

## MHC Class-II Binding Peptide Prediction Results

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### INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Thu Feb 18 13:58:02 2010
Length of input sequence	232 amino acids
Number of nanomers from input sequence	224
Number of nanomers with <a href="#">obligatory P1 anchor residue</a>	57
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	23

ALLELE:  
DRB1\_0101

Threshold for 3 % with score:  
0.14

Highest Score achievable by any  
peptide: 6

Rank	Sequence	At Position	Score	% of Highest Score
1	FASAAAIIV	92	1.1000	18.33
2	LELATPYAL	9	0.9000	15.00
3	VMNNVAPPS	155	0.4100	6.83
4	LVMNNVAPP	154	0.3400	5.67
5	WRTAAFASA	87	0.1000	1.67
6	VRRQSRWRT	81	-0.0800	0
7	LLVMNNVAP	153	-0.2000	0
8	MWLLGGAKG	170	-0.3000	0
9	FTVEPGTGS	209	-0.4100	0
10	VRETMAVVS	50	-0.6000	0
11	MAVVSAAAT	54	-0.7500	0
12	LGAGTATVV	136	-0.8100	0
13	LGGAKGPRS	173	-0.8300	0
14	MNNVAPPSR	156	-0.8800	0

15	FELLELATP	6	-1.1000	0
16	VRAVRETMA	47	-1.1600	0
17	LGASTALAF	201	-1.3000	0
18	VRTVSRPLG	129	-1.3800	0
19	LLELATPYA	8	-1.4300	0
20	VAAAPSPVA	32	-1.5300	0
21	LTDLGASTA	198	-1.6000	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LELATPYAL	9	1.9000	31.67
2	VMNNVAPPS	155	1.4100	23.50
3	LVMMNVAPP	154	1.3400	22.33
4	FASAAAIIV	92	1.1000	18.33
5	VRRQSRWRT	81	0.9200	15.33
6	LLVMNNVAP	153	0.8000	13.33
7	MWLLGGAKG	170	0.7000	11.67
8	VRETMAVVS	50	0.4000	6.67
9	MAVVSAAAT	54	0.2500	4.17
10	LGAGTATVV	136	0.1900	3.17
11	LGGAKGPRS	173	0.1700	2.83
12	MNNVAPPSR	156	0.1200	2.00
13	VRAVRETMA	47	-0.1600	0
14	LGASTALAF	201	-0.3000	0
15	VRTVSRPLG	129	-0.3800	0
16	FTVEPGTGS	209	-0.4100	0
17	LLELATPYA	8	-0.4300	0
18	VAAAPSPVA	32	-0.5300	0
19	LTDLGASTA	198	-0.6000	0
20	VVFSRDRNT	143	-0.6100	0
21	VVSAATTAE	56	-0.7100	0
22	VYQMWLLGG	167	-0.8000	0

ALLELE:	Threshold for 3 % with score:	Highest Score achievable by any
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DRB1\_0301

2.96

peptide: 9.5

Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	4.6000	48.42
2	VRTVSRPLG	129	4.3000	45.26
3	VMNNVAPPS	155	3.6000	37.89
4	LLGGAKGPR	172	3.6000	37.89
5	MNNVAPPSR	156	3.0000	31.58
6	VRRQSRWRT	81	2.8000	29.47
7	VVSAATTAE	56	2.7000	28.42
8	MGTAAVTPS	185	2.7000	28.42
9	LGVLTRPSP	107	2.4000	25.26
10	VSDDERADI	20	2.3000	24.21
11	LGASTALAF	201	2.3000	24.21
12	ILDATKPEV	73	2.0000	21.05
13	LGGAKGPRS	173	1.8000	18.95
14	VTPSTTATL	190	1.7600	18.53
15	VYQMWLLGG	167	1.7000	17.89
16	LELATPYAL	9	1.5100	15.89
17	VFSRDRNTG	144	1.3100	13.79
18	LLELATPYA	8	1.3000	13.68
19	VRETMAVVS	50	1.3000	13.68
20	LRTAILDAT	69	1.3000	13.68
21	LGAGTATVV	136	1.2000	12.63
22	VGLGAFGLG	100	1.1000	11.58
23	FSRDRNTGL	145	0.9600	10.11

ALLELE:  
DRB1\_0305Threshold for 3 % with score:  
1.7Highest Score achievable by any  
peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	2.6000	28.57
2	VMNNVAPPS	155	2.2000	24.18
3	VRTVSRPLG	129	1.9000	20.88
4	YQMWLLGGA	168	1.9000	20.88
5	MGTAAVTPS	185	1.3000	14.29
6	VRRQSRWRT	81	1.1000	12.09
7	LLGGAKGPR	172	1.1000	12.09

8	FSRDRNTGL	145	1.0000	10.99
9	WRTAAFASA	87	0.8000	8.79
10	FGLGVLTRP	105	0.8000	8.79
11	YALNAVSD	15	0.7700	8.46
12	MNNVAPPSR	156	0.5000	5.49
13	VSDDERADI	20	0.4000	4.40
14	LGVLTRPSP	107	0.4000	4.40
15	LGGAKGPRS	173	0.4000	4.40
16	LLELATPYA	8	0.3000	3.30
17	VVSAATTAE	56	0.3000	3.30
18	WLLGGAKGP	171	0.3000	3.30
19	VRETMAVVS	50	-0.1000	0
20	FASAAAIIV	92	-0.1000	0

ALLELE: DRB1_0306	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.6000	40.91
2	MGTAAVTPS	185	2.3000	26.14
3	VMNNVAPPS	155	1.8000	20.45
4	VRTVSRPLG	129	1.5000	17.05
5	VSDDERADI	20	1.4000	15.91
6	VVSAATTAE	56	1.3000	14.77
7	VRRQSRWRT	81	1.3000	14.77
8	LRTAILDAT	69	0.9000	10.23
9	LGASTALAF	201	0.9000	10.23
10	VYQMWLLGG	167	0.8000	9.09
11	VTPSTTATL	190	0.8000	9.09
12	VRETMAVVS	50	0.7800	8.86
13	VRAVRETMA	47	0.7000	7.95
14	LLGGAKGPR	172	0.7000	7.95
15	VFSRDRNTG	144	0.6000	6.82
16	VEPGTGSPQ	211	0.5000	5.68
17	LGAGTATVV	136	0.2000	2.27
18	MNNVAPPSR	156	0.1000	1.14
19	LLELATPYA	8	-0.1000	0

ALLELE: DRB1_0307	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.6000	40.91
2	MGTAAVTPS	185	2.3000	26.14
3	VMNNVAPPS	155	1.8000	20.45
4	VRTVSRPLG	129	1.5000	17.05
5	VSDDERADI	20	1.4000	15.91
6	VVSAATTAE	56	1.3000	14.77
7	VRRQSRWRT	81	1.3000	14.77
8	LRTAILDAT	69	0.9000	10.23
9	LGASTALAF	201	0.9000	10.23
10	VYQMWLLGG	167	0.8000	9.09
11	VTPSTTATL	190	0.8000	9.09
12	VRETMAVVS	50	0.7800	8.86
13	VRAVRETMA	47	0.7000	7.95
14	LLGGAKGPR	172	0.7000	7.95
15	VFSRDRNTG	144	0.6000	6.82
16	VEPGTGSPQ	211	0.5000	5.68
17	LGAGTATVV	136	0.2000	2.27
18	MNNVAPPSR	156	0.1000	1.14
19	LLELATPYA	8	-0.1000	0

ALLELE: DRB1_0308	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.6000	40.91
2	MGTAAVTPS	185	2.3000	26.14
3	VMNNVAPPS	155	1.8000	20.45
4	VRTVSRPLG	129	1.5000	17.05
5	VSDDERADI	20	1.4000	15.91
6	VVSAATTAE	56	1.3000	14.77
7	VRRQSRWRT	81	1.3000	14.77
8	LRTAILDAT	69	0.9000	10.23
9	LGASTALAF	201	0.9000	10.23

10	VYQMWLLGG	167	0.8000	9.09
11	VTPSTTATL	190	0.8000	9.09
12	VRETMAVVS	50	0.7800	8.86
13	VRAVRETMA	47	0.7000	7.95
14	LLGGAKGPR	172	0.7000	7.95
15	VFSRDRNTG	144	0.6000	6.82
16	VEPGTGSPQ	211	0.5000	5.68
17	LGAGTATVV	136	0.2000	2.27
18	MNNVAPPSR	156	0.1000	1.14
19	LLELATPYA	8	-0.1000	0

ALLELE: DRB1_0309	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 9.5
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.6000	37.89
2	VRTVSRPLG	129	3.3000	34.74
3	VMNNVAPPS	155	2.6000	27.37
4	LLGGAKGPR	172	2.6000	27.37
5	MNNVAPPSR	156	2.0000	21.05
6	FSRDRNTGL	145	1.9600	20.63
7	YQMWLLGGA	168	1.9000	20.00
8	YALNAVSDD	15	1.8700	19.68
9	VRRQSRWRT	81	1.8000	18.95
10	FGLGVLTRP	105	1.8000	18.95
11	VVSAATTAE	56	1.7000	17.89
12	MGTAAVTPS	185	1.7000	17.89
13	LGVLTRPSP	107	1.4000	14.74
14	VSDDERADI	20	1.3000	13.68
15	WLLGGAKGP	171	1.3000	13.68
16	LGASTALAF	201	1.3000	13.68
17	FELLELATP	6	1.0000	10.53
18	ILDATKPEV	73	1.0000	10.53
19	FASAAAIAV	92	0.9000	9.47
20	WRTAAFASA	87	0.8000	8.42
21	LGGAKGPRS	173	0.8000	8.42
22	VTPSTTATL	190	0.7600	8.00
23	VYQMWLLGG	167	0.7000	7.37

ALLELE: DRB1_0311	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.6000	40.91
2	MGTAAVTPS	185	2.3000	26.14
3	VMNNVAPPS	155	1.8000	20.45
4	VRTVSRPLG	129	1.5000	17.05
5	VSDDERADI	20	1.4000	15.91
6	VVSAATTAE	56	1.3000	14.77
7	VRRQSRWRT	81	1.3000	14.77
8	LRTAILDAT	69	0.9000	10.23
9	LGASTALAF	201	0.9000	10.23
10	VYQMWLLGG	167	0.8000	9.09
11	VTPSTTATL	190	0.8000	9.09
12	VRETMAVVS	50	0.7800	8.86
13	VRAVRETMA	47	0.7000	7.95
14	LLGGAKGPR	172	0.7000	7.95
15	VFSRDRNTG	144	0.6000	6.82
16	VEPGTGSPQ	211	0.5000	5.68
17	LGAGTATVV	136	0.2000	2.27
18	MNNVAPPSR	156	0.1000	1.14
19	LLELATPYA	8	-0.1000	0

ALLELE: DRB1_0401	Threshold for 3 % with score: 1.48	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.0000	34.88
2	FSRDRNTGL	145	2.0000	23.26
3	VMNNVAPPS	155	1.5000	17.44
4	VRETMAVVS	50	1.4800	17.21
5	LLVMNNVAP	153	1.4800	17.21
6	VVSAATTAE	56	1.4000	16.28
7	WRTAAFASA	87	1.1000	12.79
8	FTVEPGTGS	209	1.1000	12.79

9	MGTAAVTPS	185	1.0000	11.63
10	VTPSTTATL	190	1.0000	11.63
11	YALNAVSDDD	15	0.9000	10.47
12	LLELATPYA	8	0.8000	9.30
13	FASAAAIIV	92	-0.4200	0
14	FELLELATP	6	-0.5000	0
15	VYQMWLLGG	167	-0.6000	0
16	VAAAPSPVA	32	-0.7000	0
17	VAAAFNDEV	39	-0.7000	0
18	VSAATTAEP	57	-0.7000	0
19	VVFSRDRNT	143	-0.8000	0
20	YQMWLLGGA	168	-1.0000	0
21	WLLGGAKGP	171	-1.2000	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	2.7000	28.13
2	VVSAATTAE	56	2.6000	27.08
3	LLVMNNVAP	153	2.3000	23.96
4	MGTAAVTPS	185	2.2000	22.92
5	VRETMAVVS	50	1.4000	14.58
6	VVFSRDRNT	143	1.3000	13.54
7	LELATPYAL	9	1.0000	10.42
8	VMNNVAPPS	155	0.9000	9.38
9	VLTRPSPPP	109	0.7000	7.29
10	LTAPDVRTV	124	0.6000	6.25
11	VYQMWLLGG	167	0.4000	4.17
12	VSAATTAEP	57	0.3000	3.12
13	VRRQSRWRT	81	0.3000	3.12
14	VTPSTTATL	190	0.2000	2.08
15	LLELATPYA	8	0.1000	1.04
16	WRTAAFASA	87	0.1000	1.04
17	LATPYALNA	11	-0.3000	0
18	LGASTALAF	201	-0.5000	0
19	VRAVRETMA	47	-0.8000	0
20	LGAGTATVV	136	-0.8000	0



ALLELE: DRB1_0404	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LLVMNNVAP	153	3.2000	36.36
2	VVSAATTAE	56	2.9000	32.95
3	MGTAAVTPS	185	2.5000	28.41
4	LVMNNVAPP	154	2.4000	27.27
5	LLELATPYA	8	1.7000	19.32
6	VYQMWLLGG	167	0.9000	10.23
7	VRAVRETMA	47	0.7000	7.95
8	VRETMAVVS	50	0.7000	7.95
9	VMNNVAPPS	155	0.6000	6.82
10	VTPSTTATL	190	0.5000	5.68
11	VSAATTAEP	57	0.3000	3.41
12	LTDLGASTA	198	0.2000	2.27
13	WRTAAFASA	87	0.1000	1.14
14	LELATPYAL	9	-0.1000	0
15	MAVVSAAAT	54	-0.2000	0
16	MNNVAPPSR	156	-0.2000	0
17	VAAAFNDEV	39	-0.6000	0
18	MWLLGGAKG	170	-0.6000	0
19	YQMWLLGGA	168	-0.7500	0
20	LGASTALAF	201	-0.9000	0
21	LATPYALNA	11	-1.0000	0

ALLELE: DRB1_0405	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVSAATTAE	56	4.9000	52.13
2	YALNAVSD	15	2.7000	28.72
3	LLVMNNVAP	153	2.6000	27.66
4	LVMNNVAPP	154	1.8000	19.15
5	MGTAAVTPS	185	1.5000	15.96
6	VYQMWLLGG	167	1.2000	12.77

7	WRTAAFASA	87	1.1000	11.70
8	FSRDRNTGL	145	1.0000	10.64
9	LLELATPYA	8	0.7000	7.45
10	VTPSTTATL	190	0.5000	5.32
11	YQMWLLGGA	168	0.2500	2.66
12	FELLELATP	6	0.1000	1.06
13	LELATPYAL	9	-0.1000	0
14	FASAAAIIV	92	-0.1200	0
15	VRAVRETMA	47	-0.3000	0
16	VRETMAVVS	50	-0.3000	0
17	MAVVSAATT	54	-0.3000	0
18	VSAATTAEP	57	-0.3000	0
19	MWLLGGAKG	170	-0.3000	0
20	VMNNVAPPS	155	-0.4000	0
21	LTDLGASTA	198	-0.8000	0
22	VAAAPSPVA	32	-1.0000	0

ALLELE: DRB1_0408	Threshold for 3 % with score: 1.2	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LLVMNNVAP	153	2.2000	25.00
2	VVSAATTAE	56	1.9000	21.59
3	MGTAAVTPS	185	1.5000	17.05
4	LVMNNVAPP	154	1.4000	15.91
5	WRTAAFASA	87	1.1000	12.50
6	LLELATPYA	8	0.7000	7.95
7	YQMWLLGGA	168	0.2500	2.84
8	VYQMWLLGG	167	-0.1000	0
9	FELLELATP	6	-0.3000	0
10	VRAVRETMA	47	-0.3000	0
11	VRETMAVVS	50	-0.3000	0
12	VMNNVAPPS	155	-0.4000	0
13	FASAAAIIV	92	-0.4200	0
14	VTPSTTATL	190	-0.5000	0
15	VSAATTAEP	57	-0.7000	0
16	LTDLGASTA	198	-0.8000	0
17	VAAAPSPVA	32	-1.0000	0

18	FTVEPGTGS	209	-1.0000	0
19	LELATPYAL	9	-1.1000	0
20	MAVVSAAAT	54	-1.2000	0

ALLELE: DRB1_0410	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVSAATTAE	56	5.9000	62.77
2	LLVMNNVAP	153	3.6000	38.30
3	LVMNNVAPP	154	2.8000	29.79
4	MGTAAVTPS	185	2.5000	26.60
5	VYQMWLLGG	167	2.2000	23.40
6	LLELATPYA	8	1.7000	18.09
7	YALNAVSDDD	15	1.7000	18.09
8	VTPSTTATL	190	1.5000	15.96
9	LELATPYAL	9	0.9000	9.57
10	VRAVRETMA	47	0.7000	7.45
11	VRETMAVVS	50	0.7000	7.45
12	MAVVSAAAT	54	0.7000	7.45
13	VSAATTAEP	57	0.7000	7.45
14	MWLLGGAKG	170	0.7000	7.45
15	VMNNVAPPS	155	0.6000	6.38
16	LTDLGASTA	198	0.2000	2.13
17	WRTAAFASA	87	0.1000	1.06
18	VVFSRDRNT	143	-0.1000	0
19	MNNVAPPSR	156	-0.2000	0

ALLELE: DRB1_0421	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	4.0000	44.44
2	FSRDRNTGL	145	2.9600	32.89
3	VVSAATTAE	56	2.8000	31.11
4	LLVMNNVAP	153	2.4800	27.56

5	YALNAVSD	15	2.0000	22.22
6	VTPSTTATL	190	1.9600	21.78
7	VMNNVAPPS	155	1.9000	21.11
8	LGASTALAF	201	1.9000	21.11
9	VRETMAVVS	50	1.8800	20.89
10	FTVEPGTGS	209	1.5000	16.67
11	MGTAAVTPS	185	1.4000	15.56
12	WRTAAFASA	87	1.1000	12.22
13	LLELATPYA	8	0.8000	8.89
14	VYQMWLLGG	167	0.8000	8.89
15	FASAAAIIV	92	0.5800	6.44
16	FELLELATP	6	0.5000	5.56
17	VAAAFNDEV	39	0.3000	3.33
18	VSAATTAEP	57	0.3000	3.33
19	VVFSRDRNT	143	-0.1000	0
20	WLLGGAKGP	171	-0.2000	0
21	MWLLGGAKG	170	-0.4000	0
22	VAAAPSPVA	32	-0.7000	0

ALLELE: DRB1_0423	Threshold for 3 % with score: 1.68	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LLVMNNVAP	153	3.2000	36.36
2	VVSAATTAE	56	2.9000	32.95
3	MGTAAVTPS	185	2.5000	28.41
4	LVMNNVAPP	154	2.4000	27.27
5	LLELATPYA	8	1.7000	19.32
6	VYQMWLLGG	167	0.9000	10.23
7	VRAVRETMA	47	0.7000	7.95
8	VRETMAVVS	50	0.7000	7.95
9	VMNNVAPPS	155	0.6000	6.82
10	VTPSTTATL	190	0.5000	5.68
11	VSAATTAEP	57	0.3000	3.41
12	LTDLGASTA	198	0.2000	2.27
13	WRTAAFASA	87	0.1000	1.14
14	LELATPYAL	9	-0.1000	0
15	MAVVSAAAT	54	-0.2000	0

16	MNNVAPPSR	156	-0.2000	0
17	VAAAFNDEV	39	-0.6000	0
18	MWLLGGAKG	170	-0.6000	0
19	YQMWLLGGA	168	-0.7500	0
20	LGASTALAF	201	-0.9000	0
21	LATPYALNA	11	-1.0000	0

ALLELE: DRB1_0426	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.0000	34.88
2	FSRDRNTGL	145	2.0000	23.26
3	VMNNVAPPS	155	1.5000	17.44
4	VRETMAVVS	50	1.4800	17.21
5	LLVMNNVAP	153	1.4800	17.21
6	VVSAATTAE	56	1.4000	16.28
7	WRTAAFASA	87	1.1000	12.79
8	FTVEPGTGS	209	1.1000	12.79
9	MGTAAVTPS	185	1.0000	11.63
10	VTPSTTATL	190	1.0000	11.63
11	YALNAVSD	15	0.9000	10.47
12	LLELATPYA	8	0.8000	9.30
13	FASAAAIIV	92	-0.4200	0
14	FELLELATP	6	-0.5000	0
15	VYQMWLLGG	167	-0.6000	0
16	VAAAPSPVA	32	-0.7000	0
17	VAAAFNDEV	39	-0.7000	0
18	VSAATTAEP	57	-0.7000	0
19	VVFSRDRNT	143	-0.8000	0
20	YQMWLLGGA	168	-1.0000	0
21	WLLGGAKGP	171	-1.2000	0

ALLELE: DRB1_0701	Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LGASTALAF	201	5.3000	45.69
2	LELATPYAL	9	4.7000	40.52
3	FASAAAIIV	92	4.6000	39.66
4	VTPSTTATL	190	4.1200	35.52
5	VRETMAVVS	50	2.7000	23.28
6	FSRDRNTGL	145	2.5000	21.55
7	LGAFGLGVL	102	2.2000	18.97
8	VVFSRDRNT	143	2.0000	17.24
9	VVSAATTAE	56	1.8200	15.69
10	WRTAAFASA	87	1.4000	12.07
11	LGAGTATVV	136	1.3000	11.21
12	VRRQSRWRT	81	1.1000	9.48
13	MTEHTDFEL	0	0.9000	7.76
14	LVMNNVAPP	154	0.9000	7.76
15	MAVVAATT	54	0.8000	6.90
16	WLLGGAKGP	171	0.8000	6.90
17	LTAPDVRTV	124	0.6000	5.17
18	YQMWLLGGA	168	0.6000	5.17
19	VRAVRETMA	47	0.5000	4.31
20	LLVMNNVAP	153	0.5000	4.31
21	VRTVSRPLG	129	0.2000	1.72
22	VYQMWLLGG	167	0.2000	1.72
23	MGTAAVTPS	185	0.2000	1.72

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LGASTALAF	201	5.3000	45.69
2	LELATPYAL	9	4.7000	40.52
3	FASAAAIIV	92	4.6000	39.66
4	VTPSTTATL	190	4.1200	35.52
5	VRETMAVVS	50	2.7000	23.28
6	FSRDRNTGL	145	2.5000	21.55
7	LGAFGLGVL	102	2.2000	18.97
8	VVFSRDRNT	143	2.0000	17.24
9	VVSAATTAE	56	1.8200	15.69

10	WRTAAFASA	87	1.4000	12.07
11	LGAGTATVV	136	1.3000	11.21
12	VRRQSRWRT	81	1.1000	9.48
13	MTEHTDFEL	0	0.9000	7.76
14	LVMNNVAPP	154	0.9000	7.76
15	MAVSAATT	54	0.8000	6.90
16	WLLGGAKGP	171	0.8000	6.90
17	LTAPDVRTV	124	0.6000	5.17
18	YQMWLLGGA	168	0.6000	5.17
19	VRAVRETMA	47	0.5000	4.31
20	LLVMNNVAP	153	0.5000	4.31
21	VRTVSRPLG	129	0.2000	1.72
22	VYQMWLLGG	167	0.2000	1.72
23	MGTAAVTPS	185	0.2000	1.72

ALLELE: DRB1_0801	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	2.8000	32.56
2	VFSRDRNTG	144	2.3000	26.74
3	YQMWLLGGA	168	2.3000	26.74
4	YALNAVSDDD	15	1.9000	22.09
5	VRTVSRPLG	129	1.6000	18.60
6	VYQMWLLGG	167	1.5000	17.44
7	FELLELATP	6	1.1000	12.79
8	VVSAATTAE	56	1.0000	11.63
9	WRTAAFASA	87	0.8000	9.30
10	VRRQSRWRT	81	0.4000	4.65
11	MWLLGGAKG	170	0.2000	2.33
12	VLTRPSPPP	109	0.1000	1.16
13	VMNNVAPPS	155	0.1000	1.16
14	IDRRVAAAP	28	-0.2000	0
15	LGAFGLGVL	102	-0.3000	0
16	LGVLTRPSP	107	-0.4000	0
17	LELATPYAL	9	-0.5000	0
18	MAVSAATT	54	-0.5000	0
19	LLVMNNVAP	153	-0.7000	0

20	WLLGGAKGP	171	-0.7000	0
21	LLELATPYA	8	-0.9000	0
22	VTPSTTATL	190	-0.9000	0

ALLELE: DRB1_0802	Threshold for 3 % with score: 1.0	Highest Score achievable by any peptide: 8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	2.4000	30.00
2	YQMWLLGGA	168	2.3000	28.75
3	VFSRDRNTG	144	1.0000	12.50
4	WRTAAFASA	87	0.8000	10.00
5	FELLELATP	6	0.7000	8.75
6	VRTVSRPLG	129	0.3000	3.75
7	VYQMWLLGG	167	0.2000	2.50
8	VMNNVAPPS	155	0.1000	1.25
9	VLTRPSPPP	109	-0.3000	0
10	VRRQSRWRT	81	-0.5000	0
11	IDRRVA AAP	28	-0.6000	0
12	YALNAVSDD	15	-0.8000	0
13	LGVLTRPSP	107	-0.8000	0
14	LLELATPYA	8	-0.9000	0
15	LLGGAKGPR	172	-1.0000	0
16	MGTA AVTPS	185	-1.0000	0
17	LLVMNNVAP	153	-1.1000	0
18	MNNVAPPSR	156	-1.1000	0
19	MWLLGGAKG	170	-1.1000	0
20	WLLGGAKGP	171	-1.1000	0
21	FASAAAIAV	92	-1.3000	0
22	LGAFGLGVL	102	-1.3000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.4000	42.50



2	VFSRDRNTG	144	2.0000	25.00
3	VRTVSRPLG	129	1.3000	16.25
4	YQMWLLGGA	168	1.3000	16.25
5	VYQMWLLGG	167	1.2000	15.00
6	VMNNVAPPS	155	1.1000	13.75
7	VLTRPSPPP	109	0.7000	8.75
8	VRRQSRWRT	81	0.5000	6.25
9	IDRRVAAAP	28	0.4000	5.00
10	LGVLTRPSP	107	0.2000	2.50
11	LLELATPYA	8	0.1000	1.25
12	LLVMNNVAP	153	-0.1000	0
13	MNNVAPPSR	156	-0.1000	0
14	MWLLGGAKG	170	-0.1000	0
15	WRTAAFASA	87	-0.2000	0
16	FELLELATP	6	-0.3000	0
17	LGAFGLGVL	102	-0.3000	0
18	VRETMAVVS	50	-0.4000	0
19	MAVVSAAAT	54	-0.4000	0
20	LELATPYAL	9	-0.5000	0

ALLELE: DRB1_0806	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.8000	44.19
2	VFSRDRNTG	144	3.3000	38.37
3	VRTVSRPLG	129	2.6000	30.23
4	VYQMWLLGG	167	2.5000	29.07
5	VVSAATTAE	56	2.0000	23.26
6	VRRQSRWRT	81	1.4000	16.28
7	YQMWLLGGA	168	1.3000	15.12
8	MWLLGGAKG	170	1.2000	13.95
9	VLTRPSPPP	109	1.1000	12.79
10	VMNNVAPPS	155	1.1000	12.79
11	YALNAVSSD	15	0.9000	10.47
12	IDRRVAAAP	28	0.8000	9.30
13	LGAFGLGVL	102	0.7000	8.14
14	LGVLTRPSP	107	0.6000	6.98

15	LELATPYAL	9	0.5000	5.81
16	MAVSAATT	54	0.5000	5.81
17	LLVMNNVAP	153	0.3000	3.49
18	FELLELATP	6	0.1000	1.16
19	LLELATPYA	8	0.1000	1.16
20	VTPSTATL	190	0.1000	1.16

ALLELE: DRB1_0813	Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	VFSRDRNTG	144	3.0000	34.48
2	LVMNNVAPP	154	2.4000	27.59
3	MGTAAVTPS	185	1.8000	20.69
4	YQMWLLGGA	168	1.6000	18.39
5	YALNAVSDDD	15	1.0000	11.49
6	VVSAATTAE	56	0.8000	9.20
7	WRTAAFASA	87	0.8000	9.20
8	VYQMWLLGG	167	0.8000	9.20
9	FELLELATP	6	0.7000	8.05
10	VRAVRETMA	47	0.5000	5.75
11	VRTVSRPLG	129	0.5000	5.75
12	VMNNVAPPS	155	0.3000	3.45
13	VLTRPSPPP	109	-0.1000	0
14	LLVMNNVAP	153	-0.1000	0
15	FTVEPGTGS	209	-0.1000	0
16	FGLGVLTRP	105	-0.2000	0
17	VRETMAVVS	50	-0.4000	0
18	FASAAAIIV	92	-0.4200	0
19	LELATPYAL	9	-0.6000	0
20	IDRRVAAAP	28	-0.6000	0
21	LGVLTRPSP	107	-0.6000	0

ALLELE: DRB1_0817	Threshold for 3 % with score: 2.8	Highest Score achievable by any peptide: 10.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	VYQMWLLGG	167	3.3000	32.67
2	LVMNNVAPP	154	2.8000	27.72
3	VRTVSRPLG	129	2.7500	27.23
4	VFSRDRNTG	144	2.6000	25.74
5	YQMWLLGGA	168	2.4000	23.76
6	VVSAATTAE	56	2.1000	20.79
7	YALNAVSD	15	1.9000	18.81
8	VLTRPSPPP	109	1.2500	12.38
9	VMNNVAPPS	155	1.2500	12.38
10	VRRQSRWRT	81	1.2000	11.88
11	FELLELATP	6	1.1000	10.89
12	WRTAAFASA	87	0.8000	7.92
13	LGVLTRPSP	107	0.7500	7.43
14	FASAAAIIV	92	0.6000	5.94
15	LLELATPYA	8	0.2500	2.48
16	LELATPYAL	9	0.2000	1.98
17	MWLLGGAKG	170	0.2000	1.98
18	MGTAAVTPS	185	0.1000	0.99
19	MNNVAPPSR	156	0.0500	0.50
20	WLLGGAKGP	171	-0.1000	0
21	LGASTALAF	201	-0.1000	0
22	IDRRVAAAP	28	-0.2000	0

ALLELE: DRB1_1101	Threshold for 3 % with score: 1.1	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	2.4000	28.92
2	YQMWLLGGA	168	2.3000	27.71
3	VYQMWLLGG	167	1.6000	19.28
4	VRTVSRPLG	129	1.5500	18.67
5	VMNNVAPPS	155	1.2500	15.06
6	FELLELATP	6	1.1000	13.25
7	VRRQSRWRT	81	0.9000	10.84
8	WRTAAFASA	87	0.8000	9.64
9	LGVLTRPSP	107	0.7500	9.04
10	LLELATPYA	8	0.6500	7.83

11	FASAAAIIV	92	0.3000	3.61
12	MNNVAPPSR	156	0.1500	1.81
13	MGTAAVTPS	185	0.1000	1.20
14	LGGAKGPRS	173	-0.3500	0
15	VRETMAVVS	50	-0.5000	0
16	MWLLGGAKG	170	-0.7000	0
17	LGASTALAF	201	-0.7000	0
18	ILDATKPEV	73	-0.7500	0
19	LELATPYAL	9	-0.8000	0
20	YALNAVSD	15	-0.8000	0
21	VVSAATTAE	56	-0.9000	0
22	LLVMNNVAP	153	-1.0000	0

ALLELE: DRB1_1102	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	VRRQSRWRT	81	3.7000	44.05
2	LVMNNVAPP	154	3.5000	41.67
3	VMNNVAPPS	155	1.9000	22.62
4	MGTAAVTPS	185	1.5000	17.86
5	VFSRDRNTG	144	1.3000	15.48
6	VYQMWLLGG	167	1.3000	15.48
7	YQMWLLGGA	168	1.0000	11.90
8	VRTVSRPLG	129	0.8000	9.52
9	LGVLTRPSP	107	0.6000	7.14
10	LLELATPYA	8	0.5000	5.95
11	VRETMAVVS	50	0.5000	5.95
12	VVSAATTAE	56	0.5000	5.95
13	LELATPYAL	9	0.4000	4.76
14	LLVMNNVAP	153	0.3000	3.57
15	LTAPDVRTV	124	0.2000	2.38
16	LGGAKGPRS	173	0.2000	2.38
17	VVFSRDRNT	143	-0.1000	0
18	ILDATKPEV	73	-0.2000	0
19	WRTAAFASA	87	-0.2000	0
20	LRTAILDAT	69	-0.3000	0
21	MWLLGGAKG	170	-0.4000	0

22	VTPSTATL	190	-0.5000	0
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ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.4000	40.96
2	VYQMWLLGG	167	2.6000	31.33
3	VRTVSRPLG	129	2.5500	30.72
4	VMNNVAPPS	155	2.2500	27.11
5	VRRQSRWRT	81	1.9000	22.89
6	LGVLTRPSP	107	1.7500	21.08
7	LLELATPYA	8	1.6500	19.88
8	YQMWLLGGA	168	1.3000	15.66
9	MNNVAPPSR	156	1.1500	13.86
10	MGTAAVTPS	185	1.1000	13.25
11	LGGAKGPRS	173	0.6500	7.83
12	VRETMAVVS	50	0.5000	6.02
13	MWLLGGAKG	170	0.3000	3.61
14	LGASTALAF	201	0.3000	3.61
15	ILDATKPEV	73	0.2500	3.01
16	LELATPYAL	9	0.2000	2.41
17	FELLELATP	6	0.1000	1.20
18	VVSAATTAE	56	0.1000	1.20
19	VRAVRETMA	47	-0.1000	0
20	VAAAPSPVA	32	-0.1500	0
21	LATPYALNA	11	-0.2000	0

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.4000	40.96
2	VYQMWLLGG	167	2.6000	31.33
3	VRTVSRPLG	129	2.5500	30.72
4	VMNNVAPPS	155	2.2500	27.11

5	VRRQSRWRT	81	1.9000	22.89
6	LGVLTRPSP	107	1.7500	21.08
7	LLELATPYA	8	1.6500	19.88
8	YQMWLLGGA	168	1.3000	15.66
9	MNNVAPPSR	156	1.1500	13.86
10	MGTAAVTPS	185	1.1000	13.25
11	LGGAKGPRS	173	0.6500	7.83
12	VRETMAVVS	50	0.5000	6.02
13	MWLLGGAKG	170	0.3000	3.61
14	LGASTALAF	201	0.3000	3.61
15	ILDATKPEV	73	0.2500	3.01
16	LELATPYAL	9	0.2000	2.41
17	FELLELATP	6	0.1000	1.20
18	VVSAATTAE	56	0.1000	1.20
19	VRAVRETMA	47	-0.1000	0
20	VAAAPSPVA	32	-0.1500	0
21	LATPYALNA	11	-0.2000	0

ALLELE:  
DRB1\_1107

Threshold for 3 % with score:  
2.1

Highest Score achievable by any  
peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.6000	39.56
2	VMNNVAPPS	155	3.2000	35.16
3	VRTVSRPLG	129	2.9000	31.87
4	MGTAAVTPS	185	2.3000	25.27
5	VRRQSRWRT	81	2.1000	23.08
6	LLGGAKGPR	172	2.1000	23.08
7	MNNVAPPSR	156	1.5000	16.48
8	VSDDERADI	20	1.4000	15.38
9	LGVLTRPSP	107	1.4000	15.38
10	LGGAKGPRS	173	1.4000	15.38
11	LLELATPYA	8	1.3000	14.29
12	VVSAATTAE	56	1.3000	14.29
13	ILDATKPEV	73	1.0000	10.99
14	VRETMAVVS	50	0.9000	9.89
15	YQMWLLGGA	168	0.9000	9.89
16	VTPSTTATL	190	0.8000	8.79

17	VEPGTGSPQ	211	0.7700	8.46
18	VRAVRETMA	47	0.7000	7.69
19	VAAAPSPVA	32	0.6000	6.59
20	LRTAILDAT	69	0.6000	6.59
21	LELATPYAL	9	0.5500	6.04
22	LGASTALAF	201	0.4000	4.40
23	VYQMWLLGG	167	0.3000	3.30

ALLELE: DRB1_1114	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	VRRQSRWRT	81	2.7000	32.14
2	LVMNNVAPP	154	2.5000	29.76
3	YQMWLLGGA	168	2.0000	23.81
4	VMNNVAPPS	155	0.9000	10.71
5	WRTAAFASA	87	0.8000	9.52
6	MGTAAVTPS	185	0.5000	5.95
7	FELLELATP	6	0.4000	4.76
8	VFSRDRNTG	144	0.3000	3.57
9	VYQMWLLGG	167	0.3000	3.57
10	VRTVSRPLG	129	-0.2000	0
11	YALNAVSDD	15	-0.3000	0
12	LGVLTRPSP	107	-0.4000	0
13	LLELATPYA	8	-0.5000	0
14	VRETMAVVS	50	-0.5000	0
15	VVSAATTAE	56	-0.5000	0
16	LELATPYAL	9	-0.6000	0
17	LLVMNNVAP	153	-0.7000	0
18	LTAPDVRTV	124	-0.8000	0
19	WLLGGAKGP	171	-0.8000	0
20	LGGAKGPRS	173	-0.8000	0
21	FASAAAIIV	92	-1.0000	0
22	VVFSRDRNT	143	-1.1000	0

ALLELE:	Threshold for 3 % with score:	Highest Score achievable by any
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DRB1\_1120

2.1

peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.5000	39.77
2	VRRQSRWRT	81	3.4000	38.64
3	YQMWLLGGA	168	2.0000	22.73
4	VFSRDRNTG	144	1.7000	19.32
5	VYQMWLLGG	167	1.7000	19.32
6	FELLELATP	6	1.4000	15.91
7	VMNNVAPPS	155	1.3000	14.77
8	VRTVSRPLG	129	1.2000	13.64
9	VVSAATTAE	56	0.9000	10.23
10	MGTAAVTPS	185	0.9000	10.23
11	YALNAVSDDD	15	0.8000	9.09
12	WRTAAFASA	87	0.8000	9.09
13	LGVLTRPSP	107	0.6000	6.82
14	LELATPYAL	9	0.3600	4.09
15	LLVMNNVAP	153	0.3000	3.41
16	LTAPDVRTV	124	0.2000	2.27
17	WLLGGAKGP	171	0.2000	2.27
18	LGASTALAF	201	0.2000	2.27
19	FNDEVRAVR	43	-0.1000	0
20	VRETMAVVS	50	-0.1000	0

ALLELE:  
DRB1\_1121Threshold for 3 % with score:  
1.8Highest Score achievable by any  
peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VRRQSRWRT	81	3.7000	44.05
2	LVMNNVAPP	154	3.5000	41.67
3	VMNNVAPPS	155	1.9000	22.62
4	MGTAAVTPS	185	1.5000	17.86
5	VFSRDRNTG	144	1.3000	15.48
6	VYQMWLLGG	167	1.3000	15.48
7	YQMWLLGGA	168	1.0000	11.90
8	VRTVSRPLG	129	0.8000	9.52
9	LGVLTRPSP	107	0.6000	7.14
10	LLELATPYA	8	0.5000	5.95



11	VRETMAVVS	50	0.5000	5.95
12	VVSAATTAE	56	0.5000	5.95
13	LELATPYAL	9	0.4000	4.76
14	LLVMNNVAP	153	0.3000	3.57
15	LTAPDVRTV	124	0.2000	2.38
16	LGGAKGPRS	173	0.2000	2.38
17	VVFSRDRNT	143	-0.1000	0
18	ILDATKPEV	73	-0.2000	0
19	WRTAAFASA	87	-0.2000	0
20	LRTAILDAT	69	-0.3000	0
21	MWLLGGAKG	170	-0.4000	0
22	VTPSTTATL	190	-0.5000	0

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.4000	39.08
2	VYQMWLLGG	167	3.0000	34.48
3	VRTVSRPLG	129	2.9500	33.91
4	YQMWLLGGA	168	2.3000	26.44
5	FELLELATP	6	2.1000	24.14
6	LGVLTRPSP	107	1.7500	20.11
7	VMNNVAPPS	155	1.6500	18.97
8	MNNVAPPSR	156	1.6500	18.97
9	VRRQSRWRT	81	1.6000	18.39
10	FASAAIAV	92	1.3000	14.94
11	LGASTALAF	201	1.2000	13.79
12	WRTAAFASA	87	0.8000	9.20
13	MWLLGGAKG	170	0.7000	8.05
14	LLELATPYA	8	0.6500	7.47
15	VVSAATTAE	56	0.5000	5.75
16	MGTAAVTPS	185	0.5000	5.75
17	YALNAVSDD	15	0.3000	3.45
18	ILDATKPEV	73	0.2500	2.87
19	LELATPYAL	9	0.1600	1.84
20	LGGAKGPRS	173	0.0500	0.57
21	VRETMAVVS	50	-0.1000	0

ALLELE: DRB1_1301	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	4.5000	51.14
2	VRRQSRWRT	81	4.4000	50.00
3	VFSRDRNTG	144	2.7000	30.68
4	VYQMWLLGG	167	2.7000	30.68
5	VMNNVAPPS	155	2.3000	26.14
6	VRTVSRPLG	129	2.2000	25.00
7	VVSAATTAE	56	1.9000	21.59
8	MGTAAVTPS	185	1.9000	21.59
9	LGVLTRPSP	107	1.6000	18.18
10	LELATPYAL	9	1.3600	15.45
11	LLVMNNVAP	153	1.3000	14.77
12	LTAPDVRTV	124	1.2000	13.64
13	LGASTALAF	201	1.2000	13.64
14	YQMWLLGGA	168	1.0000	11.36
15	MWLLGGAKG	170	1.0000	11.36
16	VRETMAVVS	50	0.9000	10.23
17	MNNVAPPSR	156	0.9000	10.23
18	ILDATKPEV	73	0.8000	9.09
19	VVFSRDRNT	143	0.6000	6.82
20	LGGAKGPRS	173	0.6000	6.82
21	LLELATPYA	8	0.5000	5.68
22	VTPSTTATL	190	0.4600	5.23
23	FELLELATP	6	0.4000	4.55

ALLELE: DRB1_1302	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.5000	39.77
2	VRRQSRWRT	81	3.4000	38.64
3	YQMWLLGGA	168	2.0000	22.73
4	VFSRDRNTG	144	1.7000	19.32

5	VYQMWillGG	167	1.7000	19.32
6	FELLElATP	6	1.4000	15.91
7	VMNNVAPPS	155	1.3000	14.77
8	VRTVSRPLG	129	1.2000	13.64
9	VVSAATTAE	56	0.9000	10.23
10	MGTAAVTPS	185	0.9000	10.23
11	YALNAVSDd	15	0.8000	9.09
12	WRTAAFASA	87	0.8000	9.09
13	LGVLTRPSP	107	0.6000	6.82
14	LELATPYAL	9	0.3600	4.09
15	LLVMNNVAP	153	0.3000	3.41
16	LTAPDVRTV	124	0.2000	2.27
17	WLLGGAKGP	171	0.2000	2.27
18	LGASTALAF	201	0.2000	2.27
19	FNDEVRAVR	43	-0.1000	0
20	VRETMAVVS	50	-0.1000	0

ALLELE:  
DRB1\_1304

Threshold for 3 % with score:  
2.6

Highest Score achievable by any  
peptide: 9

Rank	Sequence	At Position	Score	% of Highest Score
1	VRRQSRWRT	81	4.6000	51.11
2	LVMNNVAPP	154	3.9000	43.33
3	VVSAATTAE	56	3.5000	38.89
4	VFSRDRNTG	144	2.6000	28.89
5	VYQMWillGG	167	2.6000	28.89
6	VRTVSRPLG	129	2.1000	23.33
7	VMNNVAPPS	155	1.9000	21.11
8	MGTAAVTPS	185	1.5000	16.67
9	LELATPYAL	9	1.4000	15.56
10	YALNAVSDd	15	1.4000	15.56
11	LGVLTRPSP	107	1.0000	11.11
12	YQMWillGGA	168	1.0000	11.11
13	MWLLGGAKG	170	0.9000	10.00
14	VVFSRDRNT	143	0.8000	8.89
15	LLVMNNVAP	153	0.7000	7.78
16	LRTAILDAT	69	0.6000	6.67
17	LLELATPYA	8	0.5000	5.56

18	VRETMAVVS	50	0.5000	5.56
19	LTAPDVRTV	124	0.5000	5.56
20	VTPSTTATL	190	0.5000	5.56
21	LGGAKGPRS	173	0.2000	2.22
22	LGASTALAF	201	0.2000	2.22
23	ILDATKPEV	73	0.1000	1.11

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.4000	39.08
2	VYQMWLLGG	167	3.0000	34.48
3	VRTVSRPLG	129	2.9500	33.91
4	YQMWLLGGA	168	2.3000	26.44
5	FELLELATP	6	2.1000	24.14
6	LGVLTRPSP	107	1.7500	20.11
7	VMNNVAPPS	155	1.6500	18.97
8	MNNVAPPSR	156	1.6500	18.97
9	VRRQSRWRT	81	1.6000	18.39
10	FASAAAIIV	92	1.3000	14.94
11	LGASTALAF	201	1.2000	13.79
12	WRTAAFASA	87	0.8000	9.20
13	MWLLGGAKG	170	0.7000	8.05
14	LLELATPYA	8	0.6500	7.47
15	VVSAATTAE	56	0.5000	5.75
16	MGTAAVTPS	185	0.5000	5.75
17	YALNAVSD	15	0.3000	3.45
18	ILDATKPEV	73	0.2500	2.87
19	LELATPYAL	9	0.1600	1.84
20	LGGAKGPRS	173	0.0500	0.57
21	VRETMAVVS	50	-0.1000	0

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	2.4000	35.29
2	YQMWLLGGA	168	2.2000	32.35
3	FELLELATP	6	1.1000	16.18
4	WRTAAFASA	87	0.8000	11.76
5	VRTVSRPLG	129	0.4000	5.88
6	VRRQSRWRT	81	0.1000	1.47
7	VMNNVAPPS	155	0.1000	1.47
8	VYQMWLLGG	167	-0.2000	0
9	LGVLTRPSP	107	-0.4000	0
10	LLELATPYA	8	-0.5000	0
11	MWLLGGAKG	170	-0.7000	0
12	YALNAVSDD	15	-0.8000	0
13	VRETMAVVS	50	-1.0000	0
14	MNNVAPPSR	156	-1.0000	0
15	MGTAAVTPS	185	-1.0000	0
16	MAVVSAAAT	54	-1.3000	0
17	FASAAAIIV	92	-1.3000	0
18	LGAFGLGVL	102	-1.4000	0
19	LELATPYAL	9	-1.5000	0
20	LLVMNNVAP	153	-1.5000	0
21	LGGAKGPRS	173	-1.5000	0
22	VTPSTTATL	190	-1.6000	0

ALLELE: DRB1_1311	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	3.4000	40.96
2	VYQMWLLGG	167	2.6000	31.33
3	VRTVSRPLG	129	2.5500	30.72
4	VMNNVAPPS	155	2.2500	27.11
5	VRRQSRWRT	81	1.9000	22.89
6	LGVLTRPSP	107	1.7500	21.08
7	LLELATPYA	8	1.6500	19.88
8	YQMWLLGGA	168	1.3000	15.66
9	MNNVAPPSR	156	1.1500	13.86
10	MGTAAVTPS	185	1.1000	13.25

11	LGGAKGPRS	173	0.6500	7.83
12	VRETMAVVS	50	0.5000	6.02
13	MWLLGGAKG	170	0.3000	3.61
14	LGASTALAF	201	0.3000	3.61
15	ILDATKPEV	73	0.2500	3.01
16	LELATPYAL	9	0.2000	2.41
17	FELLELATP	6	0.1000	1.20
18	VVSAATTAE	56	0.1000	1.20
19	VRAVRETMA	47	-0.1000	0
20	VAAAPSPVA	32	-0.1500	0
21	LATPYALNA	11	-0.2000	0

ALLELE: DRB1_1321	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.9
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Rank	Sequence	At Position	Score	% of Highest Score
1	VYQMWLLGG	167	2.9000	32.58
2	VRTVSRPLG	129	2.8500	32.02
3	LVMNNVAPP	154	2.8000	31.46
4	YQMWLLGGA	168	2.3000	25.84
5	VVSAATTAE	56	2.1000	23.60
6	YALNAVSDD	15	1.9000	21.35
7	VRRQSRWRT	81	1.8000	20.22
8	FELLELATP	6	1.5000	16.85
9	VMNNVAPPS	155	1.2500	14.04
10	LGVLTRPSP	107	1.1500	12.92
11	WRTAAFASA	87	0.8000	8.99
12	LLELATPYA	8	0.6500	7.30
13	FASAAAIIV	92	0.6000	6.74
14	MWLLGGAKG	170	0.6000	6.74
15	LELATPYAL	9	0.2000	2.25
16	LGASTALAF	201	0.2000	2.25
17	MNNVAPPSR	156	0.1500	1.69
18	MGTAAVTPS	185	0.1000	1.12
19	LGAFGLGVL	102	-0.3000	0
20	LGGAKGPRS	173	-0.3500	0
21	MAVVSAAAT	54	-0.4000	0
22	VFSRDRNTG	144	-0.4000	0

ALLELE: DRB1_1322	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	VRRQSRWRT	81	3.7000	44.05
2	LVMNNVAPP	154	3.5000	41.67
3	VMNNVAPPS	155	1.9000	22.62
4	MGTAAVTPS	185	1.5000	17.86
5	VFSRDRNTG	144	1.3000	15.48
6	VYQMWLLGG	167	1.3000	15.48
7	YQMWLLGGA	168	1.0000	11.90
8	VRTVSRPLG	129	0.8000	9.52
9	LGVLTRPSP	107	0.6000	7.14
10	LLELATPYA	8	0.5000	5.95
11	VRETMAVVS	50	0.5000	5.95
12	VVSAATTAE	56	0.5000	5.95
13	LELATPYAL	9	0.4000	4.76
14	LLVMNNVAP	153	0.3000	3.57
15	LTAPDVRTV	124	0.2000	2.38
16	LGGAKGPRS	173	0.2000	2.38
17	VVFSRDRNT	143	-0.1000	0
18	ILLDATKPEV	73	-0.2000	0
19	WRTAAFASA	87	-0.2000	0
20	LRTAILDAT	69	-0.3000	0
21	MWLLGGAKG	170	-0.4000	0
22	VTPSTTATL	190	-0.5000	0

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	VRRQSRWRT	81	2.7000	32.14
2	LVMNNVAPP	154	2.5000	29.76
3	YQMWLLGGA	168	2.0000	23.81
4	VMNNVAPPS	155	0.9000	10.71
5	WRTAAFASA	87	0.8000	9.52

6	MGTAAVTPS	185	0.5000	5.95
7	FELLELATP	6	0.4000	4.76
8	VFSRDRNTG	144	0.3000	3.57
9	VYQMWLLGG	167	0.3000	3.57
10	VRTVSRPLG	129	-0.2000	0
11	YALNAVSD	15	-0.3000	0
12	LGVLTRPSP	107	-0.4000	0
13	LLELATPYA	8	-0.5000	0
14	VRETMAVVS	50	-0.5000	0
15	VVSAATTAE	56	-0.5000	0
16	LELATPYAL	9	-0.6000	0
17	LLVMNNVAP	153	-0.7000	0
18	LTAPDVRTV	124	-0.8000	0
19	WLLGGAKGP	171	-0.8000	0
20	LGGAKGPRS	173	-0.8000	0
21	FASAAIAV	92	-1.0000	0
22	VVFSRDRNT	143	-1.1000	0

ALLELE: DRB1_1327	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	4.5000	51.14
2	VRRQSRWRT	81	4.4000	50.00
3	VFSRDRNTG	144	2.7000	30.68
4	VYQMWLLGG	167	2.7000	30.68
5	VMNNVAPPS	155	2.3000	26.14
6	VRTVSRPLG	129	2.2000	25.00
7	VVSAATTAE	56	1.9000	21.59
8	MGTAAVTPS	185	1.9000	21.59
9	LGVLTRPSP	107	1.6000	18.18
10	LELATPYAL	9	1.3600	15.45
11	LLVMNNVAP	153	1.3000	14.77
12	LTAPDVRTV	124	1.2000	13.64
13	LGASTALAF	201	1.2000	13.64
14	YQMWLLGGA	168	1.0000	11.36
15	MWLLGGAKG	170	1.0000	11.36
16	VRETMAVVS	50	0.9000	10.23



17	MNNVAPPSR	156	0.9000	10.23
18	ILDATKPEV	73	0.8000	9.09
19	VVFSRDRNT	143	0.6000	6.82
20	LGGAKGPRS	173	0.6000	6.82
21	LLELATPYA	8	0.5000	5.68
22	VTPSTTATL	190	0.4600	5.23
23	FELLELATP	6	0.4000	4.55

ALLELE: DRB1_1328	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVMNNVAPP	154	4.5000	51.14
2	VRRQSRWRT	81	4.4000	50.00
3	VFSRDRNTG	144	2.7000	30.68
4	VYQMWLLGG	167	2.7000	30.68
5	VMNNVAPPS	155	2.3000	26.14
6	VRTVSRPLG	129	2.2000	25.00
7	VVSAATTAE	56	1.9000	21.59
8	MGTAAVTPS	185	1.9000	21.59
9	LGVLTRPSP	107	1.6000	18.18
10	LELATPYAL	9	1.3600	15.45
11	LLVMNNVAP	153	1.3000	14.77
12	LTAPDVRTV	124	1.2000	13.64
13	LGASTALAF	201	1.2000	13.64
14	YQMWLLGGA	168	1.0000	11.36
15	MWLLGGAKG	170	1.0000	11.36
16	VRETMAVVS	50	0.9000	10.23
17	MNNVAPPSR	156	0.9000	10.23
18	ILDATKPEV	73	0.8000	9.09
19	VVFSRDRNT	143	0.6000	6.82
20	LGGAKGPRS	173	0.6000	6.82
21	LLELATPYA	8	0.5000	5.68
22	VTPSTTATL	190	0.4600	5.23
23	FELLELATP	6	0.4000	4.55

ALLELE: DRB1_1501	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LGAFGLGVL	102	3.6000	36.73
2	VRRQSRWRT	81	3.5000	35.71
3	VYQMWLLGG	167	3.2000	32.65
4	VRTVSRPLG	129	2.9000	29.59
5	LLVMNNVAP	153	2.4000	24.49
6	YQMWLLGGA	168	2.2000	22.45
7	LELATPYAL	9	2.1000	21.43
8	VFSRDRNTG	144	2.1000	21.43
9	LVMNNVAPP	154	1.9000	19.39
10	LGVLTRPSP	107	1.7000	17.35
11	LGASTALAF	201	1.7000	17.35
12	LATPYALNA	11	1.6000	16.33
13	VRAVRETMMA	47	1.6000	16.33
14	LRTAILDAT	69	1.5000	15.31
15	VVFSRDRNT	143	1.5000	15.31
16	MTEHTDFEL	0	1.4000	14.29
17	VMNNVAPPS	155	1.4000	14.29
18	VAPPSRGTV	159	1.3000	13.27
19	LGGAKGPRS	173	1.2000	12.24
20	MWLLGGAKG	170	1.1000	11.22
21	FASAAAIIV	92	1.0000	10.20
22	VLTRPSPPP	109	1.0000	10.20
23	LGAGTATVV	136	1.0000	10.20

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	YQMWLLGGA	168	3.2000	32.65
2	LGAFGLGVL	102	2.6000	26.53
3	VRRQSRWRT	81	2.5000	25.51
4	VYQMWLLGG	167	2.2000	22.45
5	FASAAAIIV	92	2.0000	20.41
6	WRTAAFASA	87	1.9000	19.39

7	VRTVSRPLG	129	1.9000	19.39
8	FSRDRNTGL	145	1.4000	14.29
9	LLVMNNVAP	153	1.4000	14.29
10	LELATPYAL	9	1.1000	11.22
11	VFSRDRNTG	144	1.1000	11.22
12	LVMNNVAPP	154	0.9000	9.18
13	FGLGVLTRP	105	0.8000	8.16
14	FELLELATP	6	0.7000	7.14
15	LGVLTRPSP	107	0.7000	7.14
16	LGASTALAF	201	0.7000	7.14
17	LATPYALNA	11	0.6000	6.12
18	VRAVRETMA	47	0.6000	6.12
19	WLLGGAKGP	171	0.6000	6.12
20	LRTAILDAT	69	0.5000	5.10
21	VVFSRDRNT	143	0.5000	5.10
22	MTEHTDFEL	0	0.4000	4.08
23	VMNNVAPPS	155	0.4000	4.08

ALLELE: DRB1_1506	Threshold for 3 % with score: 3.1	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LGAFGLGVL	102	3.6000	36.73
2	VRRQSRWRT	81	3.5000	35.71
3	VYQMWLLGG	167	3.2000	32.65
4	VRTVSRPLG	129	2.9000	29.59
5	LLVMNNVAP	153	2.4000	24.49
6	YQMWLLGGA	168	2.2000	22.45
7	LELATPYAL	9	2.1000	21.43
8	VFSRDRNTG	144	2.1000	21.43
9	LVMNNVAPP	154	1.9000	19.39
10	LGVLTRPSP	107	1.7000	17.35
11	LGASTALAF	201	1.7000	17.35
12	LATPYALNA	11	1.6000	16.33
13	VRAVRETMA	47	1.6000	16.33
14	LRTAILDAT	69	1.5000	15.31
15	VVFSRDRNT	143	1.5000	15.31
16	MTEHTDFEL	0	1.4000	14.29

17	VMNNVAPPS	155	1.4000	14.29
18	VAPPSRGTV	159	1.3000	13.27
19	LGGAKGPRS	173	1.2000	12.24
20	MWLLGGAKG	170	1.1000	11.22
21	FASAAAIIV	92	1.0000	10.20
22	VLTRPSPPP	109	1.0000	10.20
23	LGAGTATVV	136	1.0000	10.20

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	MNNVAPPSR	156	3.5000	35.71
2	LELATPYAL	9	2.8000	28.57
3	VYQMWLLGG	167	1.6000	16.33
4	FASAAAIIV	92	1.2000	12.24
5	VRTVSRPLG	129	0.8000	8.16
6	YQMWLLGGA	168	0.8000	8.16
7	LGASTALAF	201	0.8000	8.16
8	VRETMAVVS	50	0.7000	7.14
9	VRAVRETMA	47	0.6000	6.12
10	MWLLGGAKG	170	0.6000	6.12
11	WRTAAFASA	87	0.5000	5.10
12	VVFSRDRNT	143	0.5000	5.10
13	WLLGGAKGP	171	0.5000	5.10
14	MAVVSAAAT	54	0.4000	4.08
15	VVSAATTAE	56	0.2000	2.04
16	LLGGAKGPR	172	0.2000	2.04
17	VRRQSRWRT	81	0.1000	1.02
18	FELLELATP	6	-0.1000	0
19	LNAVSDDER	17	-0.1000	0
20	FTVEPGTGS	209	-0.1000	0
21	LDATKPEVR	74	-0.2000	0
22	LGAFGLGVL	102	-0.2000	0

ALLELE:	Threshold for 3 % with score:	Highest Score achievable by any
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DRB5\_0105

2.3

peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	MNNVAPPSR	156	3.5000	35.71
2	LELATPYAL	9	2.8000	28.57
3	VYQMWLLGG	167	1.6000	16.33
4	FASAAAIIV	92	1.2000	12.24
5	VRTVSRPLG	129	0.8000	8.16
6	YQMWLLGGA	168	0.8000	8.16
7	LGASTALAF	201	0.8000	8.16
8	VRETMAVVS	50	0.7000	7.14
9	VRAVRETMA	47	0.6000	6.12
10	MWLLGGAKG	170	0.6000	6.12
11	WRTAAFASA	87	0.5000	5.10
12	VVFSRDRNT	143	0.5000	5.10
13	WLLGGAKGP	171	0.5000	5.10
14	MAVVSAAAT	54	0.4000	4.08
15	VVSAATTAE	56	0.2000	2.04
16	LLGGAKGPR	172	0.2000	2.04
17	VRRQSRWRT	81	0.1000	1.02
18	FELLELATP	6	-0.1000	0
19	LNAVSDDER	17	-0.1000	0
20	FTVEPGTGS	209	-0.1000	0
21	LDATKPEVR	74	-0.2000	0
22	LGAFGLGVL	102	-0.2000	0