %	60
17	401	SQYPVNNNSNI	1 %	30
18	501	RRYEGPESAE	1 %	30
19	607	KQICHTSVEW	1 %	30
20	637	QQWETDIAAL	1 %	30

Table 1. The predicted peptide fragments bound and presented by HLA-B locus molecules that are similar in pocket structure to the Macaques. Fragment prediction was done using the GP160 molecule from SIV. Fragments were generated for 8mers, 9mers, and 10mers using the BIMAS algorithm.