

MHC Class-II Binding Peptide Prediction Results

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INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Apr 27 00:27:31 2010
Length of input sequence	308 amino acids
Number of nanomers from input sequence	300
Number of nanomers with obligatory P1 anchor residue	127
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	30

ALLELE: DRB1_0101	Threshold for 3 % with score: 0.14	Highest Score achievable by any peptide: 6
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Rank	Sequence	At Position	Score	% of Highest Score
1	IVLACPWF	113	2.2000	36.67
2	LISLAAILV	38	2.1000	35.00
3	FVIPAAVLF	143	2.0000	33.33
4	FYQLWAFIT	121	1.9000	31.67
5	IVMLNLAGL	207	1.9000	31.67
6	VLLELAIQI	257	1.9000	31.67
7	VGMAAGIVL	107	1.7000	28.33
8	FGFLLNLLV	187	1.7000	28.33

9	LLISLAAIL	37	1.3000	21.67
10	LVLSKALGF	160	1.3000	21.67
11	LNLLVVFGV	191	1.2000	20.00
12	MLNLAGLLT	209	1.2000	20.00
13	LFVAGAVLA	150	1.0000	16.67
14	VLFVAGAVL	149	0.9500	15.83
15	FLLTVGSDV	168	0.8000	13.33
16	MFVFAAIFT	232	0.7800	13.00
17	WRRGLIFAM	224	0.6800	11.33
18	LKVGMAAGI	105	0.6000	10.00
19	LKRLNPRNR	6	0.5900	9.83
20	VMLNLAGLL	208	0.5400	9.00
21	VVFGVSFEF	195	0.5000	8.33
22	LLVVFGVSF	193	0.4500	7.50
23	LGFLLVGS	166	0.4000	6.67
24	FLLNLLVVF	189	0.3400	5.67
25	YQRERRFAV	133	0.3000	5.00
26	LLNLLVVFG	190	0.2000	3.33
27	FVFAAIFTP	233	0.2000	3.33
28	FAMFVFAAI	230	0.0800	1.33
29	YERLKSRR	218	0.0200	0.33

ALLELE: DRB1_0102		Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6	
Rank	Sequence	At Position	Score	% of Highest Score
1	IVLACPWF	113	3.2000	53.33
2	LISLAAILV	38	3.1000	51.67
3	IVMLNLAGL	207	2.9000	48.33
4	VLELAIQI	257	2.9000	48.33
5	VGMAAGIVL	107	2.7000	45.00
6	LLISLAAIL	37	2.3000	38.33
7	LVLSKALGF	160	2.3000	38.33
8	LNLLVVFGV	191	2.2000	36.67

9	MLNLAGLLT	209	2.2000	36.67
10	FVIPAAVLF	143	2.0000	33.33
11	LFVAGAVLA	150	2.0000	33.33
12	VLVAGAVL	149	1.9500	32.50
13	FYQLWAFIT	121	1.9000	31.67
14	MFVFAAIFT	232	1.7800	29.67
15	FGLLNLLV	187	1.7000	28.33
16	LKVGMAAGI	105	1.6000	26.67
17	LKRLNPRNR	6	1.5900	26.50
18	VMLNLAGLL	208	1.5400	25.67
19	VVFGVSFEF	195	1.5000	25.00
20	LLVVFVGSF	193	1.4500	24.17
21	LGLLTVGS	166	1.4000	23.33
22	LLNLLVFG	190	1.2000	20.00
23	VIPAAVLFV	144	0.9000	15.00
24	VSFEFPLLI	199	0.9000	15.00
25	LRLKVGMAA	103	0.8900	14.83
26	VAFVIPAAV	141	0.8500	14.17
27	FLLTVGSDV	168	0.8000	13.33
28	LIVMLNLAG	206	0.8000	13.33
29	IFAMFVFAA	229	0.8000	13.33
30	MTALGAALT	248	0.7000	11.67

ALLELE: DRB1_0301	Threshold for 3 % with score: 2.96	Highest Score achievable by any peptide: 9.5		
Rank	Sequence	At Position	Score	% of Highest Score
1	VNPDATMSL	18	5.2600	55.37
2	LVLSKALGF	160	4.9000	51.58
3	IVLACPVWF	113	4.7000	49.47
4	VVFGVSFEF	195	4.7000	49.47
5	WRRGLIFAM	224	4.7000	49.47
6	LNLLVFGV	191	3.8000	40.00
7	IVMLNLAGL	207	3.6600	38.53

8	LGFLLTVGS	166	3.4000	35.79
9	FVAGAVLAY	151	3.3000	34.74
10	LLNLLVVF	190	3.3000	34.74
11	LLISLAAIL	37	3.1600	33.26
12	VRAAGLLKR	0	3.1000	32.63
13	VIPAAVLFV	144	3.1000	32.63
14	MLRLKVGMA	102	3.0000	31.58
15	VGSDVQVTA	172	2.9000	30.53
16	IQIARVHDK	263	2.9000	30.53
17	FVFAAIFTP	233	2.8000	29.47
18	FMLRLKVGM	101	2.7000	28.42
19	LKVGMAAGI	105	2.7000	28.42
20	FVIPAAVLF	143	2.7000	28.42
21	LLIVMLNLA	205	2.6100	27.47
22	ILVTTIFGF	44	2.6000	27.37
23	LRLKVGMAA	103	2.6000	27.37
24	LVVFGVSFE	194	2.5700	27.05
25	FLLNLLVVF	189	2.5000	26.32
26	LNLAGLLTY	210	2.5000	26.32
27	IFAMFVFAA	229	2.5000	26.32
28	VMLNLAGLL	208	2.3600	24.84
29	LLTYERLKS	215	2.3000	24.21
30	LAAILVTTI	41	2.2000	23.16

ALLELE: DRB1_0305	Threshold for 3 % with score: 1.7	Highest Score achievable by any peptide: 9.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	WRRGLIFAM	224	4.2000	46.15
2	VNPDATMSL	18	3.3000	36.26
3	FGLDSLGEW	60	3.1000	34.07
4	FVAGAVLAY	151	3.0000	32.97
5	FVFAAIFTP	233	2.8000	30.77
6	FAAIFTPGS	235	2.7000	29.67

7	FMLRLKVGGM	101	2.2000	24.18
8	FAVAFVIPA	139	2.1000	23.08
9	MLRLKVGMA	102	2.0000	21.98
10	LVLSKALGF	160	2.0000	21.98
11	LGFLLTVGS	166	2.0000	21.98
12	VGSDVQVTA	172	1.9000	20.88
13	IVLACPVWF	113	1.8000	19.78
14	FVIPAAVLF	143	1.8000	19.78
15	YLVLKALG	159	1.8000	19.78
16	LNLLVVFVG	191	1.8000	19.78
17	VVFGVSFEF	195	1.8000	19.78
18	IQIARVHDK	263	1.8000	19.78
19	YQRERRFAV	133	1.7000	18.68
20	IVMLNLAGL	207	1.7000	18.68
21	LLIVMLNLA	205	1.6100	17.69
22	LRLKVGMAA	103	1.6000	17.58
23	FLLNLLVVF	189	1.6000	17.58
24	IFAMFVFAA	229	1.5000	16.48
25	FPLLIVMLN	203	1.4000	15.38
26	WYSHSIFGL	54	1.3000	14.29
27	LLISLAAIL	37	1.2000	13.19
28	VIPAAVLFV	144	1.1000	12.09
29	MAAGIVLAC	109	0.9000	9.89
30	WAFITPGLY	125	0.9000	9.89

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	VNPDATMSL	18	4.0000	45.45
2	IQIARVHDK	263	3.6000	40.91
3	LVLSKALGF	160	3.5000	39.77
4	LLIVMLNLA	205	3.3000	37.50
5	LGFLLTVGS	166	2.8800	32.73

6	VGSDVQVTA	172	2.7800	31.59
7	IVMLNLAGL	207	2.7000	30.68
8	IVLACPVWF	113	2.6800	30.45
9	VIPAAVLV	144	2.6000	29.55
10	FVAGAVLAY	151	2.5000	28.41
11	MAAGIVLAC	109	2.4000	27.27
12	LLTYERLKS	215	2.4000	27.27
13	LRLKVGMAA	103	2.3000	26.14
14	LLISLAAIL	37	2.2000	25.00
15	VRAAGLLKR	0	2.1000	23.86
16	LKVGMAAGI	105	1.8000	20.45
17	LLNLLVVF	190	1.7800	20.23
18	LNLAGLLTY	210	1.7000	19.32
19	WRRGLIFAM	224	1.7000	19.32
20	MLRLKVGMA	102	1.6000	18.18
21	VLAYLVLSK	156	1.6000	18.18
22	LFVAGAVLA	150	1.3800	15.68
23	LAAILVTI	41	1.3000	14.77
24	LNLLVVFV	191	1.3000	14.77
25	VVFGVSFEF	195	1.3000	14.77
26	LLTVGSDVQ	169	1.1000	12.50
27	FMLRLKVG	101	1.0800	12.27
28	IFAMFVFAA	229	1.0000	11.36
29	ISLAAILVT	39	0.9000	10.23
30	LPQSARADI	76	0.9000	10.23

ALLELE: DRB1_0307	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8		
Rank	Sequence	At Position	Score	% of Highest Score
1	VNPDATMSL	18	4.0000	45.45
2	IQIARVHDK	263	3.6000	40.91
3	LVLSKALGF	160	3.5000	39.77
4	LLIVMLNLA	205	3.3000	37.50

5	LGFLLTVGS	166	2.8800	32.73
6	VGSDVQVTA	172	2.7800	31.59
7	IVMLNLAGL	207	2.7000	30.68
8	IVLACPWF	113	2.6800	30.45
9	VIPAAVLV	144	2.6000	29.55
10	FVAGAVLAY	151	2.5000	28.41
11	MAAGIVLAC	109	2.4000	27.27
12	LLTYERLKS	215	2.4000	27.27
13	LRLKVGMAA	103	2.3000	26.14
14	LLISLAAIL	37	2.2000	25.00
15	VRAAGLLKR	0	2.1000	23.86
16	LKVGMAAGI	105	1.8000	20.45
17	LLNLLVFG	190	1.7800	20.23
18	LNLAGLLTY	210	1.7000	19.32
19	WRRGLIFAM	224	1.7000	19.32
20	MLRLKVGMA	102	1.6000	18.18
21	VLAYLVLSK	156	1.6000	18.18
22	LFVAGAVLA	150	1.3800	15.68
23	LAAILVTTI	41	1.3000	14.77
24	LNLLVFGV	191	1.3000	14.77
25	VVFGVSFEF	195	1.3000	14.77
26	LLTVGSDVQ	169	1.1000	12.50
27	FMLRLKVGGM	101	1.0800	12.27
28	IFAMFVFAA	229	1.0000	11.36
29	ISLAAILVT	39	0.9000	10.23
30	LPQSARADI	76	0.9000	10.23

ALLELE: DRB1_0308	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8		
Rank	Sequence	At Position	Score	% of Highest Score
1	VNPDATMSL	18	4.0000	45.45
2	IQIARVHDK	263	3.6000	40.91
3	LVLKALGF	160	3.5000	39.77

4	LLIVMLNLA	205	3.3000	37.50
5	LGFLTVGS	166	2.8800	32.73
6	VGSDVQVTA	172	2.7800	31.59
7	IVMLNLAGL	207	2.7000	30.68
8	IVLACPWWF	113	2.6800	30.45
9	VIPAAVLFV	144	2.6000	29.55
10	FVAGAVLAY	151	2.5000	28.41
11	MAAGIVLAC	109	2.4000	27.27
12	LLTYERLKS	215	2.4000	27.27
13	LRLKVGMAA	103	2.3000	26.14
14	LLISLAAIL	37	2.2000	25.00
15	VRAAGLLKR	0	2.1000	23.86
16	LKVGMAAGI	105	1.8000	20.45
17	LLNLLVFG	190	1.7800	20.23
18	LNLAGLLTY	210	1.7000	19.32
19	WRRGLIFAM	224	1.7000	19.32
20	MLRLKVGMA	102	1.6000	18.18
21	VLAYLVLSK	156	1.6000	18.18
22	LFVAGAVLA	150	1.3800	15.68
23	LAAILVTTI	41	1.3000	14.77
24	LNLLVFGV	191	1.3000	14.77
25	VVFGVSFEF	195	1.3000	14.77
26	LLTVGSDVQ	169	1.1000	12.50
27	FMLRLKVGM	101	1.0800	12.27
28	IFAMFVFAA	229	1.0000	11.36
29	ISLAAILVT	39	0.9000	10.23
30	LPQSARADI	76	0.9000	10.23

ALLELE: DRB1_0309	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 9.5		
Rank	Sequence	At Position	Score	% of Highest Score
1	WRRGLIFAM	224	5.7000	60.00
2	FVAGAVLAY	151	4.3000	45.26

3	VNPDATMSL	18	4.2600	44.84
4	LVLSKALGF	160	3.9000	41.05
5	FVFAAIFTP	233	3.8000	40.00
6	FMLRLKVGGM	101	3.7000	38.95
7	IVLACPVWF	113	3.7000	38.95
8	FVIPAAVLF	143	3.7000	38.95
9	VVFGVSFEF	195	3.7000	38.95
10	FLLNLLVVF	189	3.5000	36.84
11	YLVLKALG	159	3.2000	33.68
12	FGLDSLGEW	60	3.1000	32.63
13	FAAIFTPGS	235	3.1000	32.63
14	LNLLVVFV	191	2.8000	29.47
15	YQRERRFAV	133	2.7000	28.42
16	IVMLNLAGL	207	2.6600	28.00
17	LGFLTVGS	166	2.4000	25.26
18	LLNLLVVF	190	2.3000	24.21
19	WYSHSIFGL	54	2.2600	23.79
20	WAFITPGLY	125	2.2000	23.16
21	FPLLIVMLN	203	2.2000	23.16
22	LLISLAAIL	37	2.1600	22.74
23	VRAAGLLKR	0	2.1000	22.11
24	FAVAFVIPA	139	2.1000	22.11
25	VIPAAVLFV	144	2.1000	22.11
26	MLRLKVGMA	102	2.0000	21.05
27	FVWYSHSIF	52	1.9700	20.74
28	VGSDVQVTA	172	1.9000	20.00
29	IQIARVHDK	263	1.9000	20.00
30	LKVGMAAGI	105	1.7000	17.89

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	VNPDATMSL	18	4.0000	45.45

2	IQIARVHDK	263	3.6000	40.91
3	LVLSKALGF	160	3.5000	39.77
4	LLIVMLNLA	205	3.3000	37.50
5	LGFLLTVGS	166	2.8800	32.73
6	VGSDVQVTA	172	2.7800	31.59
7	IVMLNLAGL	207	2.7000	30.68
8	IVLACPVWF	113	2.6800	30.45
9	VIPAAVLV	144	2.6000	29.55
10	FVAGAVLAY	151	2.5000	28.41
11	MAAGIVLAC	109	2.4000	27.27
12	LLTYERLKS	215	2.4000	27.27
13	LRLKVGMAA	103	2.3000	26.14
14	LLISLAAIL	37	2.2000	25.00
15	VRAAGLLKR	0	2.1000	23.86
16	LKVGMAAGI	105	1.8000	20.45
17	LLNLLVFG	190	1.7800	20.23
18	LNLAGLLTY	210	1.7000	19.32
19	WRRGLIFAM	224	1.7000	19.32
20	MLRLKVGMA	102	1.6000	18.18
21	VLAYLVLSK	156	1.6000	18.18
22	LFVAGAVLA	150	1.3800	15.68
23	LAAILVTI	41	1.3000	14.77
24	LNLLVFGV	191	1.3000	14.77
25	VVFGVSFEF	195	1.3000	14.77
26	LLTVGSDVQ	169	1.1000	12.50
27	FMLRLKVGM	101	1.0800	12.27
28	IFAMFVFAA	229	1.0000	11.36
29	ISLAAILVT	39	0.9000	10.23
30	LPQSARADI	76	0.9000	10.23

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
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1	LGFLLTVGS	166	3.7800	43.95
2	FGFLLNLLV	187	3.4000	39.53
3	VNPDATMSL	18	3.2000	37.21
4	FAAIFTPGS	235	2.7000	31.40
5	LVLSKALGF	160	2.6000	30.23
6	LIVMLNLAG	206	2.5000	29.07
7	IQIARVHDK	263	2.3000	26.74
8	VLLELAIQI	257	2.2800	26.51
9	LVDHLTELK	26	2.0000	23.26
10	FPLLIVMLN	203	1.6000	18.60
11	FAVAFVIPA	139	1.4800	17.21
12	VSFEFPLLI	199	1.4000	16.28
13	LLISLAAIL	37	1.3000	15.12
14	VIPAAVLFV	144	1.3000	15.12
15	LLNLLVVFG	190	1.2800	14.88
16	IVMLNLAGL	207	1.2000	13.95
17	IVLACPVWF	113	1.1800	13.72
18	MLRLKVGMA	102	1.1000	12.79
19	WFYQLWAFI	120	1.1000	12.79
20	FVAGAVLAY	151	1.1000	12.79
21	FVIPAAVLF	143	1.0800	12.56
22	FLLNLLVVF	189	0.8800	10.23
23	IFGLDSLGE	59	0.8000	9.30
24	LNLLVVFGV	191	0.8000	9.30
25	IFAMFVFAA	229	0.6000	6.98
26	VWYSHSIFG	53	0.5800	6.74
27	FVFAAIFTP	233	0.5000	5.81
28	LISLAAILV	38	0.4800	5.58
29	LGAALTVLL	251	0.4800	5.58
30	LFVAGAVLA	150	0.3800	4.42

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	IQIARVHDK	263	3.8000	39.58
2	LGFLITVGS	166	3.5000	36.46
3	LIVMLNLAG	206	3.5000	36.46
4	LAIQIARVH	261	2.8800	30.00
5	IFAMFVFAA	229	2.8000	29.17
6	VVFGVSFEF	195	2.7000	28.13
7	LRLKVGMAA	103	2.6000	27.08
8	VIPAAVLV	144	2.6000	27.08
9	IVLACPWF	113	2.3000	23.96
10	VLACPWFY	114	2.3000	23.96
11	VLAYLVLSK	156	2.2000	22.92
12	LVLSKALGF	160	2.1000	21.88
13	LKRLNPRNR	6	1.9000	19.79
14	LNLLVFGV	191	1.9000	19.79
15	LVDHLTEL	26	1.7000	17.71
16	LVVFGVSFE	194	1.7000	17.71
17	LRTRLLISL	33	1.6000	16.67
18	LGAALTVLL	251	1.6000	16.67
19	LLATAPFDQ	92	1.5000	15.62
20	LFVAGAVLA	150	1.5000	15.62
21	LAGLLTYER	212	1.4000	14.58
22	FVAGAVLAY	151	1.3000	13.54
23	FGLLNLLV	187	1.3000	13.54
24	LLIVMLNLA	205	1.3000	13.54
25	IFGFVWYSH	49	1.2800	13.33
26	MAAGIVLAC	109	1.2000	12.50
27	LYQRERRFA	132	1.2000	12.50
28	WRRGLIFAM	224	1.2000	12.50
29	VRAAGLLKR	0	1.1000	11.46
30	LNLLVFG	190	1.0000	10.42

ALLELE: DRB1_0404 Threshold for 3 % with score: Highest Score achievable by any peptide:

1.8

8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LGFLLTVGS	166	4.8000	54.55
2	LIVMLNLAG	206	4.0000	45.45
3	IFAMFVFAA	229	3.4500	39.20
4	LVVFGVSFE	194	3.3000	37.50
5	LNLLVVFGV	191	2.9500	33.52
6	IQIARVHDK	263	2.9000	32.95
7	LLIVMLNLA	205	2.6000	29.55
8	MLRLKVGMA	102	2.4000	27.27
9	IVMLNLAGL	207	2.4000	27.27
10	LLNLLVVFG	190	2.3000	26.14
11	FGLLNLLV	187	2.2000	25.00
12	LAAILVTTI	41	2.1000	23.86
13	IVLACPVWF	113	2.0000	22.73
14	VIPAAVLV	144	1.9000	21.59
15	LAGLLTYER	212	1.9000	21.59
16	LLTVGSDVQ	169	1.8000	20.45
17	LVLSKALGF	160	1.7000	19.32
18	FAAIFTPGS	235	1.7000	19.32
19	LISLAAILV	38	1.6800	19.09
20	VNPDATMSL	18	1.6000	18.18
21	IFGLDSLGE	59	1.6000	18.18
22	VLAYLVLSK	156	1.5000	17.05
23	LGAALTVLL	251	1.3000	14.77
24	LFVAGAVLA	150	1.2000	13.64
25	LAYLVLSKA	157	1.2000	13.64
26	MFVFAAIFT	232	1.1800	13.41
27	LKRLNPRNR	6	0.9000	10.23
28	LRLKVGMAA	103	0.9000	10.23
29	IFGFVWYSH	49	0.8800	10.00
30	LLISLAAIL	37	0.8000	9.09

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	LVVFGVSFE	194	5.3000	56.38
2	LIVMLNLAG	206	4.3000	45.74
3	LGFLLTVGS	166	3.8000	40.43
4	FPLLIVMLN	203	3.7000	39.36
5	IFGLDSLGE	59	3.6000	38.30
6	FGLLNLLV	187	3.5000	37.23
7	FAAIFTPGS	235	2.7000	28.72
8	LLNLLVVFV	190	2.6000	27.66
9	IFAMFVFAA	229	2.4500	26.06
10	IVMLNLAGL	207	2.4000	25.53
11	LNLLVVFV	191	2.2500	23.94
12	FVIPAAVLF	143	2.1000	22.34
13	IVLACPWF	113	1.9000	20.21
14	FVFAAIFTP	233	1.8500	19.68
15	VNPDATMSL	18	1.6000	17.02
16	LVLSKALGF	160	1.6000	17.02
17	LLTVGSDVQ	169	1.6000	17.02
18	YFGFLNLL	186	1.6000	17.02
19	LLIVMLNLA	205	1.6000	17.02
20	FYQLWAFIT	121	1.5500	16.49
21	FGFVWYSHS	50	1.5000	15.96
22	FAVAFVIPA	139	1.4800	15.74
23	MLRLKVGMA	102	1.4000	14.89
24	LAAILVTTI	41	1.3000	13.83
25	LGAALTVLL	251	1.3000	13.83
26	VIPAAVLFV	144	1.2000	12.77
27	FAMFVFAAI	230	1.2000	12.77
28	IQIARVHDK	263	1.2000	12.77
29	IFGFVWYSH	49	1.1000	11.70
30	YERLKSRR	218	1.1000	11.70

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	LGFLITVGS	166	3.8000	43.18
2	FGFLNLLV	187	3.2000	36.36
3	LIVMLNLAG	206	3.0000	34.09
4	FAAIFTPGS	235	2.7000	30.68
5	IFAMFVFAA	229	2.4500	27.84
6	LVVFGVSFE	194	2.3000	26.14
7	LNLLVFGV	191	1.9500	22.16
8	IQIARVHDK	263	1.9000	21.59
9	FPLLIVMLN	203	1.7000	19.32
10	LLIVMLNLA	205	1.6000	18.18
11	FGFVWYSHS	50	1.5000	17.05
12	FAVAFVIPA	139	1.4800	16.82
13	FVFAAIFTP	233	1.4500	16.48
14	MLRLKVGMA	102	1.4000	15.91
15	IVMLNLAGL	207	1.4000	15.91
16	LNLLVFG	190	1.3000	14.77
17	FVIPAAVLF	143	1.2000	13.64
18	LAAILVTTI	41	1.1000	12.50
19	YERLKSRR	218	1.1000	12.50
20	IVLACPWF	113	1.0000	11.36
21	FAMFVFAAI	230	1.0000	11.36
22	VIPAAVLFV	144	0.9000	10.23
23	LAGLLTYER	212	0.9000	10.23
24	LLTVGSDVQ	169	0.8000	9.09
25	LVLSKALGF	160	0.7000	7.95
26	LISLAAILV	38	0.6800	7.73
27	FYQLWAFIT	121	0.6500	7.39
28	VNPDATMSL	18	0.6000	6.82
29	IFGLDSLGE	59	0.6000	6.82
30	YFGFLNLL	186	0.6000	6.82

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	LVVFGVSFE	194	6.3000	67.02
2	LIVMLNLAG	206	5.3000	56.38
3	LGFLTVGS	166	4.8000	51.06
4	IFGLDSLGE	59	4.6000	48.94
5	LLNLLVVFV	190	3.6000	38.30
6	IFAMFVFAA	229	3.4500	36.70
7	IVMLNLAGL	207	3.4000	36.17
8	LNLLVVFV	191	3.2500	34.57
9	IVLACPWF	113	2.9000	30.85
10	FPLLIVMLN	203	2.7000	28.72
11	VNPDATMSL	18	2.6000	27.66
12	LVLSKALGF	160	2.6000	27.66
13	LLTVGSDVQ	169	2.6000	27.66
14	LLIVMLNLA	205	2.6000	27.66
15	FGLLNLLV	187	2.5000	26.60
16	MLRLKVGMA	102	2.4000	25.53
17	LAAILVTTI	41	2.3000	24.47
18	LGAALTVLL	251	2.3000	24.47
19	VIPAAVLFV	144	2.2000	23.40
20	IQIARVHDK	263	2.2000	23.40
21	IFGFVWYSH	49	2.1000	22.34
22	MFVFAAIFT	232	2.0800	22.13
23	LISLAAILV	38	1.9800	21.06
24	LAGLLTYER	212	1.9000	20.21
25	LAIQIARVH	261	1.9000	20.21
26	LLISLAAIL	37	1.8000	19.15
27	LWAFITPGL	124	1.8000	19.15
28	FAAIFTPGS	235	1.7000	18.09
29	MSLVDHLTE	24	1.4000	14.89
30	VWYSHSIFG	53	1.3800	14.68

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	LVLSKALGF	160	4.5000	50.00
2	FGLLNLLV	187	4.4000	48.89
3	LGFLLVGS	166	4.1800	46.44
4	VNPDATMSL	18	4.1600	46.22
5	LIVMLNLAG	206	3.9000	43.33
6	LVDHLTELR	26	3.5000	38.89
7	VLLELAIQI	257	3.1800	35.33
8	FAAIFTPGS	235	3.1000	34.44
9	IVLACPVWF	113	3.0800	34.22
10	FVIPAAVLF	143	2.9800	33.11
11	FLLNLLVVF	189	2.7800	30.89
12	LLNLLVFG	190	2.6800	29.78
13	FVAGAVLAY	151	2.4000	26.67
14	FPLLIVMLN	203	2.4000	26.67
15	IQIARVHDK	263	2.4000	26.67
16	VIPAAVLFV	144	2.3000	25.56
17	VSFEFPLLI	199	2.3000	25.56
18	LLISLAAIL	37	2.2600	25.11
19	IFGLDSLGE	59	2.2000	24.44
20	IVMLNLAGL	207	2.1600	24.00
21	WFYQLWAFI	120	2.0000	22.22
22	VWYSHSIFG	53	1.9800	22.00
23	LNLLVFGV	191	1.8000	20.00
24	YERLKSRR	218	1.7000	18.89
25	FVFAAIFTP	233	1.5000	16.67
26	LISLAAILV	38	1.4800	16.44
27	FAVAFVIPA	139	1.4800	16.44
28	LGAALTVLL	251	1.4400	16.00
29	VRAAGLLKR	0	1.3000	14.44

30	FLLTVGSDV	168	1.3000	14.44
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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	LGFLLTVGS	166	4.8000	54.55
2	LIVMLNLAG	206	4.0000	45.45
3	IFAMFVFAA	229	3.4500	39.20
4	LVVFGVSFE	194	3.3000	37.50
5	LNLLVVFGV	191	2.9500	33.52
6	IQIARVHDK	263	2.9000	32.95
7	LLIVMLNLA	205	2.6000	29.55
8	MLRLKVGMA	102	2.4000	27.27
9	IVMLNLAGL	207	2.4000	27.27
10	LNLLVVFG	190	2.3000	26.14
11	FGLLNLLV	187	2.2000	25.00
12	LAAILVTTI	41	2.1000	23.86
13	IVLACPVWF	113	2.0000	22.73
14	VIPAAVLV	144	1.9000	21.59
15	LAGLLTYER	212	1.9000	21.59
16	LLTVGSDVQ	169	1.8000	20.45
17	LVLSKALGF	160	1.7000	19.32
18	FAAIFTPGS	235	1.7000	19.32
19	LISLAAILV	38	1.6800	19.09
20	VNPDATMSL	18	1.6000	18.18
21	IFGLDSLGE	59	1.6000	18.18
22	VLAYLVLSK	156	1.5000	17.05
23	LGAALTVLL	251	1.3000	14.77
24	LFVAGAVLA	150	1.2000	13.64
25	LAYLVLSKA	157	1.2000	13.64
26	MFVFAAIFT	232	1.1800	13.41
27	LKRLNPRNR	6	0.9000	10.23
28	LRLKVGMAA	103	0.9000	10.23

29	IFGFVWYSH	49	0.8800	10.00
30	LLISLAAIL	37	0.8000	9.09

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	LGFLLTVGS	166	3.7800	43.95
2	FGFLLNLLV	187	3.4000	39.53
3	VNPDATMSL	18	3.2000	37.21
4	FAAIFTPGS	235	2.7000	31.40
5	LVLSKALGF	160	2.6000	30.23
6	LIVMLNLAG	206	2.5000	29.07
7	IQIARVHDK	263	2.3000	26.74
8	VLLELAIQI	257	2.2800	26.51
9	LVDHLTELRL	26	2.0000	23.26
10	FPLLIVMLN	203	1.6000	18.60
11	FAVAFVIPA	139	1.4800	17.21
12	VSFEFPLLI	199	1.4000	16.28
13	LLISLAAIL	37	1.3000	15.12
14	VIPAAVLFV	144	1.3000	15.12
15	LLNLLVVFG	190	1.2800	14.88
16	IVMLNLAGL	207	1.2000	13.95
17	IVLACPWWF	113	1.1800	13.72
18	MLRLKVGMA	102	1.1000	12.79
19	WFYQLWAFI	120	1.1000	12.79
20	FVAGAVLAY	151	1.1000	12.79
21	FVIPAAVLF	143	1.0800	12.56
22	FLLNLLVVF	189	0.8800	10.23
23	IFGLDSLGE	59	0.8000	9.30
24	LNLLVVFGV	191	0.8000	9.30
25	IFAMFVFAA	229	0.6000	6.98
26	VWYSHSIFG	53	0.5800	6.74
27	FVFAAIFTP	233	0.5000	5.81

28	LISLAAILV	38	0.4800	5.58
29	LGAALTVLL	251	0.4800	5.58
30	LFVAGAVLA	150	0.3800	4.42

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	LVLSKALGF	160	7.9000	68.10
2	LLISLAAIL	37	6.4000	55.17
3	WYSHSIFGL	54	6.2000	53.45
4	VGMAAGIVL	107	6.1000	52.59
5	FVIPAAVLF	143	6.1000	52.59
6	ILVTTIFGF	44	5.6000	48.28
7	VVFGVSFEF	195	5.6000	48.28
8	FGVSFEFPL	197	5.5000	47.41
9	WRRGLIFAM	224	5.4000	46.55
10	VLELAIQI	257	5.4000	46.55
11	IVLACPVWF	113	5.3000	45.69
12	FLLTVGSDV	168	5.2000	44.83
13	YFGFLLNLL	186	5.1000	43.97
14	LRTRLLISL	33	5.0000	43.10
15	VIPAAVLFV	144	4.7000	40.52
16	LAAILVTTI	41	4.5000	38.79
17	VLVAGAVL	149	4.5000	38.79
18	LLVVFGVSF	193	4.5000	38.79
19	LGAALTVLL	251	4.4200	38.10
20	FVAGAVLAY	151	4.4000	37.93
21	WLRHPYCAL	68	4.2000	36.21
22	LNLLVFGV	191	4.2000	36.21
23	IVMLNLAGL	207	4.2000	36.21
24	FAMFVFAAI	230	4.2000	36.21
25	FGFLLNLLV	187	4.1000	35.34
26	LISLAAILV	38	3.9000	33.62

27	FVFAAIFTP	233	3.9000	33.62
28	LVTTFGFV	45	3.7000	31.90
29	FLLNLLVVF	189	3.7000	31.90
30	VNPDATMSL	18	3.6200	31.21

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	LVLSKALGF	160	7.9000	68.10
2	LLISLAAIL	37	6.4000	55.17
3	WYSHSIFGL	54	6.2000	53.45
4	VGMAAGIVL	107	6.1000	52.59
5	FVIPAAVLF	143	6.1000	52.59
6	ILVTTIFGF	44	5.6000	48.28
7	VVFGVSFEF	195	5.6000	48.28
8	FGVSFEFPL	197	5.5000	47.41
9	WRRGLIFAM	224	5.4000	46.55
10	VLLELAIQI	257	5.4000	46.55
11	IVLACPWF	113	5.3000	45.69
12	FLLTVGSDV	168	5.2000	44.83
13	YFGFLLNLL	186	5.1000	43.97
14	LRTRLLISL	33	5.0000	43.10
15	VIPAAVLFV	144	4.7000	40.52
16	LAAILVTTI	41	4.5000	38.79
17	VLVAGAVL	149	4.5000	38.79
18	LLVVFVGSF	193	4.5000	38.79
19	LGAALTVLL	251	4.4200	38.10
20	FVAGAVLAY	151	4.4000	37.93
21	WLRHPYCAL	68	4.2000	36.21
22	LNLLVFGV	191	4.2000	36.21
23	IVMLNLAGL	207	4.2000	36.21
24	FAMFVFAAI	230	4.2000	36.21
25	FGFLLNLLV	187	4.1000	35.34

26	LISLAAILV	38	3.9000	33.62
27	FVFAAIFTP	233	3.9000	33.62
28	LVTTFGFV	45	3.7000	31.90
29	FLLNLLVVF	189	3.7000	31.90
30	VNPDATMSL	18	3.6200	31.21

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	FMLRLKVGM	101	5.3000	61.63
2	YLVLSKALG	159	3.8000	44.19
3	LLTYERLKS	215	3.6000	41.86
4	LRLKVGMAA	103	3.5000	40.70
5	IVMLNLAGL	207	3.4000	39.53
6	LVVFGVSFE	194	3.3000	38.37
7	LRTRLLISL	33	2.9000	33.72
8	FVWYSHSIF	52	2.8000	32.56
9	FPLLIVMLN	203	2.7000	31.40
10	LYQRERRFA	132	2.6000	30.23
11	WRRGLIFAM	224	2.4000	27.91
12	VLSKALGFL	161	2.2000	25.58
13	MLRLKVGMA	102	2.1000	24.42
14	FVAGAVLAY	151	2.1000	24.42
15	VLAYLVLSK	156	2.1000	24.42
16	LNPRNRRSR	9	1.8000	20.93
17	FVFAAIFTP	233	1.8000	20.93
18	IFGLDSLGE	59	1.6000	18.60
19	LLNLLVVFV	190	1.6000	18.60
20	IFAMFVFAA	229	1.5000	17.44
21	IVLACPVWF	113	1.4000	16.28
22	FVIPAAVLF	143	1.4000	16.28
23	LGFLITVGS	166	1.4000	16.28
24	LNLLVVFV	191	1.4000	16.28

25	LIVMLNLAG	206	1.4000	16.28
26	WAFITPGLY	125	1.2000	13.95
27	LLKRLNPRN	5	1.1000	12.79
28	VHDKRKAKR	268	1.1000	12.79
29	FLLNLLVVF	189	1.0000	11.63
30	IQIARVHDK	263	1.0000	11.63

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	FMLRLKVGM	101	4.2000	52.50
2	LLTYERLKS	215	3.6000	45.00
3	LRLKVGMAA	103	3.5000	43.75
4	VLAYLVLSK	156	2.8000	35.00
5	LYQRERRFA	132	2.6000	32.50
6	YLVLSKALG	159	2.5000	31.25
7	IVMLNLAGL	207	2.4000	30.00
8	MLRLKVGMA	102	2.1000	26.25
9	LRTRLLISL	33	1.9000	23.75
10	FVWYSHSIF	52	1.9000	23.75
11	LNPRNRRSR	9	1.8000	22.50
12	IQIARVHDK	263	1.7000	21.25
13	IFAMFVFAA	229	1.5000	18.75
14	LGFLTVGS	166	1.4000	17.50
15	FVFAAIFTP	233	1.4000	17.50
16	WRRGLIFAM	224	1.3000	16.25
17	VLSKALGFL	161	1.2000	15.00
18	LNLLVVFVGV	191	1.1000	13.75
19	VHDKRKAKR	268	1.1000	13.75
20	FVAGAVLAY	151	1.0000	12.50
21	FAVAFVIPA	139	0.9000	11.25
22	FPLLIVMLN	203	0.7000	8.75
23	LLIVMLNLA	205	0.7000	8.75

24	VIPAAVLFV	144	0.6000	7.50
25	FAAIFTPGS	235	0.6000	7.50
26	IVLACPWF	113	0.5000	6.25
27	FVIPAAVLF	143	0.5000	6.25
28	LKSWRRGLI	221	0.5000	6.25
29	LKRLNPRNR	6	0.4000	5.00
30	FGLLNLLV	187	0.4000	5.00

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	LLTYERLKS	215	4.6000	57.50
2	LRLKVGMAA	103	4.5000	56.25
3	VLAYLVLSK	156	3.8000	47.50
4	LYQRERRFA	132	3.6000	45.00
5	IVMLNLAGL	207	3.4000	42.50
6	FMLRLKVGM	101	3.2000	40.00
7	MLRLKVGMA	102	3.1000	38.75
8	LRTRLLISL	33	2.9000	36.25
9	LNPRNRRSR	9	2.8000	35.00
10	IQIARVHDK	263	2.7000	33.75
11	IFAMFVFAA	229	2.5000	31.25
12	LGFLTVGS	166	2.4000	30.00
13	VLSKALGFL	161	2.2000	27.50
14	LNLLVVFGV	191	2.1000	26.25
15	VHDKRKAKR	268	2.1000	26.25
16	LLIVMLNLA	205	1.7000	21.25
17	VIPAAVLFV	144	1.6000	20.00
18	IVLACPWF	113	1.5000	18.75
19	YLVLSKALG	159	1.5000	18.75
20	LKSWRRGLI	221	1.5000	18.75
21	LKRLNPRNR	6	1.4000	17.50
22	LNLLVVFG	190	1.3000	16.25

23	LVVFGVSFE	194	1.3000	16.25
24	VRAAGLLKR	0	1.1000	13.75
25	LIVMLNLAG	206	1.1000	13.75
26	FVWYSHSIF	52	0.9000	11.25
27	VWIFYQLWAF	119	0.9000	11.25
28	VAFVIPAAV	141	0.9000	11.25
29	LVLSKALGF	160	0.8000	10.00
30	LNLAGLLTY	210	0.7000	8.75

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	LLTYERLKS	215	4.6000	53.49
2	LRLKVGMAA	103	4.5000	52.33
3	IVMLNLAGL	207	4.4000	51.16
4	FMLRLKVGM	101	4.3000	50.00
5	LVVFGVSFE	194	4.3000	50.00
6	LRTRLLISL	33	3.9000	45.35
7	LYQRERRFA	132	3.6000	41.86
8	VLSKALGFL	161	3.2000	37.21
9	MLRLKVGMA	102	3.1000	36.05
10	VLAYLVLSK	156	3.1000	36.05
11	LNPRNRRSR	9	2.8000	32.56
12	YLVLSKALG	159	2.8000	32.56
13	IFGLDSLGE	59	2.6000	30.23
14	LLNLLVVFG	190	2.6000	30.23
15	IFAMFVFAA	229	2.5000	29.07
16	IVLACPVWF	113	2.4000	27.91
17	LGFLTVGS	166	2.4000	27.91
18	LNLLVVFGV	191	2.4000	27.91
19	LIVMLNLAG	206	2.4000	27.91
20	LLKRLNPRN	5	2.1000	24.42
21	VHDKRKAKR	268	2.1000	24.42

22	IQIARVHDK	263	2.0000	23.26
23	MSLVDHLTE	24	1.9000	22.09
24	VIPAAVLFFV	144	1.9000	22.09
25	FVWYSHSIF	52	1.8000	20.93
26	VWFYQLWAF	119	1.8000	20.93
27	LNLAGLLTY	210	1.8000	20.93
28	LVLSKALGF	160	1.7000	19.77
29	FPLLIVMLN	203	1.7000	19.77
30	LLIVMLNLA	205	1.7000	19.77

ALLELE: DRB1_0813		Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7	
Rank	Sequence	At Position	Score	% of Highest Score
1	FMLRLKVGM	101	5.2000	59.77
2	LRLKVGMAA	103	4.5000	51.72
3	LLTYERLKS	215	4.2000	48.28
4	FVWYSHSIF	52	3.7000	42.53
5	VLAYLVLSK	156	3.4000	39.08
6	LRTRLLISL	33	2.7800	31.95
7	LLIVMLNLA	205	2.7000	31.03
8	YLVLSKALG	159	2.5000	28.74
9	LGFLITVGS	166	2.4000	27.59
10	IVMLNLAGL	207	2.4000	27.59
11	IFAMFVFAA	229	2.3500	27.01
12	LYQRERRFA	132	2.3000	26.44
13	FVFAAIFTP	233	2.2500	25.86
14	IQIARVHDK	263	2.2000	25.29
15	WRRGLIFAM	224	2.1500	24.71
16	LVVFGVSFE	194	2.1000	24.14
17	LNLLVVFGV	191	1.9500	22.41
18	FAVAFVIPA	139	1.7800	20.46
19	FPLLIVMLN	203	1.7000	19.54
20	FVAGAVLAY	151	1.6000	18.39

21	LNPRNRRSR	9	1.5000	17.24
22	IVLACPVWF	113	1.5000	17.24
23	FVIPAAVLF	143	1.5000	17.24
24	FGFVWYSHS	50	1.4000	16.09
25	MLRLKVGMA	102	1.4000	16.09
26	YFGFLLNLL	186	1.4000	16.09
27	LLNLLVVFG	190	1.3000	14.94
28	VIPAAVLFV	144	1.2000	13.79
29	LAYLVLSKA	157	1.2000	13.79
30	YQRERRFAV	133	1.1500	13.22

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	FMLRLKVGM	101	5.8000	57.43
2	LLTYERLKS	215	5.4000	53.47
3	LRLKVGMAA	103	5.1000	50.50
4	LRTRLLISL	33	4.5000	44.55
5	FPLLIVMLN	203	4.3000	42.57
6	FVAGAVLAY	151	3.9000	38.61
7	VLAYLVLSK	156	3.9000	38.61
8	YLVLSKALG	159	3.8000	37.62
9	IFGLDSLGE	59	3.4000	33.66
10	IVMLNLAGL	207	3.4000	33.66
11	LVVFGVSFE	194	3.3000	32.67
12	LIVMLNLAG	206	3.2000	31.68
13	WRRGLIFAM	224	2.9000	28.71
14	FVWYSHSIF	52	2.8000	27.72
15	LYQRERRFA	132	2.8000	27.72
16	MSLVDHLTE	24	2.7000	26.73
17	VIPAAVLFV	144	2.7000	26.73
18	LNLAGLLTY	210	2.6000	25.74
19	FAVAFVIPA	139	2.5000	24.75

20	LVLSKALGF	160	2.5000	24.75
21	FGFLLNLLV	187	2.5000	24.75
22	VLSKALGFL	161	2.3000	22.77
23	FVFAAIFTP	233	2.3000	22.77
24	LLKRLNPRN	5	2.2500	22.28
25	MLRLKVGMA	102	2.2000	21.78
26	LLNLLVVFVG	190	2.1000	20.79
27	LNPRNRRSR	9	2.0000	19.80
28	IFAMFVFAA	229	2.0000	19.80
29	VRAAGLLKR	0	1.9000	18.81
30	IVLACPVWF	113	1.9000	18.81

ALLELE: DRB1_1101 Threshold for 3 % with score: 1.1 Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	YLVLSKALG	159	2.9000	34.94
2	IVMLNLAGL	207	2.8000	33.73
3	FPLLIVMLN	203	2.7000	32.53
4	MLRLKVGMA	102	2.6000	31.33
5	FGFLLNLLV	187	2.6000	31.33
6	FAVAFVIPA	139	2.5000	30.12
7	LLTYERLKS	215	2.5000	30.12
8	VIPAAVLFV	144	2.4000	28.92
9	IQIARVHDK	263	2.4000	28.92
10	FAAIFTPGS	235	2.3500	28.31
11	LRLKVGMAA	103	2.3000	27.71
12	LGFLLTVGS	166	2.3000	27.71
13	FVAGAVLAY	151	2.1000	25.30
14	LNLLVVFVG	191	2.0000	24.10
15	VRAAGLLKR	0	1.9000	22.89
16	LVLSKALGF	160	1.9000	22.89
17	FVFAAIFTP	233	1.9000	22.89
18	FMLRLKVGM	101	1.7000	20.48

19	VLAYLVLSK	156	1.7000	20.48
20	IFAMFVFAA	229	1.6000	19.28
21	LISLAAILV	38	1.5000	18.07
22	LIVMLNLAG	206	1.5000	18.07
23	LNLAGLLTY	210	1.5000	18.07
24	LLNLLVVFV	190	1.2000	14.46
25	MLNLAGLLT	209	1.2000	14.46
26	LLIVMLNLA	205	1.1000	13.25
27	WRRGLIFAM	224	1.1000	13.25
28	LKRLNPRNR	6	1.0000	12.05
29	IVLACPWWF	113	1.0000	12.05
30	IFGLDSLGE	59	0.8000	9.64

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	IQIARVHDK	263	3.9000	46.43
2	LLTYERLKS	215	3.5000	41.67
3	IFAMFVFAA	229	3.4000	40.48
4	LAIQIARVH	261	3.3800	40.24
5	LRLKVGMAA	103	3.3000	39.29
6	LYQRERRFA	132	3.3000	39.29
7	LNLLVVFGV	191	3.3000	39.29
8	LGFLTVGS	166	3.1000	36.90
9	IVMLNLAGL	207	3.1000	36.90
10	LKRLNPRNR	6	2.9000	34.52
11	VLAYLVLSK	156	2.7000	32.14
12	LNPRNRRSR	9	2.5000	29.76
13	IVLACPWWF	113	2.5000	29.76
14	VIPAAVLFV	144	2.3000	27.38
15	FMLRLKVGM	101	2.1000	25.00
16	LNLLVVVFV	190	2.0000	23.81
17	LVVFGVSFE	194	2.0000	23.81

18	WYSHSIFGL	54	1.9000	22.62
19	LVLSKALGF	160	1.9000	22.62
20	LLIVMLNLA	205	1.9000	22.62
21	FVFAAIFTP	233	1.9000	22.62
22	VRAAGLLKR	0	1.8000	21.43
23	MLRLKVGMA	102	1.8000	21.43
24	VLACPVWFY	114	1.6000	19.05
25	LLATAPFDQ	92	1.5000	17.86
26	LNLAGLLTY	210	1.4000	16.67
27	WRRGLIFAM	224	1.3000	15.48
28	LFVAGAVLA	150	1.2000	14.29
29	YLVLKALG	159	1.2000	14.29
30	LIVMLNLAG	206	1.2000	14.29

Rank	Sequence	At Position	Score	% of Highest Score
ALLELE: DRB1_1104		Threshold for 3 % with score: 2.0		Highest Score achievable by any peptide: 8.3
1	IVMLNLAGL	207	3.8000	45.78
2	MLRLKVGMA	102	3.6000	43.37
3	LLTYERLKS	215	3.5000	42.17
4	VIPAAVLFV	144	3.4000	40.96
5	IQIARVHDK	263	3.4000	40.96
6	LRLKVGMAA	103	3.3000	39.76
7	LGFLTVGS	166	3.3000	39.76
8	LNLLVVFGV	191	3.0000	36.14
9	VRAAGLLKR	0	2.9000	34.94
10	LVLSKALGF	160	2.9000	34.94
11	VLAYLVLSK	156	2.7000	32.53
12	IFAMFVFAA	229	2.6000	31.33
13	LISLAAILV	38	2.5000	30.12
14	LIVMLNLAG	206	2.5000	30.12
15	LNLAGLLTY	210	2.5000	30.12
16	LNLLVVFG	190	2.2000	26.51

17	MLNLAGLLT	209	2.2000	26.51
18	LLIVMLNLA	205	2.1000	25.30
19	LKRLNPRNR	6	2.0000	24.10
20	IVLACPWWF	113	2.0000	24.10
21	YLVLSKALG	159	1.9000	22.89
22	IFGLDSLGE	59	1.8000	21.69
23	ISLAAILVT	39	1.7000	20.48
24	FPLLIVMLN	203	1.7000	20.48
25	FGFLLNLLV	187	1.6000	19.28
26	LRTRLLISL	33	1.5000	18.07
27	FAVAFVIPA	139	1.5000	18.07
28	LKSWRRGLI	221	1.5000	18.07
29	LTVLLELAI	255	1.4000	16.87
30	FAAIFTPGS	235	1.3500	16.27

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	IVMLNLAGL	207	3.8000	45.78
2	MLRLKVGMA	102	3.6000	43.37
3	LLTYERLKS	215	3.5000	42.17
4	VIPAAVLFV	144	3.4000	40.96
5	IQIARVHDK	263	3.4000	40.96
6	LRLKVGMAA	103	3.3000	39.76
7	LGFLTVGS	166	3.3000	39.76
8	LNLLVVFGV	191	3.0000	36.14
9	VRAAGLLKR	0	2.9000	34.94
10	LVLSKALGF	160	2.9000	34.94
11	VLAYLVLSK	156	2.7000	32.53
12	IFAMFVFAA	229	2.6000	31.33
13	LISLAAILV	38	2.5000	30.12
14	LIVMLNLAG	206	2.5000	30.12
15	LNLAGLLTY	210	2.5000	30.12

16	LLNLLVVFVG	190	2.2000	26.51
17	MLNLAGLLT	209	2.2000	26.51
18	LLIVMLNLA	205	2.1000	25.30
19	LKRLNPRNR	6	2.0000	24.10
20	IVLACPWWF	113	2.0000	24.10
21	YLVLSKALG	159	1.9000	22.89
22	IFGLDSLGE	59	1.8000	21.69
23	ISLAAILVT	39	1.7000	20.48
24	FPLLIVMLN	203	1.7000	20.48
25	FGFLLNLLV	187	1.6000	19.28
26	LRTRLLISL	33	1.5000	18.07
27	FAVAFVIPA	139	1.5000	18.07
28	LKSWRRGLI	221	1.5000	18.07
29	LTVLLELAI	255	1.4000	16.87
30	FAAIFTPGS	235	1.3500	16.27

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	VNPDATMSL	18	4.3000	47.25
2	WRRGLIFAM	224	3.2000	35.16
3	MLRLKVGMA	102	3.0000	32.97
4	LVLSKALGF	160	3.0000	32.97
5	LGFLLTVGS	166	3.0000	32.97
6	VGSDVQVTA	172	2.9000	31.87
7	IVLACPWWF	113	2.8000	30.77
8	LNLLVVFVG	191	2.8000	30.77
9	VVFGVSFEF	195	2.8000	30.77
10	IQIARVHDK	263	2.8000	30.77
11	IVMLNLAGL	207	2.7000	29.67
12	LLIVMLNLA	205	2.6100	28.68
13	LRLKVGMAA	103	2.6000	28.57
14	IFAMFVFAA	229	2.5000	27.47

15	LLISLAAIL	37	2.2000	24.18
16	FGLDSLGEW	60	2.1000	23.08
17	VIPAAVLV	144	2.1000	23.08
18	FVAGAVLAY	151	2.0000	21.98
19	MAAGIVLAC	109	1.9000	20.88
20	LLNLLVFG	190	1.9000	20.88
21	LLTYERLKS	215	1.9000	20.88
22	LKVGMAAGI	105	1.8000	19.78
23	FVFAAIFTP	233	1.8000	19.78
24	FAAIFTPGS	235	1.7000	18.68
25	VRAAGLLKR	0	1.6000	17.58
26	LLATAPFDQ	92	1.5000	16.48
27	LFVAGAVLA	150	1.5000	16.48
28	VMLNLAGLL	208	1.4000	15.38
29	LAAILVTTI	41	1.3000	14.29
30	FMLRLKVGM	101	1.2000	13.19

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	FMLRLKVGM	101	3.1000	36.90
2	WYSHSIFGL	54	2.9000	34.52
3	FVFAAIFTP	233	2.9000	34.52
4	IQIARVHDK	263	2.9000	34.52
5	LLTYERLKS	215	2.5000	29.76
6	IFAMFVFAA	229	2.4000	28.57
7	LAIQIARVH	261	2.3800	28.33
8	LRLKVGMAA	103	2.3000	27.38
9	LYQRERRFA	132	2.3000	27.38
10	LNLLVFGV	191	2.3000	27.38
11	WRRGLIFAM	224	2.3000	27.38
12	YLVLSKALG	159	2.2000	26.19
13	LGFLTVGS	166	2.1000	25.00

14	IVMLNLAGL	207	2.1000	25.00
15	LKRLNPRNR	6	1.9000	22.62
16	YQRERRFAV	133	1.7000	20.24
17	VLAYLVLSK	156	1.7000	20.24
18	LNPRNRRSR	9	1.5000	17.86
19	IVLACPWF	113	1.5000	17.86
20	VIPAAVLFV	144	1.3000	15.48
21	FAVAFVIPA	139	1.2000	14.29
22	FVAGAVLAY	151	1.2000	14.29
23	FLLNLLVVF	189	1.2000	14.29
24	YFGFLLNLL	186	1.1000	13.10
25	FVIPAAVLF	143	1.0000	11.90
26	LLNLLVFG	190	1.0000	11.90
27	LVVFGVSFE	194	1.0000	11.90
28	LVLSKALGF	160	0.9000	10.71
29	LLIVMLNLA	205	0.9000	10.71
30	VRAAGLLKR	0	0.8000	9.52

ALLELE: DRB1_1120	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8		
Rank	Sequence	At Position	Score	% of Highest Score
1	FMLRLKVGM	101	4.6000	52.27
2	FVFAAIFTP	233	3.9000	44.32
3	WYSHSIFGL	54	3.8600	43.86
4	WRRGLIFAM	224	3.8000	43.18
5	YLVLSKALG	159	3.6000	40.91
6	LKRLNPRNR	6	3.4000	38.64
7	IVLACPWF	113	3.4000	38.64
8	LNLLVFGV	191	3.3000	37.50
9	FLLNLLVVF	189	3.1000	35.23
10	IVMLNLAGL	207	3.0600	34.77
11	LNPRNRRSR	9	3.0000	34.09
12	IQIARVHDK	263	3.0000	34.09

13	FVIPAAVLF	143	2.9000	32.95
14	LLTYERLKS	215	2.9000	32.95
15	LVLSKALGF	160	2.8000	31.82
16	YQRERRFAV	133	2.7000	30.68
17	FVAGAVLAY	151	2.5000	28.41
18	LGFLITVGS	166	2.5000	28.41
19	FVWYSHSIF	52	2.4000	27.27
20	LLNLLVFG	190	2.4000	27.27
21	LVVFGVSFE	194	2.4000	27.27
22	IFAMFVFAA	229	2.4000	27.27
23	VRAAGLLKR	0	2.3000	26.14
24	LRLKVGMAA	103	2.3000	26.14
25	LYQRERRFA	132	2.3000	26.14
26	VIPAAVLFV	144	2.3000	26.14
27	YFGFLLNLL	186	2.0600	23.41
28	YERLKSRR	218	2.0000	22.73
29	VLACPVWFY	114	1.9000	21.59
30	VLAYLVLSK	156	1.8000	20.45

ALLELE: DRB1_1121	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	IQIARVHDK	263	3.9000	46.43
2	LLTYERLKS	215	3.5000	41.67
3	IFAMFVFAA	229	3.4000	40.48
4	LAIQIARVH	261	3.3800	40.24
5	LRLKVGMAA	103	3.3000	39.29
6	LYQRERRFA	132	3.3000	39.29
7	LNLLVFGV	191	3.3000	39.29
8	LGFLITVGS	166	3.1000	36.90
9	IVMLNLAGL	207	3.1000	36.90
10	LKRLNPRNR	6	2.9000	34.52
11	VLAYLVLSK	156	2.7000	32.14

12	LNPRNRRSR	9	2.5000	29.76
13	IVLACPWWF	113	2.5000	29.76
14	VIPAAVLV	144	2.3000	27.38
15	FMLRLKVG	101	2.1000	25.00
16	LLNLLVFG	190	2.0000	23.81
17	LVVFGVSFE	194	2.0000	23.81
18	WYSHSIFGL	54	1.9000	22.62
19	LVLSKALGF	160	1.9000	22.62
20	LLIVMLNLA	205	1.9000	22.62
21	FVFAAIFTP	233	1.9000	22.62
22	VRAAGLLKR	0	1.8000	21.43
23	MLRLKVGMA	102	1.8000	21.43
24	VLACPWWFY	114	1.6000	19.05
25	LLATAPFDQ	92	1.5000	17.86
26	LNLAGLLTY	210	1.4000	16.67
27	WRRGLIFAM	224	1.3000	15.48
28	LFVAGAVLA	150	1.2000	14.29
29	YLVLSKALG	159	1.2000	14.29
30	LIVMLNLAG	206	1.2000	14.29

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	YLVLSKALG	159	4.3000	49.43
2	LVLSKALGF	160	3.8000	43.68
3	IVMLNLAGL	207	3.7600	43.22
4	FGLLNLLV	187	3.6000	41.38
5	FPLLIVMLN	203	3.5000	40.23
6	VRAAGLLKR	0	3.4000	39.08
7	VIPAAVLV	144	3.4000	39.08
8	FVAGAVLAY	151	3.4000	39.08
9	FMLRLKVG	101	3.2000	36.78
10	LNLLVFGV	191	3.0000	34.48

11	IVLACPVWF	113	2.9000	33.33
12	LIVMLNLAG	206	2.9000	33.33
13	LLTYERLKS	215	2.9000	33.33
14	FVFAAIFTP	233	2.9000	33.33
15	LNLAGLLTY	210	2.8000	32.18
16	FAAIFTPGS	235	2.7500	31.61
17	LGFLLVGS	166	2.7000	31.03
18	MLRLKVGMA	102	2.6000	29.89
19	LLNLLVFG	190	2.6000	29.89
20	WRRGLIFAM	224	2.6000	29.89
21	LKRLNPRNR	6	2.5000	28.74
22	LISLAAILV	38	2.5000	28.74
23	FAVAFVIPA	139	2.5000	28.74
24	FLLNLLVVF	189	2.5000	28.74
25	IQIARVHDK	263	2.5000	28.74
26	LRLKVGMAA	103	2.3000	26.44
27	IFGLDSLGE	59	2.2000	25.29
28	FVIPAAVLF	143	2.2000	25.29
29	WAFITPGLY	125	2.1000	24.14
30	MLNLAGLLT	209	1.9000	21.84

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	LKRLNPRNR	6	4.4000	50.00
2	IVLACPVWF	113	4.4000	50.00
3	LNLLVFGV	191	4.3000	48.86
4	IVMLNLAGL	207	4.0600	46.14
5	LNPRRRSR	9	4.0000	45.45
6	IQIARVHDK	263	4.0000	45.45
7	LLTYERLKS	215	3.9000	44.32
8	LVLSKALGF	160	3.8000	43.18
9	FMLRLKVGM	101	3.6000	40.91

10	LGFLLTVGS	166	3.5000	39.77
11	LLNLLVVFG	190	3.4000	38.64
12	LVVFGVSFE	194	3.4000	38.64
13	IFAMFVFAA	229	3.4000	38.64
14	VRAAGLLKR	0	3.3000	37.50
15	LRLKVGMAA	103	3.3000	37.50
16	LYQRERRFA	132	3.3000	37.50
17	VIPAAVLV	144	3.3000	37.50
18	VLACPVWFY	114	2.9000	32.95
19	FVFAAIFTP	233	2.9000	32.95
20	WYSHSIFGL	54	2.8600	32.50
21	VLAYLVLSK	156	2.8000	31.82
22	VVFGVSFEF	195	2.8000	31.82
23	WRRGLIFAM	224	2.8000	31.82
24	LAIQIARVH	261	2.8000	31.82
25	LNLAGLLTY	210	2.7000	30.68
26	LVDHLTEL	26	2.6000	29.55
27	ILVTTIFGF	44	2.6000	29.55
28	VWVYQLWAF	119	2.6000	29.55
29	YLVLSKALG	159	2.6000	29.55
30	LIVMLNLAG	206	2.6000	29.55

ALLELE: DRB1_1302	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8		
Rank	Sequence	At Position	Score	% of Highest Score
1	FMLRLKVGM	101	4.6000	52.27
2	FVFAAIFTP	233	3.9000	44.32
3	WYSHSIFGL	54	3.8600	43.86
4	WRRGLIFAM	224	3.8000	43.18
5	YLVLSKALG	159	3.6000	40.91
6	LKRLNPRNR	6	3.4000	38.64
7	IVLACPVWF	113	3.4000	38.64
8	LNLLVVFGV	191	3.3000	37.50

9	FLLNLLVVF	189	3.1000	35.23
10	IVMLNLAGL	207	3.0600	34.77
11	LNPRNRRSR	9	3.0000	34.09
12	IQIARVHDK	263	3.0000	34.09
13	FVIPAAVLF	143	2.9000	32.95
14	LLTYERLKS	215	2.9000	32.95
15	LVLSKALGF	160	2.8000	31.82
16	YQRERRFAV	133	2.7000	30.68
17	FVAGAVLAY	151	2.5000	28.41
18	LGFLLVGS	166	2.5000	28.41
19	FVWYSHSIF	52	2.4000	27.27
20	LLNLLVVFV	190	2.4000	27.27
21	LVVFGVSFE	194	2.4000	27.27
22	IFAMFVFAA	229	2.4000	27.27
23	VRAAGLLKR	0	2.3000	26.14
24	LRLKVGMAA	103	2.3000	26.14
25	LYQRERRFA	132	2.3000	26.14
26	VIPAAVLFV	144	2.3000	26.14
27	YFGFLLNLL	186	2.0600	23.41
28	YERLKSRR	218	2.0000	22.73
29	VLACPWFY	114	1.9000	21.59
30	VLAYLVLSK	156	1.8000	20.45

ALLELE: DRB1_1304	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVFGVSFE	194	5.0000	55.56
2	LAIQIARVH	261	4.6000	51.11
3	IVMLNLAGL	207	4.1000	45.56
4	LNLLVVFV	191	3.6000	40.00
5	LLTYERLKS	215	3.5000	38.89
6	IVLACPWF	113	3.4000	37.78
7	IFAMFVFAA	229	3.4000	37.78

8	LRLKVGMAA	103	3.3000	36.67
9	LYQRERRFA	132	3.3000	36.67
10	LLNLLVVFG	190	3.3000	36.67
11	FMLRLKVGM	101	3.2000	35.56
12	IQIARVHDK	263	3.2000	35.56
13	LGFLLVVGS	166	3.1000	34.44
14	IFGLDSLGE	59	3.0000	33.33
15	LKRLNPRNR	6	2.9000	32.22
16	WYSHSIFGL	54	2.9000	32.22
17	LVLSKALGF	160	2.8000	31.11
18	VLACPVWFY	114	2.7000	30.00
19	VIPAAVLV	144	2.6000	28.89
20	LNPRNRRSR	9	2.5000	27.78
21	YLVLSKALG	159	2.5000	27.78
22	LIVMLNLAG	206	2.5000	27.78
23	LNLAGLLTY	210	2.5000	27.78
24	WRRGLIFAM	224	2.4000	26.67
25	LLATAPFDQ	92	2.3000	25.56
26	FVFAAIFTP	233	2.3000	25.56
27	LRTRLLISL	33	2.1000	23.33
28	VLAYLVLSK	156	2.0000	22.22
29	LLISLAAIL	37	1.9000	21.11
30	LLIVMLNLA	205	1.9000	21.11

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	YLVLSKALG	159	4.3000	49.43
2	LVLSKALGF	160	3.8000	43.68
3	IVMLNLAGL	207	3.7600	43.22
4	FGLLNLLV	187	3.6000	41.38
5	FPLLIVMLN	203	3.5000	40.23
6	VRAAGLLKR	0	3.4000	39.08

7	VIPAAVLV	144	3.4000	39.08
8	FVAGAVLAY	151	3.4000	39.08
9	FMLRLKVGM	101	3.2000	36.78
10	LNLLVFGV	191	3.0000	34.48
11	IVLACPVWF	113	2.9000	33.33
12	LIVMLNLAG	206	2.9000	33.33
13	LLTYERLKS	215	2.9000	33.33
14	FVFAAIFTP	233	2.9000	33.33
15	LNLAGLLTY	210	2.8000	32.18
16	FAAIFTPGS	235	2.7500	31.61
17	LGFLLTVGS	166	2.7000	31.03
18	MLRLKVGMA	102	2.6000	29.89
19	LNLLVFG	190	2.6000	29.89
20	WRRGLIFAM	224	2.6000	29.89
21	LKRLNPRNR	6	2.5000	28.74
22	LISLAAILV	38	2.5000	28.74
23	FAVAFVIPA	139	2.5000	28.74
24	FLLNLLVVF	189	2.5000	28.74
25	IQIARVHDK	263	2.5000	28.74
26	LRLKVGMAA	103	2.3000	26.44
27	IFGLDSLGE	59	2.2000	25.29
28	FVIPAAVLV	143	2.2000	25.29
29	WAFITPGLY	125	2.1000	24.14
30	MLNLAGLLT	209	1.9000	21.84

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8		
Rank	Sequence	At Position	Score	% of Highest Score
1	YLVLSKALG	159	2.9000	42.65
2	IVMLNLAGL	207	2.8000	41.18
3	MLRLKVGMA	102	2.5000	36.76
4	LGFLLTVGS	166	1.8000	26.47
5	IQIARVHDK	263	1.7000	25.00

6	LNLLVVFVGV	191	1.5000	22.06
7	FVFAAIFTP	233	1.4000	20.59
8	FMLRLKVGM	101	1.2000	17.65
9	FAAIFTPGS	235	1.2000	17.65
10	FPLLIVMLN	203	1.1000	16.18
11	IFAMFVFAA	229	1.1000	16.18
12	FAVAFVIPA	139	0.9000	13.24
13	LKRLNPRNR	6	0.8000	11.76
14	FGFLLNLLV	187	0.8000	11.76
15	LLIVMLNLA	205	0.8000	11.76
16	LRLKVGMAA	103	0.7000	10.29
17	WAFITPGLY	125	0.7000	10.29
18	LNLLVVFVGV	190	0.7000	10.29
19	LLTYERLKS	215	0.7000	10.29
20	VIPAAVLV	144	0.6000	8.82
21	WRRGLIFAM	224	0.6000	8.82
22	IVLACPVWF	113	0.5000	7.35
23	LKSWRRGLI	221	0.4000	5.88
24	FVAGAVLAY	151	0.3000	4.41
25	LVVFGVSFE	194	0.2000	2.94
26	FSMTALGAA	246	0.2000	2.94
27	VRAAGLLKR	0	0.1000	1.47
28	LVLSKALGF	160	0.1000	1.47
29	FLLNLLVVF	189	0.1000	1.47
30	FAMFVFAAI	230	0.1000	1.47

ALLELE: DRB1_1311	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3		
Rank	Sequence	At Position	Score	% of Highest Score
1	IVMLNLAGL	207	3.8000	45.78
2	MLRLKVGMA	102	3.6000	43.37
3	LLTYERLKS	215	3.5000	42.17
4	VIPAAVLV	144	3.4000	40.96

5	IQIARVHDK	263	3.4000	40.96
6	LRLKVGMAA	103	3.3000	39.76
7	LGFLLTVGS	166	3.3000	39.76
8	LNLLVVFGV	191	3.0000	36.14
9	VRAAGLLKR	0	2.9000	34.94
10	LVLSKALGF	160	2.9000	34.94
11	VLAYLVLSK	156	2.7000	32.53
12	IFAMFVFAA	229	2.6000	31.33
13	LISLAAILV	38	2.5000	30.12
14	LIVMLNLAG	206	2.5000	30.12
15	LNLAGLLTY	210	2.5000	30.12
16	LLNLLVVFG	190	2.2000	26.51
17	MLNLAGLLT	209	2.2000	26.51
18	LLIVMLNLA	205	2.1000	25.30
19	LKRLNPRNR	6	2.0000	24.10
20	IVLACPWWF	113	2.0000	24.10
21	YLVLSKALG	159	1.9000	22.89
22	IFGLDSLGE	59	1.8000	21.69
23	ISLAAILVT	39	1.7000	20.48
24	FPLLIVMLN	203	1.7000	20.48
25	FGFLLNLLV	187	1.6000	19.28
26	LRTRLLISL	33	1.5000	18.07
27	FAVAFVIPA	139	1.5000	18.07
28	LKSWRRGLI	221	1.5000	18.07
29	LTVLLELAI	255	1.4000	16.87
30	FAAIFTPGS	235	1.3500	16.27

ALLELE: DRB1_1321	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.9		
Rank	Sequence	At Position	Score	% of Highest Score
1	FPLLIVMLN	203	4.7000	52.81
2	YLVLSKALG	159	4.2000	47.19
3	IFGLDSLGE	59	3.8000	42.70

4	IVMLNLAGL	207	3.8000	42.70
5	FVAGAVLAY	151	3.2000	35.96
6	LVVFGVSFE	194	3.2000	35.96
7	FGLLNLLV	187	2.9000	32.58
8	MSLVDHLTE	24	2.8000	31.46
9	FMLRLKVGM	101	2.8000	31.46
10	LVLSKALGF	160	2.8000	31.46
11	LIVMLNLAG	206	2.8000	31.46
12	VIPAAVLV	144	2.7000	30.34
13	MLRLKVGMA	102	2.6000	29.21
14	LNLAGLLTY	210	2.6000	29.21
15	FAVAFVIPA	139	2.5000	28.09
16	LLNLLVVFG	190	2.5000	28.09
17	LLTYERLKS	215	2.5000	28.09
18	FAAIFTPGS	235	2.3500	26.40
19	LRLKVGMAA	103	2.3000	25.84
20	LGFLITVGS	166	2.3000	25.84
21	LNLLVVFGV	191	2.3000	25.84
22	FVFAAIFTP	233	2.3000	25.84
23	WRRGLIFAM	224	2.2000	24.72
24	MLNLAGLLT	209	2.1000	23.60
25	VRAAGLLKR	0	1.9000	21.35
26	IVLACPVWF	113	1.9000	21.35
27	WAFITPGLY	125	1.9000	21.35
28	LISLAAILV	38	1.8000	20.22
29	IQIARVHDK	263	1.7000	19.10
30	ISLAAILVT	39	1.6000	17.98

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	IQIARVHDK	263	3.9000	46.43
2	LLTYERLKS	215	3.5000	41.67

3	IFAMFVFAA	229	3.4000	40.48
4	LAIQIARVH	261	3.3800	40.24
5	LRLKVGMAA	103	3.3000	39.29
6	LYQRERRFA	132	3.3000	39.29
7	LNLLVVFGV	191	3.3000	39.29
8	LGFLLVVGS	166	3.1000	36.90
9	IVMLNLAGL	207	3.1000	36.90
10	LKRLNPRNR	6	2.9000	34.52
11	VLAYLVLSK	156	2.7000	32.14
12	LNPRNRRSR	9	2.5000	29.76
13	IVLACPWWF	113	2.5000	29.76
14	VIPAAVLV	144	2.3000	27.38
15	FMLRLKVG	101	2.1000	25.00
16	LLNLLVVF	190	2.0000	23.81
17	LVVFGVSFE	194	2.0000	23.81
18	WYSHSIFGL	54	1.9000	22.62
19	LVLSKALGF	160	1.9000	22.62
20	LLIVMLNLA	205	1.9000	22.62
21	FVFAAIFTP	233	1.9000	22.62
22	VRAAGLLKR	0	1.8000	21.43
23	MLRLKVGMA	102	1.8000	21.43
24	VLACPWWFY	114	1.6000	19.05
25	LLATAPFDQ	92	1.5000	17.86
26	LNLAGLLTY	210	1.4000	16.67
27	WRRGLIFAM	224	1.3000	15.48
28	LFVAGAVLA	150	1.2000	14.29
29	YLVLSKALG	159	1.2000	14.29
30	LIVMLNLAG	206	1.2000	14.29

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	FMLRLKVG	101	3.1000	36.90

2	WYSHSIFGL	54	2.9000	34.52
3	FVFAAIFTP	233	2.9000	34.52
4	IQIARVHDK	263	2.9000	34.52
5	LLTYERLKS	215	2.5000	29.76
6	IFAMFVFAA	229	2.4000	28.57
7	LAIQIARVH	261	2.3800	28.33
8	LRLKVGMAA	103	2.3000	27.38
9	LYQRERRFA	132	2.3000	27.38
10	LNLLVVFGV	191	2.3000	27.38
11	WRRGLIFAM	224	2.3000	27.38
12	YLVLSKALG	159	2.2000	26.19
13	LGFLLVGS	166	2.1000	25.00
14	IVMLNLAGL	207	2.1000	25.00
15	LKRLNPRNR	6	1.9000	22.62
16	YQRERRFAV	133	1.7000	20.24
17	VLAYLVLSK	156	1.7000	20.24
18	LNPRNRRSR	9	1.5000	17.86
19	IVLACPWWF	113	1.5000	17.86
20	VIPAAVLFV	144	1.3000	15.48
21	FAVAFVIPA	139	1.2000	14.29
22	FVAGAVLAY	151	1.2000	14.29
23	FLLNLLVVF	189	1.2000	14.29
24	YFGFLLNLL	186	1.1000	13.10
25	FVIPAAVLF	143	1.0000	11.90
26	LLNLLVVFG	190	1.0000	11.90
27	LVVFGVSFE	194	1.0000	11.90
28	LVLSKALGF	160	0.9000	10.71
29	LLIVMLNLA	205	0.9000	10.71
30	VRAAGLLKR	0	0.8000	9.52

ALLELE: DRB1_1327	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8		
Rank	Sequence	At Position	Score	% of Highest Score

1	LKRLNPRNR	6	4.4000	50.00
2	IVLACPWWF	113	4.4000	50.00
3	LNLLVVFVG	191	4.3000	48.86
4	IVMLNLAGL	207	4.0600	46.14
5	LNPRNRRSR	9	4.0000	45.45
6	IQIARVHDK	263	4.0000	45.45
7	LLTYERLKS	215	3.9000	44.32
8	LVLSKALGF	160	3.8000	43.18
9	FMLRLKVGM	101	3.6000	40.91
10	LGFLTVGS	166	3.5000	39.77
11	LNLLVVFVG	190	3.4000	38.64
12	LVVFGVSFE	194	3.4000	38.64
13	IFAMVFVAA	229	3.4000	38.64
14	VRAAGLLKR	0	3.3000	37.50
15	LRLKVGMAA	103	3.3000	37.50
16	LYQRERRFA	132	3.3000	37.50
17	VIPAAVLV	144	3.3000	37.50
18	VLACPWWFY	114	2.9000	32.95
19	FVFAAIFTP	233	2.9000	32.95
20	WYSHSIFGL	54	2.8600	32.50
21	VLAYLVLSK	156	2.8000	31.82
22	VVFGVSFEF	195	2.8000	31.82
23	WRRGLIFAM	224	2.8000	31.82
24	LAIQIARVH	261	2.8000	31.82
25	LNLAGLLTY	210	2.7000	30.68
26	LVDHLTEL	26	2.6000	29.55
27	ILVTTIFGF	44	2.6000	29.55
28	VWVYQLWAF	119	2.6000	29.55
29	YLVLSKALG	159	2.6000	29.55
30	LIVMLNLAG	206	2.6000	29.55

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	LKRLNPRNR	6	4.4000	50.00
2	IVLACPWWF	113	4.4000	50.00
3	LNLLVVFGV	191	4.3000	48.86
4	IVMLNLAGL	207	4.0600	46.14
5	LNPRNRRSR	9	4.0000	45.45
6	IQIARVHDK	263	4.0000	45.45
7	LLTYERLKS	215	3.9000	44.32
8	LVLSKALGF	160	3.8000	43.18
9	FMLRLKVGM	101	3.6000	40.91
10	LGFLTVGS	166	3.5000	39.77
11	LLNLLVVFV	190	3.4000	38.64
12	LVVFGVSFE	194	3.4000	38.64
13	IFAMFVFAA	229	3.4000	38.64
14	VRAAGLLKR	0	3.3000	37.50
15	LRLKVGMAA	103	3.3000	37.50
16	LYQRERRFA	132	3.3000	37.50
17	VIPAAVLV	144	3.3000	37.50
18	VLACPWWFY	114	2.9000	32.95
19	FVFAAIFTP	233	2.9000	32.95
20	WYSHSIFGL	54	2.8600	32.50
21	VLAYLVLSK	156	2.8000	31.82
22	VVFGVSFEF	195	2.8000	31.82
23	WRRGLIFAM	224	2.8000	31.82
24	LAIQIARVH	261	2.8000	31.82
25	LNLAGLLTY	210	2.7000	30.68
26	LVDHLTEL	26	2.6000	29.55
27	ILVTTIFGF	44	2.6000	29.55
28	VWVYQLWAF	119	2.6000	29.55
29	YLVLSKALG	159	2.6000	29.55
30	LIVMLNLAG	206	2.6000	29.55

ALLELE: DRB1_1501

Threshold for 3 % with score:

Highest Score achievable by any peptide:

3.25

9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LLTYERLKS	215	6.1000	62.24
2	MFVFAAIFT	232	5.0000	51.02
3	LRLKVGMAA	103	4.7000	47.96
4	IVMLNLAGL	207	4.7000	47.96
5	LRTRLLISL	33	4.6000	46.94
6	VVFGVSFEF	195	4.5000	45.92
7	VGMAAGIVL	107	4.4000	44.90
8	LIVMLNLAG	206	4.4000	44.90
9	LVLSKALGF	160	4.3000	43.88
10	MLNLAGLLT	209	4.2000	42.86
11	YFGFLLNLL	186	3.8000	38.78
12	FGFLLNLLV	187	3.7000	37.76
13	LNLLVVFVG	191	3.7000	37.76
14	LISLAAILV	38	3.6000	36.73
15	VWIFYQLWAF	119	3.6000	36.73
16	LLIVMLNLA	205	3.6000	36.73
17	VLELAIQI	257	3.6000	36.73
18	WRRGLIFAM	224	3.4300	35.00
19	VLAYLVLSK	156	3.4000	34.69
20	LKSWRRGLI	221	3.4000	34.69
21	VRAAGLLKR	0	3.3000	33.67
22	VIPAAVLV	144	3.3000	33.67
23	FAMFVFAAI	230	3.2000	32.65
24	WYSHSIFGL	54	3.1500	32.14
25	LVVFGVSFE	194	3.1000	31.63
26	LWAFITPGL	124	3.0600	31.22
27	FVWYSHSIF	52	3.0000	30.61
28	YQRERRFAV	133	3.0000	30.61
29	VLVAGAVL	149	3.0000	30.61
30	LNLAGLLTY	210	3.0000	30.61

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	LLTYERLKS	215	5.1000	52.04
2	YFGFLLNLL	186	4.8000	48.98
3	FGFLLNLLV	187	4.7000	47.96
4	WRRGLIFAM	224	4.4300	45.20
5	FAMFVFAAI	230	4.2000	42.86
6	WYSHSIFGL	54	4.1500	42.35
7	FVWYSHSIF	52	4.0000	40.82
8	YQRERRFAV	133	4.0000	40.82
9	MFVFAAIFT	232	4.0000	40.82
10	WLRHPYCAL	68	3.7000	37.76
11	LRLKVGMAA	103	3.7000	37.76
12	IVMLNLAGL	207	3.7000	37.76
13	LRTRLLISL	33	3.6000	36.73
14	VVFGVSFEF	195	3.5000	35.71
15	VGMAAGIVL	107	3.4000	34.69
16	LIVMLNLAG	206	3.4000	34.69
17	LVLSKALGF	160	3.3000	33.67
18	FVFAAIFTP	233	3.2500	33.16
19	FVIPAAVLF	143	3.2000	32.65
20	MLNLAGLLT	209	3.2000	32.65
21	FVAGAVLAY	151	2.8000	28.57
22	FLLVGSDV	168	2.8000	28.57
23	YQLWAFITP	122	2.7000	27.55
24	LNLLVVFGV	191	2.7000	27.55
25	LISLAAILV	38	2.6000	26.53
26	VWFYQLWAF	119	2.6000	26.53
27	FYQLWAFIT	121	2.6000	26.53
28	LLIVMLNLA	205	2.6000	26.53
29	VLLELAIQI	257	2.6000	26.53
30	VLAYLVLSK	156	2.4000	24.49

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	LLTYERLKS	215	6.1000	62.24
2	MFVFAAIFT	232	5.0000	51.02
3	LRLKVGMAA	103	4.7000	47.96
4	IVMLNLAGL	207	4.7000	47.96
5	LRTRLLISL	33	4.6000	46.94
6	VVFGVSFEF	195	4.5000	45.92
7	VGMAAGIVL	107	4.4000	44.90
8	LIVMLNLAG	206	4.4000	44.90
9	LVLSKALGF	160	4.3000	43.88
10	MLNLAGLLT	209	4.2000	42.86
11	YFGFLLNLL	186	3.8000	38.78
12	FGFLLNLLV	187	3.7000	37.76
13	LNLLVVFVG	191	3.7000	37.76
14	LISLAAILV	38	3.6000	36.73
15	VWFYQLWAF	119	3.6000	36.73
16	LLIVMLNLA	205	3.6000	36.73
17	VLELAIQI	257	3.6000	36.73
18	WRRGLIFAM	224	3.4300	35.00
19	VLAYLVLSK	156	3.4000	34.69
20	LKSWRRGLI	221	3.4000	34.69
21	VRAAGLLKR	0	3.3000	33.67
22	VIPAAVLV	144	3.3000	33.67
23	FAMFVFAAI	230	3.2000	32.65
24	WYSHSIFGL	54	3.1500	32.14
25	LVVFGVSFE	194	3.1000	31.63
26	LWAFITPGL	124	3.0600	31.22
27	FVWYSHSIF	52	3.0000	30.61
28	YQRERRFAV	133	3.0000	30.61
29	VLVAGAVL	149	3.0000	30.61
30	LNLAGLLTY	210	3.0000	30.61

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	LKRLNPRNR	6	5.4000	55.10
2	IQIARVHDK	263	4.3000	43.88
3	WAFITPGLY	125	4.2000	42.86
4	YERLKSARR	218	3.8000	38.78
5	LVLSKALGF	160	3.4000	34.69
6	IVMLNLAGL	207	3.4000	34.69
7	VRAAGLLKR	0	3.3000	33.67
8	IVLACPVWF	113	3.2000	32.65
9	VGMAAGIVL	107	3.1000	31.63
10	FVIPAAVLF	143	3.0000	30.61
11	VLVAGAVL	149	2.9000	29.59
12	FYQLWAFIT	121	2.8000	28.57
13	LLATAPFDQ	92	2.7000	27.55
14	LAGLLTYER	212	2.7000	27.55
15	VVFGVSFEF	195	2.5000	25.51
16	LELAIQIAR	259	2.4000	24.49
17	IARVHDKRK	265	2.4000	24.49
18	LLISLAAIL	37	2.3000	23.47
19	FITPGLYQR	127	2.3000	23.47
20	LLVVFGVSF	193	2.2000	22.45
21	FVFAAIFTP	233	2.2000	22.45
22	ILVTTIFGF	44	2.1000	21.43
23	LLIVMLNLA	205	2.1000	21.43
24	VLLELAIQI	257	2.1000	21.43
25	LAIQIARVH	261	2.1000	21.43
26	LIVMLNLAG	206	2.0000	20.41
27	LISLAAILV	38	1.9000	19.39
28	FGVWYSHS	50	1.9000	19.39
29	WRRGLIFAM	224	1.9000	19.39
30	LNLAGLLTY	210	1.7000	17.35

ALLELE: DRB5_0105	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	LKRLNPRNR	6	5.4000	55.10
2	IQIARVHDK	263	4.3000	43.88
3	WAFITPGLY	125	4.2000	42.86
4	YERLKSRR	218	3.8000	38.78
5	LVLSKALGF	160	3.4000	34.69
6	IVMLNLAGL	207	3.4000	34.69
7	VRAAGLLKR	0	3.3000	33.67
8	IVLACPVWF	113	3.2000	32.65
9	VGMAAGIVL	107	3.1000	31.63
10	FVIPAAVLF	143	3.0000	30.61
11	VLVAGAVL	149	2.9000	29.59
12	FYQLWAFIT	121	2.8000	28.57
13	LLATAPFDQ	92	2.7000	27.55
14	LAGLLTYER	212	2.7000	27.55
15	VVFGVSFEF	195	2.5000	25.51
16	LELAIQIAR	259	2.4000	24.49
17	IARVHDKRK	265	2.4000	24.49
18	LLISLAAIL	37	2.3000	23.47
19	FITPGLYQR	127	2.3000	23.47
20	LLVVFGVSF	193	2.2000	22.45
21	FVFAAIFTP	233	2.2000	22.45
22	ILVTTIFGF	44	2.1000	21.43
23	LLIVMLNLA	205	2.1000	21.43
24	VLELAIQI	257	2.1000	21.43
25	LAIQIARVH	261	2.1000	21.43
26	LIVMLNLAG	206	2.0000	20.41
27	LISLAAILV	38	1.9000	19.39
28	FGFVWYSHS	50	1.9000	19.39
29	WRRGLIFAM	224	1.9000	19.39

30	LNLAGLLTY	210	1.7000	17.35
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