

## Table S2

Table S2. HLA-DR and -DQ binding predictions for Rv2034 p88-107 (FWTRALTGYAQLIDSEGDDT)

HLA-DR	Allele molecule	SYFPEITHI	NetMHCIIpan 2.1	NetMHCII 2.2	IEDB	IEDB
Sequence	HLA-DRB1	Score	Affinity nM	Affinity nM	arbpython (ARB) Affinity nM	SMM Affinity nM
LTGYAQLIDSEGDDT	0101	18	<b>312.24 (WB)</b> YAQLIDSEG	<b>461.4 (WB)</b> YAQLIDSEG	<b>231.3 (WB)</b> YAQLIDSEG	<b>253.0 (WB)</b> YAQLIDSEG
TRALTGYAQLIDSEG	0101	9	<b>181.26 (WB)</b> ALTGYAQLI	<b>92.6 (WB)</b> ALTGYAQLI	<b>24.6 (SB)</b> ALTGYAQLI	<b>160.0 (WB)</b> ALTGYAQLI
FWTRALTGYAQLIDS	0101	10	<b>19.73 (SB)</b> WTRALTGYA	<b>35.8 (SB)</b> TRALTGYAQ	<b>21.7 (SB)</b> WTRALTGYA	<b>199.0 (WB)</b> TRALTGYAQ
TRALTGYAQLIDSEG	0301 (17)	18	8678.79 ALTGYAQLI	8615.4 LTGYAQLID	6774.6 LTGYAQLID	12827.0 ALTGYAQLI
WTRALTGYAQLIDSE	0301 (17)	4	7642.93 ALTGYAQLI	7257.2 LTGYAQLID	6774.6 LTGYAQLID	12186.0 ALTGYAQLI
ALTGYAQLIDSEGDD	0301 (17)	1	10489.46 GYAQLIDSE	12849.8 LTGYAQLID	<b>134.5 (WB)</b> QLIDSEGDD	11880.0 ALTGYAQLI
LTGYAQLIDSEGDDT	0401	16	845.88 YAQLIDSEG	<b>298.6 (WB)</b> YAQLIDSEG	1206.2 YAQLIDSEG	910.0 YAQLIDSEG
FWTRALTGYAQLIDS	0401	6	<b>235.93 (WB)</b> WTRALTGYA	623.0 TRALTGYAQ	1500.4 WTRALTGYA	1752.0 TRALTGYAQ
FWTRALTGYAQLIDS	0701	16	<b>149.85 (WB)</b> WTRALTGYA	1010.6 ALTGYAQLI	1564.2 FWTRALTGY	1435.0 ALTGYAQLI
FWTRALTGYAQLIDS	0801	ND	<b>114.75 (WB)</b> WTRALTGYA	ND	ND	ND
FWTRALTGYAQLIDS	0901	ND	<b>49.71 (SB)</b> WTRALTGYA	<b>44.5 (SB)</b> WTRALTGYA	1575.8 WTRALTGYA	508.0 WTRALTGYA
FWTRALTGYAQLIDS	1001	ND	<b>90.27 (WB)</b> WTRALTGYA	ND	ND	ND
LTGYAQLIDSEGDDT	1101	22	5316.28 YAQLIDSEG	4891.0 YAQLIDSEG	10335.7 YAQLIDSEG	2749.0 YAQLIDSEG
FWTRALTGYAQLIDS	1101	0	<b>129.36 (WB)</b> WTRALTGYA	<b>270.2 (WB)</b> TRALTGYAQ	506.2 WTRALTGYA	1727.0 TRALTGYAQ
WTRALTGYAQLIDSE	1201	ND	<b>130.28 (WB)</b> WTRALTGYA	ND	<b>76.9 (WB)</b> GYAQLIDSE	5793.0 ALTGYAQLI
FWTRALTGYAQLIDS	1201	ND	<b>73.92 (WB)</b> WTRALTGYA	ND	<b>226.0 (WB)</b> FWTRALTGY	1436.0 FWTRALTGY
FWTRALTGYAQLIDS	1301	ND	1301.10 ALTGYAQLI	ND	ND	ND
FWTRALTGYAQLIDS	1401	ND	1119.26 WTRALTGYA	ND	ND	ND
TRALTGYAQLIDSEG	1501	<b>26</b>	1920.39 ALTGYAQLI	2419.7 ALTGYAQLI	1164.6 ALTGYAQLI	2869.0 ALTGYAQLI
LTGYAQLIDSEGDDT	1501	4	6484.58 YAQLIDSEG	7948.3 LTGYAQLID	499550.7 LIDSEGDDT	8760.0 LTGYAQLID
FWTRALTGYAQLIDS	1501	4	<b>423.74 (WB)</b> WTRALTGYA	<b>404.7 (WB)</b> WTRALTGYA	1164.6 ALTGYAQLI	1725.0 TRALTGYAQ
FWTRALTGYAQLIDS	1601	ND	<b>244.06 (WB)</b> WTRALTGYA	ND	ND	ND

HLA-DQ	Allele molecule	SYFPEITHI	NetMHCIIpan 2.1	NetMHCII 2.2	IEDB	IEDB
Sequence	HLA-DQA1-DQB1	Score	Affinity nM	Affinity nM	arbpython (ARB) Affinity nM	SMM Affinity nM
WTRALTGYAQLIDSE	0101-0501 (DQ1(5))	ND	ND	932.5 ALTGYAQLI	6495.7 RALTGYAQL	3032.0 LTGYAQLID
FWTRALTGYAQLIDS	0102-0602 (DQ1(6))	ND	ND	<b>200.7 (WB)</b> TRALTGYAQ	<b>416.4 (WB)</b> TRALTGYAQ	875.0 TRALTGYAQ
WTRALTGYAQLIDSE	0102-0602 (DQ1(6))	ND	ND	<b>278.2 (WB)</b> TGQAQLIDS	<b>416.4 (WB)</b> TRALTGYAQ	982.0 TGQAQLIDS
WTRALTGYAQLIDSE	0301-0302 (DQ3(8))	ND	ND	791.3 TRALTGYAQ	1508.9 RALTGYAQL	2218.0 ALTGYAQLI
RALTGYAQLIDSEGD	0301-0302 (DQ3(8))	ND	ND	918.5 GYAQLIDSE	1508.9 RALTGYAQL	2038.0 GYAQLIDSE
WTRALTGYAQLIDSE	0401-0402 (DQ4)	ND	ND	720.1 LTGYAQLID	8839.3 TRALTGYAQ	1907.0 LTGYAQLID
TRALTGYAQLIDSEG	0401-0402 (DQ4)	ND	ND	839.6 GYAQLIDSE	6060.8 YAQLIDSEG	1823.0 GYAQLIDSE
LTGYAQLIDSEGDDT	0501-0201 (DQ2)	ND	ND	576.6 GYAQLIDSE	2693.9 GYAQLIDSE	<b>498.0 (WB)</b> GYAQLIDSE
WTRALTGYAQLIDSE	0501-0201 (DQ2)	ND	ND	<b>383.2 (WB)</b> GYAQLIDSE	2693.9 GYAQLIDSE	1259.0 RALTGYAQL
FWTRALTGYAQLIDS	0501-0301 (DQ3(7))	ND	ND	<b>31.6 (SB)</b> TGQAQLIDS	<b>268.7 (WB)</b> RALTGYAQL	<b>116.0 (WB)</b> ALTGYAQLI

<sup>a</sup> SYFPEITHI scores  $\geq 25$  are considered positive

Affinity nM: Strong binder (SB) = between 1 and 50 nM  
Weak binder (WB) = between 50 and 500 nM

Core amino acids sequences are indicated along with Affinity nM values