MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Mar 9 00:11:07 2010
Length of input sequence	304 amino acids
Number of nanomers from input sequence	296
Number of nanomers with obligatory P1 anchor residue	95
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

Rank	Sequence	At Position	Score	% of Highest Score
1	WREAIALVA	187	1.3000	21.67
2	VRNTIGLRL	208	1.2000	20.00
3	ILHAAAVEA	41	0.9000	15.00
4	LVIEAVVEN	75	0.6000	10.00
5	YIGLDLTLA	227	0.2900	4.83
6	VVALLTQVG	156	0.2000	3.33
7	FERLATLAP	91	-0.3000	0
8	VLASAGLDV	24	-0.4000	0
9	VLPIGAVTE	109	-0.4000	0

10	LRLATLGPL	214	-0.4000	0
11	LVAAGQLGA	257	-0.4000	0
12	FIGNRLQHA	177	-0.4600	0
13	LVVRNTIGL	206	-0.6000	0
14	LAIHDAVIP	234	-0.6000	0
15	LRELVAAGQ	254	-0.7000	0
16	VPGFIGNRL	174	-0.9200	0
17	VVENLAVKQ	80	-0.9600	0
18	LATLGPLEN	216	-1.2000	0
19	LAQHIAAQL	286	-1.2000	0
20	VEVVPSART	140	-1.2500	0
21	LGPLENADY	219	-1.3000	0
22	LENADYIGL	222	-1.3000	0
23	VGKLPVRVG	163	-1.4100	0
24	LLTQVGKLP	159	-1.5000	0
25	LVAEGVCDP	193	-1.5000	0
26	VVEVVPSAR	139	-1.5500	0
27	LLRELVAAG	253	-1.6000	0
28	VVGAGLMGR	11	-1.6100	0

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	VRNTIGLRL	208	2.2000	36.67
2	ILHAAAVEA	41	1.9000	31.67
3	LVIEAVVEN	75	1.6000	26.67
4	VVALLTQVG	156	1.2000	20.00
5	VLASAGLDV	24	0.6000	10.00
6	VLPIGAVTE	109	0.6000	10.00
7	LRLATLGPL	214	0.6000	10.00
8	LVAAGQLGA	257	0.6000	10.00
9	LVVRNTIGL	206	0.4000	6.67
10	LAIHDAVIP	234	0.4000	6.67
11	WREAIALVA	187	0.3000	5.00

12	LRELVAAGQ	254	0.3000	5.00
13	VPGFIGNRL	174	0.0800	1.33
14	VVENLAVKQ	80	0.0400	0.67
15	LATLGPLEN	216	-0.2000	0
16	LAQHIAAQL	286	-0.2000	0
17	VEVVPSART	140	-0.2500	0
18	FERLATLAP	91	-0.3000	0
19	LGPLENADY	219	-0.3000	0
20	LENADYIGL	222	-0.3000	0
21	VGKLPVRVG	163	-0.4100	0
22	FIGNRLQHA	177	-0.4600	0
23	LLTQVGKLP	159	-0.5000	0
24	LVAEGVCDP	193	-0.5000	0
25	VVEVVPSAR	139	-0.5500	0
26	LLRELVAAG	253	-0.6000	0
27	VVGAGLMGR	11	-0.6100	0
28	MLTSHGFSR	0	-0.7000	0

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	IGLDLTLAI	228	5.4000	56.84
2	VGRDVPGFI	170	4.7000	49.47
3	VVRNTIGLR	207	4.3000	45.26
4	VVGAGLMGR	11	4.1000	43.16
5	VVPSARTAP	142	3.7000	38.95
6	LNHDPHPSP	244	3.6000	37.89
7	LAPDAVLAT	97	3.5000	36.84
8	LRLATLGPL	214	3.4600	36.42
9	LVIEAVVEN	75	3.4000	35.79
10	VVALLTQVG	156	3.2000	33.68
11	LQANEKGRG	294	3.2000	33.68
12	LPIGAVTER	110	3.1000	32.63
13	LVVRNTIGL	206	2.7600	29.05

14	IPVVEVVPS	137	2.5000	26.32
15	LLRELVAAG	253	2.3000	24.21
16	MLTSHGFSR	0	2.0000	21.05
17	LVAEGVCDP	193	2.0000	21.05
18	LVAAGQLGA	257	2.0000	21.05
19	VVEVVPSAR	139	1.9700	20.74
20	LHAAAVEAA	42	1.8000	18.95
21	LTQVGKLPV	160	1.8000	18.95
22	VLPIGAVTE	109	1.7000	17.89
23	VAGAGRGSV	52	1.6000	16.84
24	VLASAGLDV	24	1.5000	15.79
25	ILHAAAVEA	41	1.4000	14.74
26	VRVGRDVPG	168	1.4000	14.74
27	LAIHDAVIP	234	1.4000	14.74
28	LMGRRIAGV	16	1.3000	13.68
29	VEAARVAGA	47	1.3000	13.68
30	VAAGQLGAR	258	1.3000	13.68

ALLELE: DRB1_0305	Threshold for 3 % with score: 1.7	Highest Score achievable by any peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	IGLDLTLAI	228	3.5000	38.46
2	VGRDVPGFI	170	2.8000	30.77
3	FSRAAVVGA	6	1.8000	19.78
4	LAPDAVLAT	97	1.8000	19.78
5	VVRNTIGLR	207	1.8000	19.78
6	VVPSARTAP	142	1.7000	18.68
7	VVGAGLMGR	11	1.6000	17.58
8	LVIEAVVEN	75	1.6000	17.58
9	FIGNRLQHA	177	1.6000	17.58
10	LNHDPHPSP	244	1.6000	17.58
11	LRLATLGPL	214	1.5000	16.48
12	YIGLDLTLA	227	1.4000	15.38
13	WREAIALVA	187	1.2000	13.19

14	IPVVEVVPS	137	1.1000	12.09
15	LVAAGQLGA	257	1.0000	10.99
16	LHAAAVEAA	42	0.8000	8.79
17	VVENLAVKQ	80	0.8000	8.79
18	VVALLTQVG	156	0.8000	8.79
19	LVVRNTIGL	206	0.8000	8.79
20	LQANEKGRG	294	0.8000	8.79
21	LPIGAVTER	110	0.6000	6.59
22	FERLATLAP	91	0.5000	5.49
23	LRELVAAGQ	254	0.5000	5.49
24	ILHAAAVEA	41	0.4000	4.40
25	VEAARVAGA	47	0.3000	3.30
26	LLRELVAAG	253	-0.1000	0
27	LTQVGKLPV	160	-0.2000	0

ALLELE: DRB1_0306	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	IGLDLTLAI	228	5.0000	56.82
2	LAPDAVLAT	97	3.3000	37.50
3	VVPSARTAP	142	2.7000	30.68
4	LVAAGQLGA	257	2.5000	28.41
5	LVIEAVVEN	75	2.4800	28.18
6	VGRDVPGFI	170	2.4000	27.27
7	VVGAGLMGR	11	2.3000	26.14
8	LHAAAVEAA	42	2.2000	25.00
9	IPVVEVVPS	137	1.9800	22.50
10	VVALLTQVG	156	1.9000	21.59
11	VVENLAVKQ	80	1.6800	19.09
12	LPIGAVTER	110	1.6000	18.18
13	LRELVAAGQ	254	1.5000	17.05
14	LVVRNTIGL	206	1.4800	16.82
15	VVRNTIGLR	207	1.4000	15.91
16	VEAARVAGA	47	1.3000	14.77

17	LTQVGKLPV	160	1.3000	14.77
18	ILHAAAVEA	41	1.2800	14.55
19	LNHDPHPSP	244	1.2000	13.64
20	LRLATLGPL	214	1.1000	12.50
21	VLASAGLDV	24	1.0000	11.36
22	LVAEGVCDP	193	1.0000	11.36
23	VDLVVRNTI	204	1.0000	11.36
24	LLRELVAAG	253	0.9000	10.23
25	FIGNRLQHA	177	0.7000	7.95
26	WREAIALVA	187	0.7000	7.95
27	VRNTIGLRL	208	0.7000	7.95
28	FSRAAVVGA	6	0.6800	7.73
29	VALLTQVGK	157	0.4800	5.45
30	YIGLDLTLA	227	0.4000	4.55

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	IGLDLTLAI	228	5.0000	56.82
2	LAPDAVLAT	97	3.3000	37.50
3	VVPSARTAP	142	2.7000	30.68
4	LVAAGQLGA	257	2.5000	28.41
5	LVIEAVVEN	75	2.4800	28.18
6	VGRDVPGFI	170	2.4000	27.27
7	VVGAGLMGR	11	2.3000	26.14
8	LHAAAVEAA	42	2.2000	25.00
9	IPVVEVVPS	137	1.9800	22.50
10	VVALLTQVG	156	1.9000	21.59
11	VVENLAVKQ	80	1.6800	19.09
12	LPIGAVTER	110	1.6000	18.18
13	LRELVAAGQ	254	1.5000	17.05
14	LVVRNTIGL	206	1.4800	16.82
15	VVRNTIGLR	207	1.4000	15.91
16	VEAARVAGA	47	1.3000	14.77

17	LTQVGKLPV	160	1.3000	14.77
18	ILHAAAVEA	41	1.2800	14.55
19	LNHDPHPSP	244	1.2000	13.64
20	LRLATLGPL	214	1.1000	12.50
21	VLASAGLDV	24	1.0000	11.36
22	LVAEGVCDP	193	1.0000	11.36
23	VDLVVRNTI	204	1.0000	11.36
24	LLRELVAAG	253	0.9000	10.23
25	FIGNRLQHA	177	0.7000	7.95
26	WREAIALVA	187	0.7000	7.95
27	VRNTIGLRL	208	0.7000	7.95
28	FSRAAVVGA	6	0.6800	7.73
29	VALLTQVGK	157	0.4800	5.45
30	YIGLDLTLA	227	0.4000	4.55

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	IGLDLTLAI	228	5.0000	56.82
2	LAPDAVLAT	97	3.3000	37.50
3	VVPSARTAP	142	2.7000	30.68
4	LVAAGQLGA	257	2.5000	28.41
5	LVIEAVVEN	75	2.4800	28.18
6	VGRDVPGFI	170	2.4000	27.27
7	VVGAGLMGR	11	2.3000	26.14
8	LHAAAVEAA	42	2.2000	25.00
9	IPVVEVVPS	137	1.9800	22.50
10	VVALLTQVG	156	1.9000	21.59
11	VVENLAVKQ	80	1.6800	19.09
12	LPIGAVTER	110	1.6000	18.18
13	LRELVAAGQ	254	1.5000	17.05
14	LVVRNTIGL	206	1.4800	16.82
15	VVRNTIGLR	207	1.4000	15.91
16	VEAARVAGA	47	1.3000	14.77

17	LTQVGKLPV	160	1.3000	14.77
18	ILHAAAVEA	41	1.2800	14.55
19	LNHDPHPSP	244	1.2000	13.64
20	LRLATLGPL	214	1.1000	12.50
21	VLASAGLDV	24	1.0000	11.36
22	LVAEGVCDP	193	1.0000	11.36
23	VDLVVRNTI	204	1.0000	11.36
24	LLRELVAAG	253	0.9000	10.23
25	FIGNRLQHA	177	0.7000	7.95
26	WREAIALVA	187	0.7000	7.95
27	VRNTIGLRL	208	0.7000	7.95
28	FSRAAVVGA	6	0.6800	7.73
29	VALLTQVGK	157	0.4800	5.45
30	YIGLDLTLA	227	0.4000	4.55

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	IGLDLTLAI	228	4.4000	46.32
2	VGRDVPGFI	170	3.7000	38.95
3	VVRNTIGLR	207	3.3000	34.74
4	VVGAGLMGR	11	3.1000	32.63
5	VVPSARTAP	142	2.7000	28.42
6	LNHDPHPSP	244	2.6000	27.37
7	LAPDAVLAT	97	2.5000	26.32
8	LRLATLGPL	214	2.4600	25.89
9	LVIEAVVEN	75	2.4000	25.26
10	VVALLTQVG	156	2.2000	23.16
11	LQANEKGRG	294	2.2000	23.16
12	LPIGAVTER	110	2.1000	22.11
13	FSRAAVVGA	6	1.8000	18.95
14	LVVRNTIGL	206	1.7600	18.53
15	FIGNRLQHA	177	1.6000	16.84
16	FERLATLAP	91	1.5000	15.79

17	IPVVEVVPS	137	1.5000	15.79
18	YIGLDLTLA	227	1.4000	14.74
19	LLRELVAAG	253	1.3000	13.68
20	WREAIALVA	187	1.2000	12.63
21	MLTSHGFSR	0	1.0000	10.53
22	WNPPDLIPV	131	1.0000	10.53
23	LVAEGVCDP	193	1.0000	10.53
24	LVAAGQLGA	257	1.0000	10.53
25	VVEVVPSAR	139	0.9700	10.21
26	LHAAAVEAA	42	0.8000	8.42
27	LTQVGKLPV	160	0.8000	8.42
28	VLPIGAVTE	109	0.7000	7.37
29	VAGAGRGSV	52	0.6000	6.32
30	VLASAGLDV	24	0.5000	5.26

ALLELE: DRB1_0311	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	IGLDLTLAI	228	5.0000	56.82
2	LAPDAVLAT	97	3.3000	37.50
3	VVPSARTAP	142	2.7000	30.68
4	LVAAGQLGA	257	2.5000	28.41
5	LVIEAVVEN	75	2.4800	28.18
6	VGRDVPGFI	170	2.4000	27.27
7	VVGAGLMGR	11	2.3000	26.14
8	LHAAAVEAA	42	2.2000	25.00
9	IPVVEVVPS	137	1.9800	22.50
10	VVALLTQVG	156	1.9000	21.59
11	VVENLAVKQ	80	1.6800	19.09
12	LPIGAVTER	110	1.6000	18.18
13	LRELVAAGQ	254	1.5000	17.05
14	LVVRNTIGL	206	1.4800	16.82
15	VVRNTIGLR	207	1.4000	15.91
16	VEAARVAGA	47	1.3000	14.77

17	LTQVGKLPV	160	1.3000	14.77
18	ILHAAAVEA	41	1.2800	14.55
19	LNHDPHPSP	244	1.2000	13.64
20	LRLATLGPL	214	1.1000	12.50
21	VLASAGLDV	24	1.0000	11.36
22	LVAEGVCDP	193	1.0000	11.36
23	VDLVVRNTI	204	1.0000	11.36
24	LLRELVAAG	253	0.9000	10.23
25	FIGNRLQHA	177	0.7000	7.95
26	WREAIALVA	187	0.7000	7.95
27	VRNTIGLRL	208	0.7000	7.95
28	FSRAAVVGA	6	0.6800	7.73
29	VALLTQVGK	157	0.4800	5.45
30	YIGLDLTLA	227	0.4000	4.55

ALLELE: DRB1_0401	Threshold for 3 % with score: 1.48	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	IGLDLTLAI	228	4.2000	48.84
2	LVIEAVVEN	75	3.6800	42.79
3	FERLATLAP	91	2.9000	33.72
4	VVALLTQVG	156	2.8000	32.56
5	LVAEGVCDP	193	2.2000	25.58
6	LLRELVAAG	253	2.1000	24.42
7	VAITDTNAE	32	2.0000	23.26
8	WREAIALVA	187	1.7000	19.77
9	VLATNTSVL	102	1.4000	16.28
10	FSRAAVVGA	6	1.3800	16.05
11	VVENLAVKQ	80	1.3800	16.05
12	LRELVAAGQ	254	1.3000	15.12
13	VIPSLNHDP	240	1.2000	13.95
14	LAPDAVLAT	97	1.1000	12.79
15	FIGNRLQHA	177	1.1000	12.79
16	LHAAAVEAA	42	0.9000	10.47

17	LGPLENADY	219	0.9000	10.47
18	YIGLDLTLA	227	0.9000	10.47
19	LVVRNTIGL	206	0.6800	7.91
20	VRNTIGLRL	208	0.6000	6.98
21	LAIHDAVIP	234	0.3800	4.42
22	LWREAIALV	186	0.3000	3.49
23	VVRNTIGLR	207	0.3000	3.49
24	LVAAGQLGA	257	0.3000	3.49
25	ILHAAAVEA	41	0.2800	3.26
26	IPVVEVVPS	137	-0.2200	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVRNTIGL	206	5.0000	52.08
2	VVALLTQVG	156	3.5000	36.46
3	LQHALWREA	182	2.1000	21.88
4	VAITDTNAE	32	1.8000	18.75
5	IGLDLTLAI	228	1.8000	18.75
6	IGLRLATLG	212	1.6000	16.67
7	LAIHDAVIP	234	1.6000	16.67
8	LVAAGQLGA	257	1.6000	16.67
9	LMGRRIAGV	16	1.5000	15.62
10	VGKLPVRVG	163	1.5000	15.62
11	ILHAAAVEA	41	1.4000	14.58
12	VVENLAVKQ	80	1.2000	12.50
13	IPVVEVVPS	137	1.1000	11.46
14	VVGAGLMGR	11	1.0000	10.42
15	VEAARVAGA	47	1.0000	10.42
16	LVIEAVVEN	75	1.0000	10.42
17	VLATNTSVL	102	1.0000	10.42
18	WREAIALVA	187	1.0000	10.42
19	VIPSLNHDP	240	0.9000	9.38
20	LRELVAAGQ	254	0.9000	9.38

21	FERLATLAP	91	0.8000	8.33
22	LFERLATLA	90	0.7000	7.29
23	VRNTIGLRL	208	0.7000	7.29
24	FSRAAVVGA	6	0.5000	5.21
25	LHAAAVEAA	42	0.5000	5.21
26	LPVRVGRDV	166	0.5000	5.21
27	LGPLENADY	219	0.5000	5.21
28	LPIGAVTER	110	0.3000	3.12
29	LAQHIAAQL	286	0.2000	2.08
30	VRVGRDVPG	168	0.1000	1.04

ALLELE: DRB1_0404	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVALLTQVG	156	3.8000	43.18
2	LRELVAAGQ	254	2.5000	28.41
3	IGLDLTLAI	228	2.3000	26.14
4	LGPLENADY	219	2.1000	23.86
5	IPVVEVVPS	137	2.0000	22.73
6	LVIEAVVEN	75	1.9000	21.59
7	FERLATLAP	91	1.7000	19.32
8	VAITDTNAE	32	1.5000	17.05
9	VLATNTSVL	102	1.5000	17.05
10	LVVRNTIGL	206	1.1800	13.41
11	ILHAAAVEA	41	1.1000	12.50
12	LHAAAVEAA	42	1.0000	11.36
13	VEAARVAGA	47	1.0000	11.36
14	VVGAGLMGR	11	0.9000	10.23
15	VVEVVPSAR	139	0.9000	10.23
16	VEVVPSART	140	0.9000	10.23
17	LVAAGQLGA	257	0.9000	10.23
18	VVENLAVKQ	80	0.6000	6.82
19	VLPIGAVTE	109	0.6000	6.82
20	LVAEGVCDP	193	0.6000	6.82

21	YIGLDLTLA	227	0.6000	6.82
22	VGKLPVRVG	163	0.5000	5.68
23	LLRELVAAG	253	0.5000	5.68
24	WREAIALVA	187	0.3000	3.41
25	VIPSLNHDP	240	0.3000	3.41
26	FSRAAVVGA	6	0.2000	2.27
27	IAGVLASAG	21	0.2000	2.27
28	VALLTQVGK	157	0.1000	1.14
29	VPSARTAPD	143	-0.1000	0

ALLELE: DRB1_0405	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VVALLTQVG	156	4.1000	43.62
2	VAITDTNAE	32	3.5000	37.23
3	FERLATLAP	91	3.1000	32.98
4	LVIEAVVEN	75	2.9000	30.85
5	VLPIGAVTE	109	2.6000	27.66
6	LRELVAAGQ	254	2.3000	24.47
7	LGPLENADY	219	2.2000	23.40
8	VPSARTAPD	143	1.6000	17.02
9	YIGLDLTLA	227	1.6000	17.02
10	VENLAVKQE	81	1.5000	15.96
11	VLATNTSVL	102	1.5000	15.96
12	IGLDLTLAI	228	1.5000	15.96
13	WREAIALVA	187	1.3000	13.83
14	FSRAAVVGA	6	1.2000	12.77
15	LVVRNTIGL	206	1.1800	12.55
16	IPVVEVVPS	137	1.0000	10.64
17	LATLGPLEN	216	0.9000	9.57
18	VEVVPSART	140	0.8000	8.51
19	VGKLPVRVG	163	0.8000	8.51
20	LLRELVAAG	253	0.8000	8.51
21	IAGVLASAG	21	0.5000	5.32

22	VVENLAVKQ	80	0.4000	4.26
23	ILHAAAVEA	41	0.1000	1.06
24	VVGAGLMGR	11	-0.1000	0
25	VVEVVPSAR	139	-0.1000	0
26	LRLATLGPL	214	-0.1000	0

ALLELE: DRB1_0408	Threshold for 3 % with score: 1.2	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVALLTQVG	156	2.8000	31.82
2	FERLATLAP	91	2.7000	30.68
3	YIGLDLTLA	227	1.6000	18.18
4	LRELVAAGQ	254	1.5000	17.05
5	WREAIALVA	187	1.3000	14.77
6	IGLDLTLAI	228	1.3000	14.77
7	FSRAAVVGA	6	1.2000	13.64
8	LGPLENADY	219	1.1000	12.50
9	IPVVEVVPS	137	1.0000	11.36
10	LVIEAVVEN	75	0.9000	10.23
11	VAITDTNAE	32	0.5000	5.68
12	VLATNTSVL	102	0.5000	5.68
13	LVVRNTIGL	206	0.1800	2.05
14	ILHAAAVEA	41	0.1000	1.14
15	VVGAGLMGR	11	-0.1000	0
16	VVEVVPSAR	139	-0.1000	0
17	VEVVPSART	140	-0.1000	0
18	LVAAGQLGA	257	-0.1000	0
19	VVENLAVKQ	80	-0.4000	0
20	VLPIGAVTE	109	-0.4000	0
21	LVAEGVCDP	193	-0.4000	0
22	VGKLPVRVG	163	-0.5000	0
23	LLRELVAAG	253	-0.5000	0
24	FIGNRLQHA	177	-0.7000	0
25	VIPSLNHDP	240	-0.7000	0

26	IAGVLASAG	21	-0.8000	0
27	VALLTQVGK	157	-0.9000	0

ALLELE: DRB1_0410	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VVALLTQVG	156	5.1000	54.26
2	VAITDTNAE	32	4.5000	47.87
3	LVIEAVVEN	75	3.9000	41.49
4	VLPIGAVTE	109	3.6000	38.30
5	LRELVAAGQ	254	3.3000	35.11
6	LGPLENADY	219	3.2000	34.04
7	VPSARTAPD	143	2.6000	27.66
8	VENLAVKQE	81	2.5000	26.60
9	VLATNTSVL	102	2.5000	26.60
10	IGLDLTLAI	228	2.5000	26.60
11	LVVRNTIGL	206	2.1800	23.19
12	FERLATLAP	91	2.1000	22.34
13	IPVVEVVPS	137	2.0000	21.28
14	LATLGPLEN	216	1.9000	20.21
15	VEVVPSART	140	1.8000	19.15
16	VGKLPVRVG	163	1.8000	19.15
17	LLRELVAAG	253	1.8000	19.15
18	IAGVLASAG	21	1.5000	15.96
19	VVENLAVKQ	80	1.4000	14.89
20	ILHAAAVEA	41	1.1000	11.70
21	LHAAAVEAA	42	1.0000	10.64
22	VEAARVAGA	47	1.0000	10.64
23	LVAEGVCDP	193	1.0000	10.64
24	VVGAGLMGR	11	0.9000	9.57
25	VVEVVPSAR	139	0.9000	9.57
26	LRLATLGPL	214	0.9000	9.57
27	LVAAGQLGA	257	0.9000	9.57
28	VIPSLNHDP	240	0.7000	7.45

29	VRNTIGLRL	208	0.6000	6.38
30	YIGLDLTLA	227	0.6000	6.38

ALLELE: DRB1_0421	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9

Rank	Sequence	At Position	Score	% of Highest Score
1	IGLDLTLAI	228	5.1000	56.67
2	LVIEAVVEN	75	4.4800	49.78
3	VVALLTQVG	156	4.2000	46.67
4	FERLATLAP	91	3.9000	43.33
5	LLRELVAAG	253	3.5000	38.89
6	VAITDTNAE	32	3.4000	37.78
7	LVAEGVCDP	193	3.2000	35.56
8	VLATNTSVL	102	2.3600	26.22
9	LGPLENADY	219	2.2000	24.44
10	VIPSLNHDP	240	2.2000	24.44
11	LAPDAVLAT	97	1.8000	20.00
12	VVRNTIGLR	207	1.8000	20.00
13	WREAIALVA	187	1.7000	18.89
14	LVVRNTIGL	206	1.6400	18.22
15	VRNTIGLRL	208	1.5600	17.33
16	VVGAGLMGR	11	1.5000	16.67
17	FSRAAVVGA	6	1.3800	15.33
18	LAIHDAVIP	234	1.3800	15.33
19	LWREAIALV	186	1.3000	14.44
20	FIGNRLQHA	177	1.1000	12.22
21	LHAAAVEAA	42	0.9000	10.00
22	VGRDVPGFI	170	0.9000	10.00
23	YIGLDLTLA	227	0.9000	10.00
24	VLPIGAVTE	109	0.8800	9.78
25	VENLAVKQE	81	0.7000	7.78
26	VVENLAVKQ	80	0.6800	7.56
27	LATNTSVLP	103	0.6800	7.56
28	VKQELFERL	86	0.6600	7.33

29	LRELVAAGQ	254	0.6000	6.67
30	VGKLPVRVG	163	0.4000	4.44

ALLELE: DRB1_0423	Threshold for 3 % with score: 1.68	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVALLTQVG	156	3.8000	43.18
2	LRELVAAGQ	254	2.5000	28.41
3	IGLDLTLAI	228	2.3000	26.14
4	LGPLENADY	219	2.1000	23.86
5	IPVVEVVPS	137	2.0000	22.73
6	LVIEAVVEN	75	1.9000	21.59
7	FERLATLAP	91	1.7000	19.32
8	VAITDTNAE	32	1.5000	17.05
9	VLATNTSVL	102	1.5000	17.05
10	LVVRNTIGL	206	1.1800	13.41
11	ILHAAAVEA	41	1.1000	12.50
12	LHAAAVEAA	42	1.0000	11.36
13	VEAARVAGA	47	1.0000	11.36
14	VVGAGLMGR	11	0.9000	10.23
15	VVEVVPSAR	139	0.9000	10.23
16	VEVVPSART	140	0.9000	10.23
17	LVAAGQLGA	257	0.9000	10.23
18	VVENLAVKQ	80	0.6000	6.82
19	VLPIGAVTE	109	0.6000	6.82
20	LVAEGVCDP	193	0.6000	6.82
21	YIGLDLTLA	227	0.6000	6.82
22	VGKLPVRVG	163	0.5000	5.68
23	LLRELVAAG	253	0.5000	5.68
24	WREAIALVA	187	0.3000	3.41
25	VIPSLNHDP	240	0.3000	3.41
26	FSRAAVVGA	6	0.2000	2.27
27	IAGVLASAG	21	0.2000	2.27
28	VALLTQVGK	157	0.1000	1.14

29	VPSARTAPD	143	-0.1000	0

ALLELE: DRB1_0426	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	IGLDLTLAI	228	4.2000	48.84
2	LVIEAVVEN	75	3.6800	42.79
3	FERLATLAP	91	2.9000	33.72
4	VVALLTQVG	156	2.8000	32.56
5	LVAEGVCDP	193	2.2000	25.58
6	LLRELVAAG	253	2.1000	24.42
7	VAITDTNAE	32	2.0000	23.26
8	WREAIALVA	187	1.7000	19.77
9	VLATNTSVL	102	1.4000	16.28
10	FSRAAVVGA	6	1.3800	16.05
11	VVENLAVKQ	80	1.3800	16.05
12	LRELVAAGQ	254	1.3000	15.12
13	VIPSLNHDP	240	1.2000	13.95
14	LAPDAVLAT	97	1.1000	12.79
15	FIGNRLQHA	177	1.1000	12.79
16	LHAAAVEAA	42	0.9000	10.47
17	LGPLENADY	219	0.9000	10.47
18	YIGLDLTLA	227	0.9000	10.47
19	LVVRNTIGL	206	0.6800	7.91
20	VRNTIGLRL	208	0.6000	6.98
21	LAIHDAVIP	234	0.3800	4.42
22	LWREAIALV	186	0.3000	3.49
23	VVRNTIGLR	207	0.3000	3.49
24	LVAAGQLGA	257	0.3000	3.49
25	ILHAAAVEA	41	0.2800	3.26
26	IPVVEVVPS	137	-0.2200	0

ALLELE: DRB1_0701	Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNTIGLRL	208	8.1000	69.83
2	LVVRNTIGL	206	6.2200	53.62
3	VLATNTSVL	102	5.1200	44.14
4	VLASAGLDV	24	5.1000	43.97
5	LRLATLGPL	214	4.7000	40.52
6	IGLDLTLAI	228	4.4200	38.10
7	LENADYIGL	222	4.4000	37.93
8	ITDTNAEIL	34	3.4000	29.31
9	WNPPDLIPV	131	3.4000	29.31
10	VIEAVVENL	76	3.3000	28.45
11	VDLVVRNTI	204	3.3000	28.45
12	WREAIALVA	187	3.2000	27.59
13	VPGFIGNRL	174	3.1000	26.72
14	LTQVGKLPV	160	3.0000	25.86
15	VAITDTNAE	32	2.9200	25.17
16	VLPIGAVTE	109	2.7000	23.28
17	MGRRIAGVL	17	2.5000	21.55
18	LAQHIAAQL	286	2.5000	21.55
19	LVIEAVVEN	75	2.4000	20.69
20	MLTSHGFSR	0	2.2000	18.97
21	VKQELFERL	86	2.2000	18.97
22	LVAAGQLGA	257	2.2000	18.97
23	FSRAAVVGA	6	2.1000	18.10
24	VVPSARTAP	142	2.1000	18.10
25	IGNRLQHAL	178	2.1000	18.10
26	ILHAAAVEA	41	1.8000	15.52
27	VIGTHFWNP	125	1.7000	14.66
28	LAIHDAVIP	234	1.6000	13.79
29	VIPSLNHDP	240	1.6000	13.79
30	FERLATLAP	91	1.5200	13.10

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNTIGLRL	208	8.1000	69.83
2	LVVRNTIGL	206	6.2200	53.62
3	VLATNTSVL	102	5.1200	44.14
4	VLASAGLDV	24	5.1000	43.97
5	LRLATLGPL	214	4.7000	40.52
6	IGLDLTLAI	228	4.4200	38.10
7	LENADYIGL	222	4.4000	37.93
8	ITDTNAEIL	34	3.4000	29.31
9	WNPPDLIPV	131	3.4000	29.31
10	VIEAVVENL	76	3.3000	28.45
11	VDLVVRNTI	204	3.3000	28.45
12	WREAIALVA	187	3.2000	27.59
13	VPGFIGNRL	174	3.1000	26.72
14	LTQVGKLPV	160	3.0000	25.86
15	VAITDTNAE	32	2.9200	25.17
16	VLPIGAVTE	109	2.7000	23.28
17	MGRRIAGVL	17	2.5000	21.55
18	LAQHIAAQL	286	2.5000	21.55
19	LVIEAVVEN	75	2.4000	20.69
20	MLTSHGFSR	0	2.2000	18.97
21	VKQELFERL	86	2.2000	18.97
22	LVAAGQLGA	257	2.2000	18.97
23	FSRAAVVGA	6	2.1000	18.10
24	VVPSARTAP	142	2.1000	18.10
25	IGNRLQHAL	178	2.1000	18.10
26	ILHAAAVEA	41	1.8000	15.52
27	VIGTHFWNP	125	1.7000	14.66
28	LAIHDAVIP	234	1.6000	13.79
29	VIPSLNHDP	240	1.6000	13.79
30	FERLATLAP	91	1.5200	13.10

ALLELE: DRB1_0801	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVRNTIGL	206	3.9000	45.35
2	LMGRRIAGV	16	2.9000	33.72
3	LVIEAVVEN	75	2.3000	26.74
4	MGRRIAGVL	17	2.0000	23.26
5	VENLAVKQE	81	2.0000	23.26
6	LRELVAAGQ	254	2.0000	23.26
7	LRLATLGPL	214	1.9000	22.09
8	VVALLTQVG	156	1.7000	19.77
9	LAVKQELFE	84	1.4000	16.28
10	LQANEKGRG	294	1.3000	15.12
11	LLRELVAAG	253	1.2000	13.95
12	FERLATLAP	91	1.1000	12.79
13	VGKLPVRVG	163	1.1000	12.79
14	IGNRLQHAL	178	1.1000	12.79
15	VVRNTIGLR	207	1.0000	11.63
16	VLPIGAVTE	109	0.8000	9.30
17	WREAIALVA	187	0.7000	8.14
18	IGLRLATLG	212	0.7000	8.14
19	FSRAAVVGA	6	0.5000	5.81
20	VPSARTAPD	143	0.5000	5.81
21	LATLGPLEN	216	0.5000	5.81
22	LVAAGQLGA	257	0.5000	5.81
23	LVAEGVCDP	193	0.4000	4.65
24	VAITDTNAE	32	0.3000	3.49
25	VEAARVAGA	47	0.3000	3.49
26	FIGNRLQHA	177	0.3000	3.49
27	VVGAGLMGR	11	0.2000	2.33
28	VVENLAVKQ	80	0.1000	1.16
29	IPVVEVVPS	137	0.1000	1.16
30	LGARTGHGF	263	0.1000	1.16

ALLELE: DRB1_0802	Threshold for 3 % with score: 1.0	Highest Score achievable by any peptide: 8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVRNTIGL	206	2.9000	36.25
2	LMGRRIAGV	16	2.6000	32.50
3	LRELVAAGQ	254	1.2000	15.00
4	MGRRIAGVL	17	1.0000	12.50
5	VVRNTIGLR	207	1.0000	12.50
6	LRLATLGPL	214	0.9000	11.25
7	FERLATLAP	91	0.7000	8.75
8	WREAIALVA	187	0.7000	8.75
9	FSRAAVVGA	6	0.5000	6.25
10	LVAAGQLGA	257	0.5000	6.25
11	VVALLTQVG	156	0.4000	5.00
12	VEAARVAGA	47	0.3000	3.75
13	LVIEAVVEN	75	0.3000	3.75
14	FIGNRLQHA	177	0.3000	3.75
15	VVGAGLMGR	11	0.2000	2.50
16	IPVVEVVPS	137	0.1000	1.25
17	IGNRLQHAL	178	0.1000	1.25
18	LLRELVAAG	253	-0.1000	0
19	VGKLPVRVG	163	-0.2000	0
20	YIGLDLTLA	227	-0.2000	0
21	IGLDLTLAI	228	-0.3000	0
22	LTQVGKLPV	160	-0.4000	0
23	IGLRLATLG	212	-0.6000	0
24	VVENLAVKQ	80	-0.7000	0
25	LPVRVGRDV	166	-0.7000	0
26	LGARTGHGF	263	-0.8000	0
27	ILHAAAVEA	41	-0.9000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVRNTIGL	206	3.9000	48.75
2	LMGRRIAGV	16	3.6000	45.00
3	LRELVAAGQ	254	2.2000	27.50
4	MGRRIAGVL	17	2.0000	25.00
5	VVRNTIGLR	207	2.0000	25.00
6	LRLATLGPL	214	1.9000	23.75
7	LVAAGQLGA	257	1.5000	18.75
8	VVALLTQVG	156	1.4000	17.50
9	VEAARVAGA	47	1.3000	16.25
10	LVIEAVVEN	75	1.3000	16.25
11	VVGAGLMGR	11	1.2000	15.00
12	IPVVEVVPS	137	1.1000	13.75
13	IGNRLQHAL	178	1.1000	13.75
14	LVAEGVCDP	193	1.0000	12.50
15	LQANEKGRG	294	1.0000	12.50
16	LLRELVAAG	253	0.9000	11.25
17	VGKLPVRVG	163	0.8000	10.00
18	IGLDLTLAI	228	0.7000	8.75
19	LTQVGKLPV	160	0.6000	7.50
20	IGLRLATLG	212	0.4000	5.00
21	VVENLAVKQ	80	0.3000	3.75
22	LPVRVGRDV	166	0.3000	3.75
23	LGARTGHGF	263	0.2000	2.50
24	ILHAAAVEA	41	0.1000	1.25
25	VGRDVPGFI	170	-0.1000	0
26	LGPLENADY	219	-0.1000	0

ALLELE: DRB1_0806	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVRNTIGL	206	4.9000	56.98
2	LMGRRIAGV	16	3.9000	45.35
3	LVIEAVVEN	75	3.3000	38.37

4	MGRRIAGVL	17	3.0000	34.88
5	VENLAVKQE	81	3.0000	34.88
6	LRELVAAGQ	254	3.0000	34.88
7	LRLATLGPL	214	2.9000	33.72
8	VVALLTQVG	156	2.7000	31.40
9	LAVKQELFE	84	2.4000	27.91
10	LQANEKGRG	294	2.3000	26.74
11	LLRELVAAG	253	2.2000	25.58
12	VGKLPVRVG	163	2.1000	24.42
13	IGNRLQHAL	178	2.1000	24.42
14	VVRNTIGLR	207	2.0000	23.26
15	VLPIGAVTE	109	1.8000	20.93
16	IGLRLATLG	212	1.7000	19.77
17	VPSARTAPD	143	1.5000	17.44
18	LATLGPLEN	216	1.5000	17.44
19	LVAAGQLGA	257	1.5000	17.44
20	LVAEGVCDP	193	1.4000	16.28
21	VAITDTNAE	32	1.3000	15.12
22	VEAARVAGA	47	1.3000	15.12
23	VVGAGLMGR	11	1.2000	13.95
24	VVENLAVKQ	80	1.1000	12.79
25	IPVVEVVPS	137	1.1000	12.79
26	LGARTGHGF	263	1.1000	12.79
27	LGPLENADY	219	1.0000	11.63
28	LTQVGKLPV	160	0.9000	10.47
29	IGLDLTLAI	228	0.9000	10.47
30	VRNTIGLRL	208	0.7000	8.14

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	LVVRNTIGL	206	3.7800	43.45
2	LMGRRIAGV	16	2.6000	29.89
3	YIGLDLTLA	227	2.6000	29.89

4	IGLRLATLG	212	2.2000	25.29
5	FSRAAVVGA	6	1.5000	17.24
6	VVALLTQVG	156	1.4000	16.09
7	LVIEAVVEN	75	1.3000	14.94
8	LFERLATLA	90	1.3000	14.94
9	FERLATLAP	91	1.3000	14.94
10	FIGNRLQHA	177	1.3000	14.94
11	WREAIALVA	187	1.3000	14.94
12	VVGAGLMGR	11	1.2000	13.79
13	LRELVAAGQ	254	1.2000	13.79
14	IPVVEVVPS	137	1.1000	12.64
15	LVAAGQLGA	257	1.1000	12.64
16	IGNRLQHAL	178	0.6000	6.90
17	VVPSARTAP	142	0.5000	5.75
18	VDLVVRNTI	204	0.4000	4.60
19	MGRRIAGVL	17	0.3000	3.45
20	LHAAAVEAA	42	0.3000	3.45
21	VEAARVAGA	47	0.3000	3.45
22	VVENLAVKQ	80	0.3000	3.45
23	VVRNTIGLR	207	0.3000	3.45
24	IGLDLTLAI	228	0.3000	3.45
25	VVEVVPSAR	139	0.2000	2.30
26	LTQVGKLPV	160	0.2000	2.30
27	LRLATLGPL	214	0.2000	2.30
28	ILHAAAVEA	41	0.1000	1.15

ALLELE: DRB1_0817	Threshold for 3 % with score: 2.8	Highest Score achievable by any peptide: 10.1

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVRNTIGL	206	5.5000	54.46
2	LAVKQELFE	84	3.2000	31.68
3	LMGRRIAGV	16	2.9000	28.71
4	FERLATLAP	91	2.9000	28.71
5	LVIEAVVEN	75	2.8000	27.72

6	VENLAVKQE	81	2.6000	25.74
7	WREAIALVA	187	2.5000	24.75
8	LATLGPLEN	216	2.3000	22.77
9	LVAAGQLGA	257	2.3000	22.77
10	MGRRIAGVL	17	2.1000	20.79
11	LRLATLGPL	214	2.0000	19.80
12	LRELVAAGQ	254	2.0000	19.80
13	VVGAGLMGR	11	1.8000	17.82
14	VVALLTQVG	156	1.8000	17.82
15	IGNRLQHAL	178	1.8000	17.82
16	IGLRLATLG	212	1.8000	17.82
17	LTQVGKLPV	160	1.7000	16.83
18	IGLDLTLAI	228	1.7000	16.83
19	VRNTIGLRL	208	1.5000	14.85
20	LQANEKGRG	294	1.4000	13.86
21	VLPIGAVTE	109	1.3000	12.87
22	VGKLPVRVG	163	1.3000	12.87
23	LLRELVAAG	253	1.2000	11.88
24	VVRNTIGLR	207	1.1000	10.89
25	FSRAAVVGA	6	1.0000	9.90
26	YIGLDLTLA	227	0.9000	8.91
27	LGARTGHGF	263	0.8000	7.92
28	LAPDAVLAT	97	0.7000	6.93
29	WNPPDLIPV	131	0.7000	6.93
30	VAITDTNAE	32	0.6000	5.94

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	FERLATLAP	91	2.9000	34.94
2	WREAIALVA	187	2.5000	30.12
3	LVAAGQLGA	257	2.3000	27.71
4	VVGAGLMGR	11	1.8000	21.69
5	LRELVAAGQ	254	1.6000	19.28

6	LTQVGKLPV	160	1.5000	18.07
7	LVVRNTIGL	206	1.5000	18.07
8	YIGLDLTLA	227	1.3000	15.66
9	VVRNTIGLR	207	1.1000	13.25
10	FSRAAVVGA	6	1.0000	12.05
11	LRLATLGPL	214	1.0000	12.05
12	VVALLTQVG	156	0.9000	10.84
13	VRNTIGLRL	208	0.9000	10.84
14	IGLDLTLAI	228	0.8000	9.64
15	IPVVEVVPS	137	0.7000	8.43
16	LATLGPLEN	216	0.7000	8.43
17	VGKLPVRVG	163	0.4000	4.82
18	FIGNRLQHA	177	0.4000	4.82
19	VEAARVAGA	47	0.3000	3.61
20	LVIEAVVEN	75	0.1000	1.20
21	LQANEKGRG	294	0.1000	1.20
22	VALLTQVGK	157	-0.1000	0
23	VVENLAVKQ	80	-0.2000	0
24	LHAAAVEAA	42	-0.3000	0
25	WNPPDLIPV	131	-0.3000	0
26	LMGRRIAGV	16	-0.4000	0
27	ILHAAAVEA	41	-0.4000	0
28	VLASAGLDV	24	-0.6000	0

ALLELE: DRB1_1102	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VGKLPVRVG	163	2.3000	27.38
2	LVIEAVVEN	75	2.2000	26.19
3	LVAAGQLGA	257	2.2000	26.19
4	LVVRNTIGL	206	2.1000	25.00
5	VVALLTQVG	156	1.9000	22.62
6	LRELVAAGQ	254	1.9000	22.62
7	LAIHDAVIP	234	1.6000	19.05

8	VVGAGLMGR	11	1.5000	17.86
9	LMGRRIAGV	16	1.5000	17.86
10	VVENLAVKQ	80	1.4000	16.67
11	VEAARVAGA	47	1.3000	15.48
12	LQHALWREA	182	1.2000	14.29
13	ILHAAAVEA	41	1.1000	13.10
14	VVRNTIGLR	207	1.1000	13.10
15	LHAAAVEAA	42	1.0000	11.90
16	IGLDLTLAI	228	1.0000	11.90
17	IPVVEVVPS	137	0.9000	10.71
18	LVAEGVCDP	193	0.9000	10.71
19	LRLATLGPL	214	0.9000	10.71
20	LLRELVAAG	253	0.8000	9.52
21	VALLTQVGK	157	0.7000	8.33
22	VVPSARTAP	142	0.6000	7.14
23	FSRAAVVGA	6	0.5000	5.95
24	VENLAVKQE	81	0.5000	5.95
25	LAQHIAAQL	286	0.5000	5.95
26	WREAIALVA	187	0.4000	4.76
27	VRNTIGLRL	208	0.3000	3.57
28	FIGNRLQHA	177	0.2000	2.38
29	IGNRLQHAL	178	0.2000	2.38
30	FERLATLAP	91	0.1000	1.19

ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LVAAGQLGA	257	3.3000	39.76
2	VVGAGLMGR	11	2.8000	33.73
3	LRELVAAGQ	254	2.6000	31.33
4	LTQVGKLPV	160	2.5000	30.12
5	LVVRNTIGL	206	2.5000	30.12
6	VVRNTIGLR	207	2.1000	25.30
7	LRLATLGPL	214	2.0000	24.10

8	FERLATLAP	91	1.9000	22.89
9	VVALLTQVG	156	1.9000	22.89
10	VRNTIGLRL	208	1.9000	22.89
11	IGLDLTLAI	228	1.8000	21.69
12	IPVVEVVPS	137	1.7000	20.48
13	LATLGPLEN	216	1.7000	20.48
14	WREAIALVA	187	1.5000	18.07
15	VGKLPVRVG	163	1.4000	16.87
16	VEAARVAGA	47	1.3000	15.66
17	LVIEAVVEN	75	1.1000	13.25
18	LQANEKGRG	294	1.1000	13.25
19	VENLAVKQE	81	1.0000	12.05
20	VALLTQVGK	157	0.9000	10.84
21	VVENLAVKQ	80	0.8000	9.64
22	LHAAAVEAA	42	0.7000	8.43
23	LMGRRIAGV	16	0.6000	7.23
24	ILHAAAVEA	41	0.6000	7.23
25	VLASAGLDV	24	0.4000	4.82
26	LVAEGVCDP	193	0.3000	3.61
27	LGPLENADY	219	0.3000	3.61
28	YIGLDLTLA	227	0.3000	3.61
29	LLRELVAAG	253	0.2000	2.41
30	VAGAGRGSV	52	0.1000	1.20

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LVAAGQLGA	257	3.3000	39.76
2	VVGAGLMGR	11	2.8000	33.73
3	LRELVAAGQ	254	2.6000	31.33
4	LTQVGKLPV	160	2.5000	30.12
5	LVVRNTIGL	206	2.5000	30.12
6	VVRNTIGLR	207	2.1000	25.30
7	LRLATLGPL	214	2.0000	24.10

8	FERLATLAP	91	1.9000	22.89
9	VVALLTQVG	156	1.9000	22.89
10	VRNTIGLRL	208	1.9000	22.89
11	IGLDLTLAI	228	1.8000	21.69
12	IPVVEVVPS	137	1.7000	20.48
13	LATLGPLEN	216	1.7000	20.48
14	WREAIALVA	187	1.5000	18.07
15	VGKLPVRVG	163	1.4000	16.87
16	VEAARVAGA	47	1.3000	15.66
17	LVIEAVVEN	75	1.1000	13.25
18	LQANEKGRG	294	1.1000	13.25
19	VENLAVKQE	81	1.0000	12.05
20	VALLTQVGK	157	0.9000	10.84
21	VVENLAVKQ	80	0.8000	9.64
22	LHAAAVEAA	42	0.7000	8.43
23	LMGRRIAGV	16	0.6000	7.23
24	ILHAAAVEA	41	0.6000	7.23
25	VLASAGLDV	24	0.4000	4.82
26	LVAEGVCDP	193	0.3000	3.61
27	LGPLENADY	219	0.3000	3.61
28	YIGLDLTLA	227	0.3000	3.61
29	LLRELVAAG	253	0.2000	2.41
30	VAGAGRGSV	52	0.1000	1.20

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	IGLDLTLAI	228	4.5000	49.45
2	VGRDVPGFI	170	3.8000	41.76
3	LAPDAVLAT	97	2.8000	30.77
4	VVRNTIGLR	207	2.8000	30.77
5	VVPSARTAP	142	2.7000	29.67
6	VVGAGLMGR	11	2.6000	28.57
7	LVIEAVVEN	75	2.6000	28.57

8	LNHDPHPSP	244	2.6000	28.57
9	LRLATLGPL	214	2.5000	27.47
10	IPVVEVVPS	137	2.1000	23.08
11	LVAAGQLGA	257	2.0000	21.98
12	LHAAAVEAA	42	1.8000	19.78
13	VVENLAVKQ	80	1.8000	19.78
14	VVALLTQVG	156	1.8000	19.78
15	LVVRNTIGL	206	1.8000	19.78
16	LQANEKGRG	294	1.8000	19.78
17	LPIGAVTER	110	1.6000	17.58
18	LRELVAAGQ	254	1.5000	16.48
19	ILHAAAVEA	41	1.4000	15.38
20	VEAARVAGA	47	1.3000	14.29
21	LVAEGVCDP	193	1.0000	10.99
22	LLRELVAAG	253	0.9000	9.89
23	FSRAAVVGA	6	0.8000	8.79
24	LTQVGKLPV	160	0.8000	8.79
25	VAGAGRGSV	52	0.6000	6.59
26	VALLTQVGK	157	0.6000	6.59
27	FIGNRLQHA	177	0.6000	6.59
28	MLTSHGFSR	0	0.5000	5.49
29	VLASAGLDV	24	0.5000	5.49
30	VVEVVPSAR	139	0.4700	5.16

ALLELE: DRB1_1114	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	FSRAAVVGA	6	1.5000	17.86
2	WREAIALVA	187	1.4000	16.67
3	VGKLPVRVG	163	1.3000	15.48
4	LVIEAVVEN	75	1.2000	14.29
5	FIGNRLQHA	177	1.2000	14.29
6	LVAAGQLGA	257	1.2000	14.29
7	FERLATLAP	91	1.1000	13.10

8	LVVRNTIGL	206	1.1000	13.10
9	YIGLDLTLA	227	1.0000	11.90
10	VVALLTQVG	156	0.9000	10.71
11	LRELVAAGQ	254	0.9000	10.71
12	LAIHDAVIP	234	0.6000	7.14
13	VVGAGLMGR	11	0.5000	5.95
14	LMGRRIAGV	16	0.5000	5.95
15	VVENLAVKQ	80	0.4000	4.76
16	VEAARVAGA	47	0.3000	3.57
17	LQHALWREA	182	0.2000	2.38
18	ILHAAAVEA	41	0.1000	1.19
19	VVRNTIGLR	207	0.1000	1.19
20	IPVVEVVPS	137	-0.1000	0
21	LVAEGVCDP	193	-0.1000	0
22	LRLATLGPL	214	-0.1000	0
23	LLRELVAAG	253	-0.2000	0
24	VALLTQVGK	157	-0.3000	0
25	VVPSARTAP	142	-0.4000	0
26	VENLAVKQE	81	-0.5000	0
27	LAQHIAAQL	286	-0.5000	0

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	VGKLPVRVG	163	2.7000	30.68
2	VVALLTQVG	156	2.3000	26.14
3	FERLATLAP	91	2.1000	23.86
4	LVVRNTIGL	206	2.0600	23.41
5	VVGAGLMGR	11	2.0000	22.73
6	LVIEAVVEN	75	2.0000	22.73
7	VVRNTIGLR	207	1.6000	18.18
8	LAIHDAVIP	234	1.6000	18.18
9	FSRAAVVGA	6	1.5000	17.05
10	LMGRRIAGV	16	1.5000	17.05

11	WREAIALVA	187	1.4000	15.91
12	FIGNRLQHA	177	1.2000	13.64
13	LLRELVAAG	253	1.2000	13.64
14	LVAAGQLGA	257	1.2000	13.64
15	YIGLDLTLA	227	1.0000	11.36
16	VENLAVKQE	81	0.9000	10.23
17	LVAEGVCDP	193	0.9000	10.23
18	IGLDLTLAI	228	0.9000	10.23
19	LRLATLGPL	214	0.8600	9.77
20	VVPSARTAP	142	0.6000	6.82
21	LQANEKGRG	294	0.5000	5.68
22	LAQHIAAQL	286	0.4600	5.23
23	VEAARVAGA	47	0.3000	3.41
24	IPVVEVVPS	137	0.3000	3.41
25	VRNTIGLRL	208	0.2600	2.95
26	LQHALWREA	182	0.2000	2.27
27	IGLRLATLG	212	0.2000	2.27
28	LRELVAAGQ	254	0.2000	2.27
29	LGARTGHGF	263	0.2000	2.27
30	IGNRLQHAL	178	0.1600	1.82

ALLELE: DRB1_1121	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VGKLPVRVG	163	2.3000	27.38
2	LVIEAVVEN	75	2.2000	26.19
3	LVAAGQLGA	257	2.2000	26.19
4	LVVRNTIGL	206	2.1000	25.00
5	VVALLTQVG	156	1.9000	22.62
6	LRELVAAGQ	254	1.9000	22.62
7	LAIHDAVIP	234	1.6000	19.05
8	VVGAGLMGR	11	1.5000	17.86
9	LMGRRIAGV	16	1.5000	17.86
10	VVENLAVKQ	80	1.4000	16.67

11	VEAARVAGA	47	1.3000	15.48
12	LQHALWREA	182	1.2000	14.29
13	ILHAAAVEA	41	1.1000	13.10
14	VVRNTIGLR	207	1.1000	13.10
15	LHAAAVEAA	42	1.0000	11.90
16	IGLDLTLAI	228	1.0000	11.90
17	IPVVEVVPS	137	0.9000	10.71
18	LVAEGVCDP	193	0.9000	10.71
19	LRLATLGPL	214	0.9000	10.71
20	LLRELVAAG	253	0.8000	9.52
21	VALLTQVGK	157	0.7000	8.33
22	VVPSARTAP	142	0.6000	7.14
23	FSRAAVVGA	6	0.5000	5.95
24	VENLAVKQE	81	0.5000	5.95
25	LAQHIAAQL	286	0.5000	5.95
26	WREAIALVA	187	0.4000	4.76
27	VRNTIGLRL	208	0.3000	3.57
28	FIGNRLQHA	177	0.2000	2.38
29	IGNRLQHAL	178	0.2000	2.38
30	FERLATLAP	91	0.1000	1.19

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	FERLATLAP	91	3.9000	44.83
2	VVGAGLMGR	11	3.3000	37.93
3	VVRNTIGLR	207	2.6000	29.89
4	LTQVGKLPV	160	2.5000	28.74
5	WREAIALVA	187	2.5000	28.74
6	LVVRNTIGL	206	2.4600	28.28
7	VVALLTQVG	156	2.3000	26.44
8	LVAAGQLGA	257	2.3000	26.44
9	LRLATLGPL	214	1.9600	22.53
10	VRNTIGLRL	208	1.8600	21.38

11	VGKLPVRVG	163	1.8000	20.69
12	IGLDLTLAI	228	1.7000	19.54
13	LATLGPLEN	216	1.5000	17.24
14	LQANEKGRG	294	1.5000	17.24
15	VENLAVKQE	81	1.4000	16.09
16	YIGLDLTLA	227	1.3000	14.94
17	IPVVEVVPS	137	1.1000	12.64
18	FSRAAVVGA	6	1.0000	11.49
19	LVIEAVVEN	75	0.9000	10.34
20	LRELVAAGQ	254	0.9000	10.34
21	WNPPDLIPV	131	0.7000	8.05
22	LMGRRIAGV	16	0.6000	6.90
23	LGPLENADY	219	0.6000	6.90
24	LLRELVAAG	253	0.6000	6.90
25	VLASAGLDV	24	0.4000	4.60
26	FIGNRLQHA	177	0.4000	4.60
27	VEAARVAGA	47	0.3000	3.45
28	VLPIGAVTE	109	0.3000	3.45
29	LVAEGVCDP	193	0.3000	3.45
30	VAGAGRGSV	52	0.1000	1.15

ALLELE: DRB1_1301	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VGKLPVRVG	163	3.7000	42.05
2	VVALLTQVG	156	3.3000	37.50
3	LVVRNTIGL	206	3.0600	34.77
4	VVGAGLMGR	11	3.0000	34.09
5	LVIEAVVEN	75	3.0000	34.09
6	VVRNTIGLR	207	2.6000	29.55
7	LAIHDAVIP	234	2.6000	29.55
8	LMGRRIAGV	16	2.5000	28.41
9	LLRELVAAG	253	2.2000	25.00
10	LVAAGQLGA	257	2.2000	25.00

11	VENLAVKQE	81	1.9000	21.59
12	LVAEGVCDP	193	1.9000	21.59
13	IGLDLTLAI	228	1.9000	21.59
14	LRLATLGPL	214	1.8600	21.14
15	VVPSARTAP	142	1.6000	18.18
16	LQANEKGRG	294	1.5000	17.05
17	LAQHIAAQL	286	1.4600	16.59
18	VEAARVAGA	47	1.3000	14.77
19	IPVVEVVPS	137	1.3000	14.77
20	VRNTIGLRL	208	1.2600	14.32
21	LQHALWREA	182	1.2000	13.64
22	IGLRLATLG	212	1.2000	13.64
23	LRELVAAGQ	254	1.2000	13.64
24	LGARTGHGF	263	1.2000	13.64
25	IGNRLQHAL	178	1.1600	13.18
26	ILHAAAVEA	41	1.1000	12.50
27	FERLATLAP	91	1.1000	12.50
28	LTQVGKLPV	160	1.1000	12.50
29	VAITDTNAE	32	1.0000	11.36
30	LHAAAVEAA	42	1.0000	11.36

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	VGKLPVRVG	163	2.7000	30.68
2	VVALLTQVG	156	2.3000	26.14
3	FERLATLAP	91	2.1000	23.86
4	LVVRNTIGL	206	2.0600	23.41
5	VVGAGLMGR	11	2.0000	22.73
6	LVIEAVVEN	75	2.0000	22.73
7	VVRNTIGLR	207	1.6000	18.18
8	LAIHDAVIP	234	1.6000	18.18
9	FSRAAVVGA	6	1.5000	17.05
10	LMGRRIAGV	16	1.5000	17.05

11	WREAIALVA	187	1.4000	15.91
12	FIGNRLQHA	177	1.2000	13.64
13	LLRELVAAG	253	1.2000	13.64
14	LVAAGQLGA	257	1.2000	13.64
15	YIGLDLTLA	227	1.0000	11.36
16	VENLAVKQE	81	0.9000	10.23
17	LVAEGVCDP	193	0.9000	10.23
18	IGLDLTLAI	228	0.9000	10.23
19	LRLATLGPL	214	0.8600	9.77
20	VVPSARTAP	142	0.6000	6.82
21	LQANEKGRG	294	0.5000	5.68
22	LAQHIAAQL	286	0.4600	5.23
23	VEAARVAGA	47	0.3000	3.41
24	IPVVEVVPS	137	0.3000	3.41
25	VRNTIGLRL	208	0.2600	2.95
26	LQHALWREA	182	0.2000	2.27
27	IGLRLATLG	212	0.2000	2.27
28	LRELVAAGQ	254	0.2000	2.27
29	LGARTGHGF	263	0.2000	2.27
30	IGNRLQHAL	178	0.1600	1.82

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	LVIEAVVEN	75	4.2000	46.67
2	VGKLPVRVG	163	3.6000	40.00
3	VENLAVKQE	81	3.5000	38.89
4	VVALLTQVG	156	3.2000	35.56
5	LVVRNTIGL	206	3.1000	34.44
6	LRELVAAGQ	254	2.7000	30.00
7	VAITDTNAE	32	2.6000	28.89
8	VVENLAVKQ	80	2.2000	24.44
9	LVAAGQLGA	257	2.2000	24.44
10	LLRELVAAG	253	2.1000	23.33

11	LAIHDAVIP	234	2.0000	22.22
12	VLPIGAVTE	109	1.9000	21.11
13	LRLATLGPL	214	1.9000	21.11
14	LATLGPLEN	216	1.9000	21.11
15	LMGRRIAGV	16	1.8000	20.00
16	LAVKQELFE	84	1.6000	17.78
17	IAAQLQANE	290	1.6000	17.78
18	VVGAGLMGR	11	1.5000	16.67
19	VPSARTAPD	143	1.5000	16.67
20	LAQHIAAQL	286	1.5000	16.67
21	LQANEKGRG	294	1.4000	15.56
22	VEAARVAGA	47	1.3000	14.44
23	LVAEGVCDP	193	1.3000	14.44
24	VRNTIGLRL	208	1.3000	14.44
25	IGNRLQHAL	178	1.2000	13.33
26	LQHALWREA	182	1.2000	13.33
27	IGLDLTLAI	228	1.2000	13.33
28	ILHAAAVEA	41	1.1000	12.22
29	VVRNTIGLR	207	1.1000	12.22
30	IGLRLATLG	212	1.1000	12.22

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	FERLATLAP	91	3.9000	44.83
2	VVGAGLMGR	11	3.3000	37.93
3	VVRNTIGLR	207	2.6000	29.89
4	LTQVGKLPV	160	2.5000	28.74
5	WREAIALVA	187	2.5000	28.74
6	LVVRNTIGL	206	2.4600	28.28
7	VVALLTQVG	156	2.3000	26.44
8	LVAAGQLGA	257	2.3000	26.44
9	LRLATLGPL	214	1.9600	22.53
10	VRNTIGLRL	208	1.8600	21.38

11	VGKLPVRVG	163	1.8000	20.69
12	IGLDLTLAI	228	1.7000	19.54
13	LATLGPLEN	216	1.5000	17.24
14	LQANEKGRG	294	1.5000	17.24
15	VENLAVKQE	81	1.4000	16.09
16	YIGLDLTLA	227	1.3000	14.94
17	IPVVEVVPS	137	1.1000	12.64
18	FSRAAVVGA	6	1.0000	11.49
19	LVIEAVVEN	75	0.9000	10.34
20	LRELVAAGQ	254	0.9000	10.34
21	WNPPDLIPV	131	0.7000	8.05
22	LMGRRIAGV	16	0.6000	6.90
23	LGPLENADY	219	0.6000	6.90
24	LLRELVAAG	253	0.6000	6.90
25	VLASAGLDV	24	0.4000	4.60
26	FIGNRLQHA	177	0.4000	4.60
27	VEAARVAGA	47	0.3000	3.45
28	VLPIGAVTE	109	0.3000	3.45
29	LVAEGVCDP	193	0.3000	3.45
30	VAGAGRGSV	52	0.1000	1.15

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	LRELVAAGQ	254	1.6000	23.53
2	FERLATLAP	91	1.1000	16.18
3	VVRNTIGLR	207	1.0000	14.71
4	LRLATLGPL	214	0.9000	13.24
5	VVALLTQVG	156	0.8000	11.76
6	WREAIALVA	187	0.7000	10.29
7	FSRAAVVGA	6	0.5000	7.35
8	LVAAGQLGA	257	0.5000	7.35
9	VEAARVAGA	47	0.3000	4.41
10	FIGNRLQHA	177	0.3000	4.41

11	VVGAGLMGR	11	0.2000	2.94
12	IPVVEVVPS	137	0.2000	2.94
13	VGKLPVRVG	163	0.2000	2.94
14	YIGLDLTLA	227	0.2000	2.94
15	LVVRNTIGL	206	-0.1000	0
16	LTQVGKLPV	160	-0.3000	0
17	LMGRRIAGV	16	-0.4000	0
18	LVIEAVVEN	75	-0.4000	0
19	VENLAVKQE	81	-0.6000	0
20	VALLTQVGK	157	-0.6000	0
21	VVENLAVKQ	80	-0.7000	0
22	LVAEGVCDP	193	-0.7000	0
23	LGPLENADY	219	-0.7000	0
24	LLRELVAAG	253	-0.8000	0
25	ILHAAAVEA	41	-0.9000	0
26	VRNTIGLRL	208	-0.9000	0
27	VAGAGRGSV	52	-1.0000	0
28	IGLDLTLAI	228	-1.0000	0

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	LVAAGQLGA	257	3.3000	39.76
2	VVGAGLMGR	11	2.8000	33.73
3	LRELVAAGQ	254	2.6000	31.33
4	LTQVGKLPV	160	2.5000	30.12
5	LVVRNTIGL	206	2.5000	30.12
6	VVRNTIGLR	207	2.1000	25.30
7	LRLATLGPL	214	2.0000	24.10
8	FERLATLAP	91	1.9000	22.89
9	VVALLTQVG	156	1.9000	22.89
10	VRNTIGLRL	208	1.9000	22.89
11	IGLDLTLAI	228	1.8000	21.69
12	IPVVEVVPS	137	1.7000	20.48

13	LATLGPLEN	216	1.7000	20.48
14	WREAIALVA	187	1.5000	18.07
15	VGKLPVRVG	163	1.4000	16.87
16	VEAARVAGA	47	1.3000	15.66
17	LVIEAVVEN	75	1.1000	13.25
18	LQANEKGRG	294	1.1000	13.25
19	VENLAVKQE	81	1.0000	12.05
20	VALLTQVGK	157	0.9000	10.84
21	VVENLAVKQ	80	0.8000	9.64
22	LHAAAVEAA	42	0.7000	8.43
23	LMGRRIAGV	16	0.6000	7.23
24	ILHAAAVEA	41	0.6000	7.23
25	VLASAGLDV	24	0.4000	4.82
26	LVAEGVCDP	193	0.3000	3.61
27	LGPLENADY	219	0.3000	3.61
28	YIGLDLTLA	227	0.3000	3.61
29	LLRELVAAG	253	0.2000	2.41
30	VAGAGRGSV	52	0.1000	1.20

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	FERLATLAP	91	3.3000	37.08
2	VENLAVKQE	81	3.0000	33.71
3	LATLGPLEN	216	2.7000	30.34
4	WREAIALVA	187	2.5000	28.09
5	LVVRNTIGL	206	2.5000	28.09
6	LRELVAAGQ	254	2.4000	26.97
7	LVAAGQLGA	257	2.3000	25.84
8	VVALLTQVG	156	2.2000	24.72
9	LVIEAVVEN	75	2.1000	23.60
10	LRLATLGPL	214	2.0000	22.47
11	VLPIGAVTE	109	1.9000	21.35
12	VRNTIGLRL	208	1.9000	21.35

13	VVGAGLMGR	11	1.8000	20.22
14	LTQVGKLPV	160	1.8000	20.22
15	VGKLPVRVG	163	1.7000	19.10
16	LQANEKGRG	294	1.4000	15.73
17	YIGLDLTLA	227	1.3000	14.61
18	VVRNTIGLR	207	1.1000	12.36
19	FSRAAVVGA	6	1.0000	11.24
20	VAITDTNAE	32	1.0000	11.24
21	IGLDLTLAI	228	1.0000	11.24
22	IPVVEVVPS	137	0.7000	7.87
23	VVENLAVKQ	80	0.6000	6.74
24	VPSARTAPD	143	0.5000	5.62
25	LLRELVAAG	253	0.5000	5.62
26	LAVKQELFE	84	0.4000	4.49
27	FIGNRLQHA	177	0.4000	4.49
28	LGPLENADY	219	0.4000	4.49
29	VEAARVAGA	47	0.3000	3.37

ALLELE: DRB1_1322	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VGKLPVRVG	163	2.3000	27.38
2	LVIEAVVEN	75	2.2000	26.19
3	LVAAGQLGA	257	2.2000	26.19
4	LVVRNTIGL	206	2.1000	25.00
5	VVALLTQVG	156	1.9000	22.62
6	LRELVAAGQ	254	1.9000	22.62
7	LAIHDAVIP	234	1.6000	19.05
8	VVGAGLMGR	11	1.5000	17.86
9	LMGRRIAGV	16	1.5000	17.86
10	VVENLAVKQ	80	1.4000	16.67
11	VEAARVAGA	47	1.3000	15.48
12	LQHALWREA	182	1.2000	14.29
13	ILHAAAVEA	41	1.1000	13.10

14	VVRNTIGLR	207	1.1000	13.10
15	LHAAAVEAA	42	1.0000	11.90
16	IGLDLTLAI	228	1.0000	11.90
17	IPVVEVVPS	137	0.9000	10.71
18	LVAEGVCDP	193	0.9000	10.71
19	LRLATLGPL	214	0.9000	10.71
20	LLRELVAAG	253	0.8000	9.52
21	VALLTQVGK	157	0.7000	8.33
22	VVPSARTAP	142	0.6000	7.14
23	FSRAAVVGA	6	0.5000	5.95
24	VENLAVKQE	81	0.5000	5.95
25	LAQHIAAQL	286	0.5000	5.95
26	WREAIALVA	187	0.4000	4.76
27	VRNTIGLRL	208	0.3000	3.57
28	FIGNRLQHA	177	0.2000	2.38
29	IGNRLQHAL	178	0.2000	2.38
30	FERLATLAP	91	0.1000	1.19

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	FSRAAVVGA	6	1.5000	17.86
2	WREAIALVA	187	1.4000	16.67
3	VGKLPVRVG	163	1.3000	15.48
4	LVIEAVVEN	75	1.2000	14.29
5	FIGNRLQHA	177	1.2000	14.29
6	LVAAGQLGA	257	1.2000	14.29
7	FERLATLAP	91	1.1000	13.10
8	LVVRNTIGL	206	1.1000	13.10
9	YIGLDLTLA	227	1.0000	11.90
10	VVALLTQVG	156	0.9000	10.71
11	LRELVAAGQ	254	0.9000	10.71
12	LAIHDAVIP	234	0.6000	7.14
13	VVGAGLMGR	11	0.5000	5.95

14	LMGRRIAGV	16	0.5000	5.95
15	VVENLAVKQ	80	0.4000	4.76
16	VEAARVAGA	47	0.3000	3.57
17	LQHALWREA	182	0.2000	2.38
18	ILHAAAVEA	41	0.1000	1.19
19	VVRNTIGLR	207	0.1000	1.19
20	IPVVEVVPS	137	-0.1000	0
21	LVAEGVCDP	193	-0.1000	0
22	LRLATLGPL	214	-0.1000	0
23	LLRELVAAG	253	-0.2000	0
24	VALLTQVGK	157	-0.3000	0
25	VVPSARTAP	142	-0.4000	0
26	VENLAVKQE	81	-0.5000	0
27	LAQHIAAQL	286	-0.5000	0

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	VGKLPVRVG	163	3.7000	42.05
2	VVALLTQVG	156	3.3000	37.50
3	LVVRNTIGL	206	3.0600	34.77
4	VVGAGLMGR	11	3.0000	34.09
5	LVIEAVVEN	75	3.0000	34.09
6	VVRNTIGLR	207	2.6000	29.55
7	LAIHDAVIP	234	2.6000	29.55
8	LMGRRIAGV	16	2.5000	28.41
9	LLRELVAAG	253	2.2000	25.00
10	LVAAGQLGA	257	2.2000	25.00
11	VENLAVKQE	81	1.9000	21.59
12	LVAEGVCDP	193	1.9000	21.59
13	IGLDLTLAI	228	1.9000	21.59
14	LRLATLGPL	214	1.8600	21.14
15	VVPSARTAP	142	1.6000	18.18
16	LQANEKGRG	294	1.5000	17.05

17	LAQHIAAQL	286	1.4600	16.59
18	VEAARVAGA	47	1.3000	14.77
19	IPVVEVVPS	137	1.3000	14.77
20	VRNTIGLRL	208	1.2600	14.32
21	LQHALWREA	182	1.2000	13.64
22	IGLRLATLG	212	1.2000	13.64
23	LRELVAAGQ	254	1.2000	13.64
24	LGARTGHGF	263	1.2000	13.64
25	IGNRLQHAL	178	1.1600	13.18
26	ILHAAAVEA	41	1.1000	12.50
27	FERLATLAP	91	1.1000	12.50
28	LTQVGKLPV	160	1.1000	12.50
29	VAITDTNAE	32	1.0000	11.36
30	LHAAAVEAA	42	1.0000	11.36

ALLELE: DRB1_1328	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VGKLPVRVG	163	3.7000	42.05
2	VVALLTQVG	156	3.3000	37.50
3	LVVRNTIGL	206	3.0600	34.77
4	VVGAGLMGR	11	3.0000	34.09
5	LVIEAVVEN	75	3.0000	34.09
6	VVRNTIGLR	207	2.6000	29.55
7	LAIHDAVIP	234	2.6000	29.55
8	LMGRRIAGV	16	2.5000	28.41
9	LLRELVAAG	253	2.2000	25.00
10	LVAAGQLGA	257	2.2000	25.00
11	VENLAVKQE	81	1.9000	21.59
12	LVAEGVCDP	193	1.9000	21.59
13	IGLDLTLAI	228	1.9000	21.59
14	LRLATLGPL	214	1.8600	21.14
15	VVPSARTAP	142	1.6000	18.18
16	LQANEKGRG	294	1.5000	17.05

17	LAQHIAAQL	286	1.4600	16.59
18	VEAARVAGA	47	1.3000	14.77
19	IPVVEVVPS	137	1.3000	14.77
20	VRNTIGLRL	208	1.2600	14.32
21	LQHALWREA	182	1.2000	13.64
22	IGLRLATLG	212	1.2000	13.64
23	LRELVAAGQ	254	1.2000	13.64
24	LGARTGHGF	263	1.2000	13.64
25	IGNRLQHAL	178	1.1600	13.18
26	ILHAAAVEA	41	1.1000	12.50
27	FERLATLAP	91	1.1000	12.50
28	LTQVGKLPV	160	1.1000	12.50
29	VAITDTNAE	32	1.0000	11.36
30	LHAAAVEAA	42	1.0000	11.36

ALLELE: DRB1_1501	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNTIGLRL	208	5.3000	54.08
2	LVVRNTIGL	206	4.7600	48.57
3	LRLATLGPL	214	3.9000	39.80
4	VPGFIGNRL	174	3.8000	38.78
5	IGLDLTLAI	228	3.6600	37.35
6	VLASAGLDV	24	3.4000	34.69
7	VVGAGLMGR	11	3.2000	32.65
8	LVAAGQLGA	257	3.2000	32.65
9	LENADYIGL	222	3.0000	30.61
10	VDLVVRNTI	204	2.3000	23.47
11	VVPSARTAP	142	2.2000	22.45
12	LTQVGKLPV	160	2.1000	21.43
13	MGRRIAGVL	17	1.9000	19.39
14	WREAIALVA	187	1.9000	19.39
15	LMGRRIAGV	16	1.8500	18.88
16	LVIEAVVEN	75	1.8000	18.37

17	WNPPDLIPV	131	1.8000	18.37
18	VRVGRDVPG	168	1.8000	18.37
19	LAIHDAVIP	234	1.8000	18.37
20	VVRNTIGLR	207	1.6500	16.84
21	MLTSHGFSR	0	1.6000	16.33
22	LAQHIAAQL	286	1.6000	16.33
23	ILHAAAVEA	41	1.5000	15.31
24	VAGAGRGSV	52	1.5000	15.31
25	VAAAADLAA	60	1.5000	15.31
26	IGNRLQHAL	178	1.5000	15.31
27	VLATNTSVL	102	1.4600	14.90
28	VVALLTQVG	156	1.4600	14.90
29	LGARTGHGF	263	1.4000	14.29
30	LTSHGFSRA	1	1.3000	13.27

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNTIGLRL	208	4.3000	43.88
2	LVVRNTIGL	206	3.7600	38.37
3	WREAIALVA	187	2.9000	29.59
4	LRLATLGPL	214	2.9000	29.59
5	WNPPDLIPV	131	2.8000	28.57
6	VPGFIGNRL	174	2.8000	28.57
7	IGLDLTLAI	228	2.6600	27.14
8	VLASAGLDV	24	2.4000	24.49
9	VVGAGLMGR	11	2.2000	22.45
10	YIGLDLTLA	227	2.2000	22.45
11	LVAAGQLGA	257	2.2000	22.45
12	FERLATLAP	91	2.0600	21.02
13	LENADYIGL	222	2.0000	20.41
14	VDLVVRNTI	204	1.3000	13.27
15	VVPSARTAP	142	1.2000	12.24
16	LTQVGKLPV	160	1.1000	11.22

17	FIGNRLQHA	177	1.0000	10.20
18	MGRRIAGVL	17	0.9000	9.18
19	LMGRRIAGV	16	0.8500	8.67
20	LVIEAVVEN	75	0.8000	8.16
21	VRVGRDVPG	168	0.8000	8.16
22	LAIHDAVIP	234	0.8000	8.16
23	VVRNTIGLR	207	0.6500	6.63
24	MLTSHGFSR	0	0.6000	6.12
25	LAQHIAAQL	286	0.6000	6.12
26	ILHAAAVEA	41	0.5000	5.10
27	VAGAGRGSV	52	0.5000	5.10
28	VAAAADLAA	60	0.5000	5.10
29	FWNPPDLIP	130	0.5000	5.10
30	IGNRLQHAL	178	0.5000	5.10

ALLELE: DRB1_1506	Threshold for 3 % with score: 3.1	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNTIGLRL	208	5.3000	54.08
2	LVVRNTIGL	206	4.7600	48.57
3	LRLATLGPL	214	3.9000	39.80
4	VPGFIGNRL	174	3.8000	38.78
5	IGLDLTLAI	228	3.6600	37.35
6	VLASAGLDV	24	3.4000	34.69
7	VVGAGLMGR	11	3.2000	32.65
8	LVAAGQLGA	257	3.2000	32.65
9	LENADYIGL	222	3.0000	30.61
10	VDLVVRNTI	204	2.3000	23.47
11	VVPSARTAP	142	2.2000	22.45
12	LTQVGKLPV	160	2.1000	21.43
13	MGRRIAGVL	17	1.9000	19.39
14	WREAIALVA	187	1.9000	19.39
15	LMGRRIAGV	16	1.8500	18.88
16	LVIEAVVEN	75	1.8000	18.37

17	WNPPDLIPV	131	1.8000	18.37
18	VRVGRDVPG	168	1.8000	18.37
19	LAIHDAVIP	234	1.8000	18.37
20	VVRNTIGLR	207	1.6500	16.84
21	MLTSHGFSR	0	1.6000	16.33
22	LAQHIAAQL	286	1.6000	16.33
23	ILHAAAVEA	41	1.5000	15.31
24	VAGAGRGSV	52	1.5000	15.31
25	VAAAADLAA	60	1.5000	15.31
26	IGNRLQHAL	178	1.5000	15.31
27	VLATNTSVL	102	1.4600	14.90
28	VVALLTQVG	156	1.4600	14.90
29	LGARTGHGF	263	1.4000	14.29
30	LTSHGFSRA	1	1.3000	13.27

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNTIGLRL	208	3.6000	36.73
2	VVEVVPSAR	139	3.5000	35.71
3	MLTSHGFSR	0	3.2000	32.65
4	VVGAGLMGR	11	3.2000	32.65
5	LRLATLGPL	214	3.1000	31.63
6	VVALLTQVG	156	2.0000	20.41
7	VVRNTIGLR	207	1.8000	18.37
8	VALLTQVGK	157	1.6000	16.33
9	WREAIALVA	187	1.6000	16.33
10	LVVRNTIGL	206	1.6000	16.33
11	FLDWPAGAR	271	1.4000	14.29
12	LRELVAAGQ	254	1.3000	13.27
13	YIGLDLTLA	227	1.2000	12.24
14	LENADYIGL	222	1.1000	11.22
15	VLPIGAVTE	109	0.7000	7.14
16	VLATNTSVL	102	0.6000	6.12

17	IAGVLASAG	21	0.5000	5.10
18	VGKLPVRVG	163	0.5000	5.10
19	MGRRIAGVL	17	0.4000	4.08
20	FERLATLAP	91	0.4000	4.08
21	LATLGPLEN	216	0.4000	4.08
22	LGPLENADY	219	0.4000	4.08
23	VGRDVPGFI	170	0.3000	3.06
24	LVAAGQLGA	257	0.3000	3.06
25	VDLVVRNTI	204	0.2000	2.04
26	VAITDTNAE	32	-0.1000	0
27	ILHAAAVEA	41	-0.1000	0

ALLELE: DRB5_0105	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNTIGLRL	208	3.6000	36.73
2	VVEVVPSAR	139	3.5000	35.71
3	MLTSHGFSR	0	3.2000	32.65
4	VVGAGLMGR	11	3.2000	32.65
5	LRLATLGPL	214	3.1000	31.63
6	VVALLTQVG	156	2.0000	20.41
7	VVRNTIGLR	207	1.8000	18.37
8	VALLTQVGK	157	1.6000	16.33
9	WREAIALVA	187	1.6000	16.33
10	LVVRNTIGL	206	1.6000	16.33
11	FLDWPAGAR	271	1.4000	14.29
12	LRELVAAGQ	254	1.3000	13.27
13	YIGLDLTLA	227	1.2000	12.24
14	LENADYIGL	222	1.1000	11.22
15	VLPIGAVTE	109	0.7000	7.14
16	VLATNTSVL	102	0.6000	6.12
17	IAGVLASAG	21	0.5000	5.10
18	VGKLPVRVG	163	0.5000	5.10
19	MGRRIAGVL	17	0.4000	4.08

20	FERLATLAP	91	0.4000	4.08
21	LATLGPLEN	216	0.4000	4.08
22	LGPLENADY	219	0.4000	4.08
23	VGRDVPGFI	170	0.3000	3.06
24	LVAAGQLGA	257	0.3000	3.06
25	VDLVVRNTI	204	0.2000	2.04
26	VAITDTNAE	32	-0.1000	0
27	ILHAAAVEA	41	-0.1000	0